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WELCOME MESSAGE

Dear friends, dear colleagues,

We are thrilled to invite you to the **21st European Congress on Digital Pathology**, which will be held at the Palau de Congressos de Barcelona, situated in the heart of Barcelona, Spain. As the digital pathology community converges, we look forward to exploring cutting-edge advancements, fostering collaboration, and shaping the future of healthcare. During the event, you can engage in insightful discussions with experts in digital pathology: pathologists, image analysis engineers, quality control specialists, researchers, and industry leaders. Explore novel approaches, challenges, and breakthroughs in digital pathology. Additionally, discover the latest research, digital pathology implementations, algorithm usage, and technological advancements through cutting-edge presentations. From AI-driven diagnostics to personalized medicine, ECDP2025 promises a wealth of knowledge. Furthermore, take advantage of networking opportunities by connecting with peers from across Europe and beyond. Share experiences, exchange ideas, and build lasting relationships.

Why Barcelona?
Barcelona, overlooking the Mediterranean Sea, is not only a hub of innovation. It is a city that seamlessly blends creativity, tradition, and technological excellence. Be inspired by its stunning architecture and vibrant culture, where the iconic Sagrada Familia and bustling streets of Las Ramblas fuel creativity and curiosity. As you explore the city, bask in the warmth of the Mediterranean sun, connect with colleagues, forge new partnerships, and enjoy the renowned Spanish hospitality. And don't forget to indulge in the rich flavors of Catalan cuisine, Barcelona's gastronomy is a feast for the senses, from tapas to paella!

Join Us in Barcelona!

Mark your calendar for June 25-28, 2025, and prepare for an unforgettable congress. Welcome to Barcelona!

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Palau de Congresos de Barcelona
Av. de la Reina Maria Cristina, s/n, Sants-Montjuïc,
08004 Barcelona, Spain

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SCIENTIFIC PROGRAM OVERVIEW

	THU. 26.06.2025		FR. 27.06.2025		ST. 28.06.2025
	AUDITORIUM (1000 pax)	ROOM 6 (300 pax)	AUDITORIUM (1000 pax)	ROOM 6 (300 pax)	AUDITORIUM (1000 pax)
08:00-09:00			Breakfast Industry Symposia		Best Posters Session
09:00-09:20	Opening		Keynote II		Keynote III
09:20-09:50	Keynote I		Clinical Aplications of AI		Multimodal and Foundation models
09:50-10:45	Digital Pathology meets Oncology		Coffee Break		Coffee Break
09:20-09:50	Coffee Break				
11:00-12:00	Machine Learning and Algorithm Development I	Structure Reporting	Digital Transformation/ Workflow	Oral free Presentations III	Regulatory
12:00-12:30		Odd Couple			Generative AI
12:30-13:00	Lunch		Lunch		Closing
13:00-13:45	Industry Symposia		Industry Symposia		
13:45-14:00	Break		Break		Lunch
14:00-14:30	Global Pathology Interoperability Alliance	Machine Learning and Clinical Applications	AI Inovation Pitch: A Spotlight on Cutting-Edge Solutions	Oral Free Presentations IV	
14:30-16:00	Digital Pathology Showcase 2025: Unlocking Interoperability	Oral Free Presentations I	ESDIP AGM	Coffee Break	
16:00-16:30	Coffee Break				
16:30-17:30	Bias in AI	Oral Free Presentations II	Digital Pathology: Challenges and how to overcome them	Emerging Technologies	
17:30-18:30	Novel Interdisciplinary Approaches	How to make DP a Business Case	Digital pathology neighborhood	Machine Learning and Algorith Development II	
18:30-21:00	Networking Reception		Social Event		
21:00-23:00					

SCIENTIFIC PROGRAM JUNE 26

Auditorium

9:00 – 9:20	**Opening** | Norman Zerbe & Jordi Temprana
9:20 – 9:50	**Keynote I** | Jakob Kather
9:50 – 10:45	**Digital Pathology Meets Oncology** | Joaquin Mateo & Sabina Berezowska & Luiza Moore
10:45 – 11:15	Coffee Break
11:15 – 12:30	**Machine Learning and Algorithm Development I** | Ana Frei
12:30 – 14:00	Lunch Break
14:00 – 14:30	Global Pathology Interoperability Alliance
14:30 – 16:00	Digital Pathology Showcase 2025: Unlocking Interoperability
16:00 – 16:30	Coffee Break
16:30 – 17:30	**Bias in AI** | Saniye Gülser Corat
17:30 – 18.30	**Novel Interdisciplinary Approaches** | Geert Litjens

SCIENTIFIC PROGRAM JUNE 26

Room 6

11:15 – 12:00	**Structured Reporting** | Scott Campbell
12:00 – 12:30	**Odd Couple**
12:30 – 14:00	Lunch Break
14:00 – 15:00	**Machine Learning and Clinical Applications** | Pedro Fernandez Ruiz
15:00 – 16:00	**Oral Free Presentations I**
16:00 – 16:30	Coffee Break
16:30 – 17:30	**Oral Free Presentations II**
17:30 - 18:30	**How to Make DP a Business Case** | Frederick Deman

SCIENTIFIC PROGRAM JUNE 27

Auditorium

9:00 – 9:30	**Keynote II** | Xavier Matias-Guiu
9:30 – 10:30	**Clinical Applications of AI** | Sophie Prévot
10:30 – 11:00	Coffee Break
11:00 – 12:30	**Digital Transformation / Workflow** | Angelo dei Tos
12:30 – 14:00	Lunch Break
14:00 – 15:30	**AI Innovation Pitch: A Spotlight on Cutting-Edge Solutions**
15:30 – 16:30	Coffee Break
16:30 – 17:30	**Digital Pathology: Challenges and how to overcome them** | Juan Pablo de la Fuente
17:30 – 18.30	**Digital Pathology Neighbourhood** | Liron Pantanowitz & Hooman H. Rashidi & Etsuo Susaki & Jing Zhang & Hicham El Attar

SCIENTIFIC PROGRAM JUNE 27 | Room 6

11:00 – 12:30	**Oral Free Presentations III**
12:30 – 14:00	Lunch Break
14:00 – 15:30	**Oral Free Presentations IV**
15:30 – 16:30	Coffee Break
16:30 – 17:30	**Emerging Technologies** | Vasilis Ntziachristos & Roman Bülow
17:30 - 18:30	**Machine Learning and Algorithm Development II** | Mattias Rantalainen

SCIENTIFIC PROGRAM JUNE 28 | Auditorium

9:00 – 9:30	**Keynote III** | Raphaëlle Luisier
9:30 – 10:30	**Multimodal and Foundation Models** | Anne Martel
10:30 – 11:00	Coffee Break
11:00 – 12:00	**Regulatory** | Nick Schneider & Donald Karcher & Eric Glassy
12:00 – 12:45	**Generative AI** | Nadieh Khalili
12:45 – 13:15	**Closing** | Norman Zerbe & Jordi Temprana
13:15 – 14:00	Lunch

ORAL PRESENTATIONS

A1 Cell Detection with Transformers – A Paradigm Shift from Segmentation to Detection in Digital Pathology

Oscar Pina[1], Eduard Dorca[2], Verónica Vilaplana[1]

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Introduction

Cell nuclei detection and classification are fundamental tasks in digital pathology, enabling biomarker quantification and tumor microenvironment analysis. Although the clinically relevant objective is to detect and classify individual cells, these tasks are typically addressed using segmentation-based methods. While effective, segmentation introduces significant computational overhead. To overcome these limitations, we propose CellNuc-DETR, a transformer-based detection model that directly detects and classifies cells, offering a more efficient and scalable alternative to segmentation-based approaches.

Material and methods

CellNuc-DETR employs a Deformable-DETR backbone with a Swin Transformer encoder, leveraging multi-scale deformable attention to detect and classify individual nuclei without requiring pixel-wise segmentation. The model is trained on the PanNuke dataset and evaluated across multiple datasets, including CoNSeP and MoNuSeg, to assess generalization. Efficiency analyses are conducted by benchmarking inference speed on WSIs against segmentation-based approaches.

Results and discussion

CellNuc-DETR achieves an F1-score of 0.84 on PanNuke and 0.78 on CoNSeP, achieving state-of-the-art performance. The model reduces post-processing time by a factor of 40 compared to HoVer-Net and achieves a 2.5× speed-up in inference time compared to CellViT while maintaining comparable classification accuracy. The in-device sliding window approach further enhances efficiency, enabling rapid WSI processing with minimal GPU overhead.

Conclusion

By eliminating complex post-processing steps and reducing computational demands, CellNuc-DETR enables scalable, high-throughput cell analysis in digital pathology. These results advocate for a paradigm shift from segmentation-based methods to transformer-based detection approaches, offering a practical and efficient solution for WSI analysis in both clinical and research settings.

Key words: Cell Detection, Transformers, Deep Learning, Whole Slide Image

A2 AI-Enhanced Quantification of HER2 Low and Ultra-Low Expression in Breast Cancer Tissues

Frederik Aidt[1], Elad Arbel[2], Itay Remer[2], Oded Ben-David[2], Amir Ben-Dor[2], Daniela Rabkin[2], Kirsten Hoff[1], Karin Salomon[1], Sarit Aviel-Ronen[3], Gitte Nielsen[4], Jens Mollerup[1], Lars Jacobsen[1], Anya Tsalenko[5]

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Introduction

Recent advancements in antibody-drug conjugate therapies have expanded treatment options for breast cancer patients, particularly those with low and ultra-low HER2 expression. However, current immunohistochemistry (IHC) assays face challenges in providing reliable and quantitative HER2 evaluation in these low expression ranges. This study integrates a quantitative immunohistochemistry (qIHC) assay with AI computational techniques to objectively assess lower HER2 expression and improve IHC interpretation.

Material and methods

Serial sections of 82 formalin-fixed paraffin-embedded tissue blocks of invasive breast carcinoma with HER2 IHC scores of 0 or 1+ were stained with H&E, HercepTest™ mAb pharmDx (Dako Omnis) (HercepTest™ mAb), qIHC, and p63, scanned and aligned. Invasive tumor areas were annotated and reviewed by expert pathologists. HER2 expression was quantitatively evaluated using qIHC in 128x128µm² areas within these regions. These qIHC measurements served as ground truth for training an AI model to infer HER2 expression from HercepTest™ mAb slides. Finally, spatial maps of measured and predicted quantitative HER2 expression were created.

Results and discussion

Significant differences in slide level HER2 qIHC-based expression were observed among the HER2 null, HER2 ultra-low, and HER2 low groups. Substantial spatial heterogeneity was observed in HER2 expression levels within some slides. The expression inferred from HercepTest™ mAb by the AI model demonstrated spatial similarity to the ground-truth across the tissue and exhibited strong slide level agreement with the measured qIHC expression (Pearson correlation = 0.94, $R^2 = 0.87$).

Conclusion

The developed methodology provides an objective quantitative measure for HER2 low expression ranges, enhancing IHC assay interpretation and potentially improving therapeutic outcomes. **Disclaimer:** Research Use Only

Key words: Artificial intelligence, Deep Learning , Quantitative Immunohistochemistry, HER2 Low , Antibody-drug Conjugate Therapies, Breast Cancer

A3 MSAI-Path: Predicting Microsatellite Instability from Routine Histology Slides without Reinventing the Wheel

Elias Baumann[1], Frédérique Meeuwsen[2], Martin D. Berger[3], Richard Kirsch[4], Iris D. Nagtegaal[2], Inti Zlobec[1]

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Introduction

Microsatellite instability (MSI) / mismatch repair deficiency is a genomic biomarker of 10-15% of colorectal cancers and is used in treatment decisions. Deep learning has previously demonstrated to be able to predict MSI from hematoxylin and eosin-stained (H&E) whole slide images (WSI), yet explanations for decisions are hard to attribute. MSAI-Path predicts based on automatically quantified, individually verifiable, and morphological components aligned with Bethesda criteria, like the manual MS Path score. Validation across multiple cohorts shows performance competitive with black-box models.

Material and methods

H&E WSIs from seven retrospective cohorts were analyzed (Bern-Multislide [N=189, 18% MSI], Bern-MSI [N=175, 49% MSI], Bern-Biopsies [N=71, 14% MSI], Nijmegen [N=487, 24% MSI], SurGen [N=499, 10% MSI], Toronto [N=415, 12% MSI], TCGA [N=423, 14% MSI]). Using tissue segmentation (SRMA) and nuclei segmentation (HoVer-NeXt) models, we extracted intraepithelial lymphocytes (IEL), mucin percentage, tumor grade, and tertiary lymphoid structure counts. These features were combined with clinical data (tumor location, age, sex) to predict MSI status via logistic regression or random forest.

Results and discussion

Our approach achieves 0.87 AUC on TCGA, comparable to black box methods on identical splits. The variable importance correlates strongly with MS Path (Spearman rho=0.76). A simplified model using only IEL, location, and mucin reliably predicts MSI (0.84 AUC across cohorts). Manually assessed MS Path scores align with MSAI-Path (rho=0.76). With optimized cutoffs, MSAI-Path's clinical performance (0.45 TNR, 0.98 NPV, 0.95 sensitivity) equals CE-IVD marked MSI screening software.

Conclusion

MSAI-Path predicts MSI using verifiable morphological features, matching black-box deep learning performance while enabling pathologists to audit and fully understand each prediction.

Key words: Microsatellite Instability, Explainability, Morphology, Deep Learning

A4 A CLIDIPA multi-center validation study on deep learning-based classification of early-stage mycosis fungoides and benign inflammatory dermatoses

Thom Doeleman[1, 2], Siemen Brussee[1], Pieter Valkema[1], Werner Kempf[3], Maarten Vermeer[4], Jesper Kers[1, 5], Anne Schrader[1]

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Introduction

Mycosis fungoides (MF) is a rare primary cutaneous T-cell lymphoma presenting with patches and plaques. Diagnosing early-stage (IA to IIA) disease is challenging due to its rarity and its clinical and histopathological resemblance to benign inflammatory dermatoses (BIDs), including eczema, psoriasis, and drug reactions, leading to delayed or incorrect diagnoses, highlighting the need for deep learning (DL)-based diagnostic tools. Our proof-of-concept study (PMID: 39306030) demonstrated that weakly supervised DL models could distinguish early-stage MF from BIDs with a mean balanced accuracy of 76.2% on an internal validation dataset.

Material and methods

We trained DL models on an expanded Leiden University Medical Center dataset, comprising 633 whole-slide images (WSIs) from 317 MF patients and 1,682 WSIs from 1,446 BID patients diagnosed between 2010 and July 2024. MF diagnoses were confirmed by an expert cutaneous lymphoma panel after clinicopathological correlation. Multiple combinations of foundation model feature extractors and multiple instance learning (MIL) methods were tested. External validation was performed using datasets from the Cutaneous Lymphoma International Digital Pathology (CLIDIPA) Registry, specifically from University Medical Center Utrecht (n = 245 WSIs) and the University of Zurich (n = 216 WSIs).

Results and discussion

At 20× magnification, the H-optimus-0 or UNI feature extractor with either Attention MIL or CLAM MIL achieved the best results. The models reached mean balanced accuracies of 72-84% on external datasets, comparable to the internal validation dataset.

Conclusion

Our DL-based models demonstrated strong generalizability on external datasets but showed performance variation across centers. A reader study is warranted to evaluate the model's clinical utility and explore center-specific model calibration.

Key words: deep learning, mycosis fungoides, cutaneous lymphoma, digital pathology, whole-slide imaging

A5 Machine Learning Achieves Pathologist-Level Coeliac Disease Diagnosis

Florian Jaeckle[1, 2], James Denholm[1, 2, 3], Benjamin Schreiber[1, 3], Shelley C. Evans[1], Mike N. Wicks[4], James Y. H. Chan[5], Adrian C. Bateman[6], Shonali Natu[7], Mark J. Arends[4], Elizabeth Soilleux[1, 2]

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Introduction

The diagnosis of coeliac disease (CD), an autoimmune disorder with an estimated global prevalence of around 1%, is generally performed using duodenal biopsies. However, inter-pathologist agreement when diagnosing CD is estimated to be only 80%. We aim to improve CD diagnosis by developing a machine-learning-based diagnostic classifier.

Material and methods

We present a machine learning model that diagnoses CD from a set of duodenal biopsies representative of real-world clinical data. Our model was trained on a diverse dataset of 3383 Whole-Slide-Images of H&E-stained duodenal biopsies from four hospitals featuring five different scanners along with their clinical diagnoses. We trained our model using multiple-instance-learning and evaluated it on an independent test set featuring 644 scans from a different hospital. Additionally, we compared the model's predictions to independent diagnoses from four pathologists on a subset of the test data.

Results and discussion

Our model diagnosed CD on an independent test set from an unseen source, with accuracy, sensitivity and specificity exceeding 95% and AUC exceeding 99%. In comparing the model's predictions to diagnoses from four pathologists, on unseen test data, we found statistically indistinguishable results between pathologist-pathologist and pathologist-model inter-observer agreement ($p>96\%$).

Conclusion

Our model achieved pathologist-level performance in diagnosing CD from a representative set of duodenal biopsies, representing a significant advancement towards the adoption of machine learning in clinical practice. Additionally, it demonstrated strong generalisability, performing equally well on biopsies from an unseen hospital. Hence, our model has the potential to revolutionise the diagnosis of duodenal biopsies and significantly reduce the time required for pathologists to diagnose duodenal biopsies.

Key words: Coeliac Disease Diagnosis, Multiple-Instance Learning, Computer Vision, H&E-stained biopsies

A6 PathBench-MIL: A Comprehensive AutoML and Benchmarking Framework for Multiple Instance Learning in Histopathology

Siemen Brussee[1], Pieter A. Valkema[1], Thom Doeleman[1], Anne M.R. Schrader[1], Jesper Kers[1, 2]

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[2] Department of Pathology, Amsterdam Medical Center, The Netherlands

Introduction

Multiple Instance Learning (MIL) has become a cornerstone in computational pathology, enabling the analysis of whole slide images (WSIs) using only slide-level labels. However, the growing complexity of pipeline design, exacerbated by the release of numerous histopathology foundation models, makes it difficult to identify optimal configurations for specific tissues and tasks. Existing benchmarking frameworks often focus on isolated steps, such as feature extraction or patch aggregation, but lack support for the entire MIL pipeline.

Material and methods

We developed PathBench-MIL, the first publicly available AutoML framework specifically for computational pathology (https://github.com/Sbrussee/PathBench-MIL). PathBench-MIL covers the entire pipeline—from slide preprocessing to model outputs—allowing users to benchmark and optimize feature extractors, stain normalization methods, aggregation techniques, and loss functions. The framework also includes hyperparameter optimization and an interactive visualization application. PathBench-MIL was evaluated on the TCGA-LUSC dataset for binary classification, multiclass classification, regression, continuous survival prediction, and discretized survival prediction.

Results and discussion

PathBench-MIL demonstrated competitive performance in our case study, showcasing how it can be used for various MIL challenges in computational pathology. By streamlining end-to-end pipeline development, the framework enables robust benchmarking and facilitates insights into the impact of methodological choices.

Conclusion

PathBench-MIL democratizes MIL in computational pathology by providing a comprehensive, user-friendly framework for benchmarking and pipeline optimization. Its ability to cover the full pipeline, combined with AutoML capabilities, makes it a valuable tool for accelerating innovation and fostering reproducibility in this rapidly evolving field.

Key words: Multiple Instance Learning, Automated Machine Learning, Foundation Models, Cancer Subtyping, Survival Prediction, Benchmarking

A7 AI in diagnostic pathology: exploring the risks of over-reliance and its clinical consequences

Yaelle Bellahsen-Harrar[1, 2], Melanie Lubrano[3, 4], Charles Lepine[5, 6, 7], Aurelie Beaufrere[3], Claire Bocciarelli[7], Anais Brunet[8], Elise Decroix[9], Franck Neil El-Sissy[10], Bettina Fabiani[4], Aurelien Morini[11], Cyprien Tilmant[12], Thomas Walter[3, 13, 14], Cecile Badoual[1, 2]

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Introduction

The integration of AI algorithms into pathology practice presents both opportunities and challenges. Although it can improve accuracy and inter-rater reliability, it is not infallible and can produce erroneous diagnoses, hence the need for pathologists to always check predictions. This critical judgment is particularly important when algorithm errors could lead to high-impact negative clinical outcomes, such as missing an invasive carcinoma. However, the influence of AI tools on pathologists' decision-making is not well explored. This study aims to evaluate the impact of a previously developed AI tool on accuracy and inter-rater reliability among pathologists, while assessing whether they maintain an independent judgment.

Material and methods

Eight pathologists from different hospitals and with varying levels of experience, participated in the study. Each of them reviewed 115 slides of laryngeal biopsies, including benign epithelium, low-grade and high-grade dysplasias, and invasive squamous carcinomas.

Results and discussion

Assisted pathologists had a higher accuracy for high-grade dysplasia, invasive carcinoma and improved inter-rater reliability. However, cases of over-reliance on AI have been observed, resulting in the omission of correctly diagnosed invasive carcinomas during the unassisted examination. The false predictions on these carcinoma slides were labeled with a low confidence score, which was not taken into account by the users.

Conclusion

Our study emphasizes the potential over-reliance of pathologists on AI models and the potential harmful consequences, even with the advancement of powerful algorithms. The integration of confidence scores and the education of pathologists to use this tool could help to optimize the safe integration of AI into pathology practice.

Key words: Diagnostic computational pathology, AI Assistance, Over-reliance, Reliability, Confidence score, Clinical outcomes

A8 Temporal degradation of diagnostic artificial intelligence models in digital pathology: determinants and mitigation strategies

Anders Blilie[1, 2], Xiaoyi Ji[3], Nita Mulliqi[3], Richard Salmon[4], Einar Gudlaugsson[1], Martin Eklund[3], Emilius A.M. Janssen[1, 5, 6], Kimmo Kartasalo[7]

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Introduction

Concerns have been raised over the robustness of AI models in digital pathology, particularly in relation to various batch effects, yet few studies addressed the impact of temporal variation. This study aims to assess the phenomenon of "AI aging"—declining AI performance over time—in digital pathology, explore the underlying contributing factors and further investigate potential mitigation strategies.

Material and methods

We utilized 119 prostate core needle biopsy slides with a balanced ISUP grade distribution from Stavanger University Hospital, plus one Sierra color calibration slide. Two consecutive baseline scans were performed on a Hamamatsu NanoZoomer S60 scanner to assess reproducibility in the absence of temporal variation, followed by scans every 14 days for one year. Temporal variance's impact on AI model performance will be evaluated using a deep multiple instance learning model trained on ~46,000 whole slide images for prostate cancer diagnosis, and other state-of-the-art pathology foundation models. Model performance will be systematically compared at each timepoint, quantifying the temporal degradation.

Results and discussion

Preliminary results support the AI aging hypothesis, with a negative correlation between time intervals and model performance consistency. Several factors have been examined, including scanner variation, focus score, training data size, incorporation of target domain samples into the training set — among others to be explored. Additionally, pathologists will evaluate the slides with analysis results to provide insights into the potential determinants of variation.

Conclusion

This study pioneers the investigation of temporal degradation in digital pathology AI model performance and its influencing factors, potentially paving the way for real-time quality assurance approaches to enhance diagnostic robustness over time.

Key words: artificial intelligence, AI aging, data drift, scanner variation, quality assurance

A9 High Resolution 3D Reconstruction and Visualization of Tubulo-villous Adenoma Tissue

Mark Eastwood[1], Fayyaz Minhas[1], Sabine Tejpar[2], Zedong Hu[2], Joanne Edwards[3]

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Introduction

Tubulo-villous adenomas (TVAs) have complex 3D structures and growth patterns that give clues towards the underlying biological characteristics of the lesion. The ability to reconstruct and visualize this structure is important for understanding TVAs, and many other types of cancer and precursor lesions.

Material and methods

60 consecutive sections of TVA tissue stained with H&E were collected and scanned at 20x resolution, interleaved with a desmin IHC staining every 5 sections. These WSIs were sequentially co-registered using DeeperHistoReg, a powerful open-source registration framework. We then constructed a multi-scale volumetric representation of the stacked WSIs using CloudVolume, another open source project. CloudVolume can also be used to serve regions of this volume at a requested scale on-the-fly allowing efficient handling of very large volumetric data. This volume can be visualized and freely explored in 3D at high resolution using NeuroGlancer, a browser-based software tool developed for visualization of high-resolution MRI imaging, paired with a custom 3D shader suitable for clearly rendering H&E volumetric data.

Results and discussion

The complex 3D structure of a TVA sample has been reconstructed and visualized in a freely navigable and zoomable way, allowing better understanding of the growth patterns and biology of such lesions. This work also represents a general approach to visualize any tissue in 3D given sufficient whole slide images of consecutive stained sections.

Conclusion

We have developed a pipeline for flexible, high resolution 3D visualization of tissue samples that requires only standard H&E slide creation protocols and no specialist equipment.

Key words: Tubulo-villoous adenomas, Colorectal polyps, Visualization, 3D reconstruction

A10 Automated Registration of Prostate Whole-Mount Histopathology and Magnetic Resonance Imaging

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Introduction
Magnetic resonance imaging (MRI) is a valuable non-invasive method for assessing the extent of prostate cancer (PCa). However, the inter-observer agreement on MRI for detecting and grading PCa lesions through qualitative assessment remains only moderate. Whole-mount histopathology (WMHP) serves as a critical reference standard for detecting and grading PCa tumors.

Material and methods
We propose a new automated method for registering pre-surgical prostate MRI and WMHP. High-resolution ex vivo MRI was utilized as a reference to explore and evaluate the structural relationship between in vivo pre-surgical MRI and WMHP. A novel deep learning-based registration method was developed to register WMHP to MRI. Additionally, a new module was integrated into the pipeline to estimate and correct the distortion and motion between the prostate specimen inside and outside the human body. This proposed method was developed using images from 270 patients who underwent radical prostatectomy.

Results and discussion
The proposed method achieved a Dice similarity coefficient of 0.95 ± 0.06 on 160 test images compiled from 45 patients. In total, 90 sets of landmarks were annotated in the 45 test cases. The 2D target registration error between corresponding landmarks on in vivo MRI and WMHP measured 3.93 ± 0.80 mm before registration and improved to 1.18 ± 0.28 mm after registration (p-values < 0.001).

Conclusion
We created a registration method to align pre-surgical prostate MRI images with histopathology images, facilitating the automated mapping of PCa from WMHP to MRI. Our algorithm significantly outperformed the latest state-of-the-art method, VoxelMorph, for multimodal prostate image registration, with p-values less than 0.0001 across all metrics.

Key words: Prostate whole-mount histopathology, Prostate magnetic resonance imaging, Image registration

A11 AI-driven Spatial Transcriptomics Analysis Reveals PIGR as a Potential Prognostic Marker for Colorectal Cancer

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Introduction

The invasion front of colorectal cancer (CRC) represents an active interface for both tumor and host-related (e.g. immune cells, fibroblasts) components and constitutes a rational area to search for novel prognostic biomarkers. Here, we harness the potential of spatial transcriptomics together with AI-driven image analysis to identify new spatially resolved biomarkers which can be validated for their prognostic effect on larger patient cohorts, using standard immunohistochemistry (IHC).

Material and methods

CRCs (n=6) were subjected to spatial transcriptomic (ST) analysis using the 10x Visium platform (n≈18000 genes). A tissue segmentation model was applied to hematoxylin and eosin (H&E) images followed by alignment of spatial spots with segmented tissue areas. Cell type deconvolution was performed for spot annotation and quality check. Clustering on the BANKSY gene expression matrix identified tumor spots, validated by pathologists. Differential gene expression analysis identified a signature gene, which was then validated by IHC for prognostic effects on two independent CRC cohorts: (1) mixed stage I-IV (n= 117) and 2) stage II (n=120).

Results and discussion

ST analysis coupled with AI identified Polymeric immunoglobulin receptor (PIGR) as a candidate gene. IHC expression of PIGR was significantly associated with more aggressive tumor-related features and unfavorable outcomes, including higher tumor budding (p=0.0053) and significantly worse overall survival (88.6% vs. 73.1%) and disease-free survival (93.3% vs. 75.8%).

Conclusion

From discovery to translation, AI-driven ST identified PIGR as a potential prognostic marker in CRC patients. Validation of PIGR loss by IHC and its potential predictive value to specific therapies remain to be further elucidated.

Key words: colorectal cancer, transcriptomic, artificial intelligence, Polymeric immunoglobulin receptor (PIGR), survival analysis

A12 Advanced spatial biology and multiomic analysis – a new paradigm for pathology predictions

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Introduction

Multiomics integrates genomics, transcriptomics, epigenetics, proteomics, spatial biology, and single-cell analysis to provide a comprehensive view of molecular mechanisms underlying development, cellular responses, and disease. By combining diverse omic and modal datasets, researchers can uncover novel biological relationships and gain deeper insights into complex biological processes. Spatial biology preserves the spatial context of molecular interactions, while single-cell analysis resolves cellular heterogeneity, enabling the identification of rare cell populations and distinct states. These approaches are foundational for high-throughput, accurate data generation, ensuring the reliable output needed for multiomics research. Spatial transcriptomics, which combines sequencing and digital pathology, allows researchers to explore biological interactions at the cellular level in unprecedented detail. Computational tools, such as Illumina's DRAGEN multiomics pipelines enable seamless data preparation and analysis, while platforms like Illumina Connected Multiomics (ICM) provide powerful visualization, deeper analysis, and harmonized integration of multiomics data.

Material and methods

NA

Results and discussion

NA

Conclusion

Next-generation sequencing (NGS) technologies, such as those offered by Illumina, are fundamental to multiomics research, ensuring high-throughput and accurate data generation. As multiomics continues to evolve, the integration of spatial biology, single-cell analysis, and advanced computational tools is poised to drive breakthroughs in personalized medicine, disease research, and biomarker discovery. This approach is transforming how we understand complex biological systems, opening new frontiers in molecular biology and precision healthcare.

Key words: Multiomics, Spatial Biology, Single Cell

A13 Interoperability in the Implementation of Standardized Structured Reporting (SSR) in Pathology Practice

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Introduction

The adoption of Standardized Structured Reporting (SSR) in pathology is a transformative step toward improving diagnostic consistency, report completeness, and data interoperability. The Nictiz Layer Framework for interoperability provides a structured approach to understanding the challenges and enablers of SSR implementation. By applying this framework, this study explores the complexities of SSR adoption in pathology, particularly from the perspective of Belgian pathologists.

Material and methods

A mixed-methods approach was employed, incorporating stakeholder interviews across all interoperability layers: legal and regulatory frameworks, organizational policies, clinical workflows, information systems, applications, and IT infrastructure. This study builds on previous interviews with pathologists to provide a comprehensive assessment of SSR adoption challenges and opportunities

Results and discussion

Findings indicate that successful SSR implementation requires both vertical coordination between policy and technical layers and horizontal collaboration across institutions. Key enablers include alignment with international reporting standards, investment in robust IT infrastructure, and development of consensus-driven protocols. However, significant barriers remain, including financial constraints, resistance to workflow changes, and challenges in system integration. A hybrid approach—centralized SSR content with localized customization—emerges as a promising model.

Conclusion

Achieving interoperability in SSR requires a multi-pronged strategy, emphasizing stakeholder collaboration, targeted training programs, and policy-driven governance. By addressing both technical and organizational challenges, this study offers strategic recommendations for fostering SSR adoption, with implications for advancing digital pathology across Europe.

Key words: Standardized Structured Reporting (SSR), Pathology, Interoperability, Digital Pathology, Health IT Integration, Clinical Workflow Optimization

A14 Pathology Report Generation Using Giga-pixel Whole Slide Images for Bladder Tumors

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Introduction

Pathology reports play a crucial role in diagnostic decision-making. With advancements in digital pathology, high-resolution giga-pixel Whole Slide Images (WSIs) have become more accessible, enabling deep learning applications for automated pathology report generation. While previous studies primarily focused on localized tasks such as image classification, lesion detection, or segmentation, generating comprehensive pathology reports remains a complex challenge. Recent research has expanded into multimodal learning, integrating both slide images and reports. In response to this rapid progress, we propose a pathology report generation model fine-tuned for clinical application with high accuracy.

Material and methods

Our approach leverages 752 high-resolution H&E WSIs of bladder tumor along with paired reports from a medical center in Korea. Foundation models were employed to extract critical visual features, while structured pathology reports were processed to identify essential diagnostic attributes. The extracted features were mapped to classification-based diagnostic labels, which were subsequently utilized for pathology report generation through a language model, T5.

Results and discussion

The proposed method achieved strong performance with a ROUGE-L score of 0.92, a BLEU-4 score of 0.81, a Jaccard score of 0.84, and a BioLLM score of 0.97, further validated through Mean Opinion Score (MOS) assessments.

Conclusion

By utilizing a foundation model, our approach compensates for the limited availability of pathology data. Moreover, the proposed model enables highly accurate report generation. This model could serve as a valuable assistive tool for physicians, particularly in real-world clinical settings with a shortage of specialists, improving workflow and diagnostic support.

Key words: Whole Slide Images, Digital pathology, Generative AI, Text-to-Text Transfer Transformer

A15 Can a a Software-Based Template transform Urinary Cytology Reporting and ReduceTurnaround Time in a Tertiary Center?

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Introduction

Standardized pathology reports enhance completeness and readability, improving patient management. The Paris System for Reporting Urinary Cytology (TPS) has gained acceptance for primarily focusing on detecting high grade urothelial carcinoma. The next step at the Institute of Pathology, Faculty of Medicine, University of Ljubljana, was implementing TPS together with standardized findings on non-neoplastic changes into software-based standardized structured reporting (SBSSR).

Material and methods

SBSSR for urinary cytology was implemented at the Institute in March 2023. The template was tested and approved by all cytopathology team members before routine use, and clinicians received a briefing to enhance inter-specialty communication. Turnaround time was measured from from the receipt of the cytology sample into the lab to the time of digital signature on its diagnostic report over two consecutive 11-month periods (01/04/2022–01/03/2023 and 01/04/2023–01/03/2024), along with the quality metrics assessment.

Results and discussion

Team members quickly adopted SBSSR for urinary cytology. Reports are now generated, costs calculated, and digitally signed in a single step, eliminating dictation and administrative tasks. Average turnaround time decreased from 1.8 days (2843 samples) to 1.5 days (3438 samples), all while maintaining a stability in the prevalence of diagnoses over time.

Conclusion

SBSSR implementation improved patient care by reducing diagnosis time and enhancing report clarity.

Key words: Standardized reporting terminology, Reporting quality, Cytology, Urine, The Paris System

A16 Feature Matching Techniques for Region of Interest Registration in Whole Slide Images

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Introduction

Tumour-infiltrating lymphocytes (TILs) are scored in a region of interest (ROI) using Salgado's criteria on haematoxylin and eosin (H&E)-stained breast cancer (BC) slides. Immunohistochemistry (IHC) offers a more detailed characterisation of TIL populations, distinguishing immune cells that promote tumour progression from those that suppress it. Different biomarkers stain relevant immune cells, with scoring performed on consecutive sections of the same tissue block. However, identifying the same ROI across sections is time-consuming.

Material and methods

The cohort consists of 20 patients, each with 10 whole slide images (WSIs): one H&E-stained breast cancer (BC) tissue and nine IHC-stained WSIs of TIL-related biomarkers, which may also include axillary lymph node tissue. A pathologist annotates the ROI on the H&E slide and its corresponding counterpart on the IHC WSIs. ROI registration is assessed using traditional and deep-learning (DL) feature matching techniques without extra-tissue removal, with performance measured by the failure rate based on the relative target registration error between re-annotated and automatically registered ROI centroids across different threshold values.

Results and discussion

Robust Dense Feature Matching (RoMa), which integrates a foundational model, achieved the lowest number of failures without a staining invariance phase by combining its outdoor and indoor versions. At thresholds of 0.075, 0.05, and 0.025, the failure rates were 9/180, 9/180, and 12/180, respectively. In comparison, using SuperPoint+SuperGlue, considered state-of-the-art, resulted in 24/180, 26/180, and 31/180 failures at the same thresholds, when combining the outdoor and indoor versions.

Conclusion

The study shows that RoMa improves ROI selection on consecutive WSIs, which could be useful for more efficient TIL subtype scoring.

Key words: Tumour infiltrating lymphocyte, Region of interest, Registration, Foundation model, Immunohistochemistry, Multiple tissues

A17 A novel method for the morpho-proteomic analysis of mitotis

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Introduction

Mitosis detection is an important task in the field of digital pathology, as determination of the mitotic index (MI) plays an important role in the tumor grading of patients. Manual determination of MI is a highly demanding task for practitioners , thus, automation is needed. There has been substantial progress towards creating robust mitosis detection algorithms in recent years, primarily driven by the Mitosis Domain Generalization (MIDOG) challenges. The molecular analysis of mitosis also gained attention during the recent years to fundamentally understand the process better.

Material and methods

Here, we introduce a novel mitosis detection and single cell isolation pipeline with a domain-driven loss function. We envision a new perspective for domain generalization by improving performance of models with subtyping mitotic cells into the 5 main stages of mitosis.

Results and discussion

Our proposed detection method outperforms baseline solutions both on a subset of the MIDOG data dedicated for testing and an in-house unseen domain as well. Based on our model we present the results of a pilot experiment, where we investigate the molecular composition of dividing cells on a single cell level.

Conclusion

We believe that our work broadens the horizon generally in digital pathology: subtyping helps in solving the original, higher-level tasks while also providing promising new directions for mitotic cell detection, such as molecular analysis of the subphases on a single cell level.

Key words: mitosis detection, molecular analysis, deep learning, single cell

A18 Access to Whole Slide Images in Digital Pathology: a Canadian Perspective on Ethical, Legal and Practical Considerations

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Introduction

Digital pathology is transforming the practice of pathology by enabling computational pathology, remote work, and enhanced collaboration among healthcare professionals. However, the shift to whole slide images (WSI) introduces complex ethical, legal, and logistical challenges, including questions about image stewardship, patient access, privacy, and security.

Material and methods

Drawing lessons from medical imaging's transition to digital imaging, this discussion reviews relevant Canadian and global laws and regulatory frameworks, the implementation of DICOM standards for pathology and privacy concerns specific to WSI.

Results and discussion

WSI are part of the medical records and are subject to the laws and regulatory frameworks that govern the use and right to access personal health information. While WSI access could empower patients, enhance interdisciplinary communication and open new avenues for research and industry partnerships, it requires a cultural shift in pathology to embrace increased transparency, while making sure to establish robust privacy protocols. Widespread adoption of DICOM standards could help address interoperability issues, the need for audit trails, cybersecurity requirements for secure image transfer and preserving the integrity of the WSI. It would also foster alignment with existing medical imaging infrastructure to facilitate storage and sharing of WSI. Storage of WSI in a vendor-neutral format would also facilitate pooling of data to train computational pathology models.

Conclusion

Digital pathology can promote innovation in computational pathology and redefine the pathologist's role in modern healthcare. This work underscores the need for interdisciplinary collaboration to ensure the ethical and practical implementation of digital pathology systems that align with future patient care, patient engagement and research needs.

Key words: digital pathology, DICOM, health data stewardship, patient engagement

A19 Immune Landscape Profiling in HER2+ Breast Cancer: Predicting Pathological Complete Response Using Convolutional Neural Network

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Introduction

Breast cancer patients who achieve pathological complete response (pCR) after neoadjuvant therapy show significantly improved disease-free survival. However, predicting which patients are most likely to respond remains a challenge. We hypothesize that profiling the immune landscape of HER2+ tumours could aid in patient stratification and identify an immune profile associated with pCR.

Material and methods

Multiplex chromogenic immunohistochemistry panels targeting immune cell subpopulations and tertiary lymphoid structures (TLS) were applied to HER2+ BC tumours from patients of the neoadjuvant TCHL clinical trial (NCT01485926). Using the Aiforia® Create platform, two convolutional neural networks were trained to quantify densities of CD3+, CD20+, CD4+, CD8+, and DC-Lamp+ immune cells in invasive tumour regions. Correlations with response to neoadjuvant therapy and clinicopathological features were assessed.

Results and discussion

Deep learning models for automated analysis of CD3, CD20, and DC-Lamp (TLS model) and CD4 and CD8 (T-cell model) were developed with object detection error rates of 12.08% and 12.88%, respectively. Statistical analysis of 19 pre-treatment patient biopsies showed trends of higher pre-treatment immune cell densities in pCR vs. non-pCR patients. Higher CD3+, CD4+, and CD8+ cells were found in stage III vs. stage II tumours, and higher CD4+ and CD8+ cells in ER- vs. ER+ patients.

Conclusion

Our data suggest that immune cell densities may predict pCR to neoadjuvant therapy in HER2+ breast cancer. Convolutional neural networks for automated immune profiling provide a promising tool for patient stratification and treatment response prediction. Further validation in larger cohorts is necessary to confirm the clinical validity of these findings.

Key words: HER2+ breast cancer, immune landscape, pathological complete response, convolutional neural network, neoadjuvant therapy

A20 AI-based BRCA mutation prediction and HRD in high-grade ovarian cancer using whole slide images

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Introduction

Deleterious mutations in homologous recombination repair-related genes occur in epithelial ovarian cancers (EOC), with BRCA genes as prominent factors. Such mutations, along with homologous recombination deficiency (HRD), are now recognized as predictive biomarkers of sensitivity to poly(ADP-ribose) polymerase inhibitors (PARPi) maintenance therapy. Currently, comprehensive mutation profiling via next-generation sequencing is the norm in routine diagnostics, but it requires long-time cycles, high costs, and a large tissue for DNA. Prior studies advocate for the existence of a genotype-phenotype correlation, providing a theoretical foundation for predicting oncogenic mutations from whole slide images (WSIs). Unfortunately, existing studies rely on exhaustive annotations and are still unable to precisely localize the mutation areas.

Material and methods

In this study, we address this problem using multiple-instance learning (MIL). We developed a model of a UNI foundation model and an attention-based MIL, with a smooth operator. First, we used the TCGA-HGSOC cohort to assess the factors influencing mutation prediction, including the effect of spatial relationships induced by the Smooth to classify BRCA-mutated vs. wild-type. Second, we collected a first-of-its-kind African-Moroccan cohort of 90 patients to classify HRD-positive vs. negative.

Results and discussion

The experimental results achieved over 90% in accuracy, precision, recall, F1 score, and AUROC.

Conclusion

This demonstrates that BRCA somatic mutations have a disparate phenotypic effect that can be detected through MIL, potentially serving as a pre screening tool in the future. Additionally, we identify the patches strongly associated with mutations, providing interpretability and an analysis of the relationship with morphological features. Additional experiments are currently underway on the Moroccan cohort.

Key words: Gynecologic AI, Epithelial Ovarian Cancer, Digital & Computational Pathology, AI-biomarkers, BRCA

A21 Self-Supervised Learning Framework for Accurate Colorectal Tissue Classification Using SimCLR and ConvNext

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Introduction

Colorectal cancer (CRC) diagnosis relies heavily on histopathology image analysis, which is important for identifying and treating malignancies. CRC tumors consist of diverse tissue types, and classifying these tissues using deep learning presents challenges like limited data availability, inconsistent quality, inter-observer variability, and imbalanced datasets. A major issue is the scarcity of high-quality labeled data. Additionally, labeling histopathology images with cancer tissue types is time-intensive and demands specialized expertise.

Material and methods

We use the seven publicly available datasets including Lizard, MHIST, BreCaHD, SPIE-BreastPathQ, Colorectal, MoNuSeg, and CryoNuSeg which includes multiple tissue types. We propose a self-supervised learning (SSL) based SimCLR (Simple Framework for Contrastive Learning of Representations) approach utilising the ConvNext models with harmonic attention to extract meaningful features from unlabeled H&E patch images. With the help of unsupervised representations by contrasting augmented views of the same tissue patch, we fine-tuned downstream CRC tissue classification (tumor, stroma, complex stroma, lymphocyte, adipose, mucosa, debris and background) on CRC5000 dataset with enhanced feature representation.

Results and discussion

Our experimental results demonstrated that the proposed SimCLR-based SSL method achieved an accuracy of 93% classification, and AUC of 0.987. It outperformed our earlier developed CTCHist-Net and other state-of-the art models, by a 1.33% improvement. This approach effectively extracts high-level and spatial features (such as shape or texture) from unlabeled H&E images and improves the tissue classification.

Conclusion

The proposed approach enhances CRC tissue classification by effectively learning meaningful patterns from unlabeled H&E images and reducing the need for extensive labeled data and improving model accuracy and reliability.

Key words: Colorectal cancer, Self supervised leanring, Tissue types, Deep learning, Classification, Histopathology

A22 Validation of Stratipath Breast for risk stratification of breast cancer in over 2700 patients

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Introduction

Stratipath Breast is a CE-IVD marked artificial-intelligence based decision support tool for prognostic risk stratification of breast cancer patients. It uses deep learning-based image analysis to predict prognostic information based on the tumour's morphology from H&E-stained histopathology images. The solution enables risk stratification of invasive breast cancer, while significantly reducing costs and turn-around times compared to molecular assays. Its integration into routine clinical workflows has the potential to benefit both patients and healthcare providers, expanding the access to precision diagnostics.

Material and methods

The validation study was conducted in collaboration with Karolinska Institutet in Sweden and includes 2719 primary breast cancer patients from two Swedish hospital sites. The prognostic performance of Stratipath Breast is investigated by Kaplan-Meier plots and quantified with hazard ratios (HR) for progression-free survival (PFS) using multivariate Cox Proportional Hazards analysis.

Results and discussion

There was a significant difference in PFS between Stratipath Breast risk categories: low and high risk. The adjusted HRs for PFS between low- and high-risk categories (binary risk-classification) was 2.76 in the ER+/HER2- subgroup, and 2.20 in the NHG2 ER+/HER2- subgroup. The adjusted HR for PFS between the lowest and highest Stratipath Breast risk groups (5-level risk-classification) in the ER+/HER2- subgroup was 3.88.

Conclusion

This validation study found an independent prognostic value of Stratipath Breast, including the clinically relevant ER+/HER2- patient subgroup. Stratipath Breast provides reliable risk stratification of ER+/HER2- breast cancers directly from H&E whole slides images, with the potential to reduce over- and under-treatment of breast cancer patients.

Key words: Breast cancer, Risk stratification , Computational pathology, CE-IVD, Prognostication

A23 AI-based robust testicular cancer triaging, a promise for an efficient and cost-effective diagnostic/predictive modality.

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Introduction

Testicular cancer is the most common malignancy in males of age 20-44, and categorized into Seminoma and Non-Seminomatous Germ Cell Tumor (NSGCT). Histopathological diagnosis, though effective, is time-consuming, costly, subject to inter-observer variability, and due to the disease rarity , diverse morphology, and limited diagnostic expertise, it is susceptible to misinterpretation, potentially leading to erroneous treatment. Digital pathology with artificial intelligence (AI) promises to improve diagnostic consistency and efficiency, and importantly settings without expertise in these tumors. Here, we seek rapid and robust triaging of these subtypes leveraging AI.

Material and methods

254 retrospective multi-institutional H&E-stained slides of 149 patients, from the TCGA-TGCT collection, were used for our AI model following a training/validation/testing split of 119/15/15 patients (188/23/43 slides). We finetuned the UNI foundation model using attention-based Multiple Instance Learning (abMIL) .

Results and discussion

Independent hold-out set evaluation revealed Area Under the Curve=96%, Accuracy=94.54%, Specificity=92%, and importantly, Sensitivity=100%, which supports our model as a triaging tool, enabling faster decision-making for high-risk patients.. Specifically, all predicted NSGCT are correctly identified as NSGCT, and all Seminomas are always detected. In other words, no Seminoma case is overlooked, while just 8% of the actual NSGCT may be misclassified as Seminoma.

Conclusion

Our proposed abMIL approach leveraging a foundation model, provides a perfectly sensitive and scalable solution for clinical triaging between Seminoma and NSGCT , supporting pathologists in improving diagnostic accuracy and efficiency. Furthermore, abMIL highlighting AI decision-driving regions renders our model well-suited for large-scale clinical data, where it can make further data-driven contributions towards furthering our disease knowledge.

Key words: Testicular Cancer, ABMIL, Foundation Model, Cost-Effective, Integrative Diagnostic

A24 Cross-Cancer Generalization of Tissue Segmentation Models: Toward Pan-Cancer AI in Pathology

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Introduction
Tissue segmentation is a critical AI application in pathology, providing pixel-level precision necessary for spatial analysis. However, developing segmentation models for each tumor entity is resource-intensive and limits scalability. Cross-cancer generalization—the ability of models trained on specific tumor types to segment histologically different tumors—could reduce the need for entity-specific models and accelerate the realization of pan-cancer segmentation algorithms.

Material and methods
We assessed the cross-cancer generalization performance of five established tissue segmentation models (trained on breast, colon, lung, kidney, and prostate cancers) using 21 distinct cancer types from The Cancer Genome Atlas (TCGA), comprising over 7,700 whole slide images. Representative tumor and benign regions were selected and segmented by each model. Segmentation performance was evaluated using a pathologist-scored scale (0-10) based on tumor-stroma differentiation, boundary precision, and detection accuracy.

Results and discussion
The lung model demonstrated exceptional cross-cancer generalization, achieving mean segmentation scores of 7.9 ± 2.1 across non-native cancer types, with scores exceeding 8.5 in e.g. ovarian and esophageal carcinomas. The breast model achieved high accuracy in ovarian (8.3 ± 1.0) and prostate (8.2 ± 1.0) cancer. The colon model performed well in cholangiocarcinoma (7.2 ± 1.3). In contrast, the kidney and prostate models showed more restricted generalization, with mean scores below 5.0 in most tumor types.

Conclusion
Existing segmentation models exhibit substantial cross-domain generalization, allowing rapid adaptation to new tumor types and reducing the need for de novo model development. Our findings support the feasibility of pan-cancer segmentation models, which could streamline AI integration into pathology workflows and facilitate reproducible biomarker discovery.

Key words: AI model, histopathology, tissue segmentation, pan-cancer, generalization

A25 Artificial intelligence-based assessment of tumor-infiltrating lymphocytes as a predictor of response to neoadjuvant therapy in breast cancer

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Introduction
Tumor-infiltrating lymphocytes (TILs) are predictive and prognostic biomarker in triple-negative (TNBC) and HER2+ breast cancer (BC), but their clinical use is limited by the subjectivity of manual assessment. This study applies artificial intelligence (AI) to evaluate predictive and prognostic value of TILs in a multi-institutional cohort of TNBC and HER2+ BC patients treated with neoadjuvant chemotherapy (NACT).

Material and methods
A supervised deep learning pipeline was developed to analyze hematoxylin and eosin-stained whole-slide images from 518 BC patients. AI quantified stromal TIL percentage, stromal TIL density, and intratumoral TIL density. Associations between AI-based TIL scores, clinicopathological characteristics, and patient outcomes were assessed.

Results and discussion
AI-based scores showed high correlation with human pathologist (Spearman R = 0.61-0.77, p-val < .001). Higher AI-assessed TIL levels were significantly associated with better NACT response and both stromal and intratumoral TILs were strong and independent predictors of pathological complete response in TNBC and HER2+ subtypes. High TILs showed independent positive prognostic value for overall survival in TNBC subtype, however, no significant association with improved survival was observed for HER2+ subtype.

Conclusion
This study supports AI-driven TIL quantification as a predictive and prognostic tool in BC patients receiving NACT. AI-derived stromal and intratumoral TIL densities are independent predictors of response and survival, highlighting their potential for integration into digital pathology workflows for risk stratification.

Key words: breast cancer, neoadjuvant chemotherapy, tumor-infiltrating lymphocytes, artificial intelligence

A26 Deep Learning for detection of Mononuclear Leukocytes from PAS Stained Whole-Slide-Images of Kidney Biopsy

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Introduction

Kidney biopsies are performed to assess suspected acute or chronic rejection after transplant, where inflammatory cells play a crucial role in diagnosis. The Banff scoring system is the gold standard for evaluating transplant kidney biopsies, but it is time-consuming and lacks reproducibility as quantifying inflammatory cells manually is challenging. Moreover, the role of different subtypes of inflammatory cells in disease progression remains unclear. Automated detection and classification of mononuclear leukocytes (MNLs) using deep learning can reduce pathologists' workload, improve reproducibility in assessment and discover new insights.

Material and methods

We utilised the MONKEY challenge dataset, which contains 81 PAS-Stained whole-slide images (WSIs) of kidney tissue with annotated lymphocytes and monocytes by experienced pathologists. We developed a multi-head network architecture based on an EfficientNetV2-L encoder with three decoders each specialised in detecting a specific cell type. To enhance accuracy, the model learns to predict nuclei segmentation and contour maps. We used NuClick to generate nuclei instance segmentations and obtained nuclei contours using Sobel filters. A pixel-level weighted sampling strategy was used to address class imbalance. Additionally, we implemented a loss weighting mechanism using learnable weights to achieve optimal performance.

Results and discussion

On the MONKEY Challenge live leaderboard, our model ranked second place in overall MNLs detection and in lymphocyte and monocyte detection (FROC = 0.40, 0.41 and 0.18 for MNLs, lymphocytes and monocytes detection respectively).

Conclusion

We present a deep learning model for detecting MNLs in kidney biopsies. Future work will focus on validating our model on larger public datasets such as PanNuke.

Key words: Deep Learning, Cell Detection, Transplant Kidney Biopsy, Mononuclear Leukocytes

A27 An eye tracking dataset of pathologists' assessments on Whole Slide Images and gland images of colon cases

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Introduction

The digital revolution in pathology fosters advanced ML-based tools for CRC diagnosis, but the underlying expert gaze and decision processes remain poorly understood. Our dataset integrates 533 CRC whole slide images (WSI), real-time eye tracking collected during the assessment of 12 pathologists, the extraction of more than 6000 gland images and the corresponding gland classification and confidence decisions from 13 pathologists, enabling deeper insights into diagnostic behaviour.

Material and methods

In total, 533 WSIs of colon polyps were digitized and annotated for dysplastic and non-dysplastic glands. Based on these annotations, gland images were extracted at multiple magnifications, yielding 6361 gland images. Twelve participants assessed 14 WSIs, with the task of formulating an oral diagnosis while their gaze and viewport positions were tracked, and 13 participants classified gland images with recorded confidence levels.

Results and discussion

A preliminary ResNet18 classifier, fine-tuned on these glands, achieved 95% accuracy in differentiating dysplastic from non-dysplastic glands. Visual reconstructions confirmed the alignment of gaze data with viewport positions, validating data integrity. This comprehensive resource supports research on expert visual patterns, diagnostic confidence, and context-based interpretation in digital pathology.

Conclusion

Linking gaze behaviour with standard annotations offers insights into pathologists' diagnostic reasoning. Our dataset enables the training of explainable AI and accelerated education. Accessible through the BBMRI-ERIC CRC-ET cohort, this multi-modal data fosters novel methodologies to improve accuracy, explainability, and efficiency in digital pathology.

Key words: Eye-tracking, Artificial Intelligence, Human-Computer Interaction, Colorectal Cancer

A28 A Foundation-Model-Based Deep Learning Framework Predicts Chemo-Radiotherapy Outcomes in a Phase III Rectal Cancer Trial

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Introduction
Disease outcome prediction for cancer patients is essential for personalized treatment planning. Foundation models for digital pathology enable unsupervised feature extraction from whole-slide images. We propose a deep-learning framework integrating multi-zoom histopathological features with clinical and radiotherapy data to predict survival in locally advanced rectal cancer (LARC) patients.

Material and methods
Clinical data, radiotherapy plans and pre-treatment biopsies from 409 ARISTOTLE trial participants were divided into training (80%), validation (10%), and testing (10%). A multiple-instance-learning model with gated attention across magnification levels (20X, 10X, 5X) was trained using embeddings from foundation models (GooglePath, UNI, GigaPath), combined with nine clinical and eight dosimetric variables, and processed through a Cox-proportional-hazards head. The dosimetric variables were selected by LASSO regression for overall survival (OS) based on dose-volume histograms of planning-target volumes and organs-at-risk. Model evaluation was by C-index with standard deviation.

Results and discussion
The model with GooglePath embeddings yields a C-index of 0.742±0.05 for OS and 0.682±0.07 for disease-free survival (DFS), surpassing models with UNI (OS: 0.690±0.04, DFS: 0.645±0.08) and GigaPath (OS: 0.681±0.05, DFS: 0.632±0.07) embeddings. All multi-modal models significantly exceeded the clinical-only baseline (OS: 0.600±0.09, DFS: 0.589±0.11, $p<0.001$). In the testing set, the AI-stratified high-risk cohort had significantly worse OS (Hazard Ratio [HR]=5.02, 95% confidence interval [CI]: 1.54–16.35, p=0.003) and DFS (HR=4.43, 95% CI: 1.19–11.83, p=0.016). Tumorous tiles exhibited significantly higher attention scores ($p<0.001$).

Conclusion
Our model leveraging GooglePath feature embeddings and radiotherapy data enhances survival prediction for LARC patients receiving neoadjuvant chemo-radiotherapy. Future work includes external validation using real-world datasets and incorporating molecular and genomic markers.

Key words: Rectal cancer, Foundation model, Chemo-radiotherapy, Deep learning

A29 HALO Breast IHC AI: Demonstration of its Application as a Training Tool for Students

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Introduction

Immunohistochemical assessment of HER2, ER, PR, and Ki67 is essential in diagnosing invasive breast carcinomas and guides treatment, prognosis, and patient management. Here, we show how Indica Lab's clinical software can be utilised to undertake research projects and train medical students at the University of Bern; focussing on a recent study comparing breast cancer IHC scoring by undergraduates to that of trained pathologists, when unassisted or assisted by HALO Breast IHC AI.

Material and methods

50 (250 slides) stained for ER, PR, HER2, and Ki67 were scored twice by three students and two certified pathologists. Initial scores were obtained using manual digital pathology methods (Visual Dx), followed by reassessment with AI assistance by HALO Breast IHC AI after a 4-week washout period (AI-Assisted Dx). Accuracy and agreement of the student scores were compared to those of the pathologists.

Results and discussion

AI-Assisted Dx produced greater agreement at the clinical cutoff four all four biomarkers for both students and pathologists. Similarly, Fleiss' Kappa for all biomarkers increased for AI-Assisted Dx by an average of 0.42 for both students and pathologists. When both groups were combined, agreement at the clinical cutoff also showed improvement indicating that student scores more closely aligned with pathologists when assisted by HALO Breast IHC AI.

Conclusion

HALO Breast IHC AI provides support for both students and certified pathologists, improving agreement and consensus scores across groups with different levels of experience. HALO Breast IHC AI can objectively standardise scores and be an effective training tool for students.

Key words: Breast cancer, algorithm , scoring

A30 Image registration of H&E and IF stained Whole Slide Images using nuclei segmentation coordinates

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Introduction

Whole Slide Images are generally aligned using self-generated image features, which are subsequently matched using feature similarity. A validation procedure of these techniques transforms certain images from known datasets with their corresponding landmarks, placed by experts in the histopathological field. However, precise alignment is challenging, as lower resolutions are used. Nuclei coordinates are a common denominator in staining procedures and can thus be used as a point of interest.

Material and methods

A segmentation algorithm is used to extract nuclei coordinates of an in-house created dataset of mice lung cancer tissue, stained with IF, then re-stained using H&E. These coordinates are used as unmatched features for the alignment procedure. Complexity reduction is performed by aggregating the nuclei count on a grid. Affine transformation parameters (bidirectional translation, rotation, bidirectional scaling) are then optimized via a bounded search with Powell's method, with the cost function set as the Pearson correlation coefficient. Performance is checked by applying a random affine transformation on the detected nuclei and cross-checking the nearest-neighbor distance with the optimized transformation.

Results and discussion

After registration, the average nearest-neighbor distance between the detected nuclei was 10 pixels, corresponding to 1.1 µm of distance in the actual image. The transformed data performed considerably worse, averaging a nearest-neighbor distance of 200 pixels.

Conclusion

Registration using nuclei coordinates results in a high-precision technique that does not need to reduce image resolution for the alignment of Whole Slide Images. If no landmarks are available, simulations with nearest-neighbor distance can be used as a metric for performance.

Key words: Whole Slide Imaging, Segmentation, Image registration, Multimodality, Data Science

A31 Revolutionising Diagnostic Cytopathology Competence and Education: The Digital iEQA Scheme

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Introduction

Interpretive external quality assurance (iEQA) schemes have long been established for histopathology, but until recently, this was not the case for Diagnostic Cytopathology (DC). The traditional DC iEQA scheme, in operation since the 1990s, relied on circulating glass slide preparations from various DC cases, which became time-consuming as participant numbers grew. The process took up to 18 months, hindering efficient performance assessment. In response, UK NEQAS CPT developed a fully functional Digital Diagnostic Cytopathology iEQA scheme. This scheme provides internationally accessible, digitised cytological examples, enabling remote examination and opinion submission through a user-friendly platform.

Material and methods

The scheme utilises thin-layer technology and improved preparation techniques, offering a more suitable platform for digital transformation. In collaboration with a leading pathology digitisation provider, a unique platform was developed to offer 12 scored cases and 2 unscored cases from serous fluids, respiratory, head and neck, and urine. Clinical details accompany each case to aid diagnosis, with enhanced online software that allows participants to select specimen types and engage in self-paced learning with peers.

Results and discussion

The iEQA scheme runs two circulation cycles annually and includes features such as easy participant registration, digitised images, advanced slide viewing, and categorisation based on benign or malignant opinions. Participants receive personalised feedback, participation certificate and peer comparison feedback.

Conclusion

The DC iEQA scheme ensures compliance with international standards and promotes performance and competence for all professionals in Cytopathology. With its success, the scheme plans to expand into online educational image libraries and performance monitoring systems, ensuring continuous growth and development in professional skills, knowledge, and peer support.

Key words: Digital, Quality, Competence, iEQA, Education, Cytopathology

A32 Cancer-Associated Fibroblasts as Predictive Markers in Rectal Cancer Biopsies: A Computational Tissue Profiling Approach

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Introduction

In rectal cancer, most patients receive neo-adjuvant therapy. To better predict patient outcome from biopsies, pathologists need better tools. Histological features such as intratumoral budding (ITB) and immune infiltration have been proven to predict patient response. However, Cancer-Associated Fibroblasts (CAFs) are underexplored in rectal cancer biopsies. Here, we investigate the potential of five fibroblast markers to predict Disease-Free Survival (DFS).

Material and methods

Three Tissue Micro-Array (TMA) images consisting of 160 rectal cancer biopsy cores underwent a 31-plex seqIF™ protocol. The Pixie-pipeline applies a self-organizing map (SOM) to create meta-clusters for pixel-wise tissue classification. The tissue was further split into stromal areas using Voronoi tessellation. We identified stromal areas interacting with the epithelium using Delaunay triangulation. We subsequently extracted quantitative features for univariate (KM estimator) and multivariate survival analysis (CoxPH model).

Results and discussion

A total of four CAF meta-clusters were identified, namely “FAP+ CAFs”, “IDO1+ CAFs”, “myoCAFs” and “CD90+ CAFs”, along with eight immune meta-clusters. We found CD8+ T-cells ($p=0.072$) and M1-macrophage ($p=0.005$) infiltration as favorable features for DFS in a univariate setting. Notably, CD90+ CAFs were associated with improved DFS in a multivariate setting ($HR=0.43$, $p=0.007$), indicative of a protective role in rectal cancer progression.

A33 Lymph node cytopathology: exploring the potential of digital tools in diagnosis of lymphoproliferative disorders

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Introduction

We have recently identified a unique cellular distribution pattern in lymph node fine-needle cytology (FNC) smears from benign reactive hyperplasia (BRH), characterized by a predominance of larger lymphocytes in the center of smear and smaller ones in the periphery. Instead, low-grade non-Hodgkin lymphoma (NHL) displays an homogenous, monomorphic pattern of small/medium lymphocytes. Digital pathology could improve diagnostic accuracy by quantifying these patterns to better distinguish BRH from NHL.

Material and methods

A pilot dataset of n=16 whole slide images (WSI) FNC lymph node smears (n=8 BRH and n=8 low-grade NHL) was retrospectively collected and digitalized by Hamamatsu Nanozoomer at ×40 magnification. QuPath was used to annotate regions with progressive concentric reductions of the smear radius in 10% increments. The 10% and 20% areas were collapsed in "central-area", while the remaining areas as "peripheral-area" An instance segmentation model based on the InstanSeg framework was developed for lymphocyte identification and feature extraction.

Results and discussion

In BRH, the average mean cell area (MCA) was 58.83 μm^2 in the central area and 55.07 μm^2 in the peripheral area (Δ=-3.75 μm^2). For NHL, the average MCA was 64.03 μm^2 in the central area and 64.38 μm^2 in the peripheral area (Δ=0.34 μm^2).

Conclusion

Our preliminary findings suggest the potential of a digital approach to distinguish BRH from low-grade NHL based on lymphocyte size distribution. These results could enhance the development of deep learning algorithms for analyzing lymph node cytological specimens and creating AI-powered diagnostic tools to assess cellular patterns and predict lymphoproliferative disorders from WSI cytological images.

Key words: Digital Cytology, Lymph node cytology, Fine needle aspiration

A34 LSP-DETR: Towards Efficient and Scalable Nuclei Segmentation in Whole Slide Images

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Introduction

Cell nuclei segmentation is a critical task in digital pathology, playing a vital role in downstream tasks such as cancer diagnosis and treatment planning. Despite recent advancements in deep learning, existing approaches rely heavily on handcrafted post-processing steps, limiting their efficiency and scalability. These limitations result in slow, resource-intensive, and complex deployment pipelines, posing significant challenges for real-world adoption.

Material and methods

In this work we propose Local Star Polygon DEtection TRansformer (LSP-DETR), an end-to-end framework for cell nuclei instance segmentation and classification. LSP-DETR builds on SAP-DETR, a state-of-the-art object detection model, simplifying the segmentation process by removing the need for post-processing while enabling the direct prediction of overlapping nuclei. The model is input-size agnostic, allowing for efficient training and scalable inference on large whole-slide images.

Results and discussion

LSP-DETR achieves more than a 10-fold increase in inference speed compared to StarDist, while maintaining linear scaling with input size. Preliminary experiments on the PanNuke dataset show competitive segmentation accuracy, highlighting the model's potential for real-world histopathology applications.

Conclusion

LSP-DETR presents a promising direction for scalable and efficient nuclei segmentation. It simplifies the deployment process, reduces inference costs, and has the potential to improve accuracy. The source code, model weights, and datasets are publicly available.

Key words: panoptic segmentation, nuclei segmentation, efficient whole slide inference, DETR, end-to-en

A35 Aligning Data Annotation Workflow for AI Applications with Clinical Practice in Digital Pathology

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Introduction

We propose the workflow for creating annotated digitized histological slides that follow established familiar processes of domain experts in the histopathology field. Domain experts' knowledge gathered during the annotation process is structured to a form potentially usable for artificial intelligence (AI) development. Our proposed approach for data annotations reduces the annotation workflow refusal rate by pathologists.

Material and methods

Our proposed workflow uses a top-down approach, concentrating on annotating complex, clinically important structures at a higher level, supported by multimodal data containing other clinical information not present in the digitized histopathology specimens. This is in contrast to annotating individual low-level structures first, which is often required for training AI algorithms without any direct alignment with pathologists' routines.

Results and discussion

We adopted the proposed workflow during long-term cooperation in a multidisciplinary research team consisting of domain experts in the field of pathology, and experts in the field of applied informatics and artificial intelligence. The adopted annotation process was applied on the Nottingham grading scale for breast cancer diagnosis. We aim to spread this approach to various annotation problems within the digital histopathology domain.

Conclusion

The significant contribution of our research work is an emerging dataset for future AI applications in the field of digital pathology within Nottingham grading scale, as well as a set of defined rules verified by year-long lasting case study, based on which similar annotation workflow and data collection can be conducted effectively - without the need to make major changes to the routine actions of domain experts in the field of digitized pathology.

Key words: Digital Pathology , Data Annotations, Nottingham Grading Scale, Breast Cancer, Domain-centered AI, Multidisciplinary Research

A36 Concept Relevance Propagation for Explainability in Digital Pathology Foundation Transformers

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Introduction

Foundation models are transforming medical AI. Fine-tuning them for specific tasks reduces the need for extensive labeled data. Their potential is increasingly recognized in digital pathology, but adoption remains limited due to their black-box nature. Regulatory frameworks like the EU AI Act further emphasize the need for transparency in critical applications. Concept Relevance Propagation (CRP) has recently emerged as a powerful explainability method, allowing the identification of high-level, human-interpretable concepts in neural networks. Despite its success in convolutional models, CRP has not yet been adapted for foundation models due to challenges in handling attention mechanisms addressed in this study.

Material and methods

We extend CRP to large pre-trained vision transformers used in digital pathology. Our framework modifies the CRP workflow to accommodate attention-specific model components, making it applicable to foundation models trained on histopathological microscopy tissue data. We apply CRP to labeled histopathology tissue samples to identify diagnostically relevant concepts. The interpretability of the identified concepts is evaluated against expert histopathologist knowledge, assessing their alignment with clinically meaningful features.

Results and discussion

Our preliminary findings indicate that concepts emerge within transformer layers, in agreement with prior studies on general-purpose transformers. By applying CRP, we can distinguish whether foundation models capture diagnostically relevant structures or latent patterns of unknown clinical significance.

Conclusion

This work presents the first adaptation of CRP to explainability in digital pathology transformers and assesses their interpretability, addressing a critical gap in XAI for histopathological AI. Future research will investigate how CRP could be leveraged when labels are unavailable.

Key words: concept relevance propagation, foundation models, transformers, digital pathology

A37 Histomorphological evaluation of AI-based feature extraction in CRC specimens – from explainable AI to diagnostic pathology

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Introduction

AI technologies are revolutionizing histopathology diagnostics as well as tissue based research. For full integration of AI modules into pathologists' workflows a deep understand of the whole process is desirable. Here we have employed a post-hoc approach to manually extract tissue-based features from colorectal cancer (CRC) specimens related to two central features of cancer biology extracted by a transformer-based AI model.

Material and methods

Multimodal analysis has been performed on a cohort of metastatic colon cancer patients undergoing neoadjuvant chemotherapy. The gene expression signatures identified have been applied on the TCGA and CPTAC cohorts and prediction heatmaps have been created from the corresponding image data using gradCAM. Most influential tiles have been extracted and manually scored according to 17 key histological features associated with CRC by a pathologist.

Results and discussion

Gene expression analysis of mCRC specimens undergoing neoadjuvant chemotherapy revealed two distinct signatures (stemness and differentiation), that are closely linked to therapy response. Applying this feature on the large TCGA-COAD and READ confirms a link of the stemness signature on worse overall survial. This signature has been applied on the corresponding histology by a transformer-based AI model. The pathologist's review of highly influental tiles confirmed marked differences in histomorphological features associated with tumor architecture and the TME.

Conclusion

Gene expression signatures extracted from pretreated mCRC specimens applied on a large external test cohort identified a patient group with an adverse prognosis. Post-hoc manual assessement of histological image data can support the explainability of AI models and highlight key morphological features linked to patients' prognosis to diagnostic pathology.

Key words: colorectal cancer, explainable AI, multimodal imaging

A38 Polygenic Risk Score, Epidemiological Risk Factors, and Prostate Tissue Morphology

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Introduction
Epidemiological studies have identified several risk factors that increase a man's lifetime risk of developing prostate cancer. However, no study has systematically assessed the morphological signatures left by these factors. We examined whether prostate morphology alone could discriminate between individuals with high- and low-risk levels of a polygenic risk score (PRS), age, height, family history, and prostate-specific antigen (PSA) in patients with biopsies negative for prostate cancer from the STHLM3 diagnostic study.

Material and methods
Data on risk factors were collected via study surveys, the Swedish Registers, and bloodwork, and then linked to digitized negative biopsies (Patient N= 989). Patients were split into groups with highest and lowest quartiles for each factor, and model performance was evaluated on the test folds within a train-validation-test split in cross-validation. Pathology foundation models were adapted by adding trainable layers to a frozen encoder and training them on relevant patient data using weakly supervised learning. Inference was performed at the patient level.

Results and discussion
The examined factors had varying impacts on discriminatory performance based on tissue morphology. Strongest was age (Kappa/AUROC: 0.289/0.739) and PSA (0.254/0.659), followed by PRS (0.155/0.595), family history (0.045/0.502), and height (0.020/0.530). The ability to discriminate the PRS varied based on age (Low: 0.137/0.569; High: 0.063/0.555) and PSA (Low: 0.152/0.576, High: 0.044/0.537).

Conclusion
Epidemiological risk factors affect prostate tissue morphology in various ways and to different degrees. Understanding the interplay between genetic polymorphisms, morphological changes and cancer risk may help triage patients for genetic testing and detect cancer earlier in high-risk individuals.

Key words: Foundation Models, Prostate Cancer, Artificial Intelligence, Epidemiological Risk Factors

A39 An end-to-end whole slide image foundation model trained with slide-level labels from open-source data

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Introduction

Foundation models (FM) are transforming computational pathology, enhancing diagnostic accuracy and reducing the need for extensive, problem-specific training data. Developing state-of-the-art WSI foundation models using self-supervision demands significant data and computational resources, hindering reproducibility and increasing energy consumption. Supervised pre-training has shown promise in reducing the resources needed for robust, high-performance FMs.

Material and methods

We extended our publicly available Tissue Concepts, a multi-task supervised FM trained with patch level labels, to use weakly supervised WSI level labels. For this, the model was trained on a dataset of 33 tissue classes obtained from the NCI Imaging Data Commons (IDC), a public repository of cancer imaging data. The total data size was approximately 27 TB, necessitating the streaming download and tessellation of single images. Bags of 300 random foreground patches per WSI were created to train a patch encoder and downstream multi-head attention aggregator in an end-to-end manner to predict the respective cohort of a bag.

Results and discussion

Trained on 16,000 slides only, our extended FM achieved a validation AUC of 0.9 on a held-out validation set. Further, test performance on TCGA-LUAD TP53 mutation prediction in 5-fold cross-validation showed our model performed on par with ProvGigaPath (AUC: 0.73 vs. 0.72), which was trained on 300,000 slides. Additionally, the training took less than 500 GPU-hours (NVIDIA A100) including downloading and tessellation, compared to 3000 GPU-hours reported for ProvGigaPath.

Conclusion

Weakly supervised end-to-end training for FMs shows potential in minimizing resource requirements for scaling such models. Training with public data from the IDC facilitates reproducibility of models and results by other researchers.

Key words: Foundation Model, End-to-End, Multiple Instance Learning

A40 Use of AI in LSIL Cases with Sparse Concomitant Cells Suggestive of ASC-H/HSIL

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Introduction

LSIL with sparse ASC-H/HSIL cells is a diagnostic category in the Bethesda System (3rd edition) with clinical variability and limited literature. This study analyzes cases from our center and develops an AI algorithm to predict lesion progression using convolutional and morphological cell features.

Material and methods

We analyzed 45 LSIL cases with sparse ASC-H cells diagnosed via ThinPrep at Bellvitge University Hospital (2022-2023). Biopsy results (Negative, LSIL, HSIL) and HPV status were recorded. Slides were digitized at 40x using a 3D Histech P1000 scanner. A cytopathologist annotated ASC-H-suggestive nuclei in QuPath v.4.0. Deep convolutional features were extracted using a pre-trained InceptionV3 CNN. Morphometric features (nuclear size, circularity, irregularity, chromatin texture via GLCM) were also analyzed. Data was split (80% training, 20% testing). Two AI models were trained: XGBoost (Machine Learning) Multilayer Perceptron (Deep Learning) (512-256-128 neurons)

Results and discussion

A total of 45 cases diagnosed with LSIL with sparse ASC-H-suggestive cells were followed up with a biopsy. Among these cases, 15 progressed to HSIL, 15 remained LSIL, and 15 showed no evidence of neoplasia. The Deep Learning model achieved the following results for predicting HSIL progression: Training set: AUC = 0.75, Sensitivity = 65%, Specificity = 80% Test set: AUC = 0.7, Sensitivity = 55%, Specificity = 75% The Machine Learning model (XGBoost) yielded: Training set: AUC = 0.675, Sensitivity = 33.3%, Specificity = 80% Test set: AUC = 0.65, Sensitivity = 30%, Specificity = 70%

Conclusion

LSIL with ASC-H presents diagnostic discrepancies and variable progression. HPV status lacks statistical significance for predicting outcomes. AI models trained on larger datasets using morphological and convolutional features may enhance lesion progression prediction.

Key words: Digital Cytopathology, Algorithm development , CNN, MIL

A41 Multi-Reader Study of a Fully Automated Artificial Intelligence Solution for HER2 Scoring in Breast Cancer

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Introduction

HER2 expression is a key prognostic and treatment-guiding factor in breast cancer and is assessed for all invasive breast carcinoma (BC). This study aimed to evaluate the performance and clinical utility of an artificial intelligence (AI)-aided HER2 IHC scoring solution on whole slide images of BC.

Material and methods

The two-arm multi-reader study included 1,997 biopsies and excisions from 12 US, EU, and UK pathology laboratories. HER2 slides were stained with an anti-HER2 antibody (4B5, Roche) and scanned with various scanners. The AI solution detects the invasive tumor area, classifies HER2 staining in every invasive tumor cell, and derives a slide-level HER2 score following 2023 ASCO/CAP guidelines. Pathologists' performance (26 "readers") in HER2 scoring unassisted vs. AI-assisted was compared to ground truth (GT), established by three breast specialists.

Results and discussion

Readers' overall inter-observer agreement was significantly higher when assisted by AI: 88.6% (87.1%,90.0%) vs. 74.4% (72.4%,76.4%) without AI ($p < 0.01$). Moreover, readers' accuracy for all HER2 scores was significantly higher with AI: 81.7% (80.4%,82.9%) than without AI: 76.7% (75.3%,78.0%) ($p < 0.01$). The standalone AI performance as compared to GT was 89.4% (88.0%,90.7%), and 91.2% (89.8%,92.3%) for the respective clinical cutoffs of 0 vs. 1+/2+/3+ and 0/1+ vs. 2+/3+. User survey indicates increased pathologists' confidence in their HER2 scoring accuracy and consistency.

Conclusion

This large multi-site validation demonstrated that pathologists assisted by AI showed significant improvements in HER2 scoring consistency and accuracy. The AI solution demonstrated high accuracy and generalizability to multiple laboratories with various pre-analytics, staining protocols, and scanners.

Key words: AI, HER2, Cancer, Breast, deep learning, Image Analysis

A42 The Impact of Data Pre-Processing on Multi-Modal Deep Learning in Spatial Transcriptomics

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Introduction

There lies great potential in utilizing multi-modal data to improve performance of deep learning models. We explore best practices for fine-tuning foundation models in histology using additional spatial transcriptomics (ST) data. As raw ST data are noisy and lack a common scale, normalization is in particular focus.

Material and methods

Five cases of invasive breast cancer from the HEST-1k dataset, containing paired samples of H\&E slides and ST data, were used to fine-tune the CONCH image encoder by comparing against RNA encoder output (3-layer MLP) using multimodal contrastive alignment (InfoNCE loss). Performance evaluations were made on a downstream classification task: binary ER, PR and HER2 status of patients (n=1058) in the BNCB dataset, using logistic regression on the slide-level average embeddings. Different data preprocessing approaches were evaluated: Macenko stain normalization (histology), and total count normalization, log transformation, CPM normalization, SME normalization, and PCA (ST).

Results and discussion

The CONCH embeddings achieved a ROC-AUC score of 0.866, 0.820 and 0.780 on ER, PR and HER2 classification, respectively. The scores for stain-normalized BCNB were 0.887, 0.846 and 0.756. Fine-tuning without any preprocessing resulted in scores of 0.861, 0.796 and 0.757 while the overall best tested combination achieved 0.883, 0.831 and 0.768, with stain normalization consistently having a positive impact.

Conclusion

Our results show that for histology data, stain normalization is beneficial for learning protein expressions. Although the impact of individual ST normalization methods was inconclusive, the differences point to the importance of best practices for multi-modal learning, which could be further studied using more data for fine-tuning or variations of learning parameters.

Key words: Multimodal, Preprocessing, Spatial transcriptomics, Foundation models, Fine-tunin

A43 Using photon upconverting nanoparticles to simultaneously detect ultra-low and high biomarker expressions in tissue samples

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Introduction

With the improvement of targeted cancer therapies, such as antibody-drug conjugates, there is a growing need for highly sensitive methods to detect low levels of biomarker expression. To address this, we have developed a novel system for immunohistochemistry, which is based on upconverting nanoparticles (UCNP). The system, consisting of a scanner and reagent kit, provides superior sensitivity and dynamic range and seamlessly integrates into digital pathology workflows.

Material and methods

• System sensitivity was assessed via antibody titration, comparing UCNP with HRP/DAB. • Four HRP/DAB labelled tumour samples, evaluated by pathologists as being HER2 0, were labelled with UCNP and analysed for biomarker expression. • UCNP photostability was demonstrated by scanning a UCNP-labelled sample 500 times.

Results and discussion

• UCNP showed 10x higher sensitivity compared to HRP/DAB. • Out of the four samples classified as HER2 0, three showed significant expression of HER2 when labelled with UCNPs. • Scanning a UCNP labelled sample 500 times did not show any degradation in signal intensity.

Conclusion

The UCNP-based system shows highly improved sensitivity and a broader dynamic range in comparison to traditional techniques. Labelling of tumour samples show that the UCNP system can detect levels of HER2 expression not seen using HRP/DAB based methods. The stability of UCNP labelled samples asserts ease of use. Images and data are compatible with commonly used IHC viewers and analysis systems.

Key words: UCNP, IHC, HER2, Sensitivity, Quantitation, Stability

A44 Navigating through Noisy and Conflicting Pathologist Labels : a Gleason Patterns Segmentation Use-Case

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Introduction

Finding high quality annotation in digital pathology is a daunting task. Hence the need to adapt for both training and evaluation when dealing with noisy annotations, which is commonplace in numerous pathology tasks that suffers from high inter and intra observer variability.

Material and methods

We curated 2 datasets for this work. For the training dataset, 6 annotators labeled 1200 prostate biopsies, reviewed by 3 expert pathologists. For evaluation, each of 225 additional biopsies were labeled by 3 annotators. Three different training methods for training are compared to handle the noise at training time. First, forgotten malignant glands are handled by ignoring unlabeled tissue regions during training, learning healthy tissue representations only from healthy slides. Then, glands boundaries are improved by adding a contouring label around annotations. Finally, pseudo-labeling refines original annotations in high confidence segmented regions. Models evaluation is done on multi-annotator dataset using traditional segmentation metrics on annotators-consistent and on majority votes regions. We also use cross-entropy loss as a metric on soft labels to compare different models' ability to capture annotators' variability. Models' features capabilities to generate meaningful latent spaces are further evaluated via cluster analysis.

Results and discussion

The segmentation model performance consistently improves with each of the aforementioned steps. Intersection over Target on annotators-consistent regions and Intersection over Union on majority votes regions for each of the iterative steps steadily increase while cross-entropy on soft labels decreases.

Conclusion

Our work demonstrates high annotators' variability in the context of prostate glands' Gleason patterns segmentation, and shows examples of solutions that effectively reduce the noise burden to produce a viable model.

Key words: Digital histopathology, Deep Learning, Noisy Annotations, Segmentation, Gleason, Prostate

A45 Lack of Reimbursement as a Barrier for Global Adoption of Digital Pathology

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Introduction

Digital pathology (DP) is revolutionizing pathology practice, yet despite the promise of DP and artificial intelligence (AI), the global adoption and integration into medical practice remain low. Multiple barriers are cited for adoption of DP and AI in pathology departments that focus on pathologists' interest and trust in using these technologies. The added cost and uncertain return on investment is a major factor for the hesitancy of institutions to invest in the technology. The goal of our study was to compare reimbursement for the DP operation in two early adopter institutions in the US and the Netherlands.

Material and methods

A review of the total infrastructure, operational costs and revenues that are associated with DP was conducted at MSKCC (New York), and at UMC Utrecht using data obtained from departmental records.

Results and discussion

The cost of the additional infrastructure required for digitization and software solutions for DP/AI workflows were significantly higher in both the US and Dutch institutions in comparison to analog- no AI pathology. These added costs were reliant on internal funding at both institutions, with incomplete realization of cost savings and efficacy gain that are expected from digital pathology operations.

Conclusion

The major barrier to widespread global adoption of DP and AI is the added cost which limits their use in smaller, non-academic centers as well as in resource poor settings. The minimal reimbursement for digital workflows and incomplete return on investment, should be part of business case discussions in departments wishing to realize the benefits and improved patient care using these technologies.

Key words: Business Case, Return on Investment, Reimbursement

A46 Provision of Cloud-Based Analytical Environments for Data Ownership Protection

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Introduction

Supported by the South Korean government, the CODiPAI consortium has developed a comprehensive digital pathology dataset. Despite this accomplishment, access and analytical utilization by external researchers had remained challenging until recently. Therefore, with the objective of creating a framework enabling researchers to easily access and utilize the dataset, there was a need to adopt an approach that granted usage rights rather than transferring ownership or providing the original dataset. This approach was intended to prevent potential legal and social conflicts throughout the process.

Material and methods

The consortium developed the Safe Analysis Zone (SAZ), a cloud-based analytical environment. Via the CODiPAI website, select the datasets for analysis, and submit access requests. Upon approval, a cloud workspace is assigned for their use. Researchers bear costs and, upon completion of analysis, may retrieve their results. Importantly, the original datasets curated by the consortium are not available for extraction.

Results and discussion

In the third quarter of 2024, the consortium launched the SAZ service. The service currently provides instant access to NVIDIA A100 80GB resources or lower-performance alternatives, with plans to introduce the advanced H100 model by 2025. Storage configurations support up to 2TB per unit, with options for parallel expansion as needed.

Conclusion

The SAZ enables researchers to easily access and utilize the extensive dataset of the CODiPAI project without the need for complex analytic infrastructure development. In particular, it significantly reduces the substantial upfront costs and acquisition period associated with GPU resource deployment. The provision of the SAZ service is projected to catalyze a wide array of subsequent studies.

Key words: Digital Pathology, Cloud Platform, Big Data, Data Utilization, Analysis, Data Ownership

A47 Digital pathology servers in a multi-hospital, multi-format imaging environment with open source software. An efficient and affordable solution.

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Introduction

The design of Digital Pathology equipment must deal with the usually high costs of these facilities, especially when they are designed to serve several hospitals and incorporate scanners from different vendors.

Material and methods

Our organisation has 3 hospitals within a radius of 80 km and we implemented a single server external to the hospitals, in order to separate the hospital information systems (HIS) from the diagnostic server. This was planned by anonymizing the samples to reduce special security costs. A Xeon E5-2609 processor and a memory capacity of 50 TB was initially chosen, now increased to 400 TB. Each hospital has its own scanner: 3D-Histech Mirax Midi, Hamamatsu S210 and Aperio/Leica GT450. The three file systems, .mrxs, .ndpi, and .svs, coexist on the same server with full compatibility. Access was enabled via VPN, Tailscale, and Hamamatsu's NZconnect web server solution. The main viewer is NDP.view2. Storage control is done with TrueNAS with RAID 5.

Results and discussion

The ten pathologists in our team connect to the server's web address and set up network units via VPN from their workstations, so that the cases from the three hospitals -with their different formats- are handled as one unit in the diagnosis.

Conclusion

The cost of the entire system is around 300,000€, quite below the investment usually required for such equipment, with efficiency and convenience for the pathologists that translates into reduced response times in diagnosis and a much higher number of cases studied than with the traditional microscope model.

Key words: Multiformat, Multihospital, Open source

A48 URINE24 Model: A Novel Approach For A Suitable Cytology Cancer Diagnosis Improved By Pathomics

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Introduction

Cytology represents a growing diagnostic segment. Digital Pathology represents the alternative to the medical interpretation of the preparation in the absence of local qualified personnel. AI-assisted allows for a significant efficiency improvement and greater diagnostic sensitivity. We propose a comprehensive approach which crosses technological tools, know-how transfer and excellent clinical knowledge.

Material and methods

URINE24 project is based on a new paradigm for cancer diagnostic of the urinary tract. Basing on CYTOfast Liquid Based Cytology processing system integrated with digital pathology. URINE24 is based on self-sampling. We have started a screening campaign for bladder & urinary tract tumors adopting urine cytology, on a sample of male subjects aged 45-65, sending the sample to our laboratory, preparation of the thin-layer slide, digitization and diagnosis carried out through telepathology. Further FISH investigations are performed on the AUC-classified samples.

Results and discussion

The execution of the first hundreds tests led to the detection of bladder tumors in early stages. The evidence indicates that the proposed solution appears unique in several respects: adoption of a collecting device compliant with TPSII standard; preservation of samples enabling with transport of vials at room temperature and a wide durability; creation of standardized thin-layer preparations enabling Digital Pathology; residual sample available for further investigation. Operators involved are giving positive feedbacks on the effectiveness of the method and the easiness of use of the equipment.

Conclusion

The results support the decision to scale up recruiting new patient cohorts. We are planning to launch similar cytological screening campaigns in some sub-Saharan countries, allowing the introduction of new diagnostic options.

Key words: Urine Cytology, Pathomics, Digital Pathology, TPS, FISH, AUC

A49 Quantifying Mitotic Topology as a Pan-cancer Prognostic Biomarker Using a Deep-Learning and Network-Based Approach

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Introduction

Cancer progression is driven by uncontrolled cell division, with mitotic activity serving as a critical indicator of tumor proliferation. Current clinical methods fail to capture the spatial distribution of mitoses. To address this gap, we developed a novel framework integrating deep learning and graph-based approaches to quantify mitotic activity and topology in whole-slide images.

Material and methods

We utilized a validated deep-learning algorithm to detect mitoses in 9,141 cases from TCGA, encompassing 31 cancers. Each mitosis was treated as a node in a "Mitotic Network," with edges connecting nodes based on spatial proximity. Social network analysis techniques were applied to derive Mitotic Topological Features (MTFs), including mitotic connectivity, clustering, and proximity. Pan-cancer survival analyses were conducted using Cox Proportional Hazard models and Kaplan-Meier validation to assess the prognostic utility of MTFs for progression-free interval (PFI), disease-specific survival (DSS), overall survival (OS), and disease-free interval (DFI).

Results and discussion

MTFs significantly stratified survival outcomes in multiple cancer types, with higher mitotic activity usually correlating with worse prognosis. For PFI, MTFs were prognostic in 20 cancers, including adrenocortical, breast, kidney, esophageal, and prostate cancers. Similar trends were observed for DSS, OS, and DFI, though MTFs showed limited utility in cervical and head and neck cancers. Furthermore, MTFs outperformed standard hotspot counting in survival ranking. Clustering tumors into Mitotic-Hot and Mitotic-Cold subgroups revealed distinct proliferation landscapes, with Mitotic-Hot tumors exhibiting higher genomic instability, intratumor heterogeneity, and enrichment of cancer-related pathways.

Conclusion

Our study offers novel mitosis-based prognostic biomarkers across diverse cancer types, highlighting the clinical relevance of mitotic spatial distribution.

Key words: mitosis, social network analysis, deep learning, topology, survival, tcga

A50 Deep-learning enables standardised and reproducible assessment of tumour content at the single cell level with impact on molecular analysis

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Introduction

Accurate tumor content (TC) estimation is essential for molecular analyses such as copy number variation (CNV). Conventional pathology (CP) offers direct but subjective estimates, bioinformatic deconvolution infers TC indirectly introducing bias, highlighting a need for improved TC assessment methods. Here, we investigate the performance of molecular and DP-based TC assessment in three multi-institutional colorectal cancer (CRC) cohorts with comprehensive digital pathology and multi-omics data.

Material and methods

We analyzed three independent CRC cohorts (FOCUS, GRAMPIAN, TCGA, N=1'097 patients). In FOCUS and GRAMPIAN, serial sections alternated with tissue sampling for RNA/DNA profiling, ensuring continuity. SoftCTM, an open-source multi-organ deep-learning model, was applied to Hematoxylin and Eosin stained sections (H&Es) for tumor and non-tumor cell detection. We assessed the reproducibility of SoftCTM's TC estimation and its impact on CNV profiling compared to CP and bioinformatic deconvolution (RNA expression, DNA methylation).

Results and discussion

SoftCTM obtained perfect repeatability on the same slide (r=1.0) and excellent correlations in paired H&Es (r>0.9). TC profiled by SoftCTM correlated highly with RNA expression (r=0.59) and DNA methylation (r=0.40), while TC by CP showed a lower correlation with RNA expression (r=0.41) and DNA methylation (r=0.29). CP and deconvolution methods underestimate and overestimate TC respectively, compared to SoftCTM, resulting in 6-13% differing CNV calls.

Conclusion

In summary, SoftCTM ensures reproducible, standardized TC estimation (M=58.9%, SD=+/-16.3%) at single-cell resolution, reconciling overestimation by bioinformatic deconvolution (RNA expression: M=79.2%, SD=+/-10.5, DNA methylation: M=62.7%, SD=+/-11.8%) and underestimation by CP (M=35.9%, SD=+/-13.1%), demonstrating how computational pathology could enhance molecular analyses in research and clinics.

Key words: Tumor content estimation, Clinical application, Molecular profiling, Computational pathology

A51 AI-Driven Ki67 Scoring as a Cost-Effective Predictor of Oncotype DX Breast Recurrence Score

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Introduction

The Oncotype DX Recurrence Score (ODX-RS) guides personalized therapy decisions in HR+/HER2- breast cancer. TAILORx demonstrated that patients with ODX-RS≥26 benefit significantly from chemotherapy. Prior studies have demonstrated a moderate correlation between ODX-RS and the Ki67 proliferation index (PI), suggesting its potential as a surrogate marker. This study investigates AI-driven PI scoring as a cost-effective tool for identifying patients with ODX-RS≥26.

Material and methods

A cohort of 101 HR+/HER2- breast cancer patients (39 with ODX-RS≥26) with corresponding Ki67 IHC tissue microarrays (TMAs) was used. The PI was assessed using three state-of-the-art AI models trained and tested on independent datasets: 1) UV-Net (doi: 10.1117/12.2611212) 2) piNET (doi: 10.3390/cancers13010011) 3) deepLIIF (doi: 10.1038/s42256-022-00471-x) A breast pathologist visually assessed Ki67+ and Ki67- tumor cell counts in 20 TMAs. Absolute PI differences (ΔPI) and cell count discrepancies (ΔKi67+/-) between AI models and the pathologist were calculated for model verification. The Youden Index was used to determine optimal PI thresholds for identifying patients with ODX-RS≥26. Classification accuracy and corresponding 95% confidence intervals (CIs) were estimated using bootstrapping (10k iterations, sampled with replacement).

Results and discussion

Mean±SD for ΔKi67+, ΔKi67-, and ΔPI: 1) UV-Net: 22±12, 42±30, 9±5% 2) piNET: 40±23, 44±33, 5±2% 3) deepLIIF: 168±104, 1684±362, 6±4% Optimal PI thresholds and classification accuracy [95% CI] for ODX-RS≥26 stratification: 1) UV-Net (PI≥17%): 83.4% [76.2, 90.1] 2) piNET (PI≥18%): 78.3% [70.3, 85.1] 3) deepLIIF (PI≥15%): 70.6% [61.4, 79.2]

Conclusion

AI-driven PI scoring demonstrates promise as a cost-effective adjunct for identifying patients with ODX-RS≥26, with UV-Net achieving the highest stratification accuracy. Further model refinement and testing will be key to translating these findings into clinical practice.

Key words: Deep Learning Biomarker Quantification , Ki67 Proliferation Index, Oncotype DX, Breast Cancer, Personalized Therapy, Companion Diagnostic

A52 The Road to Clinical Implementation: A multi-institutional study evaluating AI-assisted Ki67 quantification in breast cancer in western Norway.

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Introduction
Clinical implementation of AI-assisted diagnostic tools is underway in Norway. An evaluation study in the western health region was performed prior to clinical implementation of a Ki67 counting tool for ER+/HER2-/LN- breast cancer. The study evaluated limiting factors of local and regional conditions prior to implementation.

Material and methods
The study cohort included 65 anonymised ER+/HER2-/LN- breast tumour specimens (diagnosed 2019-2022). Four sections per case were created from FFPE blocks, stained (Ki67, MIB-1 clone) and scanned (Leica GT450Dx, Hamamatsu Nanozoomer S60) at four hospitals in Norway. Ki67 scores were quantified using an AI tool. Intra-variability was assessed between scanners for each site, as was inter-variability across sites using the intraclass correlation coefficient.

Results and discussion
Digital images from each site were visibly different. One site displayed background staining which resulted in a 28-38% failure rate for slides analysed by the Ki67 algorithm. Another site had fainter scans with one scanner type (61% failed) compared to the other scanner (0% failed). Agreement between scanner types at each site varied (ICC:0.970, 0.937, 0.888, 0.597). Agreement across sites ranged from good to poor. Significant differences in mean Ki67 scores were observed between sites ($p<0.001$).

Conclusion
Standardising pre-analytical protocols is crucial for successful implementation of AI algorithms. Algorithms should be verified on multiple scanners at a single site ensuring safe performance and identify any bias. Bias introduced by differences in local protocols must be considered for multi-site implementation if fixed thresholds are used to guide patient treatment or diagnoses.

Key words: Breast cancer, Ki67, AI, Clinical implementation

A53 A Novel Digital Pathology Workflow That Increases Diagnostic Efficiency in Low-Resource Areas in Kenya

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Introduction

Developing countries, particularly those in Africa, face a significant shortage of pathologists, which in turn leads to delays in diagnosis, compromised patient outcomes, and overburdened healthcare systems. Digitising the pathology workflow creates opportunities to transform the diagnostic approach and address these deficiencies.

Material and methods

The Pathology Network developed a novel modular digital pathology workflow that was implemented in 2021. The centrally coordinated workflow utilizes a software platform to connect hospitals, laboratories and pathologists spread across Kenya, thus optimizing the coordination of institutional resources that are distributed across the country.

Results and discussion

We implemented the workflow across a network of 30 hospitals spanning both rural and urban regions of Kenya, enabling these facilities to request histopathology tests and receive results from centralized laboratories that conduct specimen processing and slide preparation, and remotely located pathologists that report on the slides. Every year, we process approximately 5,000 histopathology specimens within our network of three laboratories and a consortium of 14 reporting pathologists, with an average inter-institutional distance of 150 kilometers. Our preliminary findings demonstrate a 70 to 90% reduction in diagnostic turnaround times, alongside a marked improvement in the quality of diagnostic reports, through the adoption of standardized synoptic reporting templates aligned with CAP cancer protocols.

Conclusion

The implementation of modular digital pathology workflows offers a scalable strategy for achieving immediate gains in diagnostic efficiency and quality. Investment in digital diagnostic health systems by low to middle income countries can revolutionize access to timely, quality surgical pathology services.

Key words: Digital Pathology, Diagnostic Workflow, Africa, Access to Healthcare, Cancer, Histopathology

A54 Bridging the Gap: An Open-Source Framework for Integrating AI results from Computational Pathology into Clinical Practice using DICOM

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Introduction

Despite significant advancements in computational pathology, daily diagnostic workflows remain largely analog, limiting the integration of AI-driven innovations. To address this gap, a framework is required that digitizes manual processes while enabling seamless incorporation of novel algorithms.

Material and methods

This work presents an open-source framework that replicates routine pathology workflows while ensuring interoperability and legal compliance. Instead of proprietary solutions, open-source software facilitates transparency, adaptability, and future scalability. Vendor-specific whole slide image (WSI) formats are standardized into DICOM, ensuring compatibility with HL7 FHIR and broader healthcare integration. A modular interface of open-source tools allows switching between different analysis scripts, ensuring efficient retrieval of WSIs and enhancing image data with machine learning predictions. Established DICOM structure provides interoperability for reading WSIs and enriching meta-information. Multimodal data storage supports integrated diagnostics, bridging routine pathology and innovative science workflows.

Results and discussion

Inference results, including segmentation polylines, labels, and classifications, are stored as DICOM files. This approach ensures systematic linking of raw data, metadata, and analytical outputs, enhancing accessibility and traceability.

Conclusion

By leveraging established radiological workflows, this framework provides computational pathology with a robust digital infrastructure. Its open-source nature promotes extensibility, fostering clinical adoption of AI-driven research. This work advances the integration of computational pathology into routine diagnostics, unlocking its full potential for precision medicine.

Key words: DICOM, open-source, AI, multimodal

A55 PAPAYA; HyPerplex And sPAtial analYsis plAtform from a comprehensive immune panel setup to an automated analysis pipeline

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Introduction

To understand the mechanisms underpinning disease, it is essential to acquire comprehensive insights into the detailed molecular identity and spatial relationship between these cells. The MACSima™ platform enables the analysis of biological interactions in the cellular landscape of any pathology. This study presents the establishment of a fully automated hyperplex immunofluorescence immune panel from setup to analysis.

Material and methods

Establishment of sequential staining of 26 well-recognized lymphocyte, myeloid and stromal markers was carried out across different tissue types and protein expression was compared to diagnostic-certified clones. Optimal dilution, incubation time and cycle were tested for all targets and expression measured in three main tissue types. Analysis was carried out by use of MACS® iQ View software and in parallel by customizing the MCMICRO pipeline with Scimap.

Results and discussion

Our automated panel effectively stained and imaged tissue, generating comprehensive spatial proteomic data. Our analysis showed that both tools support spatial analysis of MACSima-generated data, including gating, clustering, and phenotyping, enabling exploration of biological neighbourhoods within tissue microenvironments. The MCMICRO pipeline, while requiring more user input, offered greater output flexibility, tailored solutions, and batch analysis, which is crucial for comparing multiple Regions Of Interest (ROIs).

Conclusion

We successfully established a backbone 26-plex immunofluorescence protein panel and two analysis pipelines. For more experienced users, the MCMICRO tool is the best option as it allows for greater customization and tailored analysis. However, the MACSiQ option is ideal for less experienced users, as it is user-friendly while still enabling comprehensive spatial analysis.

Key words: multiplex immunofluorescence, image analysis, MCMICRO, spatial analysis, pipeline, workflow

A56 AI-assisted Artifact Identification: Multi-site analytical performance validation of SlideQC BF in Digital Pathology

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Introduction

Artifacts generated during slide preparation and scanning can compromise diagnosis and hinder the performance of image analysis algorithms. AI-based artifact identification tools hold promise for streamlining quality control in digital pathology, however their performance must be rigorously validated before deployment. This study evaluates the analytical performance of SlideQC BF (Indica Labs) for automated artifact segmentation in whole slide images (WSIs) in two independent test facilities.

Material and methods

At each test facility, three qualified personnel identified 300 regions of interest (ROIs): 150 artifact-free and 150 ROIs containing artifacts. ROIs were annotated across 50 H&E- or IHC-stained WSIs (10 per artifact type comprising air bubbles, debris/dust, folds, out-of-focus regions and pen marker). Personnel delineated artifact boundaries within artifact-containing ROIs, and a majority vote annotation, representing consensus, was used as input for validation. Annotators also rated their agreement with SlideQC BF markups on a scale of 1-4 (1: <25% overlap; 4: >75% overlap).

Results and discussion

SlideQC BF achieved high sensitivity (0.91 and 0.92), specificity (0.94 and 0.98) and F1-score (0.83 and 0.88) across both facilities. High agreement with SlideQC BF markups (area overlap > 75%) was observed for artifact-containing ROIs (92.4% and 98.0%) and artifact-free ROIs (98.2% and 99.8%).

Conclusion

SlideQC BF demonstrated high performance for artifact segmentation. This tool can streamline digital pathology workflows by providing automated upfront and standardized artifact identification, aiding slide triage and excluding artifact regions in downstream image analysis.

Key words: Digital Pathology, Artifact Segmentation, Artificial Intelligence, Algorithm Validation, Quality Control

A57 A Multi-Agent Architecture with Quality Assurance for Large-Scale Cervical Cancer Screening in China

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Introduction

Cervical cancer screening in China presents significant challenges, including a population of nearly 300 million women requiring screening and a shortage of pathologists. To address these issues, we developed a multi-agent AI-human collaborative system designed to enhance screening efficiency, accuracy, and coverage.

Material and methods

The proposed workflow integrates fully digital processes and a cloud-based AI architecture. Samples are processed in centralized laboratories, digitized, and analyzed by AI agents. The system includes three key AI models: (1) an object detection model to identify suspicious cells, (2) a malignancy risk assessment model, and (3) a quality control model to identify high-risk cases for rechecking. This five-layer system optimally combines AI analysis with human expertise. Major innovations include automated slide preparation, ultra-high-throughput scanners, and a targeted risk-based evaluation approach.

Results and discussion

To date, the system has screened over 12 million women, achieving a 6.04% detection rate for positive cases. AI-assisted quality control identified an additional 9.02% of missed positives. The AI model, trained on over one billion labeled cells, achieved a sensitivity of 90.1% and a specificity of 94.8%. A population-based study demonstrated that, over four years, cervical cancer incidence and mortality were reduced by 50% in the screened group compared to unscreened group.

Conclusion

This multi-agent architecture illustrates the potential of AI-human collaboration in large-scale cervical cancer screening. By addressing resource limitations and improving diagnostic accuracy, this scalable system offers a transformative solution for public health challenges in developing regions. Future work will focus on optimizing the workflow and expanding the technology implementation to other countries and healthcare settings.

Key words: AI, Quality Assurance, Multi-Agent Architecture, Cervical cancer screening, Limited Resource Setting, Cytology

A58 Automated quality assessment in digital pathology: a multi-site study

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Introduction

While enabling new opportunities, digitization of pathology slides also presents additional challenges, particularly in ensuring consistent and reliable image quality. This study evaluates how AI can aid in quality assurance for high risk or high-impact quality issues such as tissue not being completely scanned or large areas being blurry.

Material and methods

This study developed multiple segmentation models for quality issues in whole-slide images (WSIs). Over 8,500 pixel-level annotated WSIs were used to train U-Net models from scratch. A diverse evaluation set of 200 cases was curated, sourced from four distinct sites and three WSI scanners. Aside from random real-world cases, this set included 35 incomplete tissue scans, 11 coverslips only partially covering tissue, 27 large out-of-focus regions. Furthermore, 17 challenging cases with real-world artifacts such as ink marks, stain residue, surgical markings, air bubbles, and bacteria were added. The dataset encompasses various organs and over 20 different stains.

Results and discussion

The proposed method demonstrated high performance in detecting low-quality WSIs. For missing tissue detection, the method achieved a specificity of 0.97 (CI:0.85-0.99) and sensitivity of 0.97 (CI:0.93-0.99), for inadequate coverslips, the method attained a specificity of 1.00 (CI:0.74-1.00) and sensitivity of 0.99 (CI:0.97-1.00). For blur detection, the method reported a specificity and sensitivity of 0.93 (CI:0.77-0.98) and 0.98 (CI:0.94-0.99) respectively.

Conclusion

These results indicate the potential of AI based methods for robust and accurate detection of common high-impact slide artifacts, suggesting its possible utility in automated slide quality control.

Key words: Quality, Scanning artifacts, Blur detection, Missing tissue detection, Unscanned tissue, Out-of-focus

A59 Implementation of an Integrated Electronic Health Information System: An Institutional Audit of Histopathology Requisition Data

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Introduction

The preanalytical phase, which includes patient identification and specimen collection, has consistently been identified as the most critical and error-prone phase of laboratory medicine. Electronic health information systems (eHIS) are proposed to reduce medical errors, however current literature focuses on inpatient care. Kingston Health Sciences Centre (KHSC), a tertiary hospital, recently implemented a new integrated eHIS (Cerner) which replaced handwritten paper requisitions, prone to illegibility and transcription errors, with electronic requisitions.

Material and methods

This prospective audit compares completeness and accuracy of histopathology requisitions submitted to KHSC before and after eHIS implementation. Data is collected from 6 randomized weeks between June-November 2024 (pre-implementation) and December-May 2025 (post-implementation). Data extracted include: Patient Information, Clinician Information, Specimen Information, Relevant Clinical Information, Clarity.

Results and discussion

3673 paper requisitions were evaluated "pre-implementation" and demonstrated high completions rates (>98%) of patient and clinician information. Relevant clinical information was most commonly omitted (42-65%) and 8% had illegible handwriting. Preliminary analysis of the "post-implementation" period showed 100% completion rates of patient and clinician information, and illegible handwriting was no longer an issue. Mandatory entry fields and timestamp features resulted in significant improvement in specimen information data, particularly date and time of specimen removal (>93%). Completion of relevant clinical information showed moderate improvement but remained below desired levels. These trends will be further followed until the end of the study period.

Conclusion

Incomplete clinical histories and illegible writing are important sources of pre-analytical error. Integration of an eHIS shows promise to improve these quality indicators as our centre prepares to transition to digital pathology.

Key words: Quality Improvement, Health Information Systems, Pathology Requisitions, Laboratory Workflow

A60 "AI-Driven Quality Control of Immunohistochemistry: Monitoring HER2 & PD-L1 Stain Consistency in Control Cell Lines"

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Introduction

Ensuring the quality of immunohistochemistry (IHC) slides is pivotal for reliable patient management. Traditional visual assessment of IHC slide quality relies on pathologists' experience, which can be subjective. Control tissues for IHC slides, typically derived from previous cases or tumor samples, present challenges due to limited availability and variable antigen expression. Engineered cell lines with stable antigen expression offer an alternative, with potential quality assessment improvements through artificial intelligence (AI).

Material and methods

This study investigated AI-based stain quality control of HER2 and PD-L1 IHC slides using next-generation control cell lines. Five IHC autostainers from the same manufacturer and type were used. Staining quality was evaluated weekly over 24 months using Qualitopix™, an AI algorithm designed for quantitative assessment. Additionally, inter-stainer and intra-run variations were analyzed, and calibrator slides were used to assess the lowest limit of detection for each stainer and slide slot.

Results and discussion

AI analysis revealed unexpected variations in staining quality, particularly in low and medium antigen-expressing HER2.PD-L1cell lines. Inter-stainer variability and intra-run slot-specific differences were significant. Maintenance interventions, prompted by these findings, reduced variability for the short term.

Conclusion

AI demonstrated its efficacy in monitoring IHC staining quality using next-generation cell lines engineered for constant antigen expression. By identifying and addressing variability, AI-enhanced quality control could improve the accuracy and reliability of IHC diagnostics, ultimately supporting optimal patient management.

Key words: Immunohistochemistry, AI, Qualitopix, HER2, PD-L1, Variability

A61 Customized Validation Protocol for Digital Pathology Implementation in a Multicenter Institution

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Introduction

University Health Network is a multicentre institution in Canada, serving pathology for 29 hospitals. We recently transitioned to a fully digital pathology practice.

Material and methods

To ensure a successful implementation, we designed a customized validation protocol guided by the guidelines of the Royal College of Pathologists (UK) and the College of American Pathologists, while addressing the needs of our institution, such as case sets specific to organ pathology, specific strains, and immunohistochemistry (IHC). We adopted a holistic approach for validation, including technical verification steps for instruments and software.

Results and discussion

Our protocol is formed of five phases. The first is validation planning which includes review of existing protocols and identifying change champions to lead the process. It also involves developing resources and data collection protocols. The second is individual pathologist training. The third is an evaluation phase for the confidence level and to allow additional troubleshooting. We also included a fourth phase that is a technical validation through scanning all slides to ensure connectivity and crosstalk between system components. In the fifth phase, pathologists were offered dual workflow (digital and glass slides). Specific key performance indicators were established to guide the final decision towards a digital-only pathology practice. Our protocol featured an opt-out option for validation, a resource toolkit, opportunities for follow-up and feedback and practical real-world validation.

Conclusion

Our transition to a fully digital pathology practice demonstrates the importance of a customized approach that allows for flexibility and adaptability, enabling the incorporation of institutional needs and allowing for continuous improvement.

Key words: Whole Slide Imaging (WSI), Digital Pathology (DP), Quality Assurance (QA), University Health Network (UHN)

A62 AI-Driven Efficiency: Transforming Fragment Counting in Digital Pathology

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Introduction

Fragment counting is a critical quality control process in digital pathology, ensuring that diagnostic images meet required standards. Currently performed manually twice daily, this procedure takes 4–5 hours to process 1500–1600 slides. As it is a time-consuming task, prone to variability, an automated and reproducible deep learning-based approach was developed to count the fragments, combining the YOLOv9 and Vision Transformer (ViT) architectures.

Material and methods

The dataset includes 3,253 whole-slide-images (WSIs), represented as 1024x1024 thumbnail images, annotated with spatial (bounding boxes) and numeric (fragment counts) annotations. A two-stage method combining YOLOv9 and ViT was implemented for fragment counting. In the first stage, both models detect and count sets, with ViT constraining YOLOv9 to reduce over-counting. Post-processing refines detections by removing overlaps and filtering low-confidence predictions. Each detected set is cropped and processed by a second YOLOv9 model to count fragments. Additionally, the inter-observer variability was analyzed to benchmark automated predictions against expert annotations.

Results and discussion

The proposed method was evaluated on its ability to detect and count fragments using accuracy, precision, recall, and F1-score. When tested on a subset of 100 samples annotated by seven experts, the method achieved an accuracy of 86%, falling within the observers' range (82–88%). These results demonstrate the system's efficiency and reproducibility in the fragment counting task.

Conclusion

The results highlight the potential of the automated approach to match or exceed human performance in fragment counting. By leveraging object detection and transformer-based models, this method enhances accuracy, minimizes variability, and provides a scalable solution for automated quality control in digital pathology.

Key words: Digital Pathology, Fragments, Detection, Counting, YOLO, ViT

A63 Towards the Digital Pathology Workflow: Automated Paraffin Block Recognition for Sample Traceability

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Introduction

The digital pathology workflow converts glass tissue slides into high-resolution digital images. This work presents a device for the simultaneous, large-scale decoding of barcodes on cassettes placed in tissue baskets of different shapes (rectangular, circular, and semicircular). The goal is to optimize traceability in pathology laboratories, improving efficiency and safety while reducing operator workload.

Material and methods

The device includes a Raspberry Pi 5 and a motorized optical system, while the software manages data matrix detection, camera settings, and user visualization. The initial approach captured a single image for data matrix recognition. This was then enhanced using focus stacking to merge images at different focus levels to improve decoding accuracy. We examine various parameters and configurations, including the impact of focus stacking, algorithm comparison (SIFT vs ORB), preprocessing, decoding times, and range/step variations. Finally, we compare the commercial library Dynamsoft with the open-source Libdmtx to assess processing requirements, focusing on optimizing Libdmtx's settings to enhance its performance.

Results and discussion

We set up a device capable of reading data matrices on cassettes inside a tissue basket containing slides. With a single-shot image, we achieved an accuracy rate of 0.80 in under a minute with both libraries. Using focus stacking, the best-performing settings resulted in accuracy rates of 0.94 and 0.97 with the ORB algorithm and the Libdmtx and Dynamsoft libraries, respectively.

Conclusion

This approach optimizes the process, reduces manual workload, and minimizes the risk of errors. In the future, we plan to implement a higher-resolution camera and enhanced lighting control.

Key words: Pathology workflow, Laboratory automation, Sample traceability

A64 A Transformer-Based Deep Learning Workflow for Prognostic Assessment of Uterine Smooth Muscle Tumors

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Introduction

Accurate classification and prognosis of gynecologic smooth muscle tumors (GSMT) are essential for optimizing patient management. Distinguishing leiomyoma (LM), leiomyosarcoma (LMS), and smooth muscle tumors of uncertain malignant potential (STUMP) remains challenging due to overlapping histopathological features. We propose a transformer-based deep learning workflow to automate the classification of GSMT tumors and predict the risk of relapse in LMS and STUMP cases.

Material and methods

Our workflow consists of two steps. Step 1: A transformer-based model classifies GSMT tumors into LM and LMS/STUMP using whole-slide images (WSIs). Leveraging self-attention mechanisms, the model captures critical features from WSIs to enhance classification accuracy. Step 2: A survival prediction model estimates the relapse risk for LMS and STUMP cases. The models were trained and validated on 193 LM, 115 LMS, and 36 STUMP cases, then externally tested on 35 patients (12 LM, 8 STUMP, 15 LMS).

Results and discussion

The classification model achieved an AUC of 0.9226 on internal testing and 0.8206 on external testing, demonstrating strong generalizability. The relapse prediction model outperformed traditional prognostic factors, achieving a C-index of 0.76 and 0.70 on internal and external testing. The predicted relapse risks enabled patient stratification into low-risk and high-risk groups, revealing significant differences between them in both datasets ($p = 0.001$ for internal testing, $p = 0.037$ for external testing). Additional, a visual attention maps confirmed the model's ability to focus on diagnostically relevant regions.

Conclusion

This automated, interpretable workflow improves the classification and prognosis of uterine smooth muscle tumors, aiding pathologists and refining patient stratification. Future studies will validate its clinical applicability.

Key words: Uterine cancer, Relapse-free survival, STUMP, ViT, Deep Learning

A65 Deep Learning-Based Lymph Node Segmentation for Multi-Organ Applications

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Introduction

Lymph node metastasis (LNM) assessment is critical yet labor-intensive in pathological cancer staging. For instance, AJCC TNM Staging System for gastric cancer recommends screening of at least 16 LNs to determine the pN stage. Here, we extend a LN segmentation model, initially developed for colorectal cancer, to LNs of the upper gastrointestinal (uGI) tract.

Material and methods

We annotated 196 LN whole slide images (WSIs) from 140 patients across six tissue classes (LN, primary tissue/tumor, vessels, fat, and mucin). To train a Mask2Former segmentation model, we experimented with two frozen backbones: DinoV2, pretrained on natural images, and Virchow2, a histopathology foundation model. Performance was assessed using intersection-over-union (IoU) in a 5-fold cross-validation experiment, comparing results to the original UNet trained solely on colorectal cancer data.

Results and discussion

Five-fold cross-validation yielded IoU values of 77.28 ± 4.14% (Virchow2) and 71.86 ± 9.01% (DinoV2), improving LN segmentation by 12.1% and 6.68% over UNet.

Conclusion

The results show that the performance of the model improves significantly with 1) the use of foundation models, trained on extensive and heterogeneous histopathology data, and 2) the inclusion of samples from the target tissue (uGI) in the finetuning process, which paves the way to the incorporation of additional organs to create a segmentation model for a broader use case.

Key words: multi-tissue segmentation, Lymph node metastasis detection, computer-aided diagnosis

A66 StructMe: LLM based extraction of structured data from unstructured pathology reports

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Introduction

Accurate extraction of structured data from unstructured pathology reports is critical for advancing clinical research leveraging AI. However, intrinsic variability in terminology and free text inconsistencies hinder data extraction. Here, we evaluate multiple open-source Large Language Models (LLMs) to convert unstructured pathology reports into structured data suitable for downstream analysis.

Material and methods

We sourced 3,628 pathology reports from 14 cancer types of The Cancer Genome Atlas (TCGA) collections. Closed-source LLMs (GPT-4o & Gemini-1.5 combined) were used to generate the ground truth of extracted structure data. We then systematically evaluated ten open-source LLMs for their ability to identify critical clinical details and align them with established medical standards, focusing on their cost-effectiveness and data security, which are priority considerations for deployment in healthcare settings. Performance was quantified using precision, recall, F1-score, and overall accuracy.

Results and discussion

The NVIDIA-nemotron-70B LLM demonstrated exceptional performance (Accuracy=99.85%) across the entire TCGA dataset. This model excelled in handling ambiguous phrasing, cross-referencing report sections, and interpreting domain-specific synonyms, all while preserving essential clinical information. In contrast, other LLMs exhibited inferior accuracy, struggling with complex pathological descriptions or infrequently used terminologies or hallucinating information.

Conclusion

These findings underscore the potential of LLM-driven approaches to streamline the extraction of structured data from clinical reports. By automating this task, our method accelerates large-scale retrospective analysesin clinical and research contexts.. This study illustrates the transformative potential of LLMs in extracting actionable insights from unstructured clinical narratives, facilitating further scientific research, and ultimately enhancing patient care.

Key words: LLM, GenerativeAI, Report, Structure, Pathology, FreeText

A67 Foundation model-based survival prediction of glioblastoma adjusted to evolving tumor classification

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Introduction

Glioblastoma is the most common and most aggressive malignant primary tumor of the central nervous system (CNS) in adults. Recent deep learning models have shown promise in predicting glioblastoma survival from hematoxylin and eosin-stained tissue sections. However, all existing studies were based on previous versions of the WHO classification of CNS tumors that included both IDH-wildtype and IDH-mutated glioblastoma, the latter being considered a separate tumor entity since 2021. Among IDH-wildtype glioblastoma patients, predicting survival differences appears to be more difficult due to the clinical heterogeneity and the generally poor prognosis.

Material and methods

We evaluated state-of-the-art foundation models and multiple-instance learning methods for predicting overall survival of primary IDH-wildtype glioblastoma patients. We trained 8 models using all available cases from the public TCGA and CPTAC repositories (n=544) and tested their prognostic performance on two real-world datasets from independent neuropathology departments in Germany (n=105, n=53).

Results and discussion

In a 5-fold cross validation using the public datasets, the combinations of Virchow2 resp. UNI foundation models and attention-based multiple-instance learning performed best (c-index 0.604±0.027 resp. 0.601±0.030). Both combinations showed similar performance on the larger real-word dataset (c-index 0.632±0.004 resp. 0.600±0.008), but performed substantially worse on the other (c-index 0.526±0.006 resp. 0.504±0.016).

Conclusion

The moderate c-index values obtained may suggest that foundation model-based features can provide relevant information for predicting survival differences among IDH-wildtype glioblastoma patients. To assess their potential to complement established (epi)genetic biomarkers, evaluation in larger real-world datasets is required.

Key words: Glioblastoma, Real-world data, Survival prediction, Foundation models, Multiple-instance learning

A68 Breast tumor prognostic stratification via integrative modelling of mRNA expression, clinicopathological data, and digitized histopathology

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Introduction

Improved prognostic stratification of breast cancer patients can contribute to better clinical decision-support. It is not currently established if multi-modal models can improve prognostic patient-stratification. Here, we evaluate the prognostic performance of individual data modalities (features from histopathology foundation models(FMs), gene expression data and clinical data), as well as models that integrate the different data modalities together.

Material and methods

This study included 931 patients(Clinseq-BC(N=256); TCGA breast(N=675)), with RNA-seq profiles, one hematoxylin and eosin(H&E)-stained whole slide image(WSI) per patient, and clinicopathological variables. WSI features were extracted using the UNI FM at the tile level and aggregated to the slide level via an attention mechanism. Data modalities were integrated through feature concatenation. Prognostic scores for uni- and multi-modal models were generated using an Elastic-Net regularised Cox proportional hazards model. Performance was evaluated by mean C-index over 5-fold cross-validation(Recurrence-free survival(RFS)).

Results and discussion

The multi-modal model combining WSI+clinical data achieved highest C-index(0.692,95%CI:0.632–0.752), followed by WSI+gene-expression(C-index:0.681, 95%CI:0.618-0.744), and WSI+gene-expression+clinical(0.681,95% CI:0.618–0.745). Clinical+gene-expression showed a C-index of 0.669(95%CI:0.604-0.734), while individual modalities showed comparable performance: clinical(0.678,95%CI:0.608–0.749), gene-expression(0.679,95% CI:0.603–0.751), and WSI(0.679,95%CI:0.606–0.750).

Conclusion

These results demonstrate that integrating different modalities has the potential to improve prognostic performance compared to single modalities.Future work will explore larger cohorts, additional integration strategies, and refining model architecture to further improve prognostic performance. Future work will explore larger cohorts, additional integration strategies, and refining model architecture to further improve prognostic performance.

Key words: breast cancer, computational pathology, artificial intelligence, multi-modal models, survival analysis

A69 Weakly Supervised Subtyping of Barrett's Esophagus Using Histopathological images: From Normal to Adenocarcinoma

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Introduction

Early detection of dysplasia and esophagus adenocarcinoma (EAC) can decrease the risk of progression among people with Barrett's disease. The diagnosis of most progressed stages of Barrett's esophagus relies on histopathology. Due to substantial interobserver disagreement among pathologists, there is a need to differentiate subtypes in Barrett's esophagus. We applied a deep learning approach to classify different stages of disease, from normal to neoplasm.

Material and methods

We digitized biopsy slides related to 890 cases with Barrett's diseases that have been followed up from 2013 to 2023 in a multi-center cohort across Germany. Patient- and center-wise stratification was done, which led us to use 2323 whole slide images (WSIs) for model development with a 5-fold cross-validation approach. We segmented regions of interest, followed by utilizing a pretrained foundation model for feature extraction and two deep learning models, including an attention-based multiple instance learning and Mamba classifier, to achieve accurate cancer detection and subtype classification.

Results and discussion

We included WSIs from 607 patients (933 normal, 1140 metaplasia, 101 dysplasia and 149 EAC), yielding 1667, 334, and 322 slides for training, validation and testing. With mean recall, F1 score and AUC of 0.93 ± 0.01, 94 ± 0.01, and 0.89 ± 0.09 for cancer detection, and 0.78 ± 0.03, 0.79 ± 0.03, and 0.91 ± 0.02 for subtyping, attention based multiple instance learning model outperformed Mamba.

Conclusion

Due to overlapping histopathological features and more subtle morphological differences in dysplasia compared to the other stages, the model faced challenges in classifying dysplasia with a high level of accuracy.

Key words: Barrett's disease, Deep-learning, Subtyping, Esophageal adenocarcinoma

A70 Few Shot Segmentation for Histopathology: Foundation Models do not work Wonders

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Introduction

In the domain of digital pathology, accurate segmentation of histological structures is essential for diagnostics and research. Foundation models trained in a self-supervised manner have shown promising results in tasks such as classification and gene mutation prediction. However, their application to segmentation tasks — which require detailed spatial features — has been less effective without significant architectural modifications such as specialized decoders. Additionally, foundation models often impose input size limitations, restricting the capture of larger spatial contexts at high resolution crucial for precise segmentation.

Material and methods

We compared a foundation model, H-Optimus with a ViT-G backbone (1.1 billion parameters), with a traditional Convolutional Neural Network (CNN) (EfficientNet-B0, approx. 1 million parameters) as a feature extractor for prototypical few-shot segmentation. The dataset comprises 44 images (4500 x 4500 pixels) from 33 H&E-stained colon sections and finely grained annotations of five classes (tumor, stroma, mucus, necrosis, background). 9 images were taken as a test set. Different variants of H-Optimus were tested: variations of input resolution, finetuned last transformer block, feature dimension reduction to 112. Experiments were conducted in Python leveraging the MIKAIA image analysis software's plugin API.

Results and discussion

Our findings indicate that, without substantial additions, the foundation model does not deliver satisfactory segmentation performance. The highest overall accuracy in our experiments is at 70% compared to 85% obtained with the CNN.

Conclusion

These results highlight the limitations of current self-supervised foundation models for histological segmentation tasks and underscore the efficacy of traditional CNN architectures when detailed spatial feature extraction and a large high-resolution field of view are required.

Key words: Few Shot Segmentation, Foundation model, Digital pathology

A71 Identification of cancer cells from cavity serous effusions based on hyperspectral imaging and machine learning

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Introduction

Distinction of benign and reactive conditions from malignancy represents the focus when examining cavity serous effusions. Standard cytological approach offers sometime biased results, while molecular tests are expensive and with limited accessibility. We propose here Hyperspectral Microscopy, a mix of spectroscopy and conventional microscopy, sensitive to the distinct spectral signature of each cellular structures and adequate for a simultaneous visualization and automatic classification of cells.

Material and methods

Cells were fixed with ethanol and deposited on precoated histology slides with TriPath Imaging system. Hyperspectral images (HYS) of unstained and stained (Hematoxylin-eosin or Babes Papanicolaou) samples were acquired with CytoViva® enhanced darkfield hyperspectral microscope. The maxima of the averaged spectral profiles (SP) for cells and nuclei were used in ENVI software to decompose sub-HYS at certain spectral bands. Several automated method for segmentation of cells and nuclei were assessed.

Results and discussion

HYS contains in each pixel information about intensity on 468 spectral bands between 400-1000nm were collected for different cell types. The optimal spectral bands for sub-HYS decomposition was found at 430-450nm for unstained epithelial cells and 790-810nm for unstained lymphocytes. Hyperspectral features (1D features from SP considered as vectors in a 468-dimensional space, 2D texture features from HYS, 3D spatial-spectral and morphological features from sub-HYS) were extracted and used for unstained/stained cell recognition with supervised machine learning models.

Conclusion

We demonstrated that hyperspectral cellular features constitutes a good information for automatic cell recognition for stained and unstained samples. This novel method will be further developed to detect abnormal cells from various liquid-based cytology samples.

Key words: hyperspectral microscopy, malignant cavity serous effusions, Cytoviva, spectral cellular profile, liquid-based cytology

A72 Machine Learning-Based Prediction of MammaPrint and Luminal-Type Test Results from H&E Whole Slide Images

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Introduction

Breast cancer is among the most common malignancies, with treatment decisions guided by molecular tests like MammaPrint and BluePrint. However, these tests are costly and time-consuming. Recent studies show that deep learning can help identify molecular biomarkers from histopathological whole slide images (WSIs). This study explores the use of machine learning to predict MammaPrint results and classify breast cancer into Luminal A and Luminal B subtypes directly from H&E-stained WSIs, offering a potential alternative to traditional molecular testing.

Material and methods

We employ weakly supervised learning, combining pre-trained model feature extraction with attention-based multiple instance learning (MIL) to predict MammaPrint results and Luminal A/B classification from H&E-stained WSIs. The dataset, provided by Masaryk Memorial Cancer Institute (MMCI), includes over 1000 WSIs.

Results and discussion

Our findings indicate promising performance, achieving an AUROC of 0.785 for Luminal A/B classification and a MAE of 0.213 for MammaPrint value prediction. Pathologist evaluation of attention maps revealed distinct focus patterns between models. The MammaPrint model is sensitive to invasion boundaries, while the Luminal classification model focuses on densely packed tumor cells in central tumor regions.

Conclusion

Preliminary results suggest that predicting breast cancer molecular characteristics directly from H&E WSIs is feasible. The model's attention patterns provide insights into key morphological features relevant to MammaPrint and Luminal classification. These findings indicate that machine learning could assist pathologists in distinguishing subtypes from WSIs alone, potentially reducing reliance on costly molecular tests.

Key words: genetics, breast cancer, MammaPrint, Luminal classification

A73 Refining DCIS Grading: Leveraging Morpho-Spatial Features for Improved Diagnostic Consistency

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Introduction

Ductal carcinoma in situ (DCIS) is a breast lesion that may progress to invasive cancer. Recent international clinical trials aim to reduce overtreatment by employing active surveillance. However, these trials predominantly rely on the nuclear grading system—a system known to exhibit significant variability, that may compromise patient stratification and treatment decisions. This study aims to identify morpho-spatial features driving grading disagreement and to develop an improved grading algorithm.

Material and methods

Fourteen UK expert breast histopathologists graded 1,383 ducts from 141 DCIS cases. We used our HoVer-Net-DCIS—fine-tuned with 50,000 manually annotated nuclei—and a DeepLab model with a ResNet backbone for 9-class region segmentation (distinguishing benign ducts, DCIS, fibrous stroma, among others)to extract 706 nuclear and ductal features.

Results and discussion

The DeepLab model achieved a Dice score of 0.87, and HoVer-Net an F1 score of 0.81 for nuclear classification. Inter-observer agreement for DCIS grading averaged 67% at the duct level and 71% at the slide level, with a strong correlation between these assessments ($r=0.77, p<0.001$), indicating that duct-level inconsistencies extend to overall slide evaluation. Feature analysis revealed that greater variation in duct epithelium nuclear size ($r=0.19–0.23, p<0.001$), and larger absolute nuclear size, correlated with higher agreement, reflecting higher agreement on high-grade cases. Conversely, extreme skewness and kurtosis($r=-0.19, p<0.001$) were associated with reduced agreement, suggesting uncertainty regarding the threshold of neoplastic cells for grade escalation.

Conclusion

Our findings pinpoint key morpho-spatial features that drive grading agreement. These insights provide a robust foundation for refining DCIS grading through a graph-based classifier, which has a potential to transform subjective assessments into objective and interpretable criteria.

Key words: Breast Cancer, DCIS, Morphospatial Features, Image Analysis

A74 Two Heads Are Enough: DualU-Net, a Fast and Efficient Architecture for Nuclei Instance Segmentation

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Introduction

Accurate detection and classification of cell nuclei in histopathological images are critical for both clinical diagnostics and large-scale digital pathology workflows. In this work, we introduce DualU-Net, a fully convolutional, multi-task architecture designed to streamline nuclei classification and segmentation.

Material and methods

Unlike the widely adopted three-decoder paradigm of HoVer-Net, DualU-Net employs only two output heads: a segmentation decoder that predicts pixel-wise classification maps and a detection decoder that estimates Gaussian-based centroid density maps. By leveraging these two outputs, our model effectively reconstructs instance-level segmentations. We evaluated the model on publicly available hematoxylin and eosin (HE) stained datasets, including CoNSeP and PanNuke.

Results and discussion

The proposed architecture results in significantly faster inference, reducing processing time by up to x5 compared to HoVer-Net, while achieving classification and detection performance comparable to State-of-the-Art models. Additionally, our approach demonstrates greater computational efficiency than CellViT and NuLite. We further show that DualU-Net is more robust to staining variations, a common challenge in digital pathology workflows.

Conclusion

The model has been successfully deployed in clinical settings as part of the DigiPatICS initiative, operating across eight hospitals within the Institut Català de la Salut (ICS) network, highlighting the practical viability of DualU-Net as an efficient and scalable solution for nuclei segmentation and classification in real-world pathology applications. The code and pretrained model weights are publicly available on https://github.com/davidanglada/DualU-Net.

Key words: Cell Nuclei Classification, Cell Nuclei Segmentation, Digital Pathology, MultiTask Learning, Deep Learning, Computational Efficiency

A75 Self-Supervised Deep Metric Learning for Prototypical Zero-shot Lesions Retrieval in Placenta Whole-Slide Images

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Introduction
Inflammatory lesions within the placenta, revealed through a pathological evaluation, can explain and predict postnatal adverse outcomes. However, since this evaluation is time-consuming and requires specialized skills, it isn't performed systematically. We propose an automatic placenta WSI analysis pipeline that addresses the challenges of data scarcity and lack of precise annotations.

Material and methods
Given low data availability and challenging expert annotation, we adapt an existing self-supervised learning framework to train a feature extractor without labels on normal WSIs only. This feature extractor is used to define prototype vectors for inflammatory lesions using limited pathological patches extracted from a single placenta. We can then retrieve lesions in unseen WSIs by comparing patches with the prototype vectors in the feature extractor's metric space. The similarity map thus obtained is then refined using a simple post-processing method to account for spatial patch proximity. We evaluated our method using a private dataset of 165 annotated WSIs (51 placentas) and the CAMELYON16 dataset for lymph node metastasis retrieval.

Results and discussion
We achieved a patch-level AUROC of 0.978 on our dataset and a competitive 0.985 on CAMELYON16 in the zero-shot setting. We also demonstrate the limitation of current computational pathology foundational models which cannot generalize to the specific case of the placenta.

Conclusion
The proposed method is efficient, fast and easily explainable: we find relevant regions of interest by searching for regions similar to examples provided by pathologists. It could enable a more systematic examination of placental tissue at the end of pregnancy and save pathologists considerable amounts of time.

Key words: self-supervised learning, deep metric learning, placenta, low data regime, inflammatory lesions

A76 SPIDER: A Comprehensive Multi-Organ Supervised Pathology Dataset and Baseline Models

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Introduction

Foundation models in computer vision have significantly advanced computational pathology (CPath) by enabling efficient transfer learning. While unsupervised clustering has been explored for whole slide image (WSI) segmentation, it faces limitations such as unclear biological meaning, redundant clusters, and inadequate precision for clinical applications. To address these challenges, we introduce SPIDER (Supervised Pathology Image-DEscription Repository), the largest publicly available, expert-annotated, patch-level pathology dataset spanning multiple organs. We also present a supervised baseline model designed for patch classification and WSI segmentation.

Material and methods

SPIDER consists of high-quality annotated patches from Skin, Colorectal, and Thorax tissues, with expert-validated labels ensuring accuracy. Each 224×224 patch is accompanied by 24 surrounding context patches, forming a 1120×1120 composite input, enabling improved classification performance. Professional pathologists annotated target morphologies via a semi-automatic process: initial polygon or brush annotations on WSIs, similarity-based retrieval to expand patch variety, and final binary verification under a large field of view. We fine-tuned a Hibou-L foundation model on these patches in a supervised multi-class setup, freezing the backbone and training only a lightweight attention head.

Results and discussion

Our baseline model demonstrated strong multi-class classification performance across all organ datasets with 91%+ accuracy. The model also enables efficient WSI segmentation, providing clinically meaningful feature maps for rapid diagnosis.

Conclusion

SPIDER bridges a critical gap in computational pathology by offering a large-scale, multi-organ, expertly labeled dataset with a robust benchmark model. By open-sourcing both SPIDER and its associated models, we facilitate further advancements in pathology AI, accelerating the development of clinically viable deep learning solutions.

Key words: pathology, dataset, foundation model, supervised finetuning

A77 Immunocto: a massive immune cell database auto-generated for histopathology

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Introduction

With the advent of novel cancer treatment options such as immunotherapy, studying the tumour immune micro-environment (TIME) is crucial to inform on prognosis, identify novel therapeutic targets and stratify patients for therapy. A key approach to characterising the TIME involves combining digitised images of haematoxylin and eosin (H&E) stained tissue sections obtained in routine histopathology examination with automated immune cell detection and classification methods.

Material and methods

We introduce a workflow to automatically generate robust single cell contours and labels from dually stained tissue sections with H&E and multiplexed immunofluorescence (IF) markers. The approach harnesses the Segment Anything Model and requires minimal human intervention compared to existing databases.

Results and discussion

With this methodology, we have created Immunocto, a massive automatically generated database of 2,282,818 immune cells distributed across 4 subtypes: CD4+ T-cell lymphocytes, CD8+ T-cell lymphocytes, CD20+ B-cell lymphocytes, and CD68+/CD163+ macrophages. For each cell, we provide a 64x64 pixels^2 H&E image at 40x magnification, along with a binary mask of the nucleus and a label. Deep learning models trained on Immunocto result in state-of-the-art performance for lymphocyte detection on external data. Furthermore, we find strong agreement (e.g., 90% for lymphocytes) between expert raters and Immunocto.

Conclusion

Immunocto is the largest database of automatically classified immune cells available for histopathology. Our approach demonstrates the advantages of using matched H&E and IF data to create robust databases for computational pathology applications. The database, publicly available on Zenodo (https://zenodo.org/records/11073373), can be used to train models to study the TIME on routine H&E slides.

Key words: Immunotherapy, Lymphocytes, Macrophages, Segment Anything, Dataset

A78 A workflow for AI-enabled sub-cellular compartment quantification of immunohistochemically stained biomarkers in tumor tissue

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Introduction

Accurate sub-cellular compartment detection is a priority to ensure robust quantification of immunohistochemistry (IHC) positivity for biomarker analysis. The aim of this work was to demonstrate how a workflow incorporating Artificial Intelligence (AI) can be used to segment sub-cellular compartments for detailed downstream biomarker quantification in tumor tissue.

Material and methods

Gastric and Non-Small Cell Lung Cancer (NSCLC) samples were immunohistochemically (IHC)-stained by IQVIA Laboratories to identify HER-2 or PD-L1 biomarker using DAB, with a haematoxylin counterstain. Individual HER-2 (Gastric) and PD-L1 (NSCLC) IHC-stained cell membranes were annotated and added to the Indica Labs HALO® AI Membrane Segmentation Classifier for training. This was integrated into a cell analysis algorithm alongside a Nuclear AI Segmentation Classifier, enabling biomarker quantification in individual cell membrane and cytoplasm compartments. Biomarker staining thresholds were classified per compartment as weak, moderate or strong.

Results and discussion

HER-2 exhibits a classic 'honeycomb-like' membrane structure, whereas PD-L1 exhibits membranous and cytoplasmic staining, making membrane-specific stain quantification challenging. The analysis workflow addressed this by applying a tailored algorithm to each staining profile, trained using membrane annotations reflecting the range in membrane shapes. Membrane specific stain was accurately captured for HER-2, while setting distinct thresholds for the cytoplasm and membrane IHC staining enabled greater granularity for PD-L1.

Conclusion

In conclusion, this combined workflow demonstrates a means to improve the detection of sub-cellular compartment staining presented by different biomarkers, enabling more detailed interpretation of biological changes at the cellular level associated with disease progression or therapeutic intervention.

Key words: immunohistochemistry, sub-cellular, membrane, cytoplasm, biomarker, artificial intelligence (AI)

A79 Multi-reader Study on Accuracy and Concordance of Pathologists and AI-Assisted HER2 IHC Assessment in Breast Cancer, Including HER2 ultralow Scoring.

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Introduction

The classification of HER2 status in breast cancer is evolving, presenting a greater need to reliably distinguish low levels of HER2 expression. However, the subjective interpretation of HER2 immunohistochemistry presents a diagnostic challenge. Artificial intelligence (AI) decision-support systems could enhance accuracy, especially in HER2 low and ultralow scoring, but few studies have evaluated this potential.

Material and methods

For this retrospective observational study ground truth was established on 130 consecutive HER2-stained images by three expert pathologists without AI assistance. Next, three general pathologists assessed each case without and with assistance of an AI software that provides HER2 scores on whole-slide images at individual cell resolution. HER2 0 cases were subclassified into "null" (no membrane staining) and "ultralow" (membrane staining in ≤10% of tumor cells).

Results and discussion

The AI alone achieved 94.6% accuracy in distinguishing HER2 0 from 1+/2+/3+ scores. For the four ASCO/CAP HER2 scoring categories, pathologists showed 74.4% alone and 80.3% with AI assistance. AI assistance improved inter-reader agreement from 73.3% to 79.0%. When incorporating HER2 ultralow as a scoring category, AI assistance increased pathologists' accuracy from 70.3% to 77.2% and inter-reader concordance from 67.7% to 74.4% across the 5 classes. AI-assistance reduced the number of cases that were erroneously classified as HER2-null by 44%.

Conclusion

This study demonstrates the potential of AI to enhance HER2 scoring accuracy and inter-reader agreement, particularly for HER2 ultralow cases. Integrating AI into clinical practice could thus optimize breast cancer treatment decisions.

Key words: Artificial Intelligence, Digital Pathology, HER2, Ultralow, Breast Cancer, Decision Support

A80 Application of machine learning in pathology, Experience of pathology department

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Introduction

The parallel advancement of medicine and computer science has provided revolutionary techniques in the localization and treatment of serious pathologies; however, evaluating prognosis remains a difficult task despite the precision of medical equipment. The solution that is becoming more and more apparent is to implement another computing alternative, which is artificial intelligence for cancer staging and prognosis evaluating.

Material and methods

Data was collected retrospectively in the Department of Pathology of Sahloul Hospital, Sousse, Tunisia. From slides of neuro endocrine pancreatic tumors and uveal melanoma, we took microscopic pictures. The achievement of our model was taken in four steps: Data processing (Clean and label the collected data), Model creation (organized in 5 parts: Import libraries, Load Dataset, Create the CNN Model, Train the Model and Visualize the Result), Model training and Model evaluation.

Results and discussion

Throug an Interface, the application should do the doctor task: calculate the mean of the 10 largest nucleolei for cases of uveal melanoma, calculate the estimation of KI67 for neuro endocrine tumor.

Conclusion

Artificial intelligence was a very useful and facilitating tool in this case it allowed us to calculate an important parameter with precision and it allow us to improve patients care. The training of AI methods and validation of AI models using large data sets prior to applying the methods to personal data may address many of the challenges facing the medicine today.

Key words: pathology, artificiel intelligence, proliferation index, melanoma, neuro endocrine tumor, cancer

A81 Digitalization Enhances Pathology Quality Practices in a Children Cancer Center in Egypt

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Introduction

Pathology laboratories are undergoing digital transformation, adopting innovative technologies to enhance quality and patient care.

Material and methods

The pathology laboratory at Children Cancer Hospital Egypt has adopted the use of Leica Aperio digital pathology system since 2022, raising the benchmark of pathology services in the Arab African region. We aim to scan all our department's glass slides into digitalized images, to provide reliable and fast retrieval of digital images, enable remote work as well as sharing of digital images for research and educational purposes.

Results and discussion

In routine diagnostic workflow, pathologists have access to view their cases remotely anytime to provide preliminary diagnoses to physicians and send processing instructions to technicians in a timely manner. This results in improved communication of significant findings, decreases reporting TAT and leads to efficient process workflow. Digitalized images used to estimate percentages of semiquantitative tissue markers, especially predictive markers, raised the confidence of pathologists in obtaining consistent estimation, accurate evaluation and therefore better patient management. Continuous quality monitoring and self-auditing is greatly facilitated by reviewing the digitalized images for daily and routine quality check and for peer review. For external quality assurance and proficiency testing, the stained / processed tested material are readily available as archived digital WSI for review; improving and enhancing the process of self-evaluation and exception investigation after receiving the summary evaluation reports.

Conclusion

Digital pathology system gives high level of quality and assurance to both laboratory personnel and customers.

Key words: Digital Pathology, Quality, Assurance, WSI

A82 Evaluation of Foundation Models for Feature Extraction in Graph Neural Networks for Prostate Cancer Diagnosis

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Introduction

Prostate cancer is a major global health challenge, requiring accurate and reproducible diagnostics. Graph Neural Networks (GNNs) effectively model spatial relationships in histopathology images, enhancing classification. This study evaluates foundation models as feature extractors for graph-based prostate cancer detection, comparing them to standard Convolutional Neural Networks (CNNs) pretrained on ImageNet.

Material and methods

We benchmarked ten foundation models, including Virchow2, UNI, and Prov-GigaPath, against ResNet-50, VGG-19, and DenseNet-121. Whole-slide images (WSIs) from the Automated Gleason Grading Challenge 2022 dataset, comprising biopsy and prostatectomy samples across five Gleason grades, were divided into patches. Features were extracted from these patches using foundation and standard models. The extracted features served as node attributes in graph structures, where nodes represented patches, and edges were formed based on feature similarity using k-nearest neighbors (k=5). These graphs were then processed by Graph Attention Networks (GATs) for prostate cancer classification. Performance was evaluated using accuracy, precision, F1-score and confusion matrix.

Results and discussion

Foundation models produced more discriminative feature representations, improving classification performance. Virchow2 (F1-score: 0.875) and UNI (F1-score: 0.874) outperformed standard CNNs. Prov-GigaPath (F1-score: 0.872) demonstrated robustness to class imbalance, particularly in underrepresented Gleason grades. Among standard CNNs, DenseNet-121 achieved the highest F1-score (0.804), followed by ResNet-50 (0.780) and VGG-19 (0.733), all of which underperformed compared to foundation models.

Conclusion

Foundation models improve feature extraction for graph-based prostate cancer classification, enhancing diagnostic accuracy and reproducibility with GNNs. Their superiority over CNNs, especially in handling complex tissue patterns and class imbalances, underscores their potential to advance computational pathology.

Key words: Foundation Models, Graph Neural Networks, Prostate Cancer, Histopathology

A83 Cross-institution Histological Feature Fusion Model to Predict Relapse-Free Survival in Patients with Early-Stage Urothelial Carcinoma on BCG-Therapy

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Introduction
Urothelial carcinoma, primarily presenting as non-muscle invasive papillary urothelial carcinoma (NMIPUC), exhibits significant clinical variability. Accurate pathological staging and grading are critical for effective risk stratification and treatment decisions. While artificial intelligence (AI) has the potential to enhance predictive modeling, ensuring generalizability across diverse datasets remains a challenge.

Material and methods
This study developed a cross-institution histological feature fusion AI framework using federated learning to improve NMIPUC staging, grading, and relapse prediction. By clustering ensembled histological features, a novel risk factor was derived. Retrospective data from 1,427 NMIPUC cases across two institutions in Lithuania and Taiwan were utilized for model development and analysis.

Results and discussion
The federated learning models demonstrated superior generalizability and accuracy compared to single-site models, achieving 86.2% accuracy for tumor staging and 79.2% for grading, with minimal performance variability. The novel risk factor outperformed conventional indicators in relapse-free survival (RFS) of the NMIPUC patients treated with BCG immunotherapy, with hazard ratios of 2.7 (p=0.0018) and 2.8 (p=0.0208) in the Lithuanian and Taiwanese datasets, respectively. Kaplan-Meier survival curve analysis revealed clear distinctions among risk groups identified by the histological feature fusion model, showing a greater disparity than stratification by tumor stage or grade, with a significant p-value (0.0012).

Conclusion
This study highlights the potential of federated learning and histological feature fusion AI model in providing generalizable NMIPUC risk stratification. Further integration of tumor microenvironment data may yield insights for personalized clinical interventions.

Key words: digital pathology, federated learning, relapse-free survival analysis, urothelial carcinoma

A84 Towards Automated Banff Lesion Scoring: Tissue Segmentation in Kidney Transplant Biopsies using Deep Learning

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Introduction

Inflammation and chronic changes in the different tissue structures (e.g., glomeruli, tubules, interstitium) are major contributors to kidney transplant failure and are components of the Banff classification. However, visual scoring by pathologists has suboptimal reproducibility and is labor-intensive. To address this, we developed a multi-class segmentation approach that covers all tissue structures relevant for kidney transplant biopsy diagnostics.

Material and methods

Our dataset consists of 99 Periodic-acid Schiff (PAS) stained kidney transplant biopsy slides from two pathology departments. An expert pathologist manually annotated >17,000 structures across eight classes (glomeruli, sclerotic glomeruli, empty Bowman space, proximal tubuli, distal tubuli, atrophic tubuli, capsule, arteries/arterioles, and interstitium). A separate test set was created with additional annotations for peritubular capillaries (n=10). We compared two segmentation approaches: (1) a combination of two nnU-Nets (one for tissue segmentation and one specialized for structure boundary detection) and (2) the SAM-Path foundation model. For the peritubular capillary segmentation, we used a previously developed U-Net.

Results and discussion

The two nn-Unets achieved a per-class average Dice score of 0.80, outperforming SAM-Path (0.69). Despite satisfactory performance, we observed suboptimal performances for the smaller/rarer tissue classes (e.g., atrophic tubules) and found that nnU-Net performed better overall in this regard.

Conclusion

We developed and evaluated two models for tissue segmentation in PAS-stained kidney transplant biopsies. The nnU-Net architecture outperformed SAM-Path, providing a reliable solution for all tissue structures relevant for kidney transplant biopsy diagnostics. Next, we plan to perform a reader study to investigate further the impact of AI on pathologists' performance in Banff lesion scoring.

Key words: Tissue Segmentation, Kidney Transplant Biopsies, Banff Lesion Scores, nnU-Net, SAM-Path

A85 Enabling Molecular Subtyping and Grading for Ductal Carcinoma in Situ with Foundation Models

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Introduction

Ductal Carcinoma In Situ (DCIS) is a non-obligate precursor to invasive breast cancer. Identifying patients with risk of progression remains challenging due to the lack of reliable markers. For example, histologic grading is known to be subject to interobserver variability. Grading combined with ER and HER2 status improves robustness. This combination is already used for DCIS active surveillance trials. Automated analysis of these markers from H&E whole-slide images (WSIs) allows enhanced biomarker analysis and patient risk stratification.

Material and methods

We developed a deep learning pipeline to predict ER status, HER2 status, and grade 1 and 2 vs grade 3. Models were trained and evaluated on H&E-stained WSIs from a Dutch multicenter dataset (n=761) split over 5 folds and externally validated on the UK-based Sloane dataset (n=225).

Results and discussion

ER, HER2, and grade were predicted with mean AUROCs of 0.90, 0.84, and 0.86, respectively, on the Dutch dataset, and 0.80, 0.73, and 0.75 on the external dataset. Combined into a risk group stratification based on active surveillance trial criteria (ER positive, HER2 negative, grade 1/2), the models achieved a balanced accuracy of 0.79 and 0.60, an NPV of 0.89 and 0.80 and a sensitivity of 0.78 and 0.95, on the Dutch dataset and external dataset, respectively.

Conclusion

Deep learning models using routine WSIs demonstrated consistent biomarker characterization in DCIS. These models effectively stratified patients into risk groups for active surveillance. Their performance was validated on an external dataset, showing potential for streamlining patient selection and optimizing DCIS treatment.

Key words: Deep learning, Foundation Models, DCIS, HER2, ER, Grade

A86 SmartTile: A Transformer-Based Tiling and Segmentation Tool for Digital Pathology

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Introduction

Tiling whole-slide images (WSIs) of hematoxylin and eosin–stained tissue is a critical preprocessing step in AI-driven digital pathology workflows. However, conventional tiling methods often misidentify tissue regions and inadvertently incorporate scanning artefacts—such as pen marks, dust, and tissue folds—that can bias downstream machine learning analyses and undermine the integrity of diagnostic evidence. Traditional segmentation techniques like Otsu thresholding depend on luminance-based separation, which is insufficient when artefacts are present or when specific tissue components, such as adipose tissue, exhibit intensities similar to the background.

Material and methods

We introduce SmartTile, an intelligent tiling and segmentation tool engineered to robustly identify tissue regions while systematically excluding artefacts. SmartTile employs a transformer-based architecture trained on 200 WSIs at both 40× and 20× magnifications, encompassing 23 tissue types from 39 international pathology centres. This diverse dataset reflects extensive inter-institutional, inter-scanner, and inter-tissue variability, ensuring the broad applicability of the model. We evaluated SmartTile against both conventional Otsu thresholding and an enhanced variant using an independent external dataset.

Results and discussion

On the test set of 20 WSIs, SmartTile achieved a Dice score of 96.1%, surpassing Otsu's method (93.4%) and its improved variant (94.8%). Qualitative assessments further demonstrated that SmartTile consistently identifies tissue regions across diverse histologies, while both Otsu-based approaches struggled with segmentation consistency and incomplete artefact exclusion.

Conclusion

These findings underscore SmartTile's robustness and precision in segmenting heterogeneous tissue types while minimizing the inclusion of extraneous scanning artefacts, thereby significantly enhancing its utility in AI-driven digital pathology workflows.

Key words: Intelligent Tiling, Transformer-Based Tissue Segmentation, Artifact removal

A87 Automated Evaluation of Tumor Cellularity in Pancreatic Ductal Adenocarcinoma Using Digital Image Analysis

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Introduction

Pancreatic ductal adenocarcinoma (PDAC) is a highly aggressive malignancy. Molecular profiling has identified key genetic alterations, but its clinical implementation requires accurate assessment of tumor cellularity to ensure reliable biomarker testing. PDAC presents unique challenges due to its dense desmoplastic stroma and low tumor cellularity, contributing to variability in estimation of cellularity by light microscopy. Current methods rely on subjective visual assessment by pathologists, leading to inter- and intra-observer variability. To address these limitations, we developed a machine learning-based tool for automated estimation of neoplastic cellularity in digital histological images, aiming to improve accuracy and reproducibility in molecular diagnostics.

Material and methods

We analyzed 30 PDAC cases, refining pathologist-selected regions of interest with patch-level segmentation, morphological analysis, and superpixel-based post-processing to reduce false positives. To handle large whole-slide images (WSIs), we used a sliding window with adaptive memory allocation. Additionally, we curated a high-quality PDAC dataset for nuclei classification. Predicted cellularity was compared to pathologist assessments and tumor cellularity estimation based on NGS-derived variant allele frequency (VAF).

Results and discussion

Our system provides fully automated, high-accuracy inference at multiple levels, surpassing pathologists in efficiency and demonstrating strong concordance with VAF (mean absolute error: 5.44; accuracy rate: 77.10; Pearson correlation coefficient: 0.894 ($p < 0.01$).

Conclusion

The high concordance of image analysis with pathologist assessments and even greater agreement with the estimation based on NGS-derived VAF, demonstrates that the developed tool can be used for neoplastic cellularity evaluation ensuring a greater standardization and significant time savings in molecular profiling of PDAC.

Key words: Pancreatic ductal adenocarcinoma, tumor cellularity, NGS-derived variant allele frequency, Computer vision, Cell nuclei segmentation

A88 AI identifies molecularly mandated WHO glioma subtypes solely from whole slide images

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Introduction

WHO 2021 classification of adult diffuse glioma mandates molecular profiling of glioma further to histologic assessment. Since molecular profiling is expensive, time-demanding, and when not available leads to the 'not-otherwise-specified' status, we develop an interpretable artificial intelligence (AI)-based model for classification of glioma as oligodendroglioma, astrocytoma, or glioblastoma, solely from H&E-stained whole slide images (WSI).

Material and methods

We identified retrospective glioma collections, following their reclassification according to the WHO 2021 criteria: a) TCGA-GBM/TCGA-LGG (nWSI=1,320, npatients=654) for methodology development & b) EBRAINS (nWSI=npatients=794) for independent hold-out validation. Following WSI preprocessing, a quantitative performance evaluation of glioma classification is conducted across: i) eight pathology-specific foundation models (FM) for feature extraction, ii) nine multiple-instance learning (MIL) approaches that aggregate features into slide-level representations, and (iii) 15 combinations of magnification levels (2.5x, 5x, 10x, 20x), in an attempt to mimic expert neuropathologists.

Results and discussion

Evaluation on development cohort and independent validation cohort yields average 10-fold cross-validation AUC of 0.979 and 0.963 respectively, for the best performing FM and MIL in the multi-magnification setting. Our key findings indicate: i) FMs outperform the ImageNet model, ii) Spatial-MILs yield performance improvement when used with ImageNet models than with FMs, iii) Fusion of multiple magnifications improves performance. Interpretability analysis through attention heatmaps highlights distinct identifiable morphology features.

Conclusion

AI based identification of glioma subtypes directly from H&E-stained WSI can avoid the need for molecular profiling, expedite conclusive diagnosis in clinical settings, even in underserved regions. Interpretability analysis towards distilled human-identifiable features can contribute to furthering disease understanding.

Key words: glioma, foundation models, embedding aggregation, multi-magnification

A89 Evaluating the Tumor Microenvironment Using Chromogenic Multiplexed IHC and Deep Learning

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Introduction

Current immunohistochemistry techniques quantify immune cell counts and density, but generally cannot asses the spatial relationship between tumour and immune cells. Robust, accurate, segmentation of cell nuclei for overlapping nuclei is one of the most significant unsolved issues in digital pathology. By combining a mIHC technique which enables the detection of multiple markers with deep learning segmentation methods to segment every individual cell nuclei in tissue sections with an accuracy comparable to human annotation, we can analyze the cell-cell interactions between immune and tumour cells, enhancing our ability to perform molecularly based single cell analysis of multiple cell types simultaneously within the tissue.

Material and methods

The process described integrates hyperspectral imaging, sequential labeling and spectral unmixing and can be applied on any FFPE tissue to quantify 14 biomarkers on a section. For segmentation, we have trained a deep learning segmentation method to accurately segment individual cell nuclei within overlapping clusters of nuclei using a sequential UNet application.

Results and discussion

To demonstrate the potential utility of mIHC for high-dimensional analysis, we applied our protocol to early-stage NSCLC to predict those most likely to exhibit recurrence after surgery. We further verified our results by performing sequential-immunofluorescence on adjacent sections. Specifically, we examined whether certain immune cell-cell interactions and cell neighbour frequencies correlate with recurrence and response to immune therapy. Hyperspectral mIHC preliminary results revealed several marker frequencies and cell-cell interactions which correlate with recurrence in eNSCLC.

Conclusion

Combining the two technologies has the potential to inform on the biological aggressiveness of specific cancers and the appropriate treatment strategies.

Key words: Spatial Biology, Multiplexed IHC, Tumor Microenvironment , Cell Segmentation

A90 Joint Training of a Distributed Foundation Model for Digital Pathology: Enabling Cross-Institutional Collaboration via Swarm Learning

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Introduction

Recent advances in self-supervised learning have enabled foundation models to excel in digital pathology. However, individual institutions face constraints due to limited annotated data and computational resources. Distributed training via swarm learning offers a solution that preserves patient privacy while enabling cross-institutional collaboration.

Material and methods

We developed a novel three-node framework that integrates both proprietary and open-source datasets. Our proprietary data comprise high-resolution histopathology images from 5,260 patients worldwide, augmented by open-source data from an additional 1,721 patients, totaling over 7,000 cases. Our design addresses key challenges—including communication overhead, non-IID data from variable staining protocols, synchronization, fault tolerance, and privacy risks—by employing secure aggregation, differential privacy, and dynamic load balancing across heterogeneous hardware. Performance is evaluated using linear evaluation accuracy, AUC, F1 score, cosine similarity, and top-k accuracy.

Results and discussion

Preliminary experiments show robust convergence, with our model achieving 85.0% linear evaluation accuracy, 0.88 AUC, 82.5% F1 score, 0.88 cosine similarity, and 91.0% top-5 accuracy. Our framework reduced communication overhead by ~30% and lowered memory and computational usage by ~25% compared to centralized training, thanks to optimized asynchronous aggregation and load balancing. The fault-tolerant design maintained stability during simulated node failures.

Conclusion

Our findings demonstrate that a swarm learning–based, privacy-preserving distributed training strategy can overcome key technical constraints in digital pathology. Future work will scale the framework to larger networks, refine aggregation and privacy methods, and evaluate its impact on real-world clinical outcomes.

Key words: Digital Pathology, Swarm Learning, Distributed Training, Data Heterogeneity, Privacy Preservation

A91 Foundation models for federated prostate cancer risk stratification

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Introduction

Approximately 30% of prostate cancer cases worldwide are treated with radical prostatectomy to prevent cancer spread, but about 30% of these patients experience biochemical recurrence (BCR). Current risk stratification methods, such as Gleason grading, vary due to inter-observer variability, leading to inconsistent diagnoses between centers. Deep learning can help standardize this process, but BCR data is often noisy and sparse, making it challenging for traditional methods. Foundation models show promise in handling such data, offering the potential for better stratification of BCR risk groups.

Material and methods

We fine-tuned the Tissue Concepts foundation model using multi-task learning on prostate-specific tasks to obtain a prostate-focused foundation model. This model was applied to unseen cohorts from the TCGA-PRAD and PLCO datasets in combination with an attention-based aggregator to learn time to BCR of patients, ensuring cross-center training/validation and testing splits. The architecture allows for resource efficient computation during the fine-tuning process. The separation of patch encoding from patch aggregation enabled the incorporation of private data of two German university hospitals through federated learning.

Results and discussion

In a preliminary cross-center test, our model achieved an average concordance index of 0.73±0.02 over 5 runs and thus allows for better stratification of BCR risk groups than the ISUP score with a c-index of 0.67.

Conclusion

Fine-tuned foundation models integrate additional tissue information to Gleason scoring and improve prostate cancer risk stratification with respect to BCR, while also enabling the discovery of potential new biomarkers to aid pathologists through attention weight visualization.

Key words: Prostate Cancer, Biochemical Recurrence, Foundation Model, Survival Prediction

A92 Point-cloud registration of differently stained images of consecutive slices

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Introduction

The integration of information from differently stained whole slide images (WSIs) of consecutive slices is crucial for comprehensive analysis. However, significant intensity variations and computational demands pose challenges for intensity-based registration. Point cloud (PCL) registration offers a computationally efficient and intensity-invariant alternative. We investigated its potential for registering consecutive hematoxylin and eosin (H&E) and fluorescent multiplex immunohistochemistry (fm-IHC) WSIs.

Material and methods

The first step of our pipeline involves generating PCLs for consecutive slides using the centroids of nuclei. Nuclei were segmented on hematoxylin stain for H&E WSIs and DAPI stain for fm-IHC images. Rigid registration of the generated PCLs was performed using the FilterReg probabilistic point-set registration algorithm implemented in Python. Notably, our method does not require GPU acceleration. Our method was tested using 15 pairs of WSIs, each from a different glioblastoma patient. Registration performance was quantified by comparing the average distance between closest points of the PCLs before and after registration, and measuring the computational time of the registration process.

Results and discussion

Our registration method significantly reduced the average point-to-point distance from 329.0 µm to 121.3 µm, indicating effective alignment. The registration process is computationally efficient, with an average execution time of 0.6 seconds per pair.

Conclusion

This study demonstrates that PCL-based registration offers a rapid and effective solution for aligning differently stained WSIs. By utilizing segmented nuclei as PCL points, we achieved robust registration without GPU dependency. Future work will focus on annotating corresponding landmarks on WSIs for computing target registration errors and extending the method to deformable registration to account for tissue deformations.

Key words: Point Cloud Registration, WSI Registration, Digital Pathology, Immunohistochemistry

A93 Artificial Intelligence Assisted Prostate Cancer Diagnosis for Reduced Use of Immunohistochemistry

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Introduction

Prostate cancer diagnosis heavily relies on histopathological evaluation, which is subject to variability. While immunohistochemical staining (IHC) assists in distinguishing benign from malignant tissue, it involves increased work, higher costs and diagnostic delays. Advances in artificial intelligence (AI) present a promising solution to reduce reliance on IHC by accurately classifying atypical glands and borderline morphologies in H&E-stained tissue sections.

Material and methods

In this study, we evaluated an AI model's ability to minimize IHC use without compromising diagnostic accuracy by retrospectively analysing samples from routine diagnostics at three different pathology sites. These cohorts were composed exclusively of difficult cases where the diagnosing pathologists required IHC to finalize the diagnosis.

Results and discussion

The AI model demonstrated exceptional performance, with area under the curve (AUC) values ranging from 0.951 to 0.993. Applying sensitivity-prioritized thresholding reduced the need for IHC staining by 44.4%, 42.0% and 20.7% in the three cohorts investigated, without a single false negative prediction.

Conclusion

Our work demonstrates an AI model highly adept at classifying cancer vs. benign tissue in cases where pathologists required immunohistochemical staining to make the distinction. The model's ability to make accurate benign predictions with extremely high confidence has significant potential for optimizing IHC use, streamlining decision-making, and alleviating resource burdens in prostate pathology.

Key words: Prostate biopsies, Immunohistochemistry (IHC), Artificial Intelligence (AI), Pathology, Clinical application

A94 Artificial intelligence (AI) in prostate cancer: An analysis of pre-analytic considerations for an accurate diagnosis

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Introduction
Efficacy of AI for pathological diagnosis of prostate cancer has not yet been evaluated in clinical settings. The aim of this study was to analyse the incidence of artefacts in biopsies and in digital pathology and its diagnostic performance.

Material and methods
We retrospectively performed a biopsy-based analysis of prostate cancer patients, randomly selecting 25 patients (462 biopsies). Biopsies were digitalised with p250 3DHISTECH. AI used was DEEP-DX PROSTATE.

Results and discussion
Incidence of artefacts was 224 of 462 biopsies (48.5%) (range per biopsy 1-4). Artefacts invalidated biopsy for digital diagnosis in 38 (8.2%). Types of artefacts were due to: tissue-type-related (n=5); sectioning (n=70); staining (n= 4); mounting (n=37); contamination (non-prostatic tissues) (n=2); artefacts related to digital pathology (n=119), comprising unfocused images (n=35), incomplete scanning with missing sections (n=6), and tissue scanned in slide's edge (n=78) Incorrect diagnoses reached by AI due to artefacts were: 1 false positive (FP) due to contamination (0.21%); 1 FP due to erroneously considering tumour tissue in the slide's edge (0.21%); in 6 Gleason score was overestimated (1.2%); in 2 Gleason score was underestimated (0.43%); 38 biopsies were inadequate for digital diagnosis nor AI (8.2%). However, sensitivity of AI was 98%, although concordance with expert uropathologists was low due to pattern 4 overestimation.

Conclusion
Preanalytics allows solving certain artefacts with optical microscopy, although others cannot be solved by digital pathology nor AI. Maintaining high quality standards is key to reduce the incidence of artefacts in biopsies and preclude errors with AI.

Key words: Prostate cancer , Quality, DEEP-DX PROSTATE

A95 Diagnostic Efficacy of Virtual Reality versus High-Definition Displays in Digital Pathology

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Introduction

Recent technological advancements have made Virtual Reality (VR) increasingly accessible for medical applications, potentially offering an alternative to traditional monitor-based viewing of whole slide images (WSI). This study compares modern VR technology with conventional high-definition displays for digital pathology diagnosis, focusing on diagnostic accuracy, efficiency, and user experience.

Material and methods

Twenty sentinel lymph node WSIs from breast cancer patients were randomly selected from the CAMELYON17 dataset. Two independent physicians established diagnostic baselines through consensus review (13 benign lymph nodes, 7 with micro- and macro-metastases). Eight physicians examined these slides using both a Meta Quest 3 VR headset and a 27-inch 4K monitor in randomized order, with sessions separated by a 14-day washout period. Measurements included examination time, diagnostic accuracy, confidence ratings, perceived image quality, and system usability.

Results and discussion

VR examination required significantly more time than monitor-based review (mean 69s vs 48s, range 2-267s vs 2-143s, $p<0.01$). Both modalities achieved comparable diagnostic accuracy (sensitivity and specificity >98%). Monitor-based viewing received higher ratings for image quality and diagnostic confidence, though the navigation interface of VR was preferred. Notably, all participants reported absence of adverse effects during VR usage and expressed optimism about its future applications, regardless of initial skepticism.

Conclusion

While achieving equivalent diagnostic accuracy, current VR technology presents limitations in image quality and examination efficiency compared to conventional displays. However, positive user experiences suggest promising applications for VR in diagnostic pathology, particularly as hardware capabilities continue to advance.

Key words: Virtual Reality, Diagnostic efficacy, Diagnostic confidence, Image quality, Slide examination time, User experience

A96 Application of an AI-optimised mIF workflow across multiple tumour indications to support data-driven insights within Oncology R&D

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Introduction

The Tumour Immune Cell Atlas (TICA) is a comprehensive tumour profiling database utilised by AstraZeneca to improve understanding of the tumour microenvironment (TME) and its interactions with the immune system. This study aimed to utilise multiplex immunofluorescence staining (mIF) and image analysis to profile ~1,200 TICA tumour samples across 7 cancer indications, providing insights into tumour biology and supporting data-driven decisions within AstraZeneca Oncology R&D.

Material and methods

The TICA images were stained with an Akoya Biosciences' 6-plex myeloid panel (DAPI, CD8, CD68, CD163, DC-Lamp, XCR1, and HLA-DR). OracleBio provided image analysis services to AstraZeneca through a Full-Time Equivalent service model, accessing AstraZeneca's internal digital pathology environment to develop algorithms and generate data. The workflow included image quality control (QC), algorithm development, image processing and data management. A web-based stain QC tool developed by AstraZeneca was used to exclude unsuitable images for analysis. Algorithm development involved accurate segmentation of cell lineages based on morphological features and staining to quantify macrophage and immune cell populations, using Indica Labs' HALO and HALO AI software.

Results and discussion

Generated cell data identified key phenotypes including macrophage subtypes, dendritic cells and T-cells. Spatial analysis was conducted to examine relationships between these cells, such as proximity between M1-M2 macrophages and cytotoxic T-cells to macrophage subtypes. AstraZeneca's data analytics team combined the two cell analysis algorithm outputs, enabling detailed spatial and phenotypic evaluations within the TME.

Conclusion

An optimised mIF digital pathology workflow, utilising AI, enabled characterisation of distinct cell populations, generating robust, high-quality data to enhance AstraZeneca's R&D decision-making.

Key words: Tumour Immune Cell Atlas (TICA), multiplex immunofluorescence, image quality control, myeloid cell phenotyping, spatial analysis, artificial intelligence (AI)

A97 Automated enhanced localization aids in visualisation of faint and sparse hypo-cellular LBC Pap smears

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Introduction

Hypo-cellular smears pose a great challenge for digitisation as there is a high probability of missing sparsely distributed single cells with conventional localization methods. Here we present a novel method of automated enhanced localization to improve localisation in faint and sparse hypo-cellular LBC pap smears.

Material and methods

30 cases of LBC Pap smears were scanned by Pramana Cubiq scanner at 40X magnification with sample localization using macro-image. Subsequently smears were scanned again using an automated localization algorithm based on the output of additional 4X lens to enable image capture of single cells and sparse cell clusters. WSIs from both the groups were compared with traditional light microscopy by a Pathologist to evaluate the performance of two localization methods against traditional light microscopy.

Results and discussion

For faint hypo-cellular smears with sparse cell cluster and single cells, the localization with 4X lens yielded results similar to traditional light microscopy with 100% localization of smears without missing sparsely distributed single cell, whereas the other group (localization with macroimage) shows suboptimal results with missing of few sparse and faint cell clusters. In case of normocellular and hypercellular smears, performance of both the localization methods were similar to light microscopy as both were able to capture entire smears without missing any cell clusters.

Conclusion

Robust localization using 4X lens for hypocellular faint smears with sparsely distributed cell clusters and single cells is of paramount importance for diagnosis and interpretation, it also instills more confidence in routine use of digital cytopathology for primary reporting of LBC pap smears.

Key words: Digital cytopathology, Hypocellular smear , localization, LBC smear, PAP smear, WSI

A98 Evaluating the Impact of a Deep Learning AI algorithm in the Identification of Lymph Node Metastasis in Breast, Colon and Gastric Tumor Resections

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Introduction

Screening lymph nodes (LN) for metastases, especially micrometastases, is time-consuming but essential for staging and management. This study developed a segmentation-based artificial intelligence (AI) module to enhance sensitivity and significantly reduce detection time.

Material and methods

The AI algorithm uses a deep learning-based feature extractor that produces pixel-level classifications. The model is trained on axillary LN (containing metastatic deposits from breast, colon and gastric tumors). Three expert pathologists reviewed retrospectively 314 LN whole-slide images (WSIs) (106 from gastric, 101 from breast, and 107 from colon resected specimens). The same set was analyzed by the AI module after a 3-week washout period and AI results were compared to the ground truth. Changes in their reading times, sensitivity, and specificity were assessed.

Results and discussion

The ability of three pathologists to detect metastatic deposits was evaluated both with and without AI assistance. The analysis revealed that AI support significantly improved sensitivity across all three pathologists (2% to 4.1%), while maintaining a high level of specificity (97 to 99.2%). The number of clicks to detect metastases was recorded. Colon LN metastases were identified with 2 clicks (100% sensitivity). Gastric LN detection reached 95.2% in 10 clicks, while 50 clicks identified 83.3% of breast LN metastases. Review time for WSIs with metastases was recorded with and without AI. The AI reduced review time by 50.8%, 55.7%, and 22.3% for the three pathologists.

Conclusion

The AI module improved pathologists' efficiency by reducing slide reading time and accurately detecting challenging metastases. Its intuitive workflow speeds up reviews without compromising accuracy.

Key words: Lymph node metastasis, Artificial Intelligence, Colon Cancer, Gastric cancer, Breast Cancer

A99 Comparative analysis of Automated Nuclear Pleomorphism Scoring in Breast Cancer Whole slide and Low-Resource Imaging

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Introduction

Low-resource Laboratory settings often lack access to whole-slide scanners limiting the adoption of AI-driven pathology solutions. This study aims to analyze nuclear pleomorphism scoring approaches for WSIs and low resource images using Qupath software and compare it with manual assessment by Nottingham scoring.

Material and methods

We Used Qupath software to create training images combining regions of interest for each grade (1-3) of nuclear pleomorphism, respectively. We performed nuclear morphometric measurements including nuclear circularity & nucleus cell ratio. The results from WSI and camera-captured images were compared to assess variations in nuclear feature extraction. We applied ANOVA (Analysis of Variance) to compare means. The results were then compared with expert pathologists' assessment of nuclear grades to observe the agreement.

Results and discussion

The mean ± SD for nuclear to cell ratio in WSIs was 0.287 ± 0.07689 for grade 1 ,0.3214 ± 0.094391 for grade 2 and 0.2807 ± 0.084857 for grade 3 nuclei, respectively. A p value of 0.001728 showed highly significant variation in the nuclear to cell ratio in the three groups. For nuclear circularity also, a p value of 0.00 was obtained. This highly significant variation in morphology detected by Qu path suggests agreement with the prognostic score of the Nottingham grading system. Low resource camera captured images at 10x resolution revealed similar results.

Conclusion

Our experiment revealed a very good automated morphometric assessment of nuclear morphological changes in breast cancer which lie in agreement with the Nottingham scoring system used by Pathologists to assess the grades of breast cancer.

Key words: Digital Pathology, Breast Cancer, Nottingham grading system, QuPath, Low-Resource Imaging, Nuclear Pleomorphism

A100 Multi-photon confocal scanner for label-free imaging

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Introduction

The current workflow in the Pathology Lab from sample entry to microscopy comprises grossing, processing, cutting, staining, and imaging of tissue samples. Although semi-automatized, this is lengthy and time-consuming work. To improve this workflow, we introduce a novel label-free imaging tool based on multi-photon confocal microscopy. This multi-photon scanner can generate virtual staining from slide- and stain-free samples.

Material and methods

We used the new multi-photon scanner to generate whole-slide images from breast cancer, bone and liver tissue. We included unprocessed (fresh tissue), and semi-processed samples (FFPE, unstained mounted slides, etc.) to visualize collagen, cytoplasm content information, elastin, lipids, etc. The scanner uses ultra-short pulse lasers in the near-IR to generate two- and three-photon autofluorescence, and second- and third-harmonic images. The new laser-scanning method achieves specifications (speed, field of view, etc.) comparable with typical brightfield scanners. The system is designed to fit in the lab environment with a user-friendly interface.

Results and discussion

Images from breast and bone tissue at different stages of preparation were obtained. Fresh, formalin fixed, paraffin embedded, and cut as well as bulk tissue were tested and analyzed. Images from breast cancer tissue show clear collagen structure that allows for basal lamina integrity identification. We can clearly separate extra-cellular matrix, cell cytoplasm, and nuclei. In the bone tissue images demonstrate a clear appearance of collagen fibers, lamina, canaliculi, Haversian canal, etc.

Conclusion

Our innovative multi-photon scanner shows the potential to improve the Pathology laboratory workflow at multiple stages during sample processing.

Key words: label-free, multi-photon, stain-free, slide-free, confocal, breast

A101 From Histology Slides to Understanding the Whole Picture: Investigating Placental Vessel Trees with 3D Virtual Histology

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Introduction

Three-dimensional visualizations in histopathology are often created using serial reconstructions of 2D whole-slide images or light sheet microscopy on cleared tissues [1]. A non-destructive method is 3D virtual histology of formalin fixed paraffin embedded (FFPE) tissue using X-rays [2], which does not require tissue clearing or staining, and preserves tissue for follow-up research. This technique is useful in studying twin-to-twin transfusion syndrome (TTTS), a complication in monochorionic twin pregnancies. Investigating vessel trees in placentae helps identify vascular anastomoses causing disproportionate blood flow between the twins.

Material and methods

Placentae were prepared according to Turowski. The FFPE samples were scanned using a laboratory phase-contrast X-ray tomography setup by Histomography GmbH. The FFPE samples were cut into slides and compared to segmented vessel trees after. Segmentation was performed using the 3D Slicer software, marking the dyed vessels based on thresholding of the measured intensities, followed by cleaning up artifacts.

Results and discussion

Downstream, anastomoses were identifiable in both histological slides and the unedited tomography scans. The vessel tree can be visualized based on grey levels with VG Studio Max. The segmentation performed with 3D Slicer can be used for further analysis like intervascular connectivity and blood flow simulations. Therefore, we can visualize placental vessel trees in 3D, highlighting intersections critical to understanding vessel behavior. This method can enhance understanding of TTTS and contribute to future research concerning vascular structures.

Conclusion

1. Tissue histology in 3D. Nature Methods 21, 1133–1133 (2024). 2. Reichmann, J. et al. Human lung virtual histology by multi-scale x-ray phase-contrast computed tomography. Physics in Medicine and Biology 68, (2023).

Key words: 3D Imaging, Digital Pathology, Segmentation, Histopathology, Tomography, Vessels

A102 Enhancing the iDISCO protocol for 3D cancer sample analysis with light sheet microscopy

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Introduction

Histopathology remains the gold standard for cancer grading and staging. However, conventional 2D histopathological analysis has inherent limitations, with up to 10% of cases yielding ambiguous results. A key challenge lies in the reliance on thin tissue slices, which may not fully capture the complexity of the 3D tumor architecture. Emerging non-destructive 3D pathology techniques show promise in enhancing diagnostic accuracy and sensitivity. We developed an optimized imaging pipeline comprising three steps: (1) iDISCO tissue clearing and staining, (2) high-resolution light-sheet fluorescence microscopy for 3D tissue reconstruction, and (3) computational analysis for quantitative assessment. While imaging and data processing are relatively fast, traditional tissue clearing can take several days, posing a challenge for clinical implementation.

Material and methods

FFPE biopsy samples from breast and lung cancer patients were cleared using an optimized iDISCO protocol and stained with key tumor and microenvironment markers.

Results and discussion

Our refined iDISCO method enables tissue clearing in under a single workday without compromising staining quality, significantly accelerating the process for breast and lung cancer samples.

Conclusion

This advancement brings 3D histopathology closer to clinical integration, offering a more accurate and comprehensive approach to cancer diagnosis. By improving diagnostic precision, it paves the way for personalized therapeutic strategies and better patient outcomes.

Key words: 3D histopathology , light-sheet fluorescence microscopy , tissue clearing, breast cancer, lung cancer

A103 Charting the molecular and spatial transcriptomic landscape of crypt variability in Inflammatory Bowel Disease

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Introduction

Inflammatory Bowel Diseases (IBD): Ulcerative Colitis (UC) and Crohn's Disease (CD), are characterized by persistent inflammation of the gastrointestinal tract. Alterations in crypt architecture are common in IBD, yet their precise impact on patient prognosis remains unclear and their molecular underpinnings are uncharacterised.

Material and methods

A segmentation model (SegFormer) was developed to segment IBD relevant colonic substructures. DINOv2, a self-supervised learning framework was used to learn embeddings of crypt morphology. GeoMx was used to sequence >4,500 crypts.

Results and discussion

To understand crypt structure variability in both healthy and IBD donors, we used machine learning to segment lamina propria, crypts, muscle, surface, and granulomas (IOU = 0.785, F1 score = 0.839) in >2,000 whole-slide-images. Next, we trained DINOv2 on >600,000 crypts to characterize crypt morphological variability. These embeddings revealed a continuum from normal to abnormal crypts and identified distinct clusters, such as crypts with Paneth cell metaplasia. A classification model differentiated cryptitis from crypt abscess events, demonstrating cryptitis is overrepresented in UC. Next, we generated a large spatial transcriptomic cohort of 78 UC, CD and healthy donors, and characterised the transcriptomic variability of over 4,500 individual crypts. Integration of H&E WSI, gene expression, and scRNA-seq data highlighted a crypt architectural signature implicating SLC26A2 (logFC -3.5, P=5.28×10^-8) and CHP2 (logFC -1.97, P=9.90×10^-5).

Conclusion

Leveraging large H&E datasets, we modelled the morphology of crypts across thousands of donors. Using spatial transcriptomics, we derived a previously unknown signature of crypt architectural distortion. Ongoing work focuses on learning joint image-expression embeddings of crypts.

Key words: Inflammatory Bowel Disease, crypt architecture, deep learning, DINOv2, spatial transcriptomics, multimodal embeddings

A104 The MONKEY Challenge: Machine-learning for Optimal detection of iNflammatory cells in the KidnEY

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Introduction

Because Banff classification of kidney transplant biopsies suffers from subjectivity and is time consuming, development of automated biopsy assessment is potentially useful to increase scoring consistency. We organized the MONKEY challenge, in which participants developed AI algorithms to detect individual inflammatory cells in Periodic acid-Schiff (PAS) stained kidney transplant biopsies.

Material and methods

A multicenter dataset of 116 whole slide images (WSIs) was collected, in which 31.101 monocytes and 60.629 lymphocytes were annotated within 174 ROIs. Annotations were guided by immunohistochemical (IHC) re-staining to create a robust ground truth. The publicly released training data contained 81 WSIs, scanned with three different scan profiles and a corresponding IHC restained WSI. For independent validation, 26 WSI from two centers were held back. Submissions were ranked using Free Response Operating Characteristic (FROC) analysis.

Results and discussion

MONKEY was conducted from September 2024 to February 2025. For the model with the highest FROC score, an overall inflammatory cell detection performance of 76.7%, 71.6% and 74.1% was achieved for precision, recall and F1, respectively. Visual inspection of the results of the three top-performing teams look promising to be further established in a diagnostic tool.

Conclusion

The MONKEY challenge demonstrated how a wisdom-of-the-crowd approach resulted in very promising AI applications. Eight out of 17 Banff lesion scores focus on the presence of inflammatory cells in different kidney compartments. Therefore, this study brings us a step closer to automated Banff scoring. The final best performing algorithm will be further enhanced and validated in a subsequent reader study.

Key words: Deep learning, Kidney, Transplants, Inflammation, Detection, Challenge

A105 Hierarchical Cell-to-Patch Graphs for Context-Aware Cell Classification in Digital Pathology

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Introduction

Cell classification in digital pathology requires spatial context beyond individual cell morphology, particularly for distinguishing tumor vs. normal cells in H&E-stained images. While traditional segmentation and models like CellNuc-DETR achieve high detection accuracy, their reliance on small image patches limits classification performance by excluding tissue-level context. We propose a hierarchical cell-to-patch graph framework that integrates fine-grained cell features with global spatial information using graph neural networks (GNNs) to enhance classification accuracy while maintaining computational efficiency.

Material and methods

We construct a heterogeneous graph, where cell nodes encode nuclear morphology, and patch nodes provide local tissue context extracted from CellNuc-DETR feature maps. The model is evaluated on tumor vs. normal classification in both inductive and transductive settings. Additionally, a self-supervised two-stage pipeline is introduced, where a GNN trained on unannotated H&E images extracts embeddings for classification, reducing reliance on labeled data.

Results and discussion

The hierarchical graph improves F1-score by up to 10% in tumor classification, demonstrating the importance of spatial context. In a private lung cancer dataset, classification improves by 5% in F1-score over CellNuc-DETR. The self-supervised two-stage pipeline enables classification with as few as 5 labeled cells per class, improving low-data performance by 20% over CNN-based features.

Conclusion

By leveraging graph-based hierarchical contextualization, our approach significantly enhances tumor vs. normal classification in H&E images while remaining efficient and scalable, making it ideal for real-world pathology applications with limited annotations.

Key words: Deep Learning, Cell Classification, Graph Neural Networks, Self-supervised Learning

A106 Spatial representation of intra-tumour heterogeneity based on deep-learning prognostic markers in breast cancer patients

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Introduction

Intra-tumour heterogeneity has been hypothesised to increase risk of recurrence in breast cancer patients but has not been studies systematically. Deep-learning enables systematic extraction of prognostic information from H&E histopathology whole slide images (WSI), however tile level features are typically aggregated without spatial context. Here we investigate the spatial distribution of an AI-based prognostic marker (DeepGrade) within tumour areas to identify patterns of spatial heterogeneity.

Material and methods

3325 WSIs from resected breast tumours of patients diagnosed in two hospitals in Sweden were used to predict DeepGrade status on a tile-level. Tumour regions were segmented and divided spatially into a tumour front and a tumour centre. For each tumour region, the total number of tiles, the proportion of high-risk tiles, the number of high-risk tiles in mini-clusters (regions of 25 neighbouring tiles), and Moran's I were calculated. Analyses were performed by tumour subtypes (Luminal A, Luminal B, Her2-enriched and Basal-like). Hazard ratio was performed to evaluate survival relative risk

Results and discussion

The proportion of DeepGrade-high tiles in the centre area were higher in Her2+ and basal-like patients than luminal patients, (49.6% vs 12.8% had > 80% of centre tiles DeepGrade-high). In the subgroup of luminal patients with DeepGrade-low status, those who had a cluster of DeepGrade-high tiles in the tumour front area had higher recurrence probability with a univariate hazard ratio of 3.20.

Conclusion

The spatial distribution of high-risk tumour areas in a histopathology slide can have prognostic implications and should be analysed with greater detail in the future.

Key words: Breast cancer, spatial heterogeneity , deep learning, tumour areas

A107 BMolNet identifies molecular subtypes linked to bacillus Calmette-Guerin response from bladder cancer histology images

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Introduction

Patients with high-risk non-muscle-invasive bladder cancer (HR-NMIBC) often receive intravesical BCG therapy, but 20% progress to advanced disease. Molecular subtypes (BRS1/2 vs. BRS3) predict BCG response, with BRS3 linked to poor outcomes. Traditional subtyping is expensive and slow. We developed BMolNet, a deep learning tool, to predict subtypes directly from hematoxylin and eosin (H&E)-stained slides.

Material and methods

H&E-stained slides were digitized, excluding blurry images. Areas from which RNA was extracted were annotated pixel-wise using QuPath. Image tiles of 512x512 pixels at 10X were extracted with 25% overlap. BRS1 and BRS2 images were grouped together, separate from BRS3 images. Post-normalization, patients were split 80/20 for training/validation, with 5-fold cross-validation. BMolNet was trained to classify BRS3 vs. BRS1/2 tiles. External validation included an independent test cohort and spatial transcriptomics to assess heterogeneity. Model efficacy was gauged by AUC.

Results and discussion

Of 245 H&E slides, 45 were discarded for quality. From 200 patients, distribution was 70:30 between BRS1&2 and BRS3. Cross-validation achieved a mean AUC of 0.79 for patient-level binary BRS classification. On the independent test set (83 patients), BMolNet reached an AUC of 0.71. BMolNet achieved an AUC of 0.67 in classifying BRS3 versus BRS1/2 tiles across five which ground truth was derived from spatial transcriptomics.

Conclusion

BMolNet can identify BRS3 vs. BRS1/2 subtypes from H&E images, with robust cross-validation and independent validation, and ability to detect tumor heterogeneity. This method can identify BRS3 HR-NMIBC patients who may benefit from alternative treatments than BCG in a cost and time-efficient manner. Prospective validation will further assess translation potential.

Key words: Computational pathology, Spatial transcriptomics, bladder cancer, machine learning, molcular subtype

A108 Multiple Instance Learning in the context of Annotation Variability: A Study of Gleason Grading of Histopathology Images of Prostate Cancer

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Introduction

The annotation of Whole Slide Images (WSIs) in a pixel-wise detailed manner is subject to high inter- and intra-annotator variability, making it difficult to establish a ground truth to learn from and thus to train fully-supervised (FS) models confidently. Furthermore, annotating WSIs at the pixel level can be time-consuming and costly. In contrast, slide-level annotations are much easier to provide, with significantly lower variability. In this work, we compare the performance of methods trained using either pixel-wise detailed annotations or slide-level weak annotations for the grading of prostate cancer.

Material and methods

We trained and tested a multiple instance learning (MIL) framework, commonly used for slide-level predictions, for grading prostate biopsies. We use a private dataset of 2,687 H&E-stained WSIs that were given a global Gleason Score and annotated at pixel level. We compare the MIL performance to a FS architecture trained to segment and grade glands in WSIs from which we compute a global Gleason Score.

Results and discussion

The MIL model achieves better performances for grading WSIs. In particular, it differentiates benign versus tumoral slides well, with both low false negative rate (0.014) and false positive rate (0.025), whereas the FS model often misclassifies benign slides (false positive rate of 0.335), especially when patterns of inflammation or differential diagnosis are present. Visual inspection of attention maps also shows that the MIL model correctly focuses on tumoral zones.

Conclusion

While FS models are affected by the annotation variability even with a large dataset, MIL models show encouraging results for inferring the grade of WSIs without the need for pixel-level annotations.

Key words: Multiple Instance Learning, Annotation Variability, Prostate Cancer, Deep Learning, Gleason Score, Whole-Slide Image

A109 Benchmarking Pathology Foundation Model Robustness

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Introduction

Recent pathology Foundation Models (FMs) demonstrate drastic performance improvement across a wide variety of tasks. In supervised ML, previous studies showed that models learn to represent visual signatures of medical centers unrelated to biological characteristics. This can limit generalization, bias results for subpopulations, and potentially lead to mispredictions. We systematically assessed pathology FM robustness with a new benchmark evaluating the influence of such medical center signatures.

Material and methods

Balanced multi-site patch subsets from four public histopathology datasets were distilled. We evaluated the embedding spaces of 15 FMs. We computed a novel Robustness Index measuring to what degree biological features dominate medical center features. We further quantified how confounded training data affect the generalization performance of downstream models on data from seen and unseen hospitals. Finally, we analyzed the effect of mitigation techniques such as stain normalization and domain-adversarial training.

Results and discussion

All evaluated FMs strongly encode medical center signatures; none were fully robust to medical center differences. Downstream classifiers were seen to make use of these confounding features, leading to bias and misclassification, especially on unseen data similar to the biased training distributions. Mitigation methods led to minor increases in FM robustness and reduced the performance drops of confounded downstream models.

Conclusion

Our work provides a new perspective on the evaluation of pathology FMs, paving the way towards more robust, representative, and reliable FMs and downstream models that focus on biological information. We provide our datasets and implementation as a practical benchmark for FM robustness assessment.

Key words: foundation models, robustness, bias, benchmarking, batch effects

A110 Deep Learning and Multi-Modal Analysis for Prognostic Prediction in Diffuse Large B-Cell Lymphoma

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Introduction
Diffuse large B-cell lymphoma (DLBCL) is an aggressive non-Hodgkin lymphoma (NHL) subtype with challenges in predicting treatment response. This study leverages digital pathology and deep learning to predict patient responses to immunochemotherapy (R-CHOP).

Material and methods
A total of 251 pathology slide images from 216 DLBCL patients treated with R-CHOP were collected, along with their response labels. Contrastive learning was used for feature extraction, and a multi-modal prediction model integrating clinical data and pathology image features was developed. Knowledge distillation was applied to reduce overfitting on gigapixel images, allowing pathology-based response prediction. The model's attention mechanism highlighted key histological features linked to drug responsiveness.

Results and discussion
The multi-modal model achieved an AUC of 0.856, correlating with clinical factors like Ann Arbor stage, International Prognostic Index (IPI), and bulky disease. Survival analysis confirmed its predictive value for relapse-free survival, and external validation (TCGA datasets) supported its effectiveness in distinguishing survival differences. Pathology-based predictions emerged as independent prognostic markers, with centroblastic and immunoblastic features aligning with traditional morphological classifications.

Conclusion
This study introduces a novel AI-driven approach combining digital pathology and clinical data for DLBCL treatment response prediction. The model demonstrates strong diagnostic and prognostic potential, with genomic data integration offering further improvements. This AI-powered method could enhance clinical decision-making and patient outcomes.

Key words: deep learning, diffuse large B-cell lymphoma, digital pathology

A111 Pan-Cancer Microsatellite Instability Prediction via Foundation Models and Cell Social Network Analysis Reveals Shared Tumor Microenvironment Dynamics

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Introduction
Microsatellite instability (MSI) is a critical biomarker for immunotherapy response and prognosis in multiple cancers, yet its identification via histopathology remains challenging. While deep learning models have shown promise in automating MSI prediction H&E slides, limitations persist due to scarce labeled data and poor interpretability. This study introduces a pan-cancer approach to enhance MSI prediction by leveraging cross-cancer data and investigates shared microenvironmental hallmarks of MSI (MSIness) through interpretable cell-cell interaction analysis.

Material and methods
We analyzed H&E whole-slide images (WSIs) from three TCGA cohorts: colorectal (COADREAD), gastric (STAD), and endometrial (UCEC) cancers. After extracting tiles from WSIs, UNI foundation model generated tile-level embeddings, which were aggregated into slide-level representations using different methods. A cross-validated classifier predicted MSI status across different cancer types and using different aggregation methods. To interpret results, attention maps from top-performing method guided cell social network analysis (CSNA) of tumor microenvironment (TME), quantifying spatial interactions among epithelial, inflammatory, connective, and mitotic cells.

Results and discussion
Our transformer-based aggregator achieved superior performance, with mean AUROCs of 0.95±0.05 (COADREAD), 0.96±0.04 (STAD), and 0.87±0.11 (UCEC), and a pan-cancer AUPRC of 0.854. CSNA revealed significant differences in TME connectivity between MSI and MSS cases. Furthermore, we identified similarities of molecular interactions related to MSIness that are shared across different cancer types.

Conclusion
By integrating pan-cancer data with foundation models and CSNA-driven interpretability, this work advances MSI prediction accuracy while uncovering conserved TME dynamics. The findings highlight the potential of cross-cancer learning and computational pathology to elucidate biomarkers for precision oncology.

Key words: MSI, foundation model, SNA, interpretable AI, TCGA

A112 Evaluation of Scanner-Variability Robustness of Computational Pathology Foundation Models

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Introduction

Computational pathology has the potential to enhance breast cancer diagnostics using deep learning on histopathology whole slide images (WSIs). Recently a plethora of histopathology Foundation Models (FMs) has been released. However, their robustness to technical variabilities associated with different slide-scanner has not been characterised to date. In this study we assess the robustness of multiple histopathology FMs to scanner-induced variability in multiple breast cancer classification tasks.

Material and methods

We used an in-house benchmark dataset that included 400 H&E WSIs from 400 breast cancer patients, each scanned by five different slide-scanners. Eight recent FMs were used as feature extractors, subsequently used to train models for five benchmark tasks using the TCGA-BRCA dataset. To evaluate and rank the scanner-variability robustness of the FMs, several different performance and correlation metrics were used.

Results and discussion

The FMs had the following differences in performance in the benchmarking tasks: ER (AUC) 0.88-0.92; PR (AUC) 0.73-0.77, HER2 (AUC) 0.71-0.74, Nottingham Histological Grade (NHG) (Cohen's Kappa) 0.40-0.48. UNI ranked highest on average performance for binary classification tasks, followed by Prov-Gigapath and H-Optimus-0. UNI and CONCH and CONCHv1.5 were top-ranked for 3-class NHG classification. CONCH, the smallest model, provided the highest consistency in predictions across the different scanners, albeit with slightly lower prediction performance.

Conclusion

The study reveals variable performance between FMs, and also variable robustness to scanner variabilities. Our findings highlight the need for further characterisation of the FMs under different conditions to establish robustness to technical variability, which is of high relevance for both research and clinical applications.

Key words: Computational Pathology, Foundation Models, Scanner-Variability, Breast Cancer, Deep Learning, Robustness

A113 Introducing AI Applications for Clinical Use: The Complex Intersection of the IVDR and AI Act

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Introduction

The European regulatory landscape for artificial intelligence/machine learning (AI/ML) applications is rapidly changing for device developers and users. For digital pathology, the implementation of the In Vitro Diagnostic Regulation (IVDR) and the AI Act in the European Union requires AI-driven pathology tools to navigate dual compliance requirements. The IVDR mandates clinical validation and risk management, while the AI Act imposes transparency and traceability for high-risk AI systems.

Material and methods

Most digital pathology devices are regulated under the IVDR. Devices incorporating AI must also comply with the AI Act. An exhaustive, systematic review of the IVDR and AI Act highlights mandatory requirements for performance studies and marketing authorization for AI-based digital pathology devices.

Results and discussion

The IVDR and AI Act significantly increase the complexity for commercialising AI applications, their use in clinical studies, and incorporating these devices into clinical care. AI digital pathology devices are usually Class C, requiring clinical validation and Notified Body (NB) approval. Under the AI Act, these devices will be high risk, necessitating explainability, bias mitigation, and real-time performance monitoring. Developers must meet relevant requirements prior to NB review. Clinical laboratories using AI applications are also not exempt. Users who modify devices could assume certain responsibilities and could be subject to certain regulatory requirements.

Conclusion

Lack of harmonized standards, NB backlogs, and evolving National Competent Authority interpretation, complicates the introduction of AI pathology tools. Defining the regulatory scope to use AI applications in the clinic is essential to ensure compliance and support access to important innovations for patient care.

Key words: Digital pathology, AI applications, IVDR, AI Act

A114 BRIDGE Pilot Study: A Bilateral Regulatory Investigation of Data Governance and Exchange

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Introduction

Transatlantic research collaboration offers immense potential for digital pathology by fostering access to expanded datasets, increasing diversity and reducing bias due to local patient population characteristics. However, conducting this type of research faces barriers including divergent regulatory frameworks, contrasting privacy concerns, local administrative complexities, and incompatible data models. To address these challenges, we launched the BRIDGE Pilot Study to evaluate a proposed framework to ensure regulatory compliance and ethical responsibility when performing transatlantic health data sharing.

Material and methods

Using domain expertise supplemented by ChatGPT we collected and sorted 30 relevant steps (items) separated into 3 project phases: 1) preparation and development; 2) core data; 3) data integration and analysis. Next, we collected feedback on the specific order of these items by distributing a survey among national and international societies. The results will be analyzed using a modified Delphi approach, allowing participants to refine their responses and work toward consensus.

Results and discussion

The survey was viewed by 121 participants, with 43 (35.5%) submitting complete responses. Of these, 37 participants (86.0%) modified the order of at least one item, and 12 participants (27.9%) provided further comments on the proposed order of items, their rearrangements, or additionally required items.

Conclusion

Preliminary results show mixed perspectives on the proposed framework, from broad approval to suggested rearrangements and additions. This variation highlights the lack of unified guidelines and the need for an internationally accepted framework for transatlantic health data exchange. We will use these insights to develop regulatory documents for a publicly available repository.

Key words: Transatlantic Health Data Exchange, Data Governance Framework, Structured Questionnaire

A115 From Genes to Images: Leveraging Spatial Transcriptomics for Histological Image Generation

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Introduction

Spatial Transcriptomics (ST) is a groundbreaking technology that captures gene expression within the native tissue context. Platforms such as 10x Visium and Visium HD integrate gene expression with histological imaging, offering a multi-dimensional view of tissue organisation. Motivated by the success of generative models in computer vision and natural language processing, we explore the feasibility of generating histological images conditioned on gene expression profiles.

Material and methods

Using a VisiumHD mouse kidney sample, we created a paired dataset of histological images and gene expression profiles. By applying a 10-micron stride and binning gene expression from 27×27 2-micron bins, we obtain over 300,000 paired samples. We adapted StyleGAN-T to generate histological patches conditioned on gene expression. The architecture is modified to integrate a foundational digital pathology model into the discriminator and a gene expression embedding module for conditioning. Standard 10x Visium mouse kidney samples were used for validation.

Results and discussion

Our adapted model successfully generates histological images that are morphologically plausible, as confirmed by both pathologists and non-experts. By conditioning on gene expression, the model effectively captures morphological features; similar gene expression profiles result in similar morphological patterns.

Conclusion

These results demonstrate the potential of generating histological images from gene expression, suggesting that transcriptomic profiles may encapsulate certain morphological information. Additional studies and further validation are needed to confirm the biological relevance of these images and to explore their applications in digital pathology.

Key words: spatial transcriptomics, synthetic data, generative models, contrastive pretraining

A116 Temporal degradation of diagnostic artificial intelligence models in digital pathology: determinants and mitigation strategies

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Introduction

Concerns have been raised over the robustness of AI models in digital pathology, particularly in relation to various batch effects, yet few studies addressed the impact of temporal variation. This study aims to assess the phenomenon of "AI aging"—declining AI performance over time—in digital pathology, explore the underlying contributing factors and further investigate potential mitigation strategies.

Material and methods

We utilized 119 prostate core needle biopsy slides with a balanced ISUP grade distribution from Stavanger University Hospital, plus one Sierra color calibration slide. Two consecutive baseline scans were performed on a Hamamatsu NanoZoomer S60 scanner to assess reproducibility in the absence of temporal variation, followed by scans every 14 days for one year. Temporal variance's impact on AI model performance will be evaluated using a deep multiple instance learning model trained on ~46,000 whole slide images for prostate cancer diagnosis, and other state-of-the-art pathology foundation models. Model performance will be systematically compared at each timepoint, quantifying the temporal degradation.

Results and discussion

Preliminary results support the AI aging hypothesis, with a negative correlation between time intervals and model performance consistency. Several factors have been examined, including scanner variation, focus score, training data size, incorporation of target domain samples into the training set — among others to be explored. Additionally, pathologists will evaluate the slides with analysis results to provide insights into the potential determinants of variation.

Conclusion

This study pioneers the investigation of temporal degradation in digital pathology AI model performance and its influencing factors, potentially paving the way for real-time quality assurance approaches to enhance diagnostic robustness over time.

Key words: artificial intelligence, AI aging, data drift, scanner variation, quality assurance

A117 Virtual PAS-staining of unstained tissues can visualize stain-specific details

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Introduction

Periodic-acid Schiff (PAS) staining is a commonly used histological special stain to detect certain pathologies in routine clinical practice. It, however, requires the use of harmful chemicals and time from the laboratory. In addition, it is irreversible, making the tissue unusable for subsequent analyses. Our goal is to develop and evaluate a virtual staining protocol from unstained tissue imaged with standard light microscopy to a virtual PAS-staining. This would decrease the workload of the laboratory as well as save valuable sample material.

Material and methods

Our preclinical sample set consisted of over 100 whole slide images with four different tissue types. We first imaged the samples unstained with a high-throughput scanner. After imaging, we performed PAS-staining and imaged the samples again. Virtual staining was performed using a pix2pix based image-to-image translation approach, using a training dataset where all four tissues were pooled together. Finally, we analyzed the tissues by comparing the chemically stained ground truth and virtually stained tissue by thorough histological as well as quantitative analysis.

Results and discussion

The virtually stained tissues show exceptional morphology and color accuracy. Similarly to our previous studies with HE-staining, epithelial cells and their nuclei show excellent precision. In addition, PAS-staining specific structures, such as goblet cells of the intestine are remarkably well recognized and reproduced by the algorithm.

Conclusion

These findings suggest that PAS staining could be utilized in virtual staining of unstained WSIs imaged with standard brightfield microscopy. In addition, these results show potential for histology to become more sustainable and streamlined.

Key words: PAS-staining, virtual staining, histology, whole slide imaging

A118 Histological Virtual H&E Staining using Diffusion Models

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Introduction

Histological images play a crucial role in the diagnosis and treatment of diseases, particularly cancers. However, raw histopathology sections are not sufficiently useful unless essential laboratory processes are performed. Chemical staining is a vital step required for the enhanced visualization of unstained histology images; however, despite its benefits, it is an expensive process in terms of time and substances. In recent years, with the advancement of deep learning, virtual staining has emerged as a computational and artificial intelligence-based alternative to traditional staining.

Material and methods

To address the virtual staining problem, several methods, primarily based on generative adversarial networks (GANs), have been proposed. In our approach, we employ an alternative image-to-image translation method based on diffusion models, which are state-of-the-art generative models. Specifically, we utilize the "ResShift" diffusion model to perform the translation from unstained images to Hematoxylin and Eosin (H&E) stained images.

Results and discussion

We conducted experiments using two different tissues, kidney and spleen, from images of unstained preclinical samples. Our proposed approach demonstrated promising results both numerically and visually, making it superior or at least comparable to other successful diffusion-based methods and Pix2Pix-based GAN models. The approach, in contrast to most diffusion models, uses significantly fewer diffusion steps while preserving quality and performance.

Conclusion

This study presents a fast and efficient diffusion model-based approach for translating unstained histology images into virtually stained images. The results of two distinct experiments validate the applicability and effectiveness of diffusion models in computational pathology, particularly for virtual staining.

Key words: Computational Pathology, Deep Learning, Diffusion Models, Histopathology, H&E Staining, Virtual Staining

A119 Towards an AI Co-Pathologist

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Introduction

Pathologists spend only about 25% of their time on slide interpretation. The remaining time is spent on ancillary yet critical tasks such as data validation, literature review, and report generation, leading to inefficiencies in the diagnostic workflow. To address these challenges, we present an "AI Co-Pathologist," a suite of AI-driven agents designed to automate key components of the workflow while augmenting diagnostic accuracy and efficiency.

Material and methods

The AI Co-Pathologist employs a modular architecture of specialized agents that work under the guidance of a Supervisor Agent, which dynamically orchestrates the involvement of specific agents based on the complexity of each case. Diagnostic Workflow For cases with high-confidence predictions from the initial diagnostic model, the Reporting Agent is activated to generate the report. For cases with low-confidence predictions, additional agents are deployed: Patient History Summarization Agent: Utilizes LLMs to extract and summarize relevant patient history and prior biopsies. Stain Suggestion Agent: A predictive model that proposes additional stains based on case characteristics. Literature Search Agent: Combines RAG models and knowledge graphs to suggest differential diagnoses. Report Generation Agent: Leverages LLMs to synthesize diagnostic findings dictated by the pathologist, with built-in reporting modules for drafting comprehensive reports. Evaluation The system was evaluated by three dermatopathologists, who assessed its impact on workflow efficiency, turnaround time, and overall satisfaction.

Results and discussion

The AI Co-Pathologist demonstrated a 25% reduction in case turnaround-time, while pathologist satisfaction increased by 30%.

Conclusion

The AI Co-Pathologist exemplifies the transformative potential of AI in pathology by reducing workflow inefficiencies and enhancing diagnostic precision. Automating non-interpretive tasks enables pathologists to focus on complex case evaluations and clinical decision-making.

Key words: Agentic AI, Large Language models, Diagnostic automation

POSTER PRESENTATIONS

P1 Transforming Diagnostics Through Telepathology: Insights from a Tertiary Care Center of Excellence

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Introduction
Telepathology bridges diagnostic gaps by connecting resource-limited areas with expert centers, transforming healthcare through digital innovation. The PGIMER Centre of Excellence for Telepathology, launched on November 1, 2023, under the Department of Telemedicine, aims to evaluate the implementation of telepathology services. The initiative focuses on methodology, case diversity, platform efficiency, and its impact on diagnostic accuracy, turnaround times, and accessibility to subspecialty expertise.

Material and methods
Telepathology services are provided via email, the GOI's e-Sanjeevani portal, and Onward Assist Telereporting, an AI-driven private platform. Cases from Punjab, Haryana, Himachal Pradesh, and New Delhi were accepted free of cost during a one-year trial. Referring pathologists submitted photomicrographs, videos, and requisition forms. A TP number was assigned after quality verification, and digital reports were generated within 24-48 hours.

Results and discussion
Between November 2023 and January 2025, 492 consultations were conducted, 75% (285) from private hospitals and 25% (95) from government institutions. Subspecialties included Ocular Pathology (117), Dermatopathology (77), Head and Neck Pathology (76), and others. Comprehensive diagnoses were provided in 90% (443) of cases, while 10% (49) required descriptive reports. Twelve cases initially rejected for poor image quality were resolved upon resubmission.

Conclusion
Telepathology transforms diagnostics by improving accuracy, accessibility, and turnaround times while enhancing remote education and clinical management. Its implementation at PGIMER demonstrates the potential for better healthcare outcomes through digital innovation.

Key words: Telepathology, Digital Diagnostics, Remote Pathology, Enhanced Patient Care , Diagnostic efficiency

P2 Deep Learning–Based Fixation Type Prediction for Quality Assurance in Digital Pathology

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Introduction

Accurate annotation of sample fixation type is critical in slide preparation for pathology laboratories, especially for retrospective research datasets. However, this manual process is prone to errors, impacting downstream analyses and diagnostic accuracy. Existing methods for verifying formalin-fixed, paraffin-embedded (FFPE), and frozen section (FS) fixation types typically require full-resolution whole-slide images (WSIs), limiting scalability for high-throughput quality control.

Material and methods

We propose a deep-learning approach to predict fixation types using only low-resolution thumbnails. The thumbnail is divided into 32 equally sized patches, which are processed independently to output the mean patch prediction. The model was trained on WSIs from the TUM Institute of Pathology (n=1,200, Leica GT450DX) and evaluated on a class-balanced subset of The Cancer Genome Atlas (TCGA, n=8,800, Leica AT2), as well as on class-balanced datasets from University Hospital Augsburg (UKA, n=695, Philips UFS) and University Hospital Regensburg (UKR, n=202, 3DHISTECH P1000).

Results and discussion

The model achieves an AUROC of 0.88 on TCGA, outperforming comparable pre-scan methods by 4.8%. It also achieves AUROCs of 0.72 on UKR and UKA slides, highlighting challenges related to scanner-induced domain shifts. Furthermore, the model processes each slide in 21 ms, 400× faster than existing high-magnification, full-resolution methods.

Conclusion

This approach provides an efficient solution for detecting labelling errors without relying on high-magnification scans, offering a valuable tool for quality control in high-throughput pathology workflows. Future work will improve and evaluate the model's generalisation to additional scanner types. Our findings suggest that this method can increase accuracy and efficiency in digital pathology workflows and may be extended to other slide annotation tasks.

Key words: Computational Pathology, Digital Pathology Workflow, Deep Learning, Automated Quality Control, Slide Annotation, Fixation Type

P3 Use of Information Technologies in Pathologists in Argentina: A Long Road

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Introduction

Pathology is a crucial medical specialty for the diagnosis of diseases. However, the adoption of digital technologies and information systems in pathology in Argentina faces significant inequalities and challenges, including isolated systems, lack of interoperability, and training barriers. This study evaluates the current state of the use of digital tools and proposes strategies to improve the efficiency and quality of pathological services.

Material and methods

A survey was designed in Google Forms with 26 questions distributed among pathologists members of the Argentine Society of Pathology. 93 responses were collected in July 2023, addressing topics such as software use, interoperability, quality control, and familiarity with digital pathology. Analysis included descriptive statistics and thematic coding for open-ended responses.

Results and discussion

92.5% of respondents use reporting software, but only 32.2% have interoperable systems. 84.3% lack internal traceability for samples, and 53.8% do not have direct access to patient clinical information. Furthermore, 68.2% consider that current systems do not reflect their practical needs, which highlights the lack of participatory design in technological solutions.

Conclusion

The identified barriers reflect the need to modernize information systems for pathology laboratories through the implementation of interoperable tools, continuous training and access to advanced technologies. These changes are essential to close the technological gap and ensure more accurate and efficient diagnoses.

Key words: Digital pathology, information technologies, interoperability

P4 Selecting High Throughput Scanners for Clinical Usage: A Multi-Center Institution Experience

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Introduction

The University Health Network (UHN) is a multicenter institution that serves a network of 29 hospitals. Our institution recently switched to a fully digital pathology practice for primary diagnosis, remote consultations and intraoperative diagnostics. During this intricate transition, the choice of an appropriate scanner was a critical step. However, this decision can be overcomplicated due to the complex technical language used by vendors and the limited understanding of scanner specifications which make it difficult to identify the most suitable scanner for the institution.

Material and methods

A special request for proposal (RFP) was created to compare different components of the scanning capabilities. Key factors assessed included scanning time (scanning speed), slide capacity (slides uploaded/batch), output image resolution (Microns/Pixel) and the ability for slide stacking. Additional factors including autoloading functionality and continuous loading ability were also considered and differentially scored.

Results and discussion

Our experience showed that scanner performance is dependent on speed, capacity and automation features such as tissue detection and autofocusing. Other important factors included redefining magnification by resolution (Microns/Pixel) and recognizing that 20x magnification is sufficient for most routine tasks. File size was also a critical component for long-term storage in multicenter institutions We also emphasized the importance of having open communication with vendors and thorough on-site validation of scanner performance was essential for a successful implementation.

Conclusion

In our institution, we opted for a fleet of multi-capacity scanners from various vendors, each tailored to specific applications and are fully compatible with the employed image management software and storage systems.

Key words: Whole Slide Imaging (WSI), Digital Pathology (DP), Quality Assurance (QA), University Health Network (UHN)

P5 Digital Pathology Implementation in A Multi-Site Hospital Network: The Devil is in the Details

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Introduction

University Health Network (UHN) is a Canadian multi-institutional hospital serving 29 satellite locations. Our journey to digital pathology implementation was a stepwise approach that began with remote intraoperative consultation, followed by digital pathology sign-out for remote locations and external consults, and culminating in a fully digital clinic implementation across all sites.

Material and methods

Our first step for implementation was to obtain executive leadership approval and to secure funding for the infrastructure and first five years of operations. The process focused on three components: scanners, image management software, and digital storage, with an emphasis on universally compatible systems validated through track record experience. A dedicated change management team led the project alongside pathologists, technical and IT support. Committees and working groups were established to support the transition, complemented by monthly pathologist discussion and ongoing delivery of educational material. Additionally, a customized validation protocol was developed using the guidelines set by the UK Royal College of Pathologists and the College of American Pathologists (CAP), to address the institution's needs.

Results and discussion

Our experience shows that digital pathology is a revolutionary, multi-step process that goes beyond instrument purchase, requiring modifications in workflow, QA measures and pathologist office set-up. Regular follow-up with feedback and evaluation is essential, as well as establishing key performance indicators early to ensures effective assessment before and after digitization.

Conclusion

The successful transition to digital pathology at the UHN highlights the importance of a well-structured, institution-wide approach. This process requires strategic planning and constant adaptability to ensure a successful implementation.

Key words: Whole Slide Imaging (WSI), Digital Pathology (DP), University Health Network (UHN), Digital Pathology Implementation

P6 Interpretable Machine Learning based Detection of Coeliac Disease

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Introduction

Coeliac disease, an autoimmune disorder affecting approximately 1% of the global population, is typically diagnosed on a duodenal biopsy. However, inter-pathologist agreement on coeliac disease diagnosis is only around 80%. Existing machine learning solutions designed to improve coeliac disease diagnosis often lack interpretability, which is essential for building trust and enabling widespread clinical adoption. We aim to develop an interpretable AI model capable of segmenting key histological structures in duodenal biopsies, generating explainable segmentation masks, estimating intraepithelial lymphocyte (IEL)-to-enterocyte and villus-to-crypt ratios, and diagnosing coeliac disease.

Material and methods

Semantic segmentation models were trained to identify villi, crypts, IELs, and enterocytes using 49 annotated 2048x2048 patches at 40x magnification. IEL-to-enterocyte and villus-to-crypt ratios were calculated from segmentation masks, and a logistic regression model was trained on 172 images to diagnose coeliac disease based on these ratios. Evaluation was performed on an independent test set of 613 duodenal biopsy scans from a separate NHS Trust.

Results and discussion

The villus-crypt segmentation model achieved a mean PR AUC of 80.5%, while the IEL-enterocyte model reached a PR AUC of 82%. The diagnostic model classified WSIs with 96% accuracy, 86% positive predictive value, and 98% negative predictive value on the independent test set.

Conclusion

Our interpretable AI models accurately segmented key histological structures and diagnosed coeliac disease in unseen WSIs, demonstrating strong generalization performance. These models provide pathologists with reliable IEL-to-enterocyte and villus-to-crypt ratio estimates, enhancing diagnostic accuracy. Interpretable AI solutions like ours are essential for fostering trust among healthcare professionals and patients, complementing existing black-box methodologies.

Key words: Semantic Segmentation, Coeliac Disease Diagnosis, Interpretable AI

P7 Strengthening Tumour-Infiltrating Lymphocyte Scoring in Sequential Breast Cancer Slides Using Region of Interest Registration

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Introduction
Tumour-infiltrating lymphocyte (TIL) scoring in breast cancer (BC), performed using Salgado's criteria, requires selecting a region of interest (ROI) on a haematoxylin and eosin (H&E)-stained BC slide. Scoring TILs on the same ROI across consecutive serial sections might help reduce tissue bias associated with scoring a single ROI on one slide. However, locating the same ROI across sections can be time-consuming.

Material and methods
A total of 104 BC samples were analysed, each with twelve consecutive H&E-stained whole slide images (WSIs). A pathologist manually annotated the same ROI on the first, sixth, and twelfth WSIs. This study evaluates three registration-based strategies: direct, intermediate, and serial to determine the optimal approach for identifying the most similar ROI on consecutive slides. The optimal registration strategy was selected based on geometric similarity to the pathologist's ROI on the twelfth slide and the number of registration failures. TIL scoring was performed on both manually and automatically registered ROIs using the optimal registration strategy, and statistical analysis assessed variability and agreement.

Results and discussion
The direct strategy achieved the fewest failures and the highest geometric similarity to manual ROIs on the twelfth slide. It required only a single registration step and had the lowest computational time compared to the other approaches. Strong agreement was observed between TIL scores on manually and automatically generated ROIs (ICC = 0.936).

Conclusion
The direct approach provides an efficient, reliable method for automating ROI selection across consecutive BC slides. This technique might be incorporated into digital pathology workflows to strength the TIL scoring on the same ROI across consecutive slides.

Key words: Tumour infiltrating lymphocyte, Whole slide image, Region of interest, Registration, Breast cancer

P8 Predicting the EPClin score in HER2-negative luminal breast cancer from Whole Slide Images by using transformer-based model

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Introduction

In Breast cancer, the EPClin score is a validated prognostic tool that integrates the molecular profile of tumors (EndoPredict) with clinical risk factors, such as tumor size (pT) and nodal status (pN), to provide a comprehensive risk assessment for recurrence in patients with early-stage, hormone receptor-positive, HER2-negative breast cancer. This work proposes a deep learning-based approach to predict the EPClin score combining the features from Hematoxylin, Eosin and Saffron-stained (HES) Whole Slide Images (WSIs) and risk factors (pT and pN), aiding in patient risk stratification for recurrence and treatment decisions.

Material and methods

A multi-branches transformer-based model was used to analyze the features from WSIs and clinical risk factors (pT and pN) for predicting the EPClin score of the HER2-negative breast cancer patients. The model was trained and validated on HES stained slides of 512 patients from multiple centers in 10 folds cross-validation. Then, the trained models were tested on an external cohort of 256 patients.

Results and discussion

The model achieved a mean AUC of 0.8243 (95% CI: 0.8187–0.8299) over 10-fold cross-validation, a mean AUC of 0.7927 (95% CI: 0.75 – 0.83) on the internal testing set. During the testing phase, the trained models were evaluated on an external testing cohort, where a mean AUC of 0.7414 (95% CI: 0.7394–0.7442) was obtained, demonstrating the model's generalizability.

Conclusion

The results show that HES-stained slides, combined with pT and pN status, contain valuable predictive information for estimating the EPClin score, which assesses the risk of recurrence in early-stage breast cancer patients and guides the need for adjuvant chemotherapy.

Key words: Breast cancer, EPClin score, Recurrence-free survival, Deep learning, Transformer

P9 Deep Learning in Digital Cytopathology: Evaluating Whole-Slide Images for Thyroid FNA Classification

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Introduction

Deep learning (DL) showed promising results for classifying cytological samples. We aimed to develop a DL-based framework on whole-slide images (WSIs) for the evaluation of thyroid fine-needle aspiration (FNA) samples.

Material and methods

After anonymization, 191 WSIs of thyroid FNA samples (benign: n=99, 51.8%; malignant: n=92, 48.2%) were used to develop weakly supervised (A) and supervised (B) models on a GARR Cloud virtual machine (NVIDIA A30 GPU, CUDA 12.3). Model A, a CNN-based approach using TensorFlow and Keras, classified WSIs with slide-level labels. After data augmentation, 223 WSIs were split into training (70%) and validation (30%) sets. Model B, built with the Xception DL framework, used annotated ROIs for training with Adamax optimization, binary cross-entropy loss, and three-fold cross-validation. Model performance was assessed using precision, recall, F1-score, PPV, and NPV.

Results and discussion

During training, Model A achieved a maximum accuracy of 67.0% over 30 epochs, with validation accuracy plateauing at 58.0%. Its predictive performance was limited (PPV of 46.8% and a NPV of 49.3%). In contrast, Model B demonstrated significantly superior performance, achieving 99.8% training accuracy after just 3 epochs and 83.3% validation accuracy. Its predictive metrics were significantly higher, with a PPV of 88.2% and an NPV of 80.0%.

Conclusion

These findings highlight the importance of annotated ROIs in training robust DL models for cytological evaluation. Further validation on larger datasets is necessary to assess clinical applicability and enhance generalizability. Our results support the integration of DL-based frameworks into digital pathology workflows to improve diagnostic accuracy in thyroid cytopathology.

Key words: Deep Learning, Thyroid Fine-Needle Aspiration, Whole-slide Imaging, Cytopathology, Convolutional Neural Networks, Digital Pathology

P10 Quantifying Aleatoric and Epistemic Model Uncertainty to Select Accurate Identifications of Lung Cancer

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Introduction

Pathologists can improve decision-making by comparing multiple models' uncertainty quantifications (UQs), categorized as aleatoric (caused by data randomness) and epistemic (caused by knowledge gaps in models), to identify accurate results. Previous works primarily entangle UQs and use them to avoid uncertain predictions. This study evaluates four UQs to find the most reliable output from multiple models and emphasizes the importance of disentangling them.

Material and methods

We focus on two NSCLCs from TCGA, LUAD and LUSC, using 953 WSIs for training and 100 for testing. We use multiple-instance learning with four feature extractors: ResNet50, ResNet101, and two recently released transformer-based foundational models, CONCH and UNI. Ten single-attention classifiers, trained with different seeds on the extracted features, generate outputs, and the lowest uncertainty prediction is selected. For UQ, we use two aleatoric, softmax entropy and maximum softmax, and two epistemic, Monte Carlo Dropout (MCD) entropy and MCD variance over 100 iterations.

Results and discussion

Models trained on CONCH and UNI features achieved high baseline accuracies (0.919±0.021, 0.916±0.012) and AUCs (0.988±0.001, 0.985±0.003), with MCD entropy yielding the best accuracy (0.960, 0.931) and similar AUCs (0.988). Softmax entropy and maximum softmax led to lower accuracy (0.920, 0.930) and similar AUCs. ResNet50 and ResNet101 achieved slightly lower baseline accuracies (0.853±0.012, 0.881±0.019) and AUCs (0.954±0.002, 0.963±0.006), and MCD entropy and variance improved their accuracies (0.921 for both) with AUCs up to 0.970.

Conclusion

Disentangling UQs highlighted the importance of epistemic UQs, as seen with MCD entropy and variance, which outperformed the aleatoric UQs. Overall, we generate actionable uncertainties that can help pathologists make informed decisions.

Key words: Deep learning, Model uncertainty, Lung cancer

P11 Triaging Cutaneous Melanocytic Lesions using Artificial Intelligence

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Introduction

Pathologists face a rising workload caused by a growing volume of cases and the need for more comprehensive diagnoses. We developed an artificial intelligence (AI) model for triaging cutaneous melanocytic lesions using whole slide images (WSIs) as input, with the goal of reducing workload and accelerating turnaround times.

Material and methods

The AI model was developed and evaluated using a retrospectively collected cohort from the University Medical Center Utrecht, the Netherlands. The dataset consisted of 52,202 WSIs from 27,167 unique specimens. Specimens with only common nevi were assigned to the low complexity category (86.6%) and specimens with any other melanocytic lesion subtype were assigned to the high complexity category (13.4%). The dataset was split at the patient level into a development set (80%) and test sets (20%). Predictive performance was measured using the area under the receiver operating characteristic curve (AUROC) and precision-recall curve (AUPRC). The effect of implementing AI-based triaging in the clinic was studied using a simulation experiment.

Results and discussion

The AI model reached an AUROC of 0.966 (95% confidence interval [CI], 0.960-0.972) and an AUPRC of 0.857 (95% CI, 0.836-0.877) on the primary test set. Compared to random case assignment as baseline, AI-based triaging prevented an average of 43.9 (95% CI, 36-55) initial examinations of high complexity cases by general pathologists for every 500 cases in the simulation experiment.

Conclusion

The AI model reached a strong predictive performance in distinguishing cutaneous melanocytic lesions of high complexity from low complexity ones. A substantial improvement in workflow efficiency due to AI-based triaging could be possible.

Key words: Dermatopathology, Melanocytic lesions, Artificial Intelligence, Triaging

P12 GigaPath Foundation Model For Lymphovascular Invasion Detection in Breast Cancer

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Introduction

Lymphovascular invasion (LVI) is a significant pathological feature in breast cancer, closely associated with an elevated risk of metastasis and poorer clinical outcomes. However, the manual detection of LVI remains a challenging task, often plagued by inter-observer variability. To address these challenges, this study investigates the potential of GigaPath, a state-of-the-art foundation model, for automating the detection of LVI in whole-slide images (WSIs) of breast cancer tissue.

Material and methods

We used a dataset comprising 91 Hematoxylin and Eosin (H&E)-stained breast cancer slides with expert annotations. For training, we first tessellate the input WSI and extract their features using the tile-level encoder of GigaPath. Subsequently, we fine-tune the slide-level encoder to perform binary classification, predicting the label of each tile as either LVI-positive or LVI-negative. Given the limited dataset size, we applied slide-wise color augmentation techniques to mitigate the risk of overfitting and enhance model generalization.

Results and discussion

The GigaPath model demonstrated promising performance, achieving 77% sensitivity at the slide level with an average of 7.19 false positives per slide (FPavg). The primary advantage of using GigaPath lies in its ability to generate predictions for all patches within a WSI simultaneously, as opposed to the traditional sliding window approach that requires sequential, patch-by-patch inference. This not only improves computational efficiency but also facilitates more comprehensive spatial context integration.

Conclusion

Our results highlight the potential of GigaPath, paving the way for enhanced diagnostic accuracy and reproducibility in detecting LVI. However, challenges such as false positives caused by tissue heterogeneity remain significant obstacles.

Key words: Lymphovascular invasion, Breast cancer, Whole-slide images, GigaPath

P13 AI-based Classification of Laryngeal Lesions and Lymphocytic Activity in Dysplasia

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Introduction

Laryngeal Dysplasia (LD) is a premalignant condition graded based on cytological/architectural features present in the epithelium of H&E-stained histology images. However, LD grading is highly variable and not always predictive of malignant transformation. Additionally, distinguishing LD from other laryngeal lesions, such as squamous cell carcinoma (SCC) or benign polyps, remains challenging. We propose an Artificial intelligence (AI) model to classify laryngeal lesions and highlight potential diagnostic features of LD.

Material and methods

We used 109 H&E-stained whole slide images (WSIs) from 82 cases (UHCW and Dundee) scanned at 40× magnification (0.12 microns-per-pixel, mpp; Pannoramic 250). The dataset comprised 50 LD (65 WSIs), 20 SCC (28 WSIs), and 12 benign polyp (16 WSIs) cases. A H-optimus-0 model extracted patch-level (224×224 pixels) features (0.5 mpp), and a TransMIL aggregator predicted slide-level lesion type. We derived intra-epithelial lymphocyte (IEL) and peri-epithelial lymphocyte (PEL) scores in LD cases using HoVer-NeXt nuclear and HoVer-Net+ epithelium segmentations. Scores were compared across WHO grades using Mann-Whitney tests.

Results and discussion

In Monte Carlo cross-validation (k=10), the model achieved AUROC=0.85 and AUPRC=0.73 for lesion classification. IEL and PEL scores were significantly higher in severe LD cases compared to moderate (IEL: rrb=0.09, p=0.02; PEL: rrb=0.36, p=0.02) and mild LD (IEL: rrb=0.09, p=0.01; PEL: rrb=0.36, p=0.003), linking increased lymphocyte presence/activity to higher grade.

Conclusion

We present an AI model for classifying laryngeal lesions and quantifying lymphocytic activity in LD. Our findings suggest AI's diagnostic potential in identifying LD while highlighting PEL/IEL density as a potential biomarker, not previously linked to grade. Further validation in multi-centric datasets is required.

Key words: Laryngeal Dysplasia, Early Detection, Prognostication, Classification, Malignant Transformation, Dysplasia

P14 Immunohistochemistry to Hematoxylin and Eosin Transfer Learning for Artificial Intelligence-Guided Tumor and Immune Cell Recognition Model Development

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Introduction

High-quality image annotations of large datasets for artificial intelligence (AI) development in pathology are crucial. However, this task requires extensive expert supervision, making it resource-intensive, subjective, and limiting scalability. Here, we present an automated Cross-Modality Annotation method based on Immunohistochemistry (IHC)-to-hematoxylin and eosin (H&E) transfer learning for tumor (TC) and immune cell (IC) segmentation.

Material and methods

A single slide was iteratively stained for H&E, CD3, and Pan-cytokeratin (Ker) using an in-house Next-Generation IHC (NGI) protocol. After digitalization, stainings were aligned and annotated using threshold-based segmentation for TC (Ker+) and IC (CD3+), training AI models (DeepLabv3+ for TC, U-Net for IC) on H&E slides from colorectal (CRC), breast (BC), and lung (LC) cancer datasets. Model performance was compared against manual pathologist (for TC) and image analysis (for IC) quantifications.

Results and discussion

The training set included 39 CRC, 46 BC, and 74 LC whole slide images (WSI) and 162 CRC, 118 BC, and 41 LC tissue microarray (TMA) cores. The test set included 159 CRC, 144 BC, and 32 LC WSI. AI-based CRC (0.051 loss, 124K iterations), BC (0.060 loss, 354K iterations), and LC (0.108 loss, 72K iterations) tumor recognition models correlated strongly with manual evaluations (CRC: R^2=0.9071 training, 0.8637 test; BC: R^2=0.9453 training, 0.9255 test; LC: R^2=0.9081 training, 0.845 test). AI-based IC detection achieved R^2=0.8499 in all TMA cores and 0.815 in an external 22 WSI BC, CRC and LC dataset.

Conclusion

IHC-to-H&E AI transfer learning significantly reduces manual annotation efforts, improves reproducibility and efficiency in digital pathology workflows, ultimately contributing to improved AI model development.

Key words: Digital Pathology, Artificial Intelligence, Transfer Learning, Tumor and Immune Cell Detection, Deep Learning, Image Analysis

P15 PathoPainter: Enhancing Tumor Segmentation in Histopathology with Inpainting-Based Augmentation

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Introduction

Tumor segmentation is a vital task in histopathology, yet training effective models needs pixel-wise annotations on whole slide images (WSIs). This process is labor-intensive, requiring expert knowledge to annotate gigapixel-scale WSIs with intricate structures. As a result, labeled datasets are often sparse and limited. Although image synthesis has the potential to expand data scale, it often faces challenges in ensuring accuracy between generated images and their corresponding masks.

Material and methods

To address this, we propose PathoPainter, a novel framework that reframes the image-mask generation problem as a tumor inpainting task. By preserving the image background and conditioning generation on tumor embeddings, PathoPainter ensures alignment between synthetic images and corresponding masks. To enhance dataset diversity, we introduce a conditional sampling mechanism that selects embeddings from intra-category distributions, maintaining biological plausibility. Additionally, we employ a simple filtering strategy to exclude synthetic regions with low confidence, ensuring data quality.

Results and discussion

Our method was evaluated across diverse datasets, including DCIS, CATCH, and CAMELYON16, under various training data scales. Models trained with PathoPainter-generated data showed notable improvements: segmentation performance increased from 55.12% to 58.48% on DCIS, 79.17% to 80.29% on CATCH, and 69.71% to 72.74% on CAMELYON16 with limited slides.

Conclusion

In conclusion, PathoPainter provides an effective solution for addressing the challenges of limited annotations in tumor segmentation, leveraging biologically plausible synthetic data to significantly enhance segmentation model performance.

Key words: Data augmentation, Tumor segmentation, Diffusion models

P16 Artificial Intelligence Prediction of Medulloblastoma Recurrence from Pathological Images

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Introduction

Medulloblastoma is one of the most common pediatric brain tumors, with known prognostic factors including age, histological subtype, and molecular classification. To explore additional prognostic factors, we examined whether artificial intelligence (AI) could predict the likelihood of recurrence using pathological digital images.

Material and methods

A total of 175 cases of pediatric medulloblastoma, 537 slides, resected between 2000 and 2022 from 5 Japanese hospitals were used. Patient background was M/F=1.3, mean age 6 years, recurrence rate 26%, and mortality rate 22%. Over 80% of the patients had the classic histological subtype, and 45% were molecularly classified as Group 4. Forty-five cases were randomly selected as AI model test cases, and the remaining 130 cases were used for training, based on the time to recurrence and follow-up period. Two models of the support vector machine and random forest (RF) were constructed from nuclear features and tested to predict histological subtypes and molecular classifications. Additionally, a convolutional neural network model was trained to learn tissue structure, which was then constructed and combined with the RF model to create a prognostic model.

Results and discussion

The machine learning model accuracy was approximately 85% for histological type and approximately 86% for molecular classification. For the prognostic model, the area under the curve was around 0.8, and the accuracy for the likelihood of recurrence at 3 years postoperatively was around 90%. A well-defined risk classification of high, medium, and low was achieved.

Conclusion

We created an AI model that predicted the recurrence risk with high probability from medulloblastoma pathological images.

Key words: Artificial intelligence, Medulloblastoma, Prognosis, Machine learning, Deep learning

P17 Spatial Transcriptomics and Digital Pathology-Based Biomarker Discovery in Anaplastic Thyroid Carcinoma Progression

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Introduction

The progression from papillary thyroid carcinoma (PTC) to anaplastic thyroid carcinoma (ATC) is a poorly understood process, and identifying molecular markers associated with this transformation is critical for improving diagnosis and treatment. This study aimed to discover spatially resolved biomarkers of ATC progression using spatial transcriptomics, followed by protein-level validation

Material and methods

Formalin-fixed, paraffin-embedded (FFPE) tissue samples containing PTC and ATC components were analyzed using the GeoMx® Digital Spatial Profiler (DSP) platform to obtain high-resolution spatial transcriptomic data. Regions of interest (ROIs) were carefully selected across different histologic patterns to profile differentially expressed genes. Following bioinformatic analysis, candidate biomarkers were validated at the protein level using tissue microarrays (TMAs) and immunohistochemistry (IHC). Protein expression was quantified using QuPath software, and H-scores were calculated to compare expression levels across various thyroid tumor types.

Results and discussion

Several candidate biomarkers were identified that distinguish ATC from PTC and other thyroid tumors. Functional enrichment analysis revealed their involvement in epithelial-mesenchymal transition, extracellular matrix remodeling, tumor invasion, and key ATC progression pathways. IHC validation confirmed the differential expression of these biomarkers, and H-score analysis showed statistically significant differences in expression levels across tumor subtypes. Notably, their expression patterns were independent of BRAF V600E mutation status, suggesting their potential as robust diagnostic markers.

Conclusion

This study demonstrates the power of spatial transcriptomics combined with TMA-based IHC and quantitative image analysis using QuPath to identify biomarkers associated with ATC progression. These findings provide a methodological framework for discovering spatially resolved molecular markers in aggressive thyroid cancers.

Key words: Spatial transcriptomics, Tumor progression, Anaplastic thyroid carcinoma, Papillary thyroid carcinoma, QuPath, H-score

P18 Comparison of artificial intelligence-assissted and manual quantification of PDL1 expression in non-small cell lung cancer

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Introduction

Assessment of PDL1 tumor proportion score (TPS) expression is a critical step in non-small cell carcinoma (NSCLC) patient management, helping to identify patients likely to benefit from immunotherapy. In this study, a new developed artificial intelligence (AI)-assisted scoring model was tested for PDL1 (SP263) expression in NSCLC.

Material and methods

PD-L1 expression was evaluated using TPS categorized into three levels: negative (< 1%), low (1–49%), and high (≥ 50%). To evaluate the performance of the model, 140, 135, and 205 whole slide images (WSI) of NSCLC cases were used as training, validation, and test datasets, respectively. TPS reading results from five experienced pathologists, four inexperienced pathologists and the model were analyzed on 205 PD-L1 stained WSIs. The standard for TPS was derived from the review of three expert pathologists.

Results and discussion

The model correlated strongly with the TPS standard and was comparable with the results of the experienced pathologists. In contrast, the results of inexperienced pathologists was not correlated with the TPS standard. The model performed better than the inexperienced pathologists and was comparable to experienced pathologists in both negative and low TPS groups. However, the AI model showed an unsatisfactory performance in the high TPS groups, because the false positive ratio is higher in many cases in the model. The false positive is made from misjudgement as positive about the expression in macrophage, not tumor cells

Conclusion

This AI model is believed to help pathologists determine the scoring of PDL1 expression, especially in negative and low TPS case.

Key words: Non-small cell lung cancer, PDL1, artificial intelligence

P19 Wavelet Transform and U-Net Framework for Spectral Decomposition and Noise Reduction in In Vivo Magnetic Resonance Spectroscopy

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Introduction

Magnetic Resonance Spectroscopy (MRS) provides valuable biochemical insights but is often limited by low signal-to-noise ratios (SNR) and spectral overlap. Effective spectral decomposition is crucial for improving metabolite quantification in clinical and research applications.

Material and methods

We applied a wavelet transform and U-Net deep learning framework to in-vivo MRS data. The model was trained exclusively on synthetic spectra, designed to mimic in-vivo acquisition conditions by incorporating spectral broadening, phase shifts, noise, and baseline variations. We validated its performance on multi-subject in-vivo datasets, assessing its ability to separate metabolite peaks, noise, and macromolecular components.

Results and discussion

The framework effectively decomposed in vivo MRS spectra, achieving improved SNR and accurate separation of overlapping metabolite peaks. The model successfully generalized from synthetic to in vivo data, reliably identifying key metabolites such as NAA, Cr, Glu, and macromolecule while reducing residual artifacts. Additionally, it demonstrated the ability to separate residual water and lipid signals, further enhancing spectral clarity. FSL-MRS fitting results indicate an increase in NAAG and Gln concentrations after denoising, while Glu levels decrease, highlighting the framework's capability in distinguishing overlapping signals.

Conclusion

This study validates the applicability of synthetic training-based spectral decomposition method for in-vivo MRS data. The results highlight the potential of wavelet transform and deep learning approaches for robust spectral analysis. Future work will focus on extending this approach to other nuclei, such as 31P MRS, and optimizing training strategies for improved generalization across subjects.

Key words: Magnetic Resonance Spectroscopy, Wavelet Transform, U-Net, Spectral Decomposition, Deep Learning, Noise Reduction

P20 AI caption generation model for digital pathology in endoscopic histopathology

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Introduction
Gastric adenocarcinoma is a major cause of morbidity and mortality worldwide. This study aims to develop a model to generate descriptive diagnostic reports for pathologic images of endoscopic biopsy of gastric cancer patients, encompassing histologic type and grade.

Material and methods
For training of the model, publicly available PatchGastricADC22 dataset was utilized. For validation of the model, Gil Medical Center dataset was utilized. The Multi-Instance Self-Attention Captioning model (MIAC) was utilized for caption generation. MIAC includes two primary components: an encoder and a decoder. The encoder is responsible for extracting features from patch images, while the decoder uses these features to generate diagnostic caption. The model's performance was evaluated using several standard natural language processing metrics to compare the generated captions with the reference captions.

Results and discussion
With 50 training patches per WSI, MIAC model recorded a BLEU@4 score of 0.617, ROUGE-L score of 0.731, METEOR score of 0.506, and CIDEr score of 5.588. Using validation dataset, MIAC model achieved a BLEU@4 score of 0.375 , a ROUGE-L score of 0.577 , a METEOR score of 0.336, and a CIDEr score of 4.382 at 50 patches per WSI.

Conclusion
The MIAC model demonstrated its utility in generating diagnostic captions with high accuracy in endoscopic histopathology.

Key words: Digital Pathology, Captioning Model, Multi-Instance Learning, Endoscopic histopathology

P21 Broad implementation of AI for lymph node assessment: insights from a head-to-head comparison of two applications

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Introduction

Lymph node (LN) assessment is crucial for guiding treatment in breast cancer (BC), head and neck cancer (HNC), and melanoma, but it is labor-intensive and costly. AI-assistance may improve efficiency. This study evaluates the performance of two CE-IVD-certified AI-applications, DeepPath-LYDIA© (DP) and the Metastasis-Detection-App by Visiopharm© (VP), both inside (IIU) and outside intended use (OIU).

Material and methods

Both apps were tested in positive LNs of ~100 patients for HNC (OIU) and melanoma (DP: IIU, VP: OIU), and for BC (IIU) in the 59 positive LN-samples from the CONFIDENT-B trial. Sensitivity and false alerts (FAs) were assessed.

Results and discussion

Both AI-tools detected all macro-metastases across tumor types. For BC, all 23 detectable micro-metastases on HE were identified, while ITC-detection was only moderate (8/18). In HNC, DP achieved 100% sensitivity for all metastases, while VP missed 1/22 micro-metastases and 2/3 ITC-cases. In melanoma, DP missed 1/24 micro-metastasis, while VP missed three. ITC detection remained suboptimal for both (DP: 50.0%, VP: 62.5%). FA rates were comparable in HNC/melanoma (8–9 per slide), but VP showed higher FAs in BC, particularly post-neoadjuvant therapy (17.4 vs. 6.8 for DP), which can mainly be explained by the method of annotation (more detailed versus broad outlines) and subsequent counting.

Conclusion

Two commercially available AI-tools performed similarly, both IIU and OUI, in detecting LN macro- and micro-metastases across tumor types, with moderate ITC detection. A single AI-solution for multiple indications could enhance efficiency and cost-effectiveness, thereby positively impacting the business case for individual pathology laboratories.

Key words: AI-assistance, breast cancer, head and neck cancer, melanoma, lymph node metastases, clinical implementation

P22 Enhancing Medical Education through Digital Pathology: Development of Interactive e-Learning Modules under the National Medical College Network

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Introduction

The National Medical College Network, with contributions from the e-Health division and Regional Resource Centres (RRCs), has transformed undergraduate medical education through its Learning Management Information System (LMIS). By integrating digital pathology tools, the platform enhances both conceptual learning and clinical application. Since January 2023, RRC North, PGIMER, Chandigarh, has played a key role in developing high-quality pathology e-modules aligned with the NMCN UG curriculum. These modules incorporate virtual microscopy, case-based discussions, and multimedia-driven learning aids to bridge the gap between theory and practice.

Material and methods

Hosted on the SAKSHAM platform, LMIS employs a robust database management system for seamless content delivery and access. Modules follow a structured format, including Introduction, Specific Learning Objectives, Course Material, Summary, and References. HD video production tools (OBS, Microsoft 360, Adobe Premiere Pro) are utilised by content developers and network administrators. Embedded data analytics track student engagement and feedback, enabling adaptive learning pathways.

Results and discussion

Pathology modules covering key topics such as Rheumatic Heart Disease, Aneurysms and Immunopathology have been developed, forming part of a broader repository of 100+ e-modules. The integration of digital pathology has enhanced student engagement through real-time histopathological interpretations and interactive clinical correlations provided by specialised faculty.

Conclusion

The structured implementation of pathology-based e-modules within NMCN highlights the feasibility of personalized learning, virtual simulations and open educational resources in modernising medical education. Inter-institutional collaborations ensure consistency and accuracy through resource sharing and expert validation. As LMIS evolves, it will continue integrating emerging technologies to deepen the understanding of pathology and other disciplines.

Key words: Digital Pathology, Virtual Microscopy, Medical Education, Interactive Modules, Personalized Learning, National Medical College Network

P23 Systematic review of image-based artificial intelligence algorithms for molecular diagnostics in prostate cancer pathology

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Introduction
Guidelines recommend molecular diagnostics for homologous repair (HR) and mismatch repair (MMR) deficiencies in metastatic prostate cancer, as they are targetable by PARP- (poly ADP-ribose polymerase) or immune checkpoint inhibition. Other molecular aberrations are not tested for in clinical practice. Molecular diagnostics are rarely used in prostate cancer as it is complex and expensive, especially since many patients must be tested to identify the few with molecular aberrations. To address these limitations, image-based artificial intelligence (AI) algorithms have been developed to predict molecular aberrations from hematoxylin and eosin slides. These algorithms recognize histologic patterns beyond the pathologist's visual detection. This review assesses the advancements of image-based AI algorithms predicting molecular diagnostics in prostate cancer pathology and their potential in clinical practice.

Material and methods
A search identified 4121 articles, screened by two reviewers. In total, 20 articles were selected and assessed using the QUADAS-2 criteria.

Results and discussion
Nine algorithms, focusing on specific molecular aberrations in prostate cancer, reached a mean AUC of 0.78 (range 0.67 – 0.91). These specific algorithms generally reached higher predictive performance than those focusing on multiple aberrations. Due to the lack of molecularly tested image data, most studies (17/20) used The Cancer Genome Atlas, and only five performed external validation.

Conclusion
Our review suggests that AI could serve as a prescreening molecular diagnostic tool, particularly with the recent shift towards clinically more relevant molecular aberrations (HR, MMR). Nonetheless, the AI algorithms remain in the development stage due to the limited availability of molecularly tested image data needed for proper external validation.

Key words: Prostate cancer, Molecular diagnostics, Pathology, Artificial intelligence algorithms, Systematic review

P24 Leveraging AI in Digital Pathology: Supporting Pathologists in Telepathology-Driven Diagnostics Workflows

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Introduction

In the evolving landscape of eHealth, the effective exchange of digital pathology images is becoming increasingly vital. As diagnostic complexity grows, artificial intelligence (AI) has emerged as a transformative tool, offering advanced capabilities for helping physicians analyze digital slides, detect anomalies, and triage cases with exceptional precision. These advancements are particularly critical in addressing situations where specialized anatomic pathologists may not be readily available, such as in downturn conditions, remote or under-resourced medical facilities.

Material and methods

The proposed framework combines well-established interoperability standards for reliable and secure medical imaging sharing and reporting, with the query of digital pathology AI image analysis technologies made available remotely and accessible through standard transactions. IHE profiles, including XRR, XDS-I.b and DICOM Pathology Data Model were utilized to streamline the exchange and reporting of digital pathology images. Additionally, the IHE Radiology SWF profile was integrated to optimize processes such as registration, scheduling, and image acquisition.

Results and discussion

The approach creates a robust framework for exchanging digital pathology slides in telemedicine scenarios, emphasizing interoperability in procurement strategies, integrating AI in the process as a highly available and versatile third party support actor.

Conclusion

By utilizing well-established IHE profiles and querying by sharing images with remote AI support tools, this model minimizes risks while promoting standardized image sharing and reporting in digital pathology in different conditions. These advancements make it feasible to address current limitations, enhancing diagnostic workflows and paving the way for widespread implementation in telemedicine and beyond. The time is right to embrace this transformative step.

Key words: interoperability , workflow , ai, telepathology

P25 Macrophage Scoring Algorithm with A Semi-Supervised Deep Learning Framework for Efficient Segmentation with Limited Labelled Data

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Introduction
Macrophages play a crucial role in the innate immune system and are traditionally identified by detecting specific cell surface markers. However, cell detection requires skilled experts to manually trace delineations within gigapixel images, which is both time-consuming and labour-intensive. Deep learning has shown great potential in automating cell detection, offering a promising alternative. However, these models require extensive labelled datasets, which can be costly and resource-intensive. This limitation makes it challenging to fully harness deep learning for real-world clinical applications.

Material and methods
In this study, we propose a semi-supervised deep learning approach to automate the segmentation and detection of the CD68 macrophage marker using a limited amount of labelled data. The proposed method follows a two-stage scheme. In the first stage, a model pre-trained on H&E images from the CoNIC dataset is fine-tuned to learn the visual representations of our multiplexed images. In the second stage, a convolutional model is integrated with consistency regularisation and a self-training technique. The dataset includes 530 samples, and a pathologist assigned a score at the whole slide level based on the number of CD68-positive cells. Small visual fields from 10 of these images were manually annotated for CD68 cells for training the algorithm.

Results and discussion
The results were evaluated at the WSI-level and a correlation of 0.79 between the pathologist's score and the number of detected cells was achieved. Additionally, the method outperformed the fine-tuned model ($p < 0.005$).

Conclusion
The results highlight the proposed method's potential as an efficient tool for accurate cell marker detection with reduced reliance on expert annotations.

Key words: Semi-Supervised Deep Learning, Macrophage Segmentation, Cell Marker Detection, Automated Pathology Analysis

P26 Applying deep learning models to cytospin images from intraocular biopsies of Choroidal Melanoma and Metastatic carcinomas to the choroid.

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Introduction

Metastastic carcinomas to the choroid (MCa) can be difficult to differentiate from primary Choroidal Melanoma (CM) through clinical images alone. Some specialist centres perform intraocular biopsies to provide a definitive cytological diagnosis. Artificial Intelligence has yet to be extensively applied to cytology. Our aim was to test the validity of deep learning (DL) models, applied to both segmented and non-segmented cytospin whole slide images (WSIs) of MCa and CM.

Material and methods

A total of 96 patients' May-Grunwald Giemsa (MGG)-stained slides from 38 MCa and 54 CM were obtained from the Liverpool Ocular Oncology Biobank. WSIs were split evenly into 9 smaller tiles increasing image number to 377 for MCa and 486 for CM; tiles with out-of-focus tumour cells or ones without were removed. Classification was performed using five different model architectures; both segmented and non-segmented images were trialed. Cell segmentation was performed using Cellpose's cyto3 model. Per image and patient accuracy was calculated alongside sensitivity and specificity for five different train-, test- and validation splits.

Results and discussion

ResNet50 performed the best in all categories for non-segmented images with Efficientnet-b0 being best overall for segmented images. Non-segmented images performed better on average than segmented in all categories, for all models with ResNet50 producing an average patient accuracy of 92% over the five splits.

Conclusion

DL classification models can accurately differentiate between MCa and CM on cytospin images. Segmentation did not increase the accuracy of the models. External validation is required. This model could be applied to aid cytology diagnostics.

Key words: Choroidal Melanoma, Deep Learning, AI, Cytospin, Segmentation, Metastasis

P27 Understanding Immunotherapy Resistance Mechanisms in Urothelial Carcinoma Immune Microenvironment Phenotypes

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Introduction

Muscle-invasive bladder cancer (MIBC) and metastatic urothelial carcinoma (mUC) are aggressive cancers that still have poor prognosis. Although outcomes have improved with immune checkpoint inhibitors (ICIs) and antibody-drug conjugates such as enfortumab vedotin, problems with efficacy and resistance remain persistent. Our previous research has identified spatially structured tumor immune microenvironment (TIME) phenotypes in mUC and MIBC, emphasizing their influence on survival and resistance to ICIs.

Material and methods

To characterize TIME phenotypes, we used spatial single-cell and transcriptomic analysis, employing 10x Genomics Xenium In Situ, 10x Visium Spatial, and Nanostring CosMx SMI for high-resolution spatial profiling. DESeq2, Seurat, SingleR, and Monocle3 were used for analyzing gene expression and cell identity for clustering, differential expression, cell-type identification, and trajectory analysis. Spatial tissue analysis resolved transcriptomic patterns and niche interactions. The study included N=16 tumor samples from patients with MIBC/mUC with different immunotherapy responses.

Results and discussion

Our work has established four key urothelial carcinoma immune phenotypes: Uninflamed (UI) with minimal immune infiltration, Inflamed Low (INFlow) with low adaptive immunity, Inflamed High Cytotoxic (INFhi/cyt) with abundant T-/B-cells and low exhaustion, and Inflamed High Evasion (INFhi/ev) with T-cell presence, B-cell depletion, and immune exhaustion. These phenotypes orchestrate survival outcomes following cystectomy and under immunotherapy. In particular, INFhi/ev tumors featured marked immune evasion and exhaustion, linking them to poor prognosis.

Conclusion

Spatially resolving TIME phenotypes promotes understanding of immunotherapy resistance and prognosis. Then, we could use our findings to improve immunotherapy and antibody drug conjugate treatment outcomes. Finally, immunophenotypes could be extrapolated to other cancer entities, thus broadening their utility in cancer research.

Key words: Metastatic urothelial carcinoma (mUC), Muscle-invasive Bladder Cancer (MIBC), Tumor immune microenvironment (TIME) phenotypes, Inflamed Low (INFlow), Inflamed High Evasion (INFhi/ev), Inflamed High Cytotoxic (INFhi/cyt)

P28 Computer-aided diagnostics helps to accurately determine different expression levels of claudin-18.2 in gastric cancer

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Introduction
Determination of claudin-18.2 expression by immunohistochemistry (IHC) is prerequisite for targeted treatment of gastric cancers (GC) with zolbetuximab. Precise assessment of IHC expression categories, however, may be challenging and prone to interobserver variability. Computer-aided diagnosis has a high potential of improving diagnostic accuracy and reproducibility. We established a computer-aided analysis tool for claudin-18.2 positivity scoring.

Material and methods
Analysis steps included the identification of tumour tissue on haematoxylin-3,3'-diaminobenzidine-stained tissue microarray (TMA) slides, cell segmentation, and membranous staining intensity estimation of claudin-18.2 (clone 43-14A). We analysed 2248 cores from 417 primary resected GC with detailed pathological data available.

Results and discussion
In 51.6% (1159/2248) of TMA cores, no stained tumour cells were detected. Among cases with claudin-18.2 expression, predominantly 1+ and 2+ cells, and a minority of 3+ stained cells were found, and 2+ to 3+ staining was unevenly distributed. Utilizing the SPOTLIGHT claudin-18.2 positivity threshold we identified 12% (187/1555) positive cores corresponding to 2.5% (9/365) positive cases. Lower staining intensities in tumour centre cores point to intratumoural heterogeneity.

Conclusion
Computer-aided diagnostics helps to accurately measure claudin-18.2 expression levels, allowing to precisely determine claudin-18.2 status in GC patients. Previously uncaptured categorization of staining intensities may enhance the understanding of claudin-18.2 threshold for patient stratification.

Key words: digital pathology, computer-aided diagnostics, claudin-18.2 assessment, gastric cancer

P29 Artificial Intelligence for Autonomous Detection of Lymph Node Metastasis in Prostate Cancer

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Introduction

Lymph node metastasis (LNM) is associated with a higher risk of prostate cancer (PCa)-related death, and poor prognosis, and requires modification of the treatment plan. Manual assessment of LNs on glass slides is a time-consuming task, which is prone to error and observer variability. In this study, we present a deep learning-based algorithm for the automated detection of LNM of PCa on whole-slide imaging (WSI).

Material and methods

Our dataset consists of 378 WSIs of pelvic LNM, including 59 positive and 319 negative cases. Small patches (328 cases) were extracted from training slides, and both data augmentation and under-sampling techniques were used to balance the training samples. A vision transformer was then trained using a weakly supervised learning framework, and slides with incomplete labeling were used to fine-tune the pre-trained Virchow foundation model. A hard negative mining technique was applied to identify and remove false positives from the predictions.

Results and discussion

We developed an algorithm for detecting LNM in prostate cancer. The proposed method was tested using 50 WSI including 15 positive and 35 negative cases. The proposed method achieved sensitivity and specificity of 100% and 77% at the slide level on the test cohort. The average number of false positives was 4 per slide.

Conclusion

The results of our study demonstrate that automated detection of LNM of PCa is feasible and that AI can play a significant role in this task by decreasing time consumption and providing more accuracy in detection. A more rigorous evaluation of the proposed method is the direction of our future study.

Key words: Lymph node metastasis, Prostate cancer, Deep learning, Computational pathology, Foundation model

P30 Scoring the unseen: A smarter way to evaluate clustering in digital pathology

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Introduction

Clustering is widely used in histopathology to analyse tissue architecture, but evaluating its performance remains challenging, especially in heterogeneous samples. Rapid latent space assessment is crucial for selecting foundation models in machine learning. Therefore, we introduce a Normalized Weighted Composite Score (WCS) to quantitatively assess clustering effectiveness in histopathology patches.

Material and methods

Our approach combines multiple criteria—spatial coherence, morphological consistency, and cluster compactness—into a single composite score. We apply this framework to breast tissue histopathology images. To validate our method, we conducted a qualitative visual assessment using our DimReduce software [Wilkie, P. Pathology Visions, 2024]. By benchmarking various clustering algorithms, we demonstrate that our scoring equation offers a robust and interpretable measure of clustering quality.

Results and discussion

Using WCS, we achieved a 33.65% improvement in selecting the optimal feature extractor across 20 combinations of foundation models and clustering methods on the target datasets [Rakovitch, E. Breast Cancer Research and Treatment, 2015; Martel, A.L. The Cancer Imaging Archive, 2019]. By analyzing latent space embeddings, we identified the model with the highest WCS value, ensuring compact clusters with preserved morphological consistency. WCS allows adaptive weighting to accommodate different dataset characteristics. For example, increasing morphological weighting by 10% alters cluster rankings, demonstrating its ability to prioritize biologically relevant features. This flexibility makes WCS a more comprehensive evaluation metric than traditional scores, which assess only isolated aspects of clustering quality.

Conclusion

WCS enhances objective clustering comparisons, improving the reliability of automated tissue analysis in digital pathology. It accelerates foundation model selection by identifying the most suitable latent space for a downstream dataset.

Key words: Clustering, Foundation model selection, Latent space, Feature Extraction, Clustering quality

P31 Leveraging FHIR and DICOM for Interoperable Digital Pathology and Reporting in Nonalcoholic Steatohepatitis

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Introduction

The adoption of electronic medical records (EMRs) has transformed healthcare data management, enabling efficient storage, retrieval, and analysis in digital pathology. However, data heterogeneity and the lack of interoperability among EMR systems remain major obstacles to seamless data integration and utilization.

Material and methods

We developed a research platform utilizing open standards, including Fast Healthcare Interoperability Resources (FHIR) and Digital Imaging and Communications in Medicine (DICOM), to manage pathological reports and whole slide images for non-alcoholic steatohepatitis (NASH). Open-source tools such as Raccoon, Mainecoon, and HAPI FHIR were integrated for efficient data management and visualization.

Results and discussion

This study provides a comprehensive guide for healthcare institutions to facilitate data collection and convert pathology reports and WSIs into the FHIR and DICOM formats, respectively. A total of 174 NASH pathology reports were collected and analyzed. Text extraction was performed from the section of pathological diagnosis, gross findings, and microscopic findings in a pathology report. For microscopic findings, text regular expressions were applied to extract various fatty liver assessment scoring methods, such as Microinflammatory Grading and the METAVIR Fibrosis Score, which were then converted into FHIR resources based on the designed FHIR Implementation Guide (IG).

Conclusion

We successfully integrated the NASH pathology report and DICOM WSI addressing key interoperability challenges at National Cheng Kung University Hospital providing crucial technical support for advancing digital pathology.

Key words: FHIR, DICOM, interoperability, non-alcoholic steatohepatitis

P32 Ensemble Deep Learning Model to Predict Lymphovascular Invasion in Gastric Cancer

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Introduction

Lymphovascular invasion (LVI) is one of the most important prognostic factors in gastric cancer as it indicates a higher likelihood of lymph node metastasis and poorer overall outcome for the patient. Despite its importance, the detection of LVI(+) in histopathology specimens of gastric cancer can be a challenging task for pathologists as invasion can be subtle and difficult to discern. In this study, we propose a deep learning-based LVI(+) detection method using H&E-stained whole-slide images.

Material and methods

A deep learning model, specifically the ConViT model, was employed for detecting LVI(+) in gastric cancer. The performance of the ConViT model was compared with that of the YOLOX model using AUROC and AUPRC as metrics. Additionally, an ensemble model was created by weighted averaging of the patch-level confidence scores to further enhance the detection performance.

Results and discussion

The ConViT model demonstrated the best performance with AUROC of 0.9796 and AUPRC of 0.9648 among the classification models. The YOLOX model showed slightly lower performance compared to the ConViT model (AUROC: -0.0094; AUPRC: -0.0225). The ensemble model achieved the highest scores with AUROC of 0.9880, AUPRC of 0.9769, and F1 score of 0.9280.

Conclusion

The proposed deep learning-based method for LVI(+) detection in gastric cancer exhibits high accuracy and performance, suggesting its potential to enhance precision medicine. This model can significantly save time and labor in histopathological examinations and reduce inter-pathologist variability, thus contributing to better patient outcomes.

Key words: Artificial intelligence, Digital pathology, Gastric cancer, Lymphovascular invasion

P33 Software and seminar format to jointly teach computational pathology in biomedical and computational academic curricula

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Introduction

Integration of computational pathology into academic teaching curricula is a prerequisite for successful implementation of digital workflows. We present an "odd couple's" (bioinformatician's and MD's) experience with an innovative seminar format teaching in interdisciplinary teams.

Material and methods

We developed a seminar jointly teaching third year medical and computer science master students focusing on active skill development and Artificial Intelligence (AI) for quantitative biomarker evaluation. For this, we implemented a browser-based software combining (1) interactive microscopy by formative feedback on image annotations and (2) joint design of own AI algorithms. Students learn to identify informative areas in whole slide images, annotate (outline and label) relevant structures, and jointly solve tasks in real-time online-collaboration by designing and testing segmentation or classification workflows. The software enables the innovative seminar format supporting interdisciplinary "couples", or small groups, of students jointly solving complex medical tasks.

Results and discussion

The participants showed comprehensive understanding of opportunities and potential limitations of AI-based approaches in computational pathology. In addition, we detected a significant learning progress of voluntarily participating students in a pilot phase. Particularly, drawing outlines improved understanding of histological structures in the medical context. Performance increased in final exam-like tasks from 66.0% after the regular curricular course to 79.6% after solving additional exercises using our tool. The students also reported that they liked the teaching concept.

Conclusion

The software and the seminar format improved skills and knowledge necessary for efficient interdisciplinary collaboration between students of computer science and medicine, considered essential for the emerging digitization of pathology.

Key words: education, feedback, interdisciplinary teaching, computational pathology, Artificial Intelligence, collaborative learning

P34 Feature extraction from spatial cell composition in ulcerative colitis immune microenvironment

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Introduction

Digital pathology workflows involving spatially resolved cell composition result in a growing need to analyze biologically meaningful cell-cell-interactions. We quantified interactions in two ways to improve the density-based description of immune microenvironement in ulcerative colitis (UC) and investigate consistency of the proposed metrics.

Material and methods

Cell coordinates were obtained by multiplexed immunohistochemistry for CD3, CD20, CD15, CD68, cytokeratin, and phosphorylated STAT3 (pSTAT3) in longitudinal biopsies from cohorts treated with targeted therapies to localize immune cells (ICs) and epithelial cells (ECs). To investigate cell-cell interactions, we used (1) Ripley's K in mucosal tissue compartments with tissue edge correction, and (2) neighborhood graphs reflecting simplistic adaptive and innate immune mechanisms with either lymphocytes or granulocytes as nodes. Macrophages were assigned to both graph types. A hypothetical immune pressure to an individual EC mediated by neighbored connected components of these adaptive and innate graphs was calculated. Finally, we trained machine-learning (ML) classifiers to predict therapy response.

Results and discussion

We observed more spatial dispersion of ICs around pSTAT3- ECs than around pSTAT3+ ECs based on Ripley's K. Innate graphs features showed significant differences between responders and non-responders, even when no change in Nancy Index (NI), a commonly used metric for UC activity, occurred in longitudinal examinations. Classifiers that included features from both interaction methods (Ripley's K and neighborhood graphs) reached hold-out accuracies between 60-70%.

Conclusion

Our results show that integrating spatial interaction metrics and neighborhood graphs deliver powerful features for ML algorithms. Potential applications include response prediction in UC cases with limited dynamics of conventional histologic indices such as NI under targeted therapy.

Key words: graph, Ripleys-K, distance metrics, spatial analysis, cell interactions, ulcerative colitis

P35 Deep Learning-Based End-to-End H-Score Quantification Framework for Whole Slide Images in Breast Cancer

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Introduction

The aim of our study was to develop the first end-to-end deep-learning (DL) framework for automatic H-scoring of whole slide images (WSIs).

Material and methods

We propose an end-to-end framework comprising three DL-based modules: (1) tumor-stroma segmentation using a ResNet50 encoder pretrained with a self-supervised learning scheme, paired with a segmentation head; (2) nuclei segmentation employing a modified triple U-net architecture; and (3) H-score quantification through a VGG16-based regression model. The entire framework processes IHC-WSIs as input and estimates H-scores for both the tumor and stromal compartments, while each module can also function independently for other tasks. A dataset of 301 IHC-WSIs of 133 breast cancer patients, stained with an MHC-I antibody, was used. The data was collected in the context of a multi-institutional, randomized trial, and images were digitalized at a central location. An expert pathologist segmented 109 patches (235×235 um2) for training (80%) and internal validation (20%), and two pathologists independently scored 120 WSIs in total with overlap in 20 WSIs. A dataset of 80 IHC-WSIs with HER2 score was used for external validation.

Results and discussion

Tumor-stroma segmentation achieved a sensitivity and specificity of 78% and 94% for tumor, and 92% and 75% for stroma. Tumor H-score estimation compared to average manual H-scores achieved a Spearman's rank correlation coefficient (SRC) of 0.84. SRC between pathologists was 0.84. HER2 scoring achieved 86% accuracy.

Conclusion

An end-to-end framework for automatic H-scoring of WSIs was developed, demonstrating promising results in internal validation and potential generalizability to another biomarker in an external cohort. A more extensive validation is ongoing.

Key words: Computational pathology, Deep learning, Immunohistochemistry, H-score

P36 An integrative pathology workflow to enhance molecular diagnostics in precision oncology

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Introduction

In precision oncology molecular diagnostics relies on next-generation sequencing (NGS) to generate heterogeneous omics data, whose integration and interpretation is essential for patient's therapy recommendation. This data heterogeneity often leads to fragmented analysis workflows that require continuous human intervention, with detrimental effects for patient's care management. Here, we developed an integrative strategy to automate the diagnostic workflow in molecular pathology.

Material and methods

Our integrative workflow was established both in a German and an Italian pathology department, using the TSO500 HRD gene panel as case study. Through a Python-based pipeline, the workflow fully automates all downstream bioinformatics analyses, including variant annotation and classification. Indeed, analyses are automatically started as soon as new NGS results are available. In addition, the interconnection of the pipeline with the laboratory information system (LIS) allows accessing analysis results from patient records.

Results and discussion

The pipeline for TSO500 HRD gene panel automatically creates a summary of all the quality metrics, performs functional annotation of variants, collects biological evidence from public resources, and classifies variant oncogenicity through a fully-automated implementation of the Variant Interpretation for Cancer Consortium guidelines. Furthermore, additional plots and metrics, including the genomic instability score, are provided. When interfaced with the LIS, the generated textual results and plots can be readily opened and/or visualised in the patient's gallery.

Conclusion

This workflow represents an effective solution to streamline the fragmented analysis steps in molecular diagnostics. Our integrative strategy provides the foundation for more automated molecular analyses, with the ultimate goal of enhancing patient care journey.

Key words: integrative workflow, molecular pathology, NGS-based analyses, precision oncology

P37 Deep Learning-Based Prediction of Ki-67 Expression in H&E-Stained Images

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Introduction

Ki-67 is a crucial biomarker for assessing cell proliferation in cancer diagnostics, but its detection requires costly and time-consuming immunohistochemical (IHC) staining. This study investigates whether deep learning can accurately predict Ki-67 expression directly from routine hematoxylin and eosin (H&E) stained slides. While previous computational approaches have attempted to predict biomarker expression from H&E images, they have primarily focused on hotspot detection without addressing individual cell classification.

Material and methods

We developed a two-phase deep learning pipeline: (1) HoVerNet for precise nuclei segmentation and (2) a specialized classifier trained on paired breast cancer tissue samples. The dataset was first registered then mapped to get the IHC ground truth labels in H&E, establishing a novel nuclear-level Ki-67 patch dataset. The classifier was trained using our dataset comprising 215,825 individual nuclei patches, with a balanced class distribution of 121,478 (56.3%) positive and 94,347 (43.7%) negative samples.

Results and discussion

The model demonstrated robust performance with 82.39% validation accuracy. Performance metrics showed strong predictive capability with precision of 0.795 and notably high recall of 0.925, yielding an F1-score of 0.855. Class-specific analysis revealed consistent performance across both Ki-67 positive (F1: 0.86) and negative (F1: 0.77) nuclei predictions. Beyond classification performance, the model provides precise nuclear localization through bounding boxes, enhancing clinical interpretability and enabling detailed spatial analysis of Ki-67 expression patterns.

Conclusion

Our results demonstrate that deep learning can effectively predict Ki-67 expression from H&E images alone, potentially reducing the need for additional IHC staining in routine diagnostics. The high recall rate suggests particular utility in screening applications where sensitivity is paramount.

Key words: Deep learning, Ki-67, Breast cancer, Hematoxylin and Eosin, Image Analysis

P38 Explainable AI for Foundation Models in Digital Pathology

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Introduction

Foundation Models, powered by self-supervised learning that does not require explicit labels, offer new opportunities for digital pathology. However, the lack of labels makes reliable assessment more difficult. Moreover, the EU AI Act requires transparency in high-stake tasks, yet few Explainable AI (XAI) methods address label-free scenarios. Besides, label-free methods can help verify whether Foundation Models have learned diagnostically important features, thereby offering a mechanism to validate and potentially discover new concepts.

Material and methods

Addressing this gap, we extend the work on Label-Free Activation Maps by Karjauv and Albayrak (2024) by adapting Layer-wise Relevance Propagation (LRP), originally designed for supervised settings. We propose propagating relevance directly from the model embeddings, eliminating the need for labels, thereby preserving the label-free nature essential for self-supervised settings, and delivering more fine-grained feature attribution crucial for medical image interpretation.

Results and discussion

Preliminary investigations indicate that the LRP-enhanced method generates higher-resolution saliency maps that more accurately attribute critical features compared to existing methods. Although these findings are promising, deeper evaluation in digital pathology is required to rigorously assess clinical applicability. This process remains challenging due to the difficulty of obtaining datasets with appropriate annotations, introducing significant obstacles for systematic evaluation.

Conclusion

This study highlights the potential of adapting LRP for Foundation Models in digital pathology, addressing the limitations of low-resolution and architecture-specific XAI methods. The proposed method can enhance transparency and open avenues for knowledge discovery. Future research will explore the effectiveness of this method across various datasets and investigate its capacity to uncover and validate latent semantic concepts essential for clinical decision-making.

Key words: XAI, Foundation Models, Self-supervised learning

P39 IMPLEMENTATION OF ARTIFICIAL INTELLIGENCE FOR THE DIAGNOSIS OF INTRAHEPATIC DUCTULAR LESIONS

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Introduction

Intrahepatic cholangiocarcinoma (iCCA) is the second most common primary malignancy of the liver, for which anatomopathological diagnosis is required in order to adapt therapeutic management. It presents numerous differential diagnoses, including benign ductular tumors such as biliary adenomas (BDA) and biliary hamartomas (BDH). The aim of this study was to explore the performance of deep learning based on the use of convolutional neural networks (CNN) in the classification of intrahepatic ductular lesions.

Material and methods

This bi-centric study tested the binary and multi-class classification performances of 7 models: VGG16, VGG19, MobileNetV2, ResNet50, InceptionV3, Xception and DenseNet on 261 cases comprising the classes « normal liver », « benign tumor » including BDA and BDH and « malignant tumor » consisting of iCCA.

Results and discussion

The VGG16 model achieved 90% diagnostic accuracy in multi-class classification, with F1 scores of 89%, 68% and 94% for the normal liver, benign tumor and malignant tumor classes respectively. Following this processing, we built a complete automatic pipeline from whole image (WSI) to characterization.

Conclusion

Our study showed good performance of the VGG16 model, with promising results for the use of AI in routine medical practice. An improvement in prediction using the introduction of new classes, model fusion and the use of a confidence score are being considered. This approach could be applied to other tumor locations that present diagnostic difficulties.

Key words: anatomopathology, classification, iCCA, BDA, BDH, VGG16

P40 Self-Supervision Enhances Instance-based Multiple Instance Learning Methods in Digital Pathology

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Introduction

Multiple instance learning (mil) has emerged as the best solution for whole slide image (wsi) classification. It consists of dividing each slide into patches, which are treated as a bag of instances labeled with a global label. The mil includes two main approaches: instance-based and embedding-based. In the former, each patch is classified independently, and then the patch scores are aggregated to predict the bag label. In the latter, bag classification is performed after aggregating patch embeddings. Even if instance-based methods are naturally more interpretable, embedding-based mils have usually been preferred in the past, due to their robustness to poor feature extractors. Recently, the quality of feature embeddings has drastically increased using self-supervised learning (ssl). Nevertheless, many authors continue to endorse the superiority of embedding-based mil and remain focused on them.

Material and methods

We conduct 710 experiments across 4 datasets, comparing 10 mil strategies, 6 self-supervised methods with 4 backbones, 4 foundation models and various pathology-adapted techniques. Furthermore, we introduce 4 instance-based mil methods, never used before in the pathology domain.

Results and discussion

We show that with a good SSL feature extractor, simple instance-based MILs, with very few parameters, obtain similar or better performance than complex, state-of-the-art (sota) embedding-based MIL methods, setting new sota results on the BRACS and Camelyon16 datasets.

Conclusion

Since simple instance-based mil methods are naturally more interpretable and explainable to clinicians, our results suggest that more effort should be put into well-adapted ssl methods rather than into complex embedding-based mil methods.

Key words: Whole Slide Image Classification, Self-Supervised Learning, Multiple Instance Learning, Digital Pathology

P41 Algorithm pathologist correlation: Quantitative comparison of immunohistochemical staining for claudin 6 in ovarian carcinoma TMA

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Introduction

Scoring of immunohistochemistry (IHC) is critical for validating the expression of tumour surface antigens and offering insights into clinically relevant targets for antibody-drug conjugates, which we explored in this study through a comparative analysis of two digital image analysis software applications, QuPath and HALO, and evaluating their performance against pathologist assessments of the tumour cell membrane marker claudin 6 in an ovarian cancer tissue microarray.

Material and methods

Single-plex DAB IHC was employed for immunostaining claudin-6 in 94 cases of ovarian cancer in a commercially available TMA. H-score analysis of claudin-6 was performed in 173 viable tumour cores using Qupath and Halo software, and semi-quantitatively by a pathologist. Whole slide digital images obtained were used to annotate tumour cores followed by classification of tumour and non-tumour cells using the object classifier and DenseNet networks. The mean membrane DAB intensities were quantified for H-score evaluation.

Results and discussion

Comparison of both Qupath and Halo with pathologist H-scores demonstrated high Spearman's correlations of 0.82 and 0.81 respectively, whilst further agreement was observed when comparing Qupath with Halo. The bias (Bland-Altman) between Qupath and Halo H-scores was low (3.6; -32.6 – 39.8) indicating high concordance whilst further increases in bias were observed when comparing Qupath and Halo with pathologist scoring.

Conclusion

The increases in bias observed between pathologist H-score over image analysis were attributable to cases with apical only staining of claudin-6 which included mucinous cases. The analysis highlights potential limitations to consider when comparing digital with manual pathologist membrane H-scores in certain tumour histotypes.

Key words: membrane H-score, object classifier, Bland-Altman analysis, algorithm-pathologist correlation, claudin 6

P42 First Steps in Digital Pathology for Higher Non-University Students

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Introduction
The revolution of digital pathology must be transferred to the classrooms of future histotechnicians and cytotechnologists to prepare them for their future work environment. This project, driven by the Institut Hospital del Mar, teaches our students how convolutional neural networks (CNN) help us detect anomalies in medical images with precision through clinical decision support systems based on Artificial Intelligence (AI).

Material and methods
Our students were challenged with creating a basic image classification model into gynaecological cytology module using the Google Teachable Machine (TM) application. This tool allows training image classification models using neural networks trained with user-provided images. To perform it, students must integrate the logic of the algorithms with their knowledge in gynaecological cytology. Working in groups, they are training TM with cytology images selected by them, using whole slide images (WSI) from our own Virtual Microscopy, which will feed the virtual machine algorithm to predict diagnostic results. After that, the reliability of the models will be analysed.

Results and discussion
Students understood the importance of selecting representative fields for a CNN making the necessary inferences to achieve the desired results. Additionally, it enhances our student's ability to analyse images representing malignancy and benignity within the gynaecological cytology field.

Conclusion
Understanding AI will help technicians use it in their future professional environment. Our mission as educators goes through assisting them to acquire professional skills and knowledge about the field current reality, promoting synergies between technicians, pathologists and computer scientists, which plays an important role in their future career.

Key words: CNN, IA, WSI, gynaecological cytology , training

P43 A comparison of AI-detected tumor-infiltrating lymphocytes and foundation models for immune checkpoint inhibitor response prediction in melanoma

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Introduction
Biomarkers predicting melanoma response to immune checkpoint inhibition (ICI) are limited. This study evaluates foundation models and AI-detected tumor-infiltrating lymphocytes (TILs) on pretreatment metastatic specimens as a biomarker for response in ICI response.

Material and methods
Patients with advanced cutaneous melanoma receiving first-line ICI were retrospectively identified across 11 Dutch melanoma centers. Pre-treatment H&E-stained metastatic specimens were analyzed at 20× magnification using Slideflow for feature extraction with six foundation models, followed by Attention-based MIL. For comparison, TILs were quantified using Hover-NeXt, trained on 166,718 pathologist-verified nuclei, and averaged per 200 µm² tumor area. Data were split into five folds based on treatment centers. The primary outcome was ICI response per RECIST 1.1. Mean AUROC and standard deviation were calculated across all validation folds for both Attention-based MIL and a logistic regression model trained on TILs in the training dataset.

Results and discussion
A total of 1,220 metastases were included, mainly from lymph nodes (n=342), followed by skin and soft tissue. Biopsies accounted for 47.5% of samples, whereas the remainder was resection material. The overall objective response rate was 57%. Among the foundation models, Phikon demonstrated the highest AUC (0.552±0.041), whereas Uni had the lowest (0.496±0.085). The AUC values for other models were as follows: CTransPath (0.536±0.030), Gigapath (0.513±0.088), PLIP (0.504±0.075), and Virchow2 (0.498±0.033). Scoring of AI-quantified TILs resulted in an AUC of 0.587±0.024.

Conclusion
AI-quantified TILs demonstrated higher predictive performance for treatment response compared to foundation models. This may be due to variability in biopsies from different locations and hospitals to which foundation models might not be robust.

Key words: Melanoma, Pre-treatment metastatic sample, ICI response prediction, TILs, Foundation models

P44 Support vector machine model including computational pathology to predict early recurrence of hepatocellular carcinoma after surgical resection

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Introduction
Although surgical resection for hepatocellular carcinoma (HCC) is considered curative in early stages, the high recurrence rate emphasizes the need for accurate risk assessment to guide potential adjuvant biotherapies. This study aims to develop a predictive model for early HCC recurrence after resection.

Material and methods
We collected a series of 196 patients who underwent curative hepatic resection for HCC during the period 2016-2022 across three hospitals (105/43/48). 969 HES-stained slides were digitized on three different scanners (646/125/189) and automatically pre-processed for resolution and color adjustments. Recurrence prediction was performed through a Gaussian Support Vector Machine integrating features delivered by pretrained deep neural networks. The main cohort (n = 105) was split into a training (n = 74) and a test set (n = 31). The two other cohorts were used for external validation. 64 out of 122 patients in the test and external cohorts experienced recurrence within a couple of years. Model inputs included clinical (tumour size, serum AFP, multinodular pattern, number of nodules), AI-based tumour architectural, nuclear, and inflammatory descriptors.

Results and discussion
Our model validated through 5-fold cross-validation achieved 0.935 accuracy, and 0.935 F1-score on the test set. The cross-validation confirmed the model's robustness across various splits. External validation yielded an accuracy of 0.907/0.917 and a F1-score of 0.906/0.917 for the two cohorts. Ablation studies highlighted the contribution of all descriptors to the model's performance.

Conclusion
Our model's predictive performance offers a valuable tool for personalized adjuvant biotherapies in patients with high recurrence risk.

Key words: hepatocellular carcinoma, tumor recurrence, deep learning, prediction model, support vector machine

P45 Pathology Foundation Models to Reveal Prognostic Features and Molecular Correlations in Head and Neck Squamous Cell Carcinoma

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Introduction

Head and neck squamous cell carcinoma (HNSC) diagnosis is complicated by tumor heterogeneity and subjective evaluations. Emerging AI-driven pathology foundation models which are trained on diverse whole-slide images (WSIs) could be used to more accurate diagnoses, reduced inter-observer variability, and improved patient outcomes in HNSC.

Material and methods

WSIs, clinical, and mRNA expression data for HNSC were obtained from TCGA and CPTAC. Three pathology foundation models (PRISM, Prov-GigaPath, and MADELEINE) were applied for feature extractions of whols slide images. Log-rank tests were runned in all features of each pathology foundation models and identified prognostically significant features using a best p-value cutoff method. Spearman's correlation (≥ 0.3) linked features to mRNA expression, followed by GO-BP enrichment with FDR corrections.

Results and discussion

A total of 589 cases (447 TCGA, 142 CPTAC) showed similar survival distributions. Across models, 10–11% of extracted features were inter-correlated. A smaller subset (0.89–2.09%) exhibited strong correlations with mRNA expression, repeatedly highlighting genes like PXYLP1 and BCL10. GO enrichment revealed biological processes such as epidermis development and keratinocyte differentiation, underscoring the clinical relevance of these AI-derived features.

Conclusion

The potential of pathology foundation models in HNSC to identify morphological features for overall survival is a subject that has been the focus of much recent research. Despite the presence of variations in cohort and model features, these approaches show great promise in significantly enhancing patient care through earlier and more accurate diagnostics.

Key words: Pathology Foundation model, Head and neck squamous cell carcinoma, Gene Ontology, mRNA expression

P46 Annotation Discrepancies in Prostate Cancer Gleason Grading: Implications for Deep Learning Training

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Introduction

Supervised learning is the predominant approach for training deep learning models in Gleason pattern segmentation on histopathology slides. However, precise annotations are essential, and inter-observer variability in the evaluation of Gleason score remains a major challenge, with reported kappa values as low as 0.34 and a concordance rate of 57% at the slide level (Ozkan et al., 2016). This variability raises critical questions on how to construct robust training and test datasets for deep learning applications.

Material and methods

We collected 200 tumoral prostate slides and had three independent pathologists annotate each slide at the gland group, gland and cellular level using six labels: Gleason 3, Gleason 4, Gleason 5, IDC, HGPIN, ASAP. Annotations were reviewed by senior prostate specialists to ensure consistency. Pathologists underwent specialized training, and both pathologists and data scientists reviewed annotations to align methodologies. A multi-reader test set was created to estimate local annotation variability, and a consensus ground truth was derived by merging annotations.

Results and discussion

Our analysis quantified annotation discrepancies: the concordance area ratio between two pathologists was 33% on average, while 42% of the regions were labeled by only one pathologist. Additionally, 50% of the annotated regions had conflicting labels, with the most frequent confusion occurring between Gleason 3 and Gleason 4 patterns. The derived slide-wise Gleason score yielded an inter-observer kappa of 0.2.

Conclusion

Local gland-level annotation exhibits higher variability than slide-wise Gleason scoring. This variability must be explicitly considered in model training and evaluation to ensure robustness in automated Gleason grading.

Key words: Annotation variability, Deep learning, dataset, gleason grading, prostate cancer

P47 Comparing Foundation Models Across Key Diagnostic and Prognostic Tasks: Endometrial Cancer as a Use Case

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Introduction

Deep learning has revolutionized histopathology by predicting histopathological subtypes, molecular alterations, and prognosis from whole slide images (WSIs). A key step is feature extraction using disease-specific or foundation models (FMs) trained on large pan-cancer datasets. FMs show strong performance across tasks, but model selection and comparisons to disease-specific models for cancer research remain underexplored. Here, we leveraged the largest endometrial cancer (EC) biobank to evaluate FMs alongside an EC-specific model across key diagnostic and prognostic tasks.

Material and methods

We utilized H&E WSIs of 3,292 EC patients from seven clinical cohorts and three randomized trials. Seven FMs (H-Optimus-0, GigaPath, Virchow2, Hibou-L, UNI, CONCH, CTransPath) and an EC-specific model (EsViT, 3.7M training patches, 1,837 EC patients) were included. Attention multiple-instance learning models were trained and evaluated using five-fold cross-validation on 1,451 patients across three morphological (histotyping, grading), four molecular classification tasks (POLE mutations, mismatch-repair deficiency, p53 abnormality and estrogen receptor status) using AUC, and a prognostic task (distant recurrence) assessed by C-index.

Results and discussion

H-Optimus-0 achieved the highest mean performance across tasks (0.864±0.073), followed by CONCH (0.862±0.066) and Virchow2 (0.860±0.072), with CTransPath and Hibou-L lowest (0.817±0.095 and 0.821±0.095). The best-performing FM varied by task and correlated with the number of WSIs used in self-supervised learning (Spearman Rho=0.710, P=0.032) and model size (Rho=0.710, P=0.032). The top FM outperformed the EC-specific model across all tasks with a mean delta of 0.067.

Conclusion

Performance varied by task, with FMs outperforming the EC-specific model. This study highlights the need to evaluate multiple FMs, guiding selection for EC research and precision diagnostics.

Key words: Computational pathology, Foundation models, Multiple-instance learning, Slide-level classification, Survival prediction, Endometrial cancer

P48 AI-based molecular classification of a real-world endometrial cancer cohort on H&E whole-slide-images for prognostic stratification

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Introduction

AI-based biomarker prediction from whole-slide images (WSI) has shown impressive results across a wide range of cancer types. Endometrial cancer is classified into four molecular subtypes with understudied morpho-molecular correlations. We aimed to predict these subtypes directly from H&E WSIs.

Material and methods

H&E WSIs, molecular, and clinicopathological data were obtained from n=1115 patients diagnosed with endometrial cancer, composed of three independent cohorts from TCGA-UCEC (n=529), CPTAC-UCEC (n=254) and our real-world cohort from clinical routine diagnostic from University Hospital Erlangen (n= 332). We performed feature extraction using several different state-of-the-art histopathology foundation models. We trained a transformer-based multiple-instance learning model on reference datasets from TCGA-UCEC and CPTAC-UCEC and tested on our local cohort. Patch-level classification scores and attention weights from representative samples were interpreted by expert pathologists. Highly ranked image areas from both correctly and incorrectly classified samples were segmented on single-cell level for downstream analysis, interpretability and morpho-molecular correlations. Overall survival and disease-free survival are correlated with classified subtypes.

Results and discussion

Our model showed fair performance at molecular subtype prediction, achieving an AUC-ROC score of 0.742 (macro-average) on our local, real-world independent test cohort. Further improvement may be achieved by model fine tuning. High-attention regions correlate with tumor tissue, while low-attention is placed on normal myometrium, necrosis, and artefacts, which underlines our model's ability to focus on specific histopathological features.

Conclusion

We suggest that deep-learning-based biomarker prediction shows robust classification results on real-world data and can highlight the relevance of the morphology for prognostic stratification of endometrial cancer.

Key words: AI-based biomarker prediction, molecular classification, endometrial cancer, clinical translation, prognostic stratification, real-world cohort

P49 The Role of Sample Quality and Digitization in AI-Driven Digital Pathology

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Introduction

High-quality sample digitisation in the pathology field is essential for archiving, visualising, and interpreting images, especially by predictive artificial intelligence (AI) models.

Material and methods

We conducted a pilot study to validate an AI model that predicts the histological tumour subtype—fibroadenoma, in situ carcinoma, and invasive carcinoma—from digitised H&E-stained breast biopsies. The model was trained on a private database digitised following strict guidance, including only artefact-free samples. In contrast, for the pilot study, 130 new samples were retrieved and digitised with the same scan by technicians new to the digital pathology workflow without any guidance. We performed inference on these images, followed by a detailed analysis of the sensitivity and specificity of the model, along with an extensive study of the characteristics of the digital images included in the pilot.

Results and discussion

The model achieved a mean sensitivity of 0.78 [per class: 0.95, 0.54, 0.84] and a mean specificity of 0.92 [per class: 0.98, 0.91, 0.88] on the pilot samples, which was lower than model metrics on the development phase. After the visual and computational study of the images, we identified 23 samples with artefacts such as pen marks, text labels, or blacked-out corners. We removed these cases, and both sensitivity and specificity improved to 0.85 [0.95, 0.60, 1.00] and 0.93 [0.98, 0.91, 0.92], respectively, highlighting the impact of high-quality digitisation.

Conclusion

The findings underscore the vital importance of a meticulous digitisation process, as poor-quality digital images can significantly compromise the performance of AI models.

Key words: Sample digitisation, Sample quality, Artificial intelligence

P50 "Nuclear Diagnostics": Intelligent System for Personalized Diagnosis of Breast Oncology

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Introduction

Breast cancer is the most common malignant cancer in the world among the female population. This paper presents an algorithm for screening the pathology of breast tumour cell nuclei using cytological features analysis by an information-extreme algorithm.

Material and methods

A dataset of 167 cell images (magnification x400) was collected to train the algorithm. We identified 21 cytological features that can be divided into two types: "Shape" (Area, Eccentricity, Solidity, Extent, Orientation, Major and Minor Axis Length, Elongation, Perimeter, Convex area, and Circularity) and "Texture" (Mean intensity, Absorbance, Contrast, Dissimilarity, Homogeneity, Angular Second Moment, Energy, Correlation, Standard Deviation, Histogram Peaks, and Histogram Valleys).

Results and discussion

Our approach allows us to unify the cell recognition process since the number of scenarios for developing cytopathology is limited for most types of tissues. The decision rules were unified by transferring them to the binary Hamming space using the machine learning method, namely the information-extreme algorithm. The study results showed that the proposed algorithm can accurately classify cells into healthy and malignant. 16 malignant cells were identified on the example of a breast tissue slide. Moreover, 40 suspicious areas were initially identified, but not all contained sufficient cytological signs for verification using the intelligent component.

Conclusion

First of all, this approach contributes to the unification of the diagnostic process since the development of cell pathology is generally similar, regardless of the tissue type. In the future, it is planned to expand the vector of features, in particular, by assessing the tumour microenvironment and the intercenter distance between cells for more accurate classification.

Key words: nuclear pathology, breast cancer, artificial intelligence, digital pathology, whole slide imaging, nuclear morphology

P51 PathProfiler as a Quantitative Quality Control Software for Prostate Biopsies – Pilot Study in Centro de Anatomia Patológica Germano de Sousa

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Introduction

The Quality of Whole Slide Images (WSI) is a determining factor for a proper diagnosis and prognosis and to an enhanced performance of Digital and Computational Pathology. In a context where diagnoses are increasingly quantitative, an automated, precise, effective and rapid quality control is of adamant importance. PathProfiler is a deep learning-based software trained on prostate biopsies that provides a 'usability score' of WSI, evaluating its suitability for diagnosis. The Centro de Anatomia Patológica Germano de Sousa receives around 2500 prostate biopsies a year, which are distributed to Pathologists remotely. Hence, it becomes crucial to investigate the viability of PathProfiler for automated and quantitative quality control of WSI and its monitorization for diagnostic purposes.

Material and methods

In the last 3 months of 2024, 234 H&E WSI from prostate biopsies were retrospectively analyzed by PathProfiler. Usability score, focus and H&E quality were registered numerically.

Results and discussion

WSIs had an average usability score of 0.6, focus score of 9.5 and an H&E quality score of 9.5. A usability score of 0.4 or more was obtained for 77% of the WSIs, while 23% needed to be revised. Artefacts such as mounting media, folded and no detected tissue were the major issues detected since the algorithm provides a lower rating.

Conclusion

PathProfiler is a valuable tool in the automatic quality control of prostate biopsies, allowing quick evaluation and identification of cases that need to be reviewed before being handed over to the pathologist. Moreover, it also promotes recognition of opportunities to improve laboratory quality.

Key words: Digital Pathology, Quality Control, WSI, Prostate Biopsies

P52 Satisfaction of Pathologists with the Implementation of Digital Pathology in a Secondary-Level Hospital: A Cross-Sectional Survey Study

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Introduction
Digital pathology is transforming pathology workflows by improving accessibility, collaboration, and efficiency. However, successful integration depends on user aceptance and adaptation. This study evaluates pathologists and residents satisfaction with DP implementation in a secondary-level hospital, focusing on usability, workflow impact, and diagnostic confidence.

Material and methods
A cross-sectional survey was conducted among 7 pathologists and 3 residents at Hospital Son Llàtzer. The questionnaire included Likert scale and multiple-choice questions assessing ease of use, workflow impact, diagnostic confidence, and barriers. Data were analyzed descriptively to identify preferences.

Results and discussion
• Ease of use: 60% found DP easier or equivalent to microscopy; 40% found it more difficult. • Workflow impact: 50% reported improved efficiency due to faster case access and better collaboration. • Diagnostic confidence: 30% felt more confident with DP; one participant reported decreased confidence. • Barriers: Main challenges were image artifacts, slow loading times, and accessibility issues. • Preference: 60% preferred digital diagnosis, while 40% depended on the case type.

Conclusion
The implementation of DP in a secondary hospital enhanced workflow efficiency and accessibility, yet challenges remain. Technical issues and adaptation variability indicate the need for ongoing training and system improvements. Ensuring optimal image quality and interface responsiveness will be crucial for broader acceptance. Additionally, personalized training programs could mitigate resistance and maximize the benefits of DP, ultimately contributing to more consistent and reliable diagnoses.

Key words: Digital pathology, user satisfaction, workflow efficiency, diagnostic confidence, pathology informatics

P53 Closing the Loop: Continuous AI Model Improvement Through Pathologist-Guided Feedback

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Introduction

AI integration in digital pathology requires continuous refinement, not just initial deployment. Annotating large datasets is time-consuming, and training an optimal model upfront is impractical. As part of the DigiPatICS project, our approach enables ongoing improvement of deployed algorithms through collaboration between pathologists and data scientists in a structured feedback loop with minimal workflow disruption. This accelerates database growth with task-specific annotations. Moreover, involving different end users reduces bias and enhances diversity and generalizability.

Material and methods

Pathologists diagnose patients by reviewing whole-slide images (WSIs) alongside algorithmic results and annotate good and bad inferences. Only the singled out WSI regions and corresponding results are then extracted through a feedback tool. Corrections are made, verified, and added to the database for retraining. A key challenge is selecting images, integrating them effectively, and measuring their impact. In order to maintain model robustness and prevent overfitting, the database improvement targets general weaknesses rather than rare corner cases. WSI and annotation retrieval are managed through a secure web platform, while QuPath is used for visualization, correction, and tile extraction. Data conversion is handled via Python scripts.

Results and discussion

This iterative feedback loop has significantly increased the volume of curated data specific to the project. Incorporating expert-reviewed corrections ensures that the model remains unbiased while improving accuracy.

Conclusion

This methodology supports long-term model convergence, enhancing performance over time, and makes AI-assisted pathology more precise and flexible to diagnostic evolution over time, while reducing annotation costs. The structured feedback loop corrects systematic errors, enhances model reliability, and strengthens the AI-pathologist partnership.

Key words: Digital Pathology, Pathologist-AI Collaboration, HITL, Incremental Dataset Augmentatio

P54 Automated Invasive Area Detection Algorithm for Breast Cancer

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Introduction

The Nottingham Histological Grading (NHG) is performed on invasive regions of breast cancer, omitting non-invasive areas. To automate our NHG algorithm we developed a solution to identify invasive areas. This study evaluates the performance of the algorithm with the pathologists' assessments.

Material and methods

100 WSIs are randomly retrieved from TCGA-BRCA. Five experienced pathologists independently assessed the overlap between the algorithm-generated invasive mask and their own visual assessment of invasive regions using a web-based study platform. Ratings are provided using categorical intervals (0 to 100% overlap), and 500 individual assessments are collected. Inter-rater reliability is assessed using weighted kappa to measure agreement between experts.

Results and discussion

67% of the scores fell within the 81-100% range, reflecting strong agreement between algorithm and pathologist. In 43 cases, 5 pathologists rated the algorithm mask as 81-99%. However, inter-rater agreement was low (kappa 0.39-0.57). There was 1 case where the algorithm masked some areas as invasive, which was a false positive. There are 2 cases where the algorithm missed the invasive area as a false negative and 5 pathologists agreed. The false positive case was a slide with non-malignant tissue. The false negative cases are one slide with a mucinous pattern and one with a tubular pattern. In addition, 0.6% of the assessments are classified as 0-20% overlap.

Conclusion

Our algorithm for identifying invasive areas in breast cancer WSIs shows promising performance with a high proportion of ratings in the 81-100% overlap range. However, the poor inter-rater reliability (kappa 0.32-0.52) and the occurrence of isolated false results suggest that further refinement is required.

Key words: Invasive Detection, Deep Learning, Evaluation, Nottingham Histological Grading, Breast Cancer , Algorithm performance

P55 Leveraging foundation models to improve lymph node segmentation in colorectal cancer whole slide images

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Introduction

We recently developed "MetAssist", a deep learning model for detecting lymph node metastases in colorectal cancer and integrated it into our routine diagnostic workflow for quality control. Post-integration usability feedback from pathologists shows that MetAssist often struggles to differentiate between lymph nodes and other surrounding tissues (mainly vessels, primary tumour and normal). This study presents the preliminary results of improving lymph node segmentation by exploring the potential of recent, Virchow2, a foundation model in combination with mask2former.

Material and methods

We performed several experiments with recent segmentation approaches and found that the Mask2former with Virchow2 (a foundation model) as the backbone encoder provides excellent improvements in lymph node segmentation. We used 119 whole slide images from 63 colorectal cancer patients. These images were annotated for lymph node, adipose, vessel, primary tumour, primary normal and mucin tissue regions. We performed a 5-fold cross-validation approach and used intersection over union (IoU) as the evaluation criteria.

Results and discussion

When comparing the results of the new approach with our previous UNet model, the lymph node segmentation on IoU improved from 68.13±7.60 to 87.93±3.25. Our results show that the new approach can well differentiate between primary tumour, normal tissue, vessels and lymph nodes.

Conclusion

This study demonstrates the potential of the proposed approach to be used for higher resolution morphology such as metastasis detection as a next step to improve the overall workflow of MetAssist. In addition, we are extending this approach to other types of lymph nodes including upper gastrointestinal, lung, breast, endometrial, head and neck and melanoma.

Key words: colorectal cancer, lymph nodes, metastasis, segmentation, foundation models

P56 Artificial Intelligence-Based Prediction of Molecular Subtypes in Breast Cancer Using Hematoxylin and Eosin-Stained Whole Slide Images

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Introduction
The primary objective of this study is to determine whether an artificial intelligence (AI) model can accurately classify molecular subtypes of breast cancer based solely on hematoxylin and eosin (H&E)-stained whole slide images (WSI).

Material and methods
A total of 250 WSI from invasive ductal carcinoma cases were collected, with 50 slides per subtype: Luminal A-like, Luminal B-like (HER2-negative), Luminal B-like (HER2-positive), HER2-positive (non-luminal), and Triple-negative. A carefully designed framework for genetic mutation prediction in WSI was implemented, consisting of three stages: (i) Cancerous area segmentation via supervised learning to filter non-malignant regions, (ii) Patch clustering using contrastive learning-derived representations to ensure patch selection completeness, and (iii) Mutation classification through a hierarchical deep multiple-instance learning (HDMIL) approach, optimizing patch selection accuracy.

Results and discussion
The AI model achieved classification accuracies of 78.4% for Luminal A-like, 61.6% for Luminal B-like (HER2-negative), 72.5% for Luminal B-like (HER2-positive), 87.8% for HER2-positive (non-luminal), and 92% for Triple-negative cases in the test set.

Conclusion
Pathomics-based AI analysis demonstrated a revolutionary potential for molecular subtype determination in breast cancer. By analyzing H&E-stained WSI, molecular insights traditionally requiring costly analyses can be obtained, highlighting AI's role in advancing digital pathology.

Key words: Breast cancer, Deep learning, predictive, algorithm

P57 Development and features of Digital Pathology Diagnostic System among our group hospitals including Vietnam

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Introduction

Our university is the newest medical school in Japan, and when we built affiliated Narita Hospital, we built a pathology laboratory based on a digital pathology system. We are also moving forward with the digitalization of our affiliated hospitals and building a network that enables mutual diagnostics. Today, we will introduce our digital pathology system and its features.

Material and methods

We digitize all the histology slides including biopsy, resected specimen, and autopsy slides. A significant feature of our system is its independence from specific WSI scanners. Our Image Information System (Infinitt) converts all original WSI files from each scanner to DICOM format for observation. Currently, Hamamatsu, Leica, and Evident scanners are in use, allowing hospitals to choose scanners based on their size and characteristics. The pathological diagnosis network operates through a closed network among three of the nine hospitals in the Tokyo area and is under expansion. As part of this interhospital network, we have been conducting international remote pathology diagnosis with a Vietnamese hospital Since 2018. Because we are university facility, we also provide microscopes as well as digital pathology systems to enable microscopic diagnosis. Glass specimens are submitted for study. Cases are selected using QR codes on the glass slide labels, enabling diagnosis through both digital and microscopic methods. Regarding AI integration, we have recently connected HALO for use.

Results and discussion

There are so many benefits including easy refer to diagnostic histories, faster diagnosis report, expert double-check across hospitals, and so on.

Conclusion

We are now planning to actively incorporate AI into our diagnostics.

Key words: digital pathology diagnostic system, DICOM, experts double-check through interhospital network, International digital pathology

P58 Integrating spatial multi-omics to investigate metal-driven tumour evolution in gliomas

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Introduction

Gliomas exhibit significant heterogeneity, with low-grade gliomas (LGGs) often progressing into high-grade malignancies (HGGs). Copper is a key driver of tumour progression and immune evasion, shaping a pro-tumorigenic tumour microenvironment (TME). Our work repurposes copper chelation as a safe strategy to disrupt tumour growth by reshaping metabolic and immune landscapes. Notably, our findings in neuroblastoma led to an ongoing clinical trial combining copper chelation with immune-checkpoint therapy. We hypothesise that targeting copper homeostasis in gliomas may mitigate disease progression, reduce relapse risk, and prevent LGG-to-HGG transition.

Material and methods

We employ a spatial multi-omics approach, integrating Akoya PhenoCycler-Fusion spatial proteomics, CosMx 6K spatial transcriptomics, and spatial metallomics across tissue microarrays (TMAs) of LGGs and HGGs. This unprecedented combination of transcriptomic, proteomic, and metallomic data allows us to map metal ion distribution in the TME and investigate its influence on tumour evolution and immune interactions.

Results and discussion

We observed significant copper-driven signalling across TMAs, with distinct effects on tumour and immune cell populations. Copper metabolism was linked to key immune-evasive mechanisms and tumour-immune crosstalk. Additionally, we identified novel copper-driven cell populations with grade-specific functional roles in glioma progression.

Conclusion

This study establishes a rationale for metal-targeted therapies in gliomas by defining copper's role within the TME. Targeting copper signalling could halt LGG progression, maintaining tumours in a more manageable state. This approach is particularly critical for young patients, where standard treatments pose neurodevelopmental risks.

Key words: Glioma, Copper metabolism, Spatial multi-omics, Tumour microenvironment, Immune system, Metallomics

P59 Adoption and Impact of Digital Pathology and AI at a Mid-Sized Pathology Department: Experience from the University of Texas Medical Branch (UTMB)

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Introduction

Large institutions have led digital pathology adoption, while mid-sized academic departments have lagged due to distinct challenges. At UTMB, we are a mid-sized department that successfully transitioned to digital pathology, followed by AI-assisted integrated diagnostics.

Material and methods

In 2021 we went live with digital pathology for diagnosis after a one-year implementation phase. Key elements of the process included securing approvals, optimizing workflows, selecting platforms, IT integration and validation. In 2024 we integrated and validated AI applications for prostate and breast cancer diagnosis. In 2025 we harnessed generative AI, using iterative prompt engineering to develop custom LLMs to produce comprehensive integrative diagnostic reports.

Results and discussion

Digital pathology was embraced by all 12 faculty and 24 residents. We had a hybrid workflow for two years before switching to a fully digital mode in 2023. In these four years, our surgical volume has nearly doubled without increasing faculty, productivity gains attributable to digital pathology, a remarkable return on investment. Validated AI models now support all prostate and breast cancer diagnoses. LLM-powered integrative reports combine clinical, imaging, and pathology data and provide guidelines-based risk stratification to inform patient management. Remote access, digital consultations and AI assistance have boosted morale and helped retain and recruit faculty. Our training program is now preferred by applicants seeking future-ready skills.

Conclusion

With the right team and mindset, mid-sized departments can successfully implement digital and AI-driven diagnostics. Our experience demonstrates that digital transformation improves diagnostic accuracy, increases staff productivity, helps with recruitment and retention, and positions a department for long-term success in a rapidly evolving field.

Key words: Integrative Diagnostics, Clinical Application of AI, Generative AI, Digital Pathology Business case, Return on Investment, Validation of Digital Pathology and AI tools

P60 Comparative Analysis of State-of-the-Art Extractive Question Answering Models for Histopathology Report Information Extraction

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Introduction
Accurate retrieval of key parameters from unstructured pathology reports is essential to guide clinical management. Transformer-based extractive question-answering models can efficiently automate this process.

Material and methods
We compared six state-of-the-art transformer models in extracting eight parameters (ER status, PR status, HER-2 status, Ki-67 index, histologic grade, tubule formation score, nuclear pleomorphism grade, and mitotic rate) from histopathology reports. One-hundred-fifty-one surgical pathology reports were divided into training (n=91), validation (n=30), and test (n=30) sets. Six models were fine-tuned for extractive question answering: medicalai-ClinicalBERT, deepset-RoBERTa-base-squad2, google-BERT-large-uncased, Iserinol-Turkish-question-answering, timpal0l-mdeberta-v3-base-squad2, and deepset-deberta-v3-large-squad2. Model performance on the test set was evaluated using Word Error Rate (WER) and categorized error types (substitutions, insertions, deletions) based on 240 questions.

Results and discussion
deepset-deberta-v3-large-squad2 achieved the lowest WER of 2.91% with 6 substitutions, 0 insertions, and 1 deletion. Iserinol-Turkish-question-answering and timpal0l-mdeberta-v3-base-squad2 followed with a WER of 3.75% (8 substitutions, 1 insertion, 0 deletions; and 7 substitutions, 0 insertions, 2 deletions, respectively). google-BERT-large-uncased and deepset-RoBERTa-base-squad2 reported a WER of 4.16% (8 substitutions, 0 insertions, 2 deletions; and 9 substitutions, 1 insertion, 0 deletions, respectively). medicalai-ClinicalBERT had the highest WER of 6.25% (11 substitutions, 4 insertions, 0 deletions).

Conclusion
We found that transformer-based models such as deepset-deberta-v3-large-squad2 can effectively extract key parameters from histopathology reports. These results support further investigation of domain-specific extensions and larger datasets to optimize automated pathology reporting.

Key words: Extractive Question Answering, Transformer Models, Natural Language Processing, Pathology Reports, Clinical Information Extraction

P61 Validating Conformal Prediction for Cervical Atypia Classification

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Introduction
Managing uncertainty in cervical cytology is essential and is addressed in the Bethesda system, where ambiguous findings can be classified as atypical squamous cells. Conformal prediction (CP) allows models to do the same by providing several potential labels. However, CP often lacks thorough validation. This study collects four experts' tile-level labels (non-atypia, low-grade atypia, high-grade atypia, and artifact) to validate three CP methods on cervical atypia classifier models.

Material and methods
We use a labeled tiles dataset from 279 whole-slide images (WSIs) to train EfficientNetB0, ResNet18, and ResNet50 models. The experts annotated a different set of 438 tiles selected from 25 WSIs using a pre-trained model; we use these and their annotation consensus for CP validation. We generate CP sets using the least ambiguous set-valued classifier (LAC), adaptive prediction sets (APS), and regularized adaptive prediction sets (RAPS) methods. We then use the expert annotations containing multiple labels per tile to validate CP sets using mean precision, mean recall, mean f1-score, and Jaccard similarity. CP metrics---coverage, size stratified coverage (SSC), and mean width---are computed using consensus annotations.

Results and discussion
Across all the models, RAPS scored the highest coverage (0.98) and SSC (0.93) when applied to ResNet18. The runner-up approach was APS. Evaluated on expert annotations, the LAC method applied to ResNet50 achieved the highest mean precision (0.82), while RAPS with EfficientNetB0 scored the highest mean recall (0.79).

Conclusion
We validated CP methods in generating sets that accurately capture expert opinions. LACS produced concise CP sets, minimizing inaccurate extra labels, whereas RAPS demonstrated stronger alignment with experts.

Key words: Cervical atypia, Conformal prediction, Model uncertainty, Deep learning

P62 A Synthetic Data Framework for Benchmarking Single-Cell Computational Methods in Image-Based Spatial Transcriptomics

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Introduction

As spatial transcriptomics gains popularity for its ability to map gene expression within tissue architecture at subcellular resolution, many studies have adapted existing scRNA-Seq pipelines for image-based spatial transcriptomics (iST) analysis. However, these pipelines were not designed to handle spatial dependencies or the targeted nature of iST panels, which can lead to biases in gene expression quantification and misinterpretation of spatial patterns, raising concerns about the validity of current analyses in the field. To address this gap, the aim of this study is to evaluate how scRNA-Seq methods perform when applied to iST data. We simulated scRNA-seq data with a negative binomial distribution to generate synthetic iST data with known ground truth, using real spatial transcriptomics datasets as references to assign spatial coordinates and introduce realistic batch effects across multiple fields of view. This controlled setup allowed us to evaluate the performance of standard scRNA-Seq normalization, batch correction, and highly variable gene selection workflows for spatially distributed data. Early results indicate that the simulated distributions of gene-level mean expression closely mirror the real data (Jensen–Shannon-Divergence=0.007). In this case, a dataset consisting of liver cancer samples—was used to estimate the parameters necessary for the data generation. By enabling comparisons against a predefined ground truth, our synthetic framework highlights the necessity of spatially aware processing strategies. These findings illustrate the potential pitfalls of relying on conventional scRNA-Seq methods for iST data and emphasize the importance of new integrative tools designed to preserve spatial context, which is crucial for interpreting cellular interactions and tissue microenvironments.

Material and methods

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Results and discussion

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Conclusion

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Key words: Digital Pathology, Cancer, Spatial Transcriptomics, Generative AI, Machine Learning, Statistics

P63 Automated Cell Segmentation for Oligodendroglioma

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Introduction

Oligodendroglioma diagnosis requires molecular testing according to current WHO classification of tumours of the central nervous system (CNS). These include analysis of 1p/19q co-deletion, which is mainly worldwide tested by Fluorescence In Situ Hybridization (FISH) in Formalin Fixed Parafin Embedded samples. The evaluation of this test demands high precision and trained profesionals, who recognize evaluable cells by DAPI nuclear staining prior to probes quantification. To address this first step, our project introduces an automated solution that applies advanced machine learning techniques to improve diagnostic accuracy and streamline laboratory workflows.

Material and methods

We developed an advanced cell segmentation model based on the « Harmony of Data-Centric and Model-Centric for Multi-Modality Microscopy » (MEDIAR) architecture. The model underwent fine-tuning and supervised training to achieve both precise cell counting and instance segmentation, differentiating adjacent cells. The training process utilized a dataset comprising 25 high-resolution FISH images of samples tested for 1p or 19q deletions, taken with Leica Aplication Suite (version 4.8.0) for red and green double detection. Development and validation were executed on the Google Colab platform. The trained model was integrated into a desktop application via a dedicated API.

Results and discussion

The automated model demonstrated a segmentation accuracy of 0.83, marking a significant improvement over traditional manual methods of non-expert evaluators, combining state of the art machine learning with an intuitive user interface.

Conclusion

The application developed is a first step that could be easily incorporated in routine SNC FISH evaluations in both digital pathology scanned or microspy images without requirements of DAPI evaluation.

Key words: semantic segmentation, cell segmentation, Fluorescence In Situ Hybridization, Oligodendroglioma

P64 Lung Cancer Segmentation on Macro Images with Deep Learning

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Introduction

The recent implementation of the NHS lung cancer screening program has led to an increase in early-stage diagnoses, increasing the workload for histopathology departments. Macroscopic assessment is critical yet time-consuming step in pathology, requiring expertise to accurately identify and sample tumour regions. This study aims to develop an AI tool to analyse macro photographs of lung specimens, providing automated detection, classification, and mapping of lung tumours to support histopathology teams.

Material and methods

Images of lung tissue specimens were collected using the Macro-Imager® Image Capturing System. A total of 184 images from 117 samples were acquired, representing a mix of benign and malignant cases. Each image was labelled with segmentation annotations to mark abnormal areas. We developed and tested multiple deep learning segmentation models to identify abnormal regions, comparing their performance in detecting and classifying lung lesions.

Results and discussion

The benchmark U-Net model trained for segmentation of abnormal regions achieved F1 and Dice scores of 0.20 and 0.25, respectively. In contrast, ConvNeXtV2 achieved scores of 0.72 and 0.63. Our proposed fine-tuned Segment Anything Model outperformed both benchmark models, achieving F1 and Dice scores of 0.77 each.

Conclusion

This AI tool demonstrates significant potential in streamlining the macroscopic assessment of lung cancer specimens improving consistency in tumour sampling. Integrating AI into macroscopic analysis, may contribute to faster, standardised specimen processing and improved diagnostic workflows supporting histopathologists in managing increasing case volumes. Further validation on a larger dataset is essential to refine its clinical applicability and integration into routine practice.

Key words: Lung cancer, Deep learning, Macroscopic image analysis, Pathology specimen dissection, Segmentation

P65 Real-world performance of AI-based tumor cell content quantification

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Introduction

Quantifying the tumor cell content (TCC) in molecular tumor diagnostics is a crucial step for subsequent analyses, especially copy number variation inference. However, in practice, pathologists' estimations of TCC are often flawed, as evidenced by insufficient correlation with other quantification methods, low repeatability, and high intra- and inter-observer biases (Smits et al., 2014). While manually counting individual cells within a region of interest could improve accuracy, this approach is prohibitively labor-intensive. Thus, practitioners face a trade-off between significantly higher costs and suboptimal diagnostic quality. To overcome this challenge, artificial intelligence solutions have been developed to automate the identification and quantification of tumor cells.

Material and methods

We implemented the PathAI AIM-TC algorithm (AI) and evaluated its TCC quantification of digitalized diagnostic whole slide images against the estimation by pathologists (Pathol), and Foundation Medicine's bioinformatics-based approach (FMI) across 491 tumor cases, including breast, colon, lung, pancreas, and prostate carcinomas.

Results and discussion

We found that correlations between Pathol and AI (rs=0.48), and Pathol and FMI (rs=0.49) were the weakest, whereas AI and FMI (rs=0.65) correlated more strongly, despite their distinct methodologies, suggesting robust AI performance. Discrepancies between Pathol and AI were most pronounced near the low-end of the AI-based tumor cell estimations, where pathologists consistently provided higher estimates. Furthermore, discrepancies seemed dependent on excision-related artifacts, cancer site, and specimen type.

Conclusion

We will present causes that explain these discrepancies, and our analyses will contribute to the development and implementation of AI solutions for the automated TCC assessment into molecular pathology workflows.

Key words: artificial intelligence, diagnostic molecular pathology, personalised medicine, tumor purity, automated tumor cell quantification

P66 The Impact of Tissue Section Thickness on Image Quality and Computational Feature Extraction in Digital Pathology

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Introduction

Tissue Section Thickness (TST) impacts tissue presentation in digital pathology (DP), influencing both the visual assessment of whole slide images (WSIs) and computationally derived features. Despite its relevance, TST remains underexplored. We aimed to examine how TST affects image quality and the extraction of computational features at both a nuclear and WSI level.

Material and methods

To investigate the effects of TST, n=144 thyroid tissue samples from 9 patients were prepared at thicknesses ranging from 0.5 µm to 10 µm. Care was taken to minimize preanalytical artifacts and batch-effects. WSI quality was evaluated using HistoQC, nuclear segmentation was performed via HoverFast, and Scikit-Learn alongside Mahotas were employed for extraction of texture, intensity, and morphological features.

Results and discussion

TST demonstrated a significant effect on both WSI and nuclear-level features. Visual assessment showed thinner sections displayed enhanced transparency and sharper cellular details, whereas thicker sections appeared darker with increased staining intensity and more artifacts. As thickness increased from 0.5 µm to 10 µm the Haralick texture feature, difference entropy, computed from segmented nuclei declined by 13.7%, indicating a reduction in textural complexity, likely related to increased overlap of chromatin fibers and nucleoli. Additionally, intensity levels decreased by 26.1% and 30.4% at WSI and nuclear levels, respectively, while WSI contrast increased by 92.6%.

Conclusion

Our results underscore the influence of TST on qualitative assessments and computational measurements in DP. Real biological signals are likely confounded by presentational variability imparted by TST. These findings advocate for standardized sectioning procedures and routine reporting of TST to ensure reproducible analyses.

Key words: Tissue Thickness, Digital Pathology, Quality -Control

P67 Path-omics: Computational pathology approach to predict Barrett's esophagus progression using aneuploidy and ecological microenviromental metrics

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Introduction

Barrett's esophagus (BE) is precancerous metaplastic transformation of the esophageal epithelium due to chronic reflux. Although significant insights into molecular and immune changes in BE have emerged, reliable pathology-level indicators for carcinoma progression risk are lacking. We propose an integrated computational pathology approach that leverages molecular data and spatial ecological immune metrics to predict cancer progression.

Material and methods

We utilised H&E-stained 742 biopsy slides from 138 patients with BE, including 125 slides from 26 patients with aneuploid cell populations identified by flow cytometry. Notably, training and test slides were digitized at different institutions. Our pipeline employed a multiple-instance learning framework, CLAM with the REMEDIS foundation model, for aneuploidy prediction and an ACformer-based single-cell detection model.

Results and discussion

The aneuploidy prediction model achieved a balanced accuracy of 74.3% (0.81 AUC) on 388 test slides. Aneuploidy showed modest, yet limited, correlation with cancer outcomes as determined by both flow cytometry (balanced accuracy 74.7%, p=1.83e-09) and our model's predictions (73.5%, p=5.93e-06). The single-cell model reached 98.3% accuracy across epithelium, lymphocyte, plasma, eosinophil, neutrophil, and stroma cells. Ecological metrics (Morisita-Horn, Getis-Ord, Moran, kNN, Ripley) quantified the spatial distribution of cells and served as inputs for a lasso regression model that predicts cancer progression (balanced accuracy 85.4%, p <1e-5) in aneuploid samples.

Conclusion

Integrating computational pathology with spatial ecological analysis effectively predicts BE progression. By coupling slide-level aneuploidy prediction with ecological metric-based regression, our approach offers a novel framework for risk stratification using routine BE pathology slides, highlighting the interaction between molecular alterations and microenvironment, paving the way for improved image-based prognostic tools.

Key words: Immune microenvironment, Precancer, Clinical prediction, Barrett's esophagus, Aneuploid, Ecology

P68 A Multicenter Validation of a Novel Digital Pathology Molecular Workflow for Minimal Residual Disease Testing of Oncologic Specimens

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Introduction

With the rise in cancer diagnoses, specialized molecular testing is crucial. A minimal residual disease (MRD) assay using cell-free DNA can be customized to detect relapse earlier than traditional methods. However, current labs still rely on physical glass slide assessments, limiting capacity to onsite pathologists. To address this, we validated a digital pathology molecular workflow.

Material and methods

We purchased and calibrated two Phillips digital scanners (SG60 and SG300) in line with specifications across two sites. Sixty retrospective H&E slides from different tumor types were reviewed by two board-certified US based pathologists using both glass slides (GS) and digital slides (DS). The pathologists evaluated slide quality, tumor percentage, and suitability for macrodissection. A two-week washout period between GS and DS assessments ensured unbiased results. Validation concordance was set at >95%.

Results and discussion

One pathologist achieved 100% concordance (60/60), and the other reached 98% (59/60), at both sites confirming the viability of the digital workflow. Pathologists now use digital tools for annotating tumors on H&E slides, facilitating macrodissection and DNA extraction. We also incorporated tablet tools for precise resizing of annotated slides to match unstained ones during macrodissection.

Conclusion

Digital pathology is an approved medium for primary histopathologic diagnosis, however, implementation in the pre-analytic component of molecular labs is less common. We were able to successfully validate a digital pathology workflow and include digital annotation tools for use by in-house pathologists and consultants. This workflow will enable us in the future to track fundamental data metrics such as DNA tumor yields, failure rates, and turnaround times.

Key words: Digital Pathology, Molecular, MRD, Genomics, Liquid Biopsy

P69 Optimizing Telepathology Workflows: A Data-Driven Approach to Digital Case Submission and Quality Assessment

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Introduction

PGIMER, Chandigarh, a designated Centre of Excellence in Telepathology, serves as a hub for digital pathology services across North India. Its telepathology workflow streamlines digital case submission, quality assessment, and remote diagnostics for spoke centers. By integrating multiple platforms- Official Email, eHealth GoI Portal, and Onward Assist with AI-driven workflows-the system ensures standardized imaging, secure data management, and real-time specialist diagnostic support.

Material and methods

From November 2023 to January 2025, 492 cases were submitted in DICOM, PNG, and MP4 formats, including clinical details, photomicrographs (approx 22 per case), and videos. Each case was assigned a Telepathology Number and underwent an initial image quality assessment. Optimization was requested in 20% of cases before final acceptance. Ancillary tests, such as immunohistochemistry (IHC), were recommended based on diagnostic requirements. Data was systematically categorized by patient ID to facilitate retrieval and review.

Results and discussion

Cases were received from six states/regions, with an average turnaround time of 18–24 hours. The digital submission process reduced physical slide transport by approximately 250 km per case, saving an estimated ₹12,30,000 in logistics costs. Notably, 30% of cases were submitted outside standard working hours, demonstrating the model's flexibility. Video submissions significantly improved diagnostic accuracy, particularly in enucleation and large resection specimens.

Conclusion

The hub-spoke telepathology model at PGIMER offers a scalable, efficient solution for remote diagnostics. Standardized imaging protocols, real-time feedback, and AI-driven triage can further optimize workflows, enhance accessibility, and improve diagnostic accuracy across diverse pathology cases.

Key words: By integrating multiple platforms- Official Email, eHealth GoI Portal, and Onward Assist with AI-driven workflows-the system, reduced physical slide transport by approximately 250 km per case, Data was systematically categorized by patient ID to facilitate retrieval and review.

P70 Patch Engineering: Novel Data Augmentation for Multi-Tissue Transitional Region Segmentation with Sparse Annotations

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Introduction

Transitional regions in histopathological images—such as interfaces between tumor and benign tissues—are crucial yet most challenging for semantic segmentation. Deep learning techniques typically require dense, labor-intensive annotations for optimal performance. We propose a novel, straightforward data augmentation strategy called Patch Engineering (PE) that enables robust segmentation with sparse, easier-to-obtain annotations and limited tissue volume.

Material and methods

PE generates training patches by stitching existing patches along organically shaped binary masks, simulating transitional regions. Models are trained on datasets from prostate cancer (n=19,000 patches) and colorectal cancer (n=3,300 patches) WSIs, with our PE augmentation adapted to annotation sparsity. Evaluation is performed on whole datasets and subsets of transitional regions across seven datasets, and four network architectures, primarily using Dice scores. Furthermore, we examine the impact of our method on three different training case numbers.

Results and discussion

PE significantly improves segmentation in transitional regions, with average tumor and benign gland Dice gains of ≥0.1 ($p<0.001$) across all four prostate segmentation datasets and average Dice improvements of ≥0.03 ($p<0.05$) on both colorectal datasets. Segmentation performance on whole datasets improves, partially significantly ($p<0.05$ or $p<0.001$), for all six segmentation datasets. PE improves prostate tumor detection AUROC on a dataset of simulated biopsies from 0.988 to 0.99, corresponding to a 16% reduction in error. Performance gains persist across multiple architectures and training case sizes, with only slight limitations at higher case numbers.

Conclusion

Our PE augmentation strategy enables high-accuracy segmentation of histopathological transitional regions using sparse annotations and limited tissue volume, requiring as few as five sparsely annotated cases.

Key words: AI, Segmentation, Augmentation, Sparse Annotations , Tissue Interfaces

P71 Optimizing a Scanning Protocol for Liquid-Based Cervical Cytology on Whole Slide Images Using Z-Stack

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Introduction

In the field of gynecological cytology whole-slide imaging without using Z-stack to focus on 3-dimensional (3D) cell groups is limited. Z-Stack has many options for layer selection. We aimed to optimize a protocol with small file size and fast scan time using Z-stack by comparing different layers to increase confidence of pathologists' diagnosis on WSIs on 3D clusters.

Material and methods

Sixteen PAP smear cases diagnosed AIS(n=1), HSIL(n=2), LSIL(n=2), AGC (n=1) and NILM(n=10) were selected for our study. All glass slides were scanned with NanoZoomer S360 used at ×40 magnification with a pixel resolution of 0.23 µm. Four different protocols (13 layers with 0,6 µm distance (A), 7 layers with 1 µm distance (B), 5 layers with 1,5 µm distance (C), and 3 layers with 2 µm distance (D)) were created. All protocols were compared by their scanning time, file size and quality (1-poor to 5-excellent) regarding pathologists' confidence.

Results and discussion

No significant differences were seen between the protocols, concordance rates for all categories were good to near perfect. Protocol A, B, C, D took 341, 209, 132, and 77 minutes respectively and file sizes followed this order. In addition, the quality score for A, B, C and D protocols were 4.1, 3.9, 3.3, and 3.3 respectively.

Conclusion

Protocol A is the best for pathologists' confidence. However, when considering all results the optimized protocol for routine scanning has been shown to be Protocol B. Our next step would be to use this protocol on more cases by involving more pathologists to get additional data such as diagnosis time

Key words: Cytology, Scan protocol, Z-stack, PAP smear

P72 Multicolor, fast volumetric imaging of cancer samples with multi-confocal light-sheet microscopy

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Introduction

Non-destructive 3D histopathology holds promise for revolutionizing clinical practice, providing a comprehensive view of biopsies and surgical samples less prone to sampling errors. Light-sheet fluorescence microscopy (LSFM) is a promising technique for volumetric tissue imaging; however, being based on fluorescence emission, it can introduce crosstalk between multiple markers leading to confused interpretation of results. For this reason, standard LSFM approaches are based on sequential imaging of multiple fluorophores, reducing throughput and posing potential misalignment issues between channels.

Material and methods

We developed a new method for fast, crosstalk-free multi-color imaging in LSFM based on multi-confocal line detection. The system generates the light sheet by scanning an illumination line. To remove crosstalk between different colors, the laser beams exciting different fluorophores are slightly displaced, and each one is synchronized to the rolling shutter of a distinct imaging camera. This system was used to image volumetric tissue samples from breast and lung cancer, as well as lymph nodes from colorectal cancer patients.

Results and discussion

The multi-confocal LSFM enables fast, crosstalk-free 3D imaging of cleared cancer tissue samples. We show how this new feature allows avoiding false colocalizations of different markers that may arise from fluorescence crosstalk in standard LSFM systems. We demonstrate its capabilities by imaging the distribution of multiple cell types within the tumor and in its microenvironment.

Conclusion

This advancement represents an important step towards the use of 3D histopathology for assessing the spatial distribution of multiple biomarkers simultaneously. The high speed guaranteed by this approach makes it suitable also for future clinical use.

Key words: 3D histology, Light-sheet microscopy, Multiplexed imaging

P73 H&E-Based TIL Assessment in OSCC: A Novel AI Approach Bypassing Immunohistochemistry

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Introduction

Our study presents a novel method for assessing tumor-infiltrating lymphocytes (TILs) in oral squamous cell carcinoma (OSCC) using artificial intelligence (AI) and hematoxylin and eosin (H&E)-stained whole-slide images (WSI), bypassing the need for immunohistochemistry (IHC). Current IHC-based TIL quantification is prone to inter- and intra-observer variability. To address this, we developed a StarDist-based deep learning model for T-cell detection, classification, and segmentation in H&E-stained WSI.

Material and methods

The model was trained using a dataset of annotated histological slides from the University of Naples "Federico II" pathology archive, with IHC-derived ground truth annotations generated in QuPath. The trained model was then implemented in QuPath and applied to an independent OSCC dataset from The Cancer Genome Atlas (TCGA).

Results and discussion

Correlation of AI-predicted TIL density with clinicopathological data, including survival analysis using Kaplan-Meier curves and Cox regression, demonstrated a significant association between TIL infiltration and patient prognosis, consistent with established findings. This "virtual immunohistochemistry" approach offers an accessible and accurate solution for automated TIL assessment in OSCC, potentially improving risk stratification and requiring only basic informatics knowledge for implementation by pathologists.

Conclusion

This "virtual immunohistochemistry" approach, using H&E staining and AI, offers a novel method for image annotation and model training, enabling automated TIL assessment for OSCC risk stratification. Developed using user-friendly tools, this accurate and accessible solution empowers pathologists with basic informatics knowledge to perform sophisticated image analysis.

Key words: OSCC, TIL, StarDist

P74 Explainable AI for Weakly Supervised Membrane Expression Scoring

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Introduction

Deep learning enables accurate, scalable solutions for automated scoring of cell membrane expression from immunohistochemistry slides. Due to the "black box"-nature of deep learning models, which entirely learn from data, it is non-trivial to understand on which image features the scoring is based. Classic approaches first segment the membrane and compute the expression from its optical density. Such approaches, although interpretable, are often less accurate and require laborious pixel-level annotations.

Material and methods

We explore explainable AI (XAI) for combining the best of both worlds. First, 7,901 image patches from 78 WSIs are extracted around tumor cells and labeled by a pathologist into 4 different levels of membrane expression and used to train a neural network (recall 90%). Next, we compute XAI heatmaps using IntegratedGradients which highlight pixels that the model deemed most important for predicting membrane expression. From this, a pseudo-segmentation mask is derived and used to compute an optical density per cell.

Results and discussion

The XAI-derived optical densities correlated well with the pathologist labels (rho=0.79). A review of the XAI heatmaps exhibited several interesting properties of the model, e.g. that the model indeed correctly focuses on membranes, however sometimes not only on the cell of interest.

Conclusion

We showed that XAI heatmaps allow to segment cell membranes, solely reusing an existing expression classification model. This can be seen as a weakly supervised learning setup, where pixel-wise targets are learned from annotations on patch level, which are typically cheaper. Moreover, this approach helps to identify model shortcomings and explain mispredictions and can thus be used for model improvement.

Key words: Explainable AI, immunohistochemistry, expression scoring, segmentation, weak supervision

P75 Deep Learning Reveals Stromal Signatures of Prognosis in Oral Squamous Cell Carcinoma

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Introduction

In the present study we used deep learning to investigate the prognostic value of stromal features in oral squamous cell carcinoma (OSCC).

Material and methods

We trained ResNet18, ResNet50, and ResNet152 models to classify OSCC hematoxylin and eosin (H&E)-stained whole-slide images (WSI) from The Cancer Genome Atlas (TCGA) into good (S0) and poor (S1) prognosis groups.

Results and discussion

Gradient-weighted Class Activation Mapping (Grad-CAM) was employed to visualize the models' attention and identify key histological features. Our analysis revealed that both prognostic groups consistently highlighted the extracellular matrix (ECM). Notably, in S0, attention maps predominantly focused on small cell clusters, likely indicative of immune cell infiltration, associated with favorable outcomes. Conversely, in S1, the models emphasized linearized collagen fibers, a feature linked to tumor progression and metastasis. Furthermore, we validated these findings with a weakly supervised approach by training a classification model using CLAM (Cluster Attention Multiple-Instance Learning) on a ResNet50 architecture. The resulting heatmaps from the CLAM model corroborated the previously observed patterns, confirming the critical role of ECM structure, particularly immune cell distribution and collagen organization, in OSCC prognosis.

Conclusion

These findings suggest that ECM structure, particularly immune cell distribution and collagen organization, plays a critical role in OSCC prognosis. Future research will further characterize the specific stromal and cellular components contributing to these prognostic differences.

Key words: TME, AI, prognosis

P76 Beyond Attention Heatmaps: Better Explanations for Multiple Instance Learning Models in Histopathology

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Introduction

Multiple instance learning (MIL) is a powerful weakly supervised learning approach that has led to breakthroughs in computational histopathology. Attention heatmaps are commonly used to interpret MIL models. However, they tend to be unspecific and suffer from various limitations in reflecting model decisions. Therefore, we aimed to improve the explainability of MIL models.

Material and methods

We formulated Explainable MIL (xMIL), a framework for interpreting and evaluating MIL attribution heatmaps. We then adopted gradient-, perturbation-, and propagation-based explanation methods to xMIL, and implemented them for Attention-, Transformer-, and Mamba-based MIL models in the context of classification, regression, and survival analysis. We extensively assessed explanation faithfulness across 10 benchmark tasks, covering diagnosis, biomarker, and survival prediction. For biological validation, a Transformer-based MIL model was trained to predict VEGF pathway activity from H&E-stained TCGA HNSCC histopathology images and tested on the CPTAC dataset. The model was then deployed on an in-house dataset, where validation proxies for VEGF were created using CD34 staining as a vessel marker. We analyzed whether model heatmaps overlap with protein expression quantified via QuPath.

Results and discussion

Our xMIL-LRP approach consistently outperformed other explanation methods in producing faithful heatmaps across models and tasks, excelling for Transformer-based biomarker and survival prediction. We could derive spatial locations of CD34 activations for 10 out of 14 patients using xMIL-LRP heatmaps from our VEGF prediction model.

Conclusion

Our work underscores the importance of advancing XAI in digital histopathology beyond traditional attention heatmaps to enhance model validation and knowledge discovery. Our code is provided in a public GitHub repository.

Key words: explainable AI, knowledge discovery, histopathology, multiple instance learning

P77 AI-powered Classification of Thymic Epithelial Tumors Using Histopathological Analysis of H&E Whole Slide Images

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Introduction

Thymic Epithelial Tumors (TETs) are rare, complex neoplasms. The World Health Organization (WHO) classifies them as thymomas (A, AB, B1, B2, B3) and Thymic Carcinoma (TC). Accurate diagnosis is challenging due to interobserver variability and overlapping histological features. This study aimed to develop a tool to assist pathologists in accurate subtyping, facilitating treatment decisions and improving patient outcomes.

Material and methods

The EMC dataset (n=669 patients) of TETs was used, with diagnoses from a panel of eight pathologists. Patients with less than 70% consensus and other thymoma types were excluded (n=498). For training, 76 cases were selected, and 95 cases were used for testing. Tumor regions were annotated and 512×512-pixel tiles extracted at 10x magnification using QuPath. Vahadane's staining normalization method addressed staining variability. A multiclass weakly supervised CNN was developed to classify A, AB, B1, B2, B3, and TC. Multiscale and transfer learning enhanced feature extraction, while stratified 3-fold cross-validation ensured robustness.

Results and discussion

The model achieved an AUC of 0.96 ± 0.02 on the validation set. For the 70-100% consensus test set, it attained an AUC of 0.88 ± 0.03, accurately classifying subtypes A and TC, but misclassifying B2, often confusing it with B1, AB, and B3. Grad-CAM activation maps highlighted salient features.

Conclusion

The model demonstrated high accuracy in distinguishing TETs subtypes, providing valuable support to pathologists and informing treatment decisions. However, similar to challenges faced by pathologists, the model's performance decreased in ambiguous cases with mixed histological features. Future research will incorporate external validation datasets to enhance generalizability.

Key words: Thymic Epithelial Tumors, AI classification, Histopathology, Deep Learning, Subtyping

P78 Color Standardization in Digital Pathology: A Comparative Study of Stain Normalization Methods for H&E Whole Slide Images

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Introduction
Stain variability in whole slide images (WSIs) across different scanners significantly impacts the generalization of machine and deep learning models in digital pathology. This study evaluates the effectiveness of stain normalization methods to address this challenge.

Material and methods
Fifty H&E-stained slides were scanned using six scanners (VS200 Olympus, Aperio AT2, Ventana DP200, and NanoZoomer 2.0HT) across institutions in Spain, Italy, and France, producing 300 WSIs in various formats. Five fragments from each scanner were randomly selected, and two stain normalization methods, Reinhard and Vahadane, were applied. A reference fragment from one scanner was used to calculate the Euclidean distance between its average LAB color space intensities and those of corresponding same fragments from other scanners, both before and after normalization.

Results and discussion
Reinhard's method produced visually homogeneous images, clustering closely in the HS space, while Vahadane's method resulted in inhomogeneous outputs. Reinhard's method introduced a yellowish tint, whereas Vahadane reduced it. Magnification differences (20x vs. 40x) in NanoZoomer 2.0 scanners did not significantly affect color consistency, with Euclidean distances of 0 (20x) and 8 (40x) for original images, and 16 and 15.8 for Reinhard-normalized images. Other scanners exhibited greater variability, with Euclidean distances ranging from 11.9 to 22.9 for original images and 13.8 to 27.4 for normalized images.

Conclusion
Reinhard's method provides superior stain normalization, ensuring consistent color representation across scanners, which is essential for robust computational analysis in digital pathology.

Key words: Digital pathology, stain normalization, whole slide imaging, color standardization, Reinhard method, Vahadane method

P79 Intelligent procedure based on digital holographic imaging for colonic polyps and adenocarcinomas grading

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Introduction

The use of endogenous malignancy biomarkers extracted from unstained samples would increase the diagnostics accuracy in Digital Pathology . Digital Holographic Microscopy (DHM) is a non-invasive technique already validated in various clinical areas (hematology, oncology, infectious diseases, etc.). DHM provides quantitative phase maps (QPMs) of the optical phase shift values induced by transparent native samples in the transmitted laser wavefront, particularly the dry mass values of the samples, in case of tissue sections of constant thickness.

Material and methods

Serial slides were prepared from 2µm-thick 2 consecutive sections of colonic adenomatous polyps collected during colonoscopy. One slide was H&E stained and the other was left unstained. The stained slide was used as reference for malign features after being examined by the Pathologist. The unstained slide was used for QPMs reconstruction with an off-axis DHM set-up (Lyncee Tec). An U-Net type CNN was adapted and trained for automatic recognition of the structures (layers, cells, nuclei, crypts) in QPMs. Customized MATLAB codes were developed to characterize the tissue structures and classify the samples by using statistical, shape, and texture parameters.

Results and discussion

The HoloPath data set contained 400 QPMs of colonic adenomas was collected and analyzed. Statistically significant alteration of the quantitative phase-parameters was found for samples with malignant characteristics. An average 90% accuracy was obtained for grading the samples based on QPMs.

Conclusion

This pilot study confirm that DHM offers objective optical cancer biomarkers when applied on unstained samples, being a promising solution for a faster and accurate automate diagnostic in the support of digital pathology.

Key words: colonic adenomas, cancer grading, digital holographic microscopy, optical phase biomarkers

P80 Enhancing Digital Pathology Interoperability with Meditecs DICOMPath: Insights from the DICOM WG-26 2025 Connectathon

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Introduction

While interoperability remains a challenge in digital pathology, standardized protocols are becoming increasingly prevalent. Our modular middleware, Meditecs DICOMPath, facilitates communication between diverse systems, enabling them to participate in standardized workflows and achieve compliance with standards like the IHE PaLM DPIA profile, which relies on standards like HL7 and DICOM and is crucial for integrating AP-LIS, WSI scanners, PACS, and viewers.

Material and methods

At the DICOM WG-26 2025 Connectathon, the middleware will be tested in the Acquisition Manager role, supporting IHE PaLM DPIA transactions. The most important tasks will include: - Responding to and initiating LAB-81 and LAB-80 transactions to provide the Acquisition Modality with Work Orders or canceling them in both query and broadcast modes. - Accurately conveying patient, specimen, and slide identifiers, including fixation, embedding, and staining information. - Communicating with heterogeneous imaging devices.

Results and discussion

At ECDP 2025, the middleware is expected to showcase its capabilities in processing and exchanging structured pathology metadata by leveraging IHE PaLM DPIA transactions and ensuring compliance with the standard. Seamless integration should be achieved with WSI scanners and image archives, validating metadata consistency and enhancing workflow automation.

Conclusion

Data exchange is essential for digital pathology. Since individual integrations for every system are not scalable, using standards simplifies the process, making connections easier for systems, enabling faster workflow implementations, optimized data exchange, and long-term adaptability.

Key words: Connectathon, Interoperability, IHE, DPIA, DICOM, HL7

P81 A scoping review of automated tumor-stroma ratio assessment in colorectal cancer: Current approaches and challenges

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Introduction
Tumour-Stroma Ratio (TSR) is a prognostic biomarker in colorectal cancer (CRC). Recent AI-driven approaches aim to reduce inter-observer variability and improve accuracy, yet challenges remain in their validation and integration into clinical workflows.

Material and methods
A scoping review following PRISMA-ScR guidelines was conducted to analyse automated TSR scoring methods. A literature search across PubMed and Scopus, followed by the application of exclusion criteria, identified twenty relevant studies on automated TSR scoring for CRC, published between 2018 and 2025.

Results and discussion
Fifteen studies developed semi-automated approaches, using expert-defined regions of interest (ROIs), while six developed fully automated pipelines. TSR calculation follows three key steps: ROI selection, tissue identification, and TSR estimation. Regarding ROI selection, four of six studies analysed the entire tumour bulk. Two studies used a circular hotspot region, replicating the manual approach, and possibly increasing accuracy. Tissue identification was performed using thresholding, machine learning, and deep learning, with the latter exceeding 95% accuracy in patch-wise and pixel-wise classification. TSR estimation was influenced by the selected ROI and tissue identification errors. The variability between automated TSR and human observers was reflected in kappa scores ranging from 0.239 to 0.472, evaluated in five studies.

Conclusion
Automated TSR evaluation represents a promising approach. While segmentation methods have shown strong performance in tissue identification, significant challenges remain, particularly in ROI selection and reducing discrepancies between automated and human-derived TSR scores. To identify the exact source of this discrepancy, each component of the scoring pipeline should be evaluated independently.

Key words: tumour-stroma ratio, colorectal carcinoma, computational pathology, artificial intelligence, scoping review

P82 Quantitative image analysis of CD4 and CD8 in colon medullary carcinoma

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Introduction

Medullary carcinoma shows microsatellite instability, frequent right localization, prominent lymphocytic infiltration and lacks glandular differentiation. Despite some morphological similarities to poorly differentiated and undifferentiated adenocarcinomas it shows a good prognosis. We analysed tumour immune response in medullary carcinoma compared to adenocarcinoma NOS via quantitative image analysis.

Material and methods

We collected 5 poorly differentiated adenocarcinomas and 5 CRC medullary carcinomas. Cases were selected based on their microsatellite instability. Moreover, in contrast to adenocarcinoma NOS, medullary subtype showed positive or focal expression of calretinin and negative expression of ARID1A and CDX2. CD4 and CD8 were performed to identify tumor infiltrating lymphocytes. Sections were scanned using the Ventana DP200 scanner and images were loaded on HALO software (Indica Labs) for lymphocyte quantification. HALO Multiplex IHC v3.4.9 settings have been configurated for nuclear segmentation and tumor-infiltrating lymphocyte quantification.

Results and discussion

Halo software showed differences on lymphocyte infiltration between the two subgroups. • Medullary carcinomas showed about 17-10.4%, of CD4 and 12,8-3% of CD8 • Poorly differentiated adenocarcinomas showed about 8,8-2,2% of CD4 and 7-0,05% of CD8.

Conclusion

Halo software permitted to establish more accurate lymphocyte quantification on two different colon carcinoma subtypes. We found a prominent lymphocyte infiltration on medullary subtype when compared with poorly differentiated adenocarcinoma NOS. Further analysis needs to be performed for statistical analysis. In future digital pathology could improve the diagnostic accuracy of this specific histotype.

Key words: Medullary carcinoma , Lymphocytic infiltrate, Image analysis

P83 Aging of AI Caused by Scanner Drift Can Be Rescued by Color Calibration

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Introduction

A recent study demonstrated standardizing WSI color by calibration increases AI robustness and reliability. Concerns exist over 'AI aging' as scanners change color over time, impacting AI post-validation performance and potentially compromising safety.

Material and methods

We employed a color calibration technology that corrects WSI to ground truth color of real glass slides using ICC profiles. To assess impacts of temporal color variation, 119 prostate cores with balanced ISUP grade distribution were scanned alongside the color calibration slide on one scanner every 14 days for one year. The tissue color was measured for change. Scanner-induced temporal variance on pathologist concordance and AI model performance was evaluated on a deep learning model trained on over 46,000 WSI for prostate cancer diagnosis.

Results and discussion

The RGB color stability of the scanner degraded over even short timepoints, discernable by humans and revealing traceable events needing quality assurance that caused sudden changes. Timepoint ICC profiles recovered to stable, accurate color resulting in better AI concordance with pathologist ISUP grading, and actual tissue did not change color. With only scanner color uncontrolled, AI performance linearly regressed which ICC color calibration rescued to intended consistency.

Conclusion

Frequent color calibration provides a universal solution to the variation introduced by scanners drifting, making AI-based cancer diagnostics more reliable in the real world. In future studies, introducing more scanners will investigate impacting AI reliability exponentially and grade-specific rescuing of AI-aging for ISUP 2-4 is expected to have significant diagnostic impact. This study pioneers real-time quality assurance for stable and scalable performance of scanners and AI over time.

Key words: QA, standardisation, AI, color, calibration, validation

P84 Using Large Language Models for Extracting Slide-level Information from Pathological Reports

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Introduction

Pathology reports contain detailed information for a case, aggregated over multiple slides. Accessing slide-level information thus is challenging, but valuable for automated processing. We explore large language models (LLMs) to facilitate the extraction of slide information from case reports.

Material and methods

As a gold-standard, we manually extracted slide information from 20 prostate cancer reports. Each report contains three sections: macroscopy, microscopy and critical findings. Each case includes 11 slides potentially mentioned in each section, totaling 660 slide-level descriptions. We used one-shot prompting with nine locally executable multilingual LLMs from different publishers and sizes: Llama by Meta (1B, 8B and 70B parameters), Gemma 2 by Google (2B, 9B and 27B parameters), and Qwen 2.5 by Alibaba Cloud (1.5B, 7B and 72B parameters) to extract the slide information for a given section and report. For evaluation, we compared the prompted outputs to the manually extracted descriptions using BLEU-4 and ROUGE-L metrics.

Results and discussion

The median slide description length was 103 characters . The largest Llama model showed a BLEU-4 score of 0.74 and ROUGE-L of 0.84, while the smallest model scored 0.11 and 0.27, respectively. The best performing Gemma 2 model achieved 0.60 (BLEU-4) and 0.70 (ROUGE-L), whereas Qwen2.5 scored 0.69 and 0.78, respectively.

Conclusion

Our experiment shows that general-purpose LLMs can extract slide-level information from given pathological reports. The performance deteriorates significantly for smaller models, as they struggle to capture the context in the rather lengthy sections of a report. Interestingly, the deterioration can look very different with the Llama model family having the best and worst performing model simultaneously.

Key words: Large Language Models, Pathological Reports, Label Extraction, Natural Language Processing

P85 Biological information derived from clinical samples is hindered by upstream processing steps in Image-based Spatial Transcriptomics data

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Introduction

Image-based Spatial Transcriptomics (iST) allows single-molecule RNA readout. Current iST processing strategies rely on single cell RNA-sequencing (scRNA-seq) specific methods. The ability of these pipelines to retrieve unbiased biological information has just started to be investigated.

Material and methods

We investigated the effects of upstream processing methods of scRNA-seq data, when applied to iST. We evaluated differences in the ability to characterize cell populations and gene expression heterogeneity in a set of 6 public datasets, representing different pathological conditions across 2 technologies: CosMx Spatial Molecular Imaging (SMI, Nanostring) and Xenium (10XGenomics). We built a validation cohort of 13 colorectal cancer (CRC) patients with matched liver metastasis (LM) on a tissue microarray (TMA). CosMx generated a transcriptomic readout of 1000-plex. AtoMx was used for cell segmentation. Quality control was performed to discard cells with low expression or area below 5th percentile, low-quality cores, and genes with low signal-to-noise ratio. Seven normalization workflows accounting for the cell area, library size and gene variance across cells were tested. Highly Variable Genes (HVG) were identified followed by automatic cell annotation using Insitutype.

Results and discussion

Our results show that HVG identification is impacted by the upstream analysis, with only 50% HVGs being consistently detected. The disparity in HVG identification results in inconsistent cell phenotyping. This creates a bottleneck for the identification of sample differences that might be clinically relevant.

Conclusion

In conclusion, iST-specific methods are needed to account for the differences between iST and scRNA-seq for the application of iST for clinically relevant research questions.

Key words: spatial transcriptomics, clinical bias, single cell, benchmarking

P86 Self-supervised learning identifies cellular neighbourhoods from multiplex immunofluroescence images

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Introduction

Multiplex immunofluroescence (mIF) allows for the simultaneous interrogation of multiple protein-directed antibodies from a single tissue section. In contrast to classical chromogenic immunohistochemistry, mIF images are information-dense and analysis pipelines are evolving. Self-supervised learning (SSL) is a form of deep learning which allows the extraction of meaningful image features without costly annotation and is free of the need of an up-front hypothesis. SSL is well-established in the analysis of H&E images, but its utility in fluorescent images has yet to be explored.

Material and methods

We applied SSL to two internal mIF datasets of lung adenocarcinoma (LUAD), each approximately 3000 cores from 1000 patients. The first panel, the 'hallmarks' panel is an 8-plex assay comprised of protein markers of key hallmarks of cancer. The second panel, the 'immuno-oncology' panel, is a 6-plex panel examining the tumour microenvironment. We used Leiden community detection to discover clusters from image features, where clusters are groups of images which appear similar. We then aligned single cell data, allowing us to characterise each cluster with cell frequencies and quantitative measures of protein expression. We associated cluster frequency with clinicopathological variables.

Results and discussion

We encode cancer modules of interpretable phenomena, such as regional enrichment for markers of hypoxia or immune evasion; or neighbourhoods of immune engagement.

Conclusion

We apply SSL to a novel image modality, enabling us to quantitatively encode interpretable biological modules in LUAD which we can relate to prognosis. This allows to extract salient features from information-dense images, offering us rich hypothesis-generating material.

Key words: self-supervised learning, spatial biology, lung adenocarcinoma

P87 A Deep Active Learning Framework for Mitotic Figure Detection with Minimal Manual Annotation and Labelling

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Introduction

Accurately and efficiently identifying mitotic figures (MFs) is crucial for diagnosing and grading various cancers, including glioblastoma (GBM). GBM is a highly aggressive brain tumor requiring precise and timely intervention. Traditional manual counting of MFs in whole slide images (WSIs) is labor-intensive and prone to interobserver variability. Recent advances in deep learning offer potential solutions, yet they often require large labeled datasets, which are costly and time-consuming to produce.

Material and methods

Our study introduces a deep active learning framework that addresses these challenges by iteratively training a model with minimal human intervention. We utilized a dataset of GBM WSIs from The Cancer Genome Atlas (TCGA). Our framework integrates convolutional neural networks (CNNs) with an active learning strategy. At first, a CNN is trained on a small, annotated dataset. The framework then identifies uncertain samples from the unlabeled data pool, which are subsequently reviewed by experts. These ambiguous cases will be verified and then used for model retraining. This iterative process continues until the model achieves satisfactory performance.

Results and discussion

Our deep active learning approach achieved promising results in this study. For MF detection, it reached 81.75% precision and 82.48% recall. For MF subclass classification, it attained an accuracy of 84.1%. Additionally, this approach reduced the annotation time to nearly half, approximately 900 minutes across 66 WSIs. These results demonstrate a substantial improvement over traditional methods.

Conclusion

By reducing the dependency on large annotated datasets, our approach reduces manual effort while maintaining high accuracy.

Key words: mitotic figure, glioma, web application, Active Learning, convolutional neural networks

P88 FL-Net: Fast and lightweight Network for Breast Cancer Segmentation

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Introduction

This abstract presents a fast and lightweight network for Breast Cancer segmentation. The proposed approach focuses on a multi-scale feature extraction and manipulation strategy to achieve the best performance on different disease datasets.

Material and methods

In the proposed model, we employed a pre-trained MobileNet-V2 encoder for feature extraction, taking into account the significance of the model's lightweight nature and inference speed for real-time applications. In addition to the encoder, the proposed model consists of two other components to address the scale variance problems and camouflage properties of objects in medical images. Multi_Scale Feature Fusion Module (MSFFM) is proposed to deal with the scale variance issues of objects, while Feature Refinement and Fusion Module (FRFM) is designed to improve the important feature representation to deal with camouflage issues. To train, validate, and test the proposed model for both binary and multi-class segmentation tasks, we employed the publicly available BCSS dataset.

Results and discussion

In our experimental study,among trained baseline models on the same dataset for binary segmentation, U-Net with MobileNet-V3-L performed best among the other versions of the U-Net model, and the achieved mean Dice and mean IoU (68.8%, 55.77%), respectively. However, We achieved the best mean Dice (76.51%), and mean IoU (66.43%) from the version V2 of our proposed model. In contrast, multi-class segmentation has no clear winner.

Conclusion

The proposed model seems to obtain adequate results with also good efficiency, which could make it more easily deployable in real world scenarios.

Key words: machine learning, breast cancer, segmentation

P89 Unsupervised Domain Adaptation for Cell Detection Across Histopathological Stains

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Introduction

Deep learning models trained on hematoxylin and eosin (H&E) stained images often fail to generalize to immunohistochemistry (IHC) stains due to domain shifts. The scarcity of annotated IHC datasets limits the applicability of supervised learning. To address this challenge, we propose an unsupervised domain adaptation approach that enables CellNuc-DETR to generalize from H&E to IHC without requiring additional manual annotations.

Material and methods

We leverage Adversarial Query Transformers (AQT) to align feature representations between H&E and IHC domains, enhancing generalization without explicit supervision. The model is pre-trained on PanNuke (H&E) and fine-tuned using unannotated IHC patches from 93 WSIs across four stains: ER, PR, Ki-67, and HER2. Performance is evaluated using F1-score on annotated test patches.

Results and discussion

The AQT-adapted CellNuc-DETR significantly outperforms the source-only model, improving F1-score from 0.42 to 0.74, 0.46 to 0.80 and 0.46 to 0.80 on Ki-67, ER and PR, demonstrating strong cross-stain generalization. Compared to CycleGAN-based stain translation, AQT achieves a 20% improvement in F1-score. Additionally, we find that adapting to all IHC stains at once leads to better generalization than adapting to each stain individually, suggesting that learning shared stain-invariant features is more effective than stain-specific adaptation. However, adaptation remains challenging for HER2, where the stain highlights cell membranes rather than nuclei, leading to poor performance and indicating the need for further adaptation techniques.

Conclusion

Our results highlight the potential of adversarial domain adaptation to extend deep learning models to new histological stains without requiring extensive re-annotation. This approach enables scalable, generalizable computational pathology workflows, improving automated biomarker quantification across different staining modalities.

Key words: Cell Detection, Unsupervised Domain Adaptation, Deep Learning, Transformers

P90 Automated AI-assisted Ashcroft scoring of lung fibrosis in a bleomycin-induced and spirometry-confirmed mouse model of IPF

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Introduction

Ashcroft scoring of lung fibrosis is commonly applied to preclinical models of idiopathic pulmonary fibrosis (IPF). Manual Ashcroft scoring is prone to inter- and intra-observer variability which influences accuracy and reproducibility. We developed and validated a deep learning-assisted platform for automated assessment of Ashcroft score in the bleomycin-induced and spirometry-confirmed mouse model of IPF.

Material and methods

Masson's trichrome stained lung sections (n=93) from mice receiving a single intratracheal installation of bleomycin (1.5mg/kg) or saline were scanned. Images were downscaled and split into tiles of 512x512 pixels (n=4,666). An expert histopathologist scored all tiles according to the Ashcroft criteria from grade 0 to 8 (normal lung tissue to total fibrous obliteration). An automated AI-assisted pathology scoring pipeline (GHOST) was developed in Python 3.7.

Results and discussion

The data was resampled to balance the classes and divided into training, validation, and test sets. GHOST was trained based on the Inception-v3 network architecture using the Keras library to predict the tile score. The training was performed for 25 epochs, and the accuracy was computed at every iteration. The Adam optimizer was used during training, and data augmentation was applied in the form of rotations, flips, and brightness. The CNN trained model was used to compute the Ashcroft score in lung samples using the test set. The analysis indicated a high degree of agreement between automated and manual scoring (Kappa value=0.83).

Conclusion

GHOST shows high agreement with manual scoring model providing unbiased, fast, accurate and reproducible histopathological scoring of pulmonary fibrosis in the BLEO-IPF mouse.

Key words: Ashcroft score, AI, Machine learning, Fibrosis, IPF

P91 Transitioning to a Paperless Pathology Workflow

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Introduction

Request forms are a major source of paper waste and inefficiency in pathology laboratories. The integration of Laboratory Information Management Systems (LIMS) with automation enables a transition to a paperless workflow, promising increased accuracy, reduced waste and improved turnaround times in digital pathology. This study evaluates its implementation and environmental benefits.

Material and methods

We measured the paper waste from pathology request forms at Prof. Dr. Cemil Taşcıoğlu City Hospital between 2022 and 2024. In 2022, forms for 30,000 biopsies and 15,000 cytologies were weighed, totalling 583 kilograms. These forms, which included patient identification, biopsy details and preliminary diagnoses, were archived and manually re-typed for digital reporting. We analysed trends and projected annual waste over the three-year period.

Results and discussion

The average annual paper waste was approximately 0.63 tons. Transitioning to a paperless system will eliminate these forms and reduced transcription errors and preanalytical errors such as barcode mismatches. In addition, the digital workflow will shorten report turnaround times and reduce archival storage requirements. An environmental assessment shows that the reduction of 1.9 tons of paper in 3 years saves approximately 38 trees and thousands of pages.

Conclusion

Switching to a paperless digital pathology system will provide significant operational and environmental benefits. Eliminating paper-based request forms will improve workflow efficiency, reduce errors, and reduce storage requirements while conserving forest resources. Our 2025 goal is to completely eliminate paper forms and further integrate a unified LIMS to improve data accessibility and interdepartmental communication. These environmental improvements represent a significant advancement in modern pathology.

Key words: paperless pathology workflow, Laboratory Information Management Systems, environmental sustainability

P92 AI-Based Detection and Quantification of Fibrosis in Kidney Biopsies Stained with Masson's Trichrome

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Introduction

Fibrosis, marked by excessive collagen accumulation from chronic inflammation, is a key indicator of chronic kidney disease (CKD) progression. Traditional assessment using Masson's Trichrome-stained slides is subjective and prone to inter-observer variability. Consequently, there is an evident need for standardized quantification of fibrosis.

Material and methods

Two ResNest CNN models were developed: (1) a kidney anatomy segmentation model, and (2) a fibrosis detection model trained to distinguish background, glomerular fibrosis, interstitial fibrosis, normal non-fibrotic interstitial collagen, and normal glomerular collagen. The models were trained using 80 kidney biopsies from the publicly available Kidney Precision Medicine Project (KPMP) dataset. Tile-wise classification was performed on 512 × 512 image patches extracted from whole-slide images and annotated by four pathologists.

Results and discussion

The fibrosis detection model alone achieved an accuracy of 89% and an F1-score of 0.83. On the other hand, kidney anatomy segmentation model achieved an accuracy of 96% and an F1-score of 0.91, demonstrating high precision in distinguishing kidney structures. When both models were integrated into the pipeline, the overall system achieved an accuracy of 94% and an F1-score of 0.89. This indicates that the combination of anatomical segmentation and fibrosis classification enhances overall performance, likely by reducing the misclassification of fibrosis in ambiguous regions.

Conclusion

Our approach demonstrates high accuracy in detecting and quantifying kidney fibrosis from Masson's trichrome-stained biopsies. It offers a reproducible solution for future clinical integration in CKD diagnosis and monitoring. Future improvements will focus on expanding datasets and enhancing model generalization to ensure broader applicability in pathology workflows.

Key words: CNN, AI, Fibrosis, CKD, Masson's Trichrome

P93 Enhancing Forensic Pathology: AI and Computational Histopathology in Coronary Autopsy Analysis

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Introduction

Computational histopathology (CH) usually focuses on improving clinical pathology, where we analyze whole slide images (WSI) to assess biopsy outcomes. In this work, we evaluate the use of CH in a forensic application, where we use artificial intelligence to detect cases of thrombosis and atherosclerosis in the coronary artery.

Material and methods

The North Branch of the National Institute of Legal Medicine and Forensic Sciences provided the dataset used in this study. It contains 250 WSIs with multiple cross-sections from coronary arteries with 125 WSIs labeled as normal by conventional histopathology, 45 as thrombosis, and 80 as atherosclerosis. We employed UNI and CONCH Vision-Language Foundation Models to extract features from 512 × 512 patches, and CLAM for classification. We also evaluated the use of only a low-resolution version of the WSIs (thumbnails) where we manually extracted the regions of interest (ROI). ResNET-50, VGG-16, and ViT-16 were used for ROI classification. If all ROIs of a WSI are predicted as normal, the global decision is normal. When this is not the case, the global decision is determined by soft-voting the non-normal predictions.

Results and discussion

We obtained a balanced accuracy of 0.815 for UNI+CLAM and 0.852 for CONCH+CLAM. Using the thumbnails, ResNET-50 reached a balanced accuracy of 0.937, VGG-16 0.875 and ViT-16 0.827.

Conclusion

Current CH techniques can be used for coronary analysis to assess autopsy outcomes. We also conclude that the low-resolution versions of the WSIs are sufficient to identify cases of thrombosis and atherosclerosis in the coronary artery.

Key words: Computational histopathology diagnosis, Coronary artery disease, Legal forensic medicine

P94 Large language models outperform human experts in pathology multiple choice questions

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Introduction

Large language models (LLMs) based on generative AI have recently emerged as powerful tools for various natural language-related tasks including medicine. LLMs may potentially have added value particularly in pathology, which covers an overwhelming amount of literature expected to be adapted by human experts.

Material and methods

The performance of seven different LLMs was evaluated with 100 multiple-choice questions covering various pathology subspecialties: 1. breast, 2. genitourinary, 3. gastrointestinal, 4. thoracic, and 5. dermatopathology. Twenty questions were selected for each subspecialty, and points were assigned as follows: 2 points for a correct answer, -0.5 points for a wrong answer, and 0 points for a skipped question. The test was repeated in three rounds. The questions were benchmarked by five board-certified consultant-level pathology subspecialists.

Results and discussion

The three best performing LLMs scored from 86.8 % to 96.3 % of the total points, clearly outperforming human experts (74.0%), whereas the least accurate LLM reached 52.3 % of the total points. The consistency of LLMs was evaluated through assessing the number of questions with inconsistent answers (range 0-56 /100). The number of tactically skipped questions varied between 0 and 21, depending on LLMs self-reflecting capacity.

Conclusion

The most advanced LLMs clearly outperformed human experts in pathology multiple choice questions with a high consistency, suggesting that a pathologist could get a more reliable second opinion from LLM than from a colleague. In addition, the latest generative pre-trained transformer achieved an almost perfect score, indicating that the rapid development of LLMs may eliminate the need for fine-tuning with domain specific literature.

Key words: LLM, pathology , general pre-trained transformer, benchmarking

P95 Morphometric assessment of cardiac interstitial mature collagen network depending on age

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Introduction

Aging and diseases, with their subsequent lesions, cause cardiac wall remodeling consisting of changes of its structural and functional components. The authors compared the variations of interstitial mature collagen fibers-IMFCOL amount-% between the different cardiac wall regions during patients´ ageing.

Material and methods

Five epicardium-to-endocardium cross sections (left ventricle anterior-LV_AW, lateral-LV_LW and posterior-LV_PW, interventricular septum-IVS and right ventricle-RVW) were taken during autopsy from 95 patients with different ages (0-24 years-AP_01, 25-44 years-AP_02, 45-64 years-AP_03 and >64 years-AP_04) died in the hospital. Tissue samples were processed and stained with Picro-Sirius_Red. Slides were digitized. The IMFCOL amount was measured with an "in-house" designed software. Average values-AV were compared using Pearson's test.

Results and discussion

The IMFCOL percentage is the lowest in elderly, increases significantly towards the younger periods of age. The IMFCOL amount is the highest in the RV_W, excepting the AP_04, and the lowest in the IVS. In LVW, it has a general increasing trend from anterior to posterior in AP_01 and AP_03 and in men and a decreasing trend from anterior to posterior in AP_02 and AP_04 and in women_AW. IMFCOL amount has a general decreasing pattern with age, the most pronounced in RVW both in men and women, excepting men` LV_PW where it remains almost constant and women` LV_AW where it slightly increases.

Conclusion

The remodeling process of IMFCOL amount along the cardiac wall`s regions and with aging follows a general decreasing pattern in both sexes mostly with higher values in men than in women, but with variations along different regions.

Key words: heart, interstitial collagen, ageing, morphometry

P96 HASD: Hierarchical Adaption for pathology Slide-level Domain-shift

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Introduction

Domain shift is a critical problem for pathology AI as pathology data is heavily influenced by center-specific conditions. Current pathology domain adaptation methods focus on image patches rather than WSI, thus failing to capture global WSI features required in typical clinical scenarios.

Material and methods

In this work, we address the challenges of slide-level domain shift by proposing a Hierarchical Adaptation framework for Slide-level Domain-shift (HASD). HASD has two key components: (1) a hierarchical adaptation framework that integrates a Domain-level Alignment Solver for feature alignment, a Slide-level Geometric Invariance Regularization to preserve the morphological structure, and a Patch-level Attention Consistency Regularization to maintain local critical diagnostic cues; and (2) a prototype selection mechanism that reduces computational overhead.

Results and discussion

We validate our method on two slide-level tasks across five datasets, achieving a 4.1\% AUROC improvement in a Breast Cancer HER2 Grading cohort and a 3.9\% C-index gain in a UCEC survival prediction cohort.

Conclusion

Our method achieves multi-scale feature consistency and computationally efficient slide-level domain adaptation. It provides a practical and reliable slide-level domain adaption solution for pathology institutions, minimizing both computational and annotation costs.

Key words: slide-level tasks, domain shift, domain adaption

P97 Impact of TLR9 Expression and Tumor Microenvironment on Survival Outcomes in Glioma Patients: A Histological and Molecular Analysis

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Introduction

Toll-like receptor 9 (TLR9), an intracellular receptor recognizing unmethylated CpG motifs, has been linked to glioma progression and poor patient survival. Its activation influences the tumor microenvironment by modulating immune cell infiltration and inflammatory responses. TLR9 agonists, such as CpG oligodeoxynucleotides, have shown potential in enhancing T cell-mediated cytotoxicity, highlighting its relevance as both a prognostic marker and therapeutic target in glioma.

Material and methods

Adult diffuse glioma samples from IDH-wildtype (n=161, WHO grade 4) and IDH-mutant (n= 43, WHO grade 2-4) tumors were analyzed on tissue microarrays. Sections were stained for immune cell markers, TLR9, and a hypoxia-related protein CA9. QuPath software-quantified immune cell densities were compiled with metadata, which included tumor grade, IDH status, and survival. Data were processed and analyzed in Python to assess the relationship between immune cell infiltration and survival outcomes.

Results and discussion

All the tumor samples included a subpopulation of TLR9-positive cells representing different cell types. Kaplan-Meier survival analysis revealed that the density of TLR9-positive immune cells was associated with distinct survival patterns across cell types. Notably, high density of CD163- or CD163+ microglia in IDH-mutant tumors is significantly associated with worse overall patient survival ($p= 0.0098$ and $p=0.018$, respectively, log-rank test). These findings highlight the role of TLR9-positive microglia in tumor regulation, warranting further investigation into their clinical significance.

Conclusion

Our findings suggest that TLR9-positive microglia densities are associated with worse survival outcomes especially in IDH-mutant diffuse astrocytomas. These results highlight the potential prognostic value of TLR9-positive immune cells and the need for further research into their clinical significance.

Key words: TLR9 Expression, Brain tumor, Immune Cells, Tumor Microenvironment

P98 Quantitative assessment of interstitial mature collagen network depending on cause of death

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Introduction

Myocardial tissue responds to the increasingly diverse range of diseases causing death with structural and functional changes. The authors compared the variations of interstitial mature collagen fibres-IMFCOL amount-% between the different cardiac wall regions depending on patients' cause of death.

Material and methods

Five epicardium-to-endocardium cross sections (left ventricle anterior-LV_AW, lateral-LV_LW and posterior-LV_PW, interventricular septum-IVS and right ventricle-RVW) were taken during autopsy from 95 patients died with different causes of death (vascular diseases-V_P, non-vascular diseases-NV_P, and suspect/violent cause of death-S/V_Dth) in the hospital. Tissue samples were processed and stained with Picro-Sirius_Red. Slides were digitized. The IMFCOL amount was measured with a dedicated software. Average values-AV were compared using chi square test.

Results and discussion

The IMFCOL percentage was the highest in NV_P in all cardiac main regions and the lowest in V_P, excepting LV, in both sexes. It was also the highest in the RVW and the lowest in IVS in all types of diseases. In LV, IMFCOL amount was the highest in NV_P but the lowest in S-V_Dth in all its segments. It was also the highest in LV_LW and the lowest in LV_AW of V_P and S-V-Dth and vice versa in NV_P. IMFCOL amount was higher in men than in women in all cardiac main regions in NV_P and S-V_Dth but vice versa in V_P.

Conclusion

The remodelling process of IMFCOL amount has the same distribution patterns in the three types of diseases and in each of them along the cardiac regions, with higher values in men than in women, excepting left ventricle.

Key words: heart, interstitial collagen, cause of death, morphometry

P99 Graph Neural Networks for Spatially-Aware Phenotyping of Breast Cancer Whole Slide Images

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Introduction

Intratumour heterogeneity, originating from factors such as subclonality and variations in cancer cell subpopulations, are potential causes for treatment resistance and poor survival in breast cancer patients. Traditional computational histopathology treats whole slide images (WSIs) as unordered collections of tiles, disregarding spatial relationships. We propose a graph neural network (GNN) framework that captures spatial variability within breast WSIs, enabling the identification of morphologically distinct phenotypes with potential prognostic value.

Material and methods

We employ a GNN trained using contrastive learning to model intratumour heterogeneity in hematoxylin and eosin-stained WSIs. Nodes correspond to 224×224 pixel tiles at 20X magnification, with features extracted from the UNI foundation model, providing morphological and potentially prognostic attributes, while edges encode spatial connectivity between tiles. The GNN is trained in a contrastive manner to extract meaningful representation of morphological structures; defined as subgraphs in the slides. By leveraging subgraph representations, the GNN learns embeddings that reflect spatially-aware histomorphological patterns within the breast tumours.

Results and discussion

We hypothesise that the learned embedding space captures spatial histomorphology in breast cancer WSIs, enabling the identification of phenotypic subgroups. We report prognostic association of subgroups as well as association with clinicopathological factors. The GNN model is validated in an external dataset including 1,500 breast cancer patients.

Conclusion

Our approach integrates spatial context into whole slide image analysis. By leveraging contrastive learning in a GNN framework, we aim to identify biologically, or clinically, relevant phenotypes linked to patient outcomes. This method has the potential to refine patient stratification and contribute to improved clinical decision support for breast cancer.

Key words: Breast cancer, Graph neural network, Intratumour heterogeneity, Phenotyping, Prognostic biomarker, Foundation model

P100 End-to-end Deep Learning Model for Predicting Recurrence-Free Survival after Radical Prostatectomy

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Introduction

Biochemical recurrence (BCR) after prostate cancer treatment is a clinical concern, impacting long-term patient outcomes. Accurate prediction of BCR-free survival (BCR-FS) could improve post-treatment decisions. This study develops a deep learning-based model utilizing pseudo-observations to predict BCR-FS at clinically relevant time points after radical prostatectomy (RP) from histopathology whole slide images (WSIs). The model's prognostic performance is compared with Gleason grades assigned by pathologists and an in-house AI Gleason Grading model.

Material and methods

The study includes 472 men (n_BCR=66) from the STHLM3 trial who underwent RP. A total of 2218 cancer WSIs were included for training and validation. An attention-based model, pre-trained on a large prostate cancer dataset for Gleason grading, was fine-tuned on 10 cross-validation (CV) folds, to predict BCR-FS at 5 years from patient WSIs. Model prognostic performance was compared to baseline approaches, including Gleason grades assigned by pathologists and an in-house AI Gleason grading model. Prognostic performance was measured by the weighted C-index (at 5 years) using 10-fold CV.

Results and discussion

The proposed pseudo-observation-based model demonstrated superior prognostic performance (C-index = 0.650 ± 0.109) compared to Cox models fitted on pathologist-assigned Gleason grades (C-index = 0.550 ± 0.132) and AI-derived Gleason grades (C-index = 0.561 ± 0.079).

Conclusion

We propose an end-to-end prognostic deep learning model that outperforms Gleason-based grading for BCR-FS prediction, demonstrating potential clinical utility for guiding post-treatment decisions. Future work will validate the model across multiple endpoints and competing events to further assess its robustness.

Key words: artificial intelligence, prostate cancer, recurrence-free survival, deep learning, histopathology

P101 Deep multiple instance learning for predicting BRCA gene mutations from digitized prostate cancer pathology slides

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Introduction

Testing for BRCA mutations is crucial for identifying prostate cancer patients who may benefit from poly ADP-ribose polymerase inhibitors (PARPi). Despite clinical guidelines recommending genetic testing for BRCA in metastatic prostate cancer, testing is hindered due to various barriers, including resource limitations, costs, and the lack of adequate candidate identification. To overcome these barriers and enhance the accessibility of BRCA testing, we aim to develop a deep learning model that predicts BRCA mutations directly from digitized histopathology sections.

Material and methods

We attempted to solve the binary classification problem with three multiple instance learning (MIL) models: CLAM, HIPT, and Prov-GigaPath. All three rely on pre-extracted tile features, for which we compared several foundation models, such as Virchow2, H-optimus0, and UNI2. By exploring multiple pairings of feature extraction models and MIL models for aggregation, we aimed to obtain robust insights into the feasibility of solving the problem with MIL and, ultimately, into the patterns potentially predictive of BRCA mutations. Our dataset included 576 wild-type prostate cancer patients (1196 slides) and 38 mutant cases (116 slides) split into a training and validation set (80%-20%).

Results and discussion

We achieved an average area under the receiver operating characteristic curve of 0.772 by pairing Virchow2 with CLAM and 0.749 for Prov-GigaPath across eight-fold internal validation.

Conclusion

This proof-of-concept study demonstrates the potential of MIL-based classification models to predict BRCA gene mutations from pathology slides of metastatic prostate cancer patients. We are currently expanding this study with a larger dataset and external validation.

Key words: BRCA mutation, Prostate cancer pathology, Deep learning , Multipe instance learning

P102 Digital quantification of Ki67 and PRAME in challenging melanocytic lesions: A novel diagnostic tool

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Introduction
Diagnosing melanocytic lesions can be difficult, even for experienced pathologists. In challenging cases, immunohistochemistry (IHC) with Ki67 and PRAME often serve as diagnostic aids. Yet, their interpretation is challenged by their potential expression in non-melanocytic cells, and the time-consuming, non-reproducible nature of their manual evaluation. The study aimed to evaluate the diagnostic performance of digitally quantified Ki67 and PRAME in challenging melanocytic lesions utilizing double-nuclear IHC with SOX10.

Material and methods
Formalin-fixed, paraffin-embedded tissue from 156 melanocytic lesions subdivided into WHO and MPATH-Dx V2.0 classes were initially stained with H&E; then physical Ki67/SOX10 double-nuclear IHC and virtual PRAME/SOX10 IHC performed on the same tissue slide. AI-driven image analysis (U-net) quantified number-based indices in epidermis, dermis, a dermal-epidermal border region, and the entire lesion.

Results and discussion
ROC AUC of Ki67/SOX10 (0.87, 95%CI: 0.81;0.94) was considerably higher compared with non-specific Ki67 indices (0.75, 95%CI: 0.66;0.84; P<0.001), as opposed to ROC AUC of PRAME/SOX10 (0.73, 95%CI:0.64;0.82) compared with non-specific PRAME indices (0.80, 95%CI: 0.72;0.89; P=0.090). The diagnostic performance was highest for the dermal-epidermal border region. Median indices of both Ki67 and PRAME differed significantly for overall WHO and MPATH-Dx V2.0 classes (P<0.001), and by combining markers the number of misclassified melanomas was reduced.

Conclusion
Double-nuclear IHC improved the diagnostic performance of Ki67, but not PRAME. The combination of digitally quantified Ki67 and PRAME may potentially serve as a diagnostic tool for challenging melanocytic lesions. To aid the pathologist in the most optimal way, the proposed diagnostic tool may present results both visually, graphically, and quantitatively for relevant tissue regions.

Key words: Melanoma, Immunohistochemistry, Convolutional neural network, Diagnosis, Ki67, PRAME

P103 H&E to IHC virtual staining in breast cancer: methods, benchmarking, and challenges

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Introduction

Breast cancer (BC) treatment relies on immunohistochemistry (IHC)-based biomarkers, but traditional methods are time-consuming and expensive. Deep generative models (DGM) offer a cost-effective alternative by generating virtual IHC stainings, e.g. from a H&E-stained sample. This study examines the state-of-the-art in virtual staining for BC IHC panel and compares three widely used models on two public datasets.

Material and methods

After an initial search and manual cross-checking, we identified 28 publications. Most models use cycleGAN or Pix2Pix variants with specialized loss functions to preserve pathological information. The most promising models are PyramidPix2Pix and ASP, which also introduce the BCI and MIST (public) datasets, featuring paired tiles from consecutive H&E and IHC slides. Thus, we benchmarked PyramidPix2Pix, ASP, and PSPStain (designed to enforce pathological consistency). The models were trained and validated on the BCI dataset using published hyperparameters and tested for generalization on the MIST HER2 dataset.

Results and discussion

On BCI, PyramidPix2Pix recorded the highest SSIM (0.590±0.171), outperforming ASP (0.512±0.141) and PSPStain (0.520±0.162). However, a visual inspection revealed that PyramidPix2Pix produces blurred images, which inflated the SSIM values. On MIST, overall performance dropped, highlighting generalization challenges, but PyramidPix2Pix still led (0.333±0.110), followed by PSPStain (0.303±0.100) and ASP (0.300±0.094).

Conclusion

IHC virtual staining in BC is an emerging field, but despite the variety of proposed DGM, their maturity remains limited, particularly in preserving pathology-specific content and consistency. Our findings reveal a discrepancy between metrics and the visual quality of generated images, underscoring the necessity for high-quality "same-slide" datasets. Whether pathology-specific loss functions can improve downstream performance remains unclear.

Key words: virtual staining, deep generative models, benchmarking analysis, breast cancer, HER2

P104 Volumetric scanning enhances the mitosis algorithm performance by using shape and texture analysis across Z stacks similar to fine focus of microscopy

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Introduction

Mitosis is an important diagnostic and prognostic factor for solid tumor and it also acts as a decisive factor for tumor classification and grading. So it's imperative that mitosis detection algorithms have higher accuracy with less false positives. Here we are presenting a novel approach of utilising the z stacks data generated from volumetric scanning to improve the mitosis detection algorithm performance.

Material and methods

Thirty cases of Solid tumors were volumetrically scanned using Pramama Cubiq scanner. Mitosis detection algorithm was run inline on all the WSI, 1st on best focus images and afterwards it was run inline on the individual Z stack layers. Comparative evaluation of algorithm output of both the run was done by the Pathologist.

Results and discussion

For all the cases, the results for the mitosis detection algorithm were better when the algorithm was run inline across the Z stack layers in comparison to algorithm output on best focus image. Volumetric scanning aids in running the mitosis algorithm inline across Z stacks which helps to capture change in the shape and texture of mitosis across the Z plane, mimicking Pathologists approach of using fine focus of microscope across Z axis to differentiate between mitosis and false positives. The overall mitosis count was higher in Z stack images in comparison to best focus images.

Conclusion

Volumetric scanning captures fine details of change in shape and texture of mitotic cell across the Z stack layers similar to fine focus of microscope, thus improving the mitosis algorithm performance when compared to algorithm performance in best focus image.

Key words: Mitosis, Volumetric scanning, Z stacks, Mitotic count, WSI

P105 Deep Learning in Bone Marrow Diagnostics: The BaMBo & BoMBR Datasets for Segmentation and Reticulin Quantification

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Introduction

Bone marrow cellularity and reticulin fibrosis are key pathological features in diagnosing, prognosing, and managing hematological conditions. Current diagnostic methods rely on subjective visual assessments, leading to significant inter-observer variability and inefficiencies. Artificial intelligence (AI)-based approaches show promise for consistent and accurate diagnostics, but progress has been hindered by the lack of publicly available, high-quality annotated datasets for bone marrow biopsy analysis.

Material and methods

BaMBo (Bone Marrow Biopsy): Consists of 185 high-resolution bone marrow biopsy images annotated for four classes: bony trabeculae, adipocytes, cellular regions, and background. Annotations were refined using a U-Net-based deep learning (DL) model to support accurate bone marrow cellularity estimation. BoMBR (Bone Marrow Biopsy Reticulin): Comprises 201 bone marrow biopsy images annotated for reticulin fiber segmentation and myelofibrosis (MF) grading. Preliminary annotations were generated using DL models and image processing techniques, subsequently refined by two experienced hematopathologists using the Computer Vision Annotation Tool (CVAT).

Results and discussion

The BaMBo dataset enabled precise estimation of bone marrow cellularity, achieving a Dice Score of 0.831 ± 0.099 for semantic segmentation and 96% accuracy in object classification. The BoMBR dataset demonstrated significant potential for fibrosis grading, with a mean Dice score of 0.92 achieving 70% overall accuracy.

Conclusion

The BaMBo and BoMBR datasets represent groundbreaking efforts to standardize annotated resources for bone marrow biopsy analysis. Together, they address critical gaps in AI-based diagnostics and provide a robust foundation for developing advanced DL models. These resources hold the potential to transform bone marrow evaluation with ongoing research aiming to refine and validate their clinical utility for improved patient outcomes.

Key words: Bone Marrow, Reticulin, Artificial Intelligence, Deep Learning, Semantic Segmentation, Fibrosis Grading

P106 Mapping the immune-cell landscape for optimal index calculation using AI-powered image analysis of multiplexed immunohistochemistry in breast cancer

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Introduction

Immune-cell indices of immunohistochemistry (IHC) are calculated in countless research studies; often to identify prognostic or predictive biomarkers in cancer patients. The study aimed to investigate how the location of immune cells and the amount of tumor epithelia may affect their calculation in breast cancer (BC) patients whilst exploring multiple digital sample techniques for IHC immune-cell quantification.

Material and methods

Formalin-fixed, paraffine-embedded pretreatment tumor tissue (N=227) from BC patients was stained with two multiplexed chromogenic IHC using CK7/19, CD8, CD4, FOXP3, CD20, CD66b, and CD68. AI-powered image analysis (U-net) determined area-based indices in reference spaces: total tumor area, tumor stroma, tumor epithelia, a stromal tumor brim, and a fixed area for each lesion using multiple subsamples within tumor stroma (1 mm2) and epithelia (1 mm2).

Results and discussion

Immune cells were predominantly situated in tumor stroma and rarely epithelia ($P<0.01$). The most infiltrative cell type was CD68 with a mean index of 3% for epithelia, yet 32% for stroma. In remainder cells, indices were <0.7% for epithelia. The amount of epithelia ranged from 1-60%, which strongly affected index calculations that included the total area of epithelia ($P<0.01$). In addition, solidity of tumor islands was highly associated with the number of infiltrative CD8, CD66b, and CD68 cells ($P<0.01$).

Conclusion

The location (stroma vs epithelia) of each immune cell of interest should be considered in connection to its index calculation because the amount of tumor epithelia may skew the result. Alternatively, the effects of tumor epithelia can be overcome by employing the digital subsampling techniques developed in this study.

Key words: Breast cancer, Immunohistochemistry, Immune system, Prognostic biomarkers, Immune-cell quantification, Convolutional neural network

P107 Deep Learning-Based, Fully Automated Analysis of histological biomarkers of ER, PgR, HER2 and Ki-67 on Invasive Breast Carcinoma

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Introduction

Breast cancer (BC) treatment is stratified by immunohistochemical staining for estrogen receptor (ER), progesterone receptor (PgR), HER2, and Ki-67. The interpretation of these biomarkers presents challenges of increasing workload on pathologists and concerns about reproducibility. These challenges have highlighted the need for fully automated image analysis solutions.

Material and methods

Consecutive 204 invasive BC stained for ER/PgR/HER2 was retrieved, with original reports as a reference. Additionally, 100 HER2 and 202 Ki-67 samples were included from prior studies, which board-certified pathologists assessed following established guidelines. Deep learning-based analysis was performed using the Breast Cancer AI APP (Visiopharm APP 10185) in a fully automated manner on whole-slide images scanned with a NanoZoomer XR (Hamamatsu Photonics).

Results and discussion

The median scores for ER/PgR assigned by pathologists were 75.8/53.8%, with the AI software demonstrating a strong positive correlation (R^2=0.953/0.909). HER2 score of null/ultra-low/1+/2+/3+ was identified by pathologists as 4/15/31/41/9 cases, while the AI software reported 2/6/49/31/12 (weighted kappa=0.974). Exact concordance was observed in 65%, with one-step discordance in 33%. One case revealed a potential pitfall where intraductal components were misclassified as strong positive. For Ki-67, the AI software quantified a large number of cells (mean=385,985) and showed a strong correlation with pathologists' assessments (R^2=0.911). Reproducibility was perfect between Japanese laboratory technicians and Danish engineers.

Conclusion

We have developed fully automated AI applications for the analysis of BC biomarkers, demonstrating concordance with experienced pathologists. While further confirmation of clinical value is required and specific pitfalls need to be addressed, these innovations free up pathologists' time, and precise biology will support clinicians and patients in selecting optimal treatment.

Key words: breast cancer, deep learning, IHC biomarkers

P108 Evaluating a Web-Based AI Algorithm for Pap Smear Pre-Screening: A Multicenter Pilot Study in Korea and India

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Introduction

With advancements in the field of information technology, AI solutions are transforming cervical cancer cytology screening. These algorithms enable users to focus on areas of abnormalities rather than diagnosing the complete slide of each specimen. identify.bio's PSx2 is one such cloud-based viewer that assists pathologist's diagnosis of LBC Pap smear specimens. A validation of this algorithm has been conducted on slides from Korea's Quality Assurance Program at 2 institutions in South Korea and 1 in India.

Material and methods

100 slides were used, 50 ThinPrep® and 50 SurePath™ slides. The ground truth was the original lab diagnosis of the slides. In total there were 20 Squamous Cell Carcinoma, 20 Adenocarcinoma, 18 HSIL, 20 LSIL, 2 ASCUS and 20 Negative slides. This study included 2 arms. 10 pathologists reviewed each of the 100 slides in an online slide viewer with and without AI assistance.

Results and discussion

Sensitivity of the pathologist increased from 83% to 96% with AI assistance but specificity reduced from 75% to 70% on using algorithm. Overall accuracy increased and Negative Predictive value sharply increased with the use of the algorithm. Pathologists took on average 6 hours to diagnose the 100 slides manually and 3.33 hours with AI assistance.

Conclusion

There is the opportunity to use this algorithm as an aid to the pathologist to help reduce the overall time taken for diagnosis and reduce the number of False Positive diagnoses. Areas for improvement include a reduction in the number of normal cells being flagged as abnormal.

Key words: Cervical Cancer, Artificial Intelligence, Pap smear , Screening

P109 Automated IHC distinguishes risk groups in DLBCL

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Introduction

Gene expression profiles have great clinical utility in diffuse large B-cell lymphoma (DLBCL) though, are commonly predicted using the immunohistochemistry (IHC) Hans algorithm. Manual assessment of IHC can add to pathologist workloads and suffers from poor inter-observer agreement. We compare two automated routes for IHC quantification in DLBCL, with survival differences observed between groups.

Material and methods

IHC panels of 13 lymphoma markers, including BCL2, CD10 and Ki-67 were obtained for 330 DLBCL patients of the population HMRN cohort (n > 3,400 slides total). IHC staining was quantified at a tissue level using Macenko stain separation and application of a positive threshold. At a cell level, IHC was quantified using DeepLIIF stain prediction. Stain quantities were compared against pathologist estimates (CD10, BCL6, MUM1). Patients were clustered on predicted IHC, with comparison against expression profile and overall survival (OS).

Results and discussion

Both tissue- and cell-level quantification correlated well with pathologist estimates of CD10 staining (Pearson r: 0.73-0.77) but less well for nuclear markers (BCL6 r: 0.40-0.59; MUM1 r: 0.55-0.64). Clustering of tissue-level IHC resulted in 3 groups. One cluster was enriched for low-risk expression (GCB), with good outcome (HR vs. Rest: 0.64; p=0.03). Another cluster was enriched for high-risk (ABC) expression, demonstrated poor outcome (HR vs. Rest: 1.75; p = 0.004) and high event rate within 12 months of diagnosis (33% patients experiencing OS event vs. 19% in rest).

Conclusion

Automated methods correlated well with pathologist for some IHC markers. Clustering of predicted IHC into risk-associated groups evidence potential for use in triage of high-risk DLBCL patients.

Key words: Immunohistochemistry, Lymphoma, Expression profiles, Automation

P110 Diffusion-based H&E-to-HER2 virtual staining: the impact of data alignment

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Introduction

Immunohistochemistry biomarkers play an important role in breast cancer diagnosis and treatment, making virtual staining a promising approach in computational pathology. While Generative Adversarial Networks (GANs) have been widely used for hematoxylin & eosin (H&E) to immunohistochemistry (IHC) virtual staining, Diffusion Models (DMs) are gaining traction.

Material and methods

This study assesses the performance of a Brownian Bridge Diffusion Model (BBDM) trained and validated on two distinct datasets: an imperfectly aligned dataset of consecutive H&E and HER2-stained Whole Slide Images (WSIs) and a well-registered, curated dataset of same-section re-stained WSIs. For the first setting, we used the Breast Cancer Immunohistochemistry (BCI) dataset, containing 3896 (training) and 977 (test) paired tiles. For the latter, we used an in-house dataset containing 3000 (training) and 977 (test) paired tiles.

Results and discussion

The BBDM trained on the BCI dataset yielded better SSIM (0.548±0.199 vs. 0.395±0.133) and PSNR (19.5±6.3 vs. 18.1±4.9), while the model trained on the in-house dataset outperformed in perceptual metrics such as LPIPS (0.361±0.116 vs. 0.461±0.099) and FID (153.7 vs. 205.6). The qualitative evaluation indicated that the in-house dataset produced much stronger content and style consistency.

Conclusion

Accurately curated and registered ground-truth data are crucial, particularly when training models like DMs, which may be less robust to misalignments. This is demonstrated by our study, the first to apply a BBDM for the virtual staining of HER2 from H&E samples. While the model showed good content and effective style transformation, future work should focus on improving pathological consistency, which is key for real-world application.

Key words: virtual staining, diffusion models, data quality, HER2

P111 Combining unsupervised and active learning in training a classifier for global glomerulosclerosis detection

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Introduction

Deep learning models for classifying global glomerulosclerosis are typically trained using supervised learning. However, acquiring and labeling glomeruli represents a very time-consuming task for pathologists. Thus, datasets are often limited in size and potentially not reflecting much of the existing clinical or staining-related variability, severely hampering the training of robust models. In the current study, we propose a strategy combining unsupervised and active learning to provide more representative datasets while keeping labeling manageable.

Material and methods

We previously demonstrated that clustering can separate globally and non-globally sclerosed glomeruli, while highlighting difficult borderline images. Using this approach, we sampled a vast collection of unlabeled glomeruli to identify a small subset of images that (i) captures the overall distribution of glomerular features and (ii) includes the images most difficult to cluster. Through this prefiltering, the pathologist's limited time can then be dedicated to labeling only the particular images that might be most valuable for facilitating model accuracy and generalizability.

Results and discussion

So far, we sampled over 350000 glomeruli across five different stains, utilizing the approach to select a subset of roughly 3000 representative glomeruli for downstream deep learning. Labeling of these glomeruli by a panel of nephropathologists has not fully concluded at this time, but preliminary training experiments with the selected glomeruli demonstrated excellent classification accuracies (>97%) across six labeled validation datasets from diverse sources and histological stains.

Conclusion

In summary, we believe that the outlined approach could enable better use of pathologists' time by directing labeling to images more representative and informative for deep learning.

Key words: Glomeruli, Glomerulosclerosis, Deep learning, Active learning, Unsupervised learning, Nephropathology

P112 An Equivalency Study of Digital Pathology for Clinical Routine Diagnostics

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Introduction

The transition to digital pathology (DP) is reshaping histopathology workflows, offering AI integration, remote diagnostics, and improved data sharing. Despite benefits, challenges include scanner integration, personnel adaptation, and workflow validation. We analyzed case sign-out times before and after DP adoption at our accredited pathology center. Our phased approach optimized efficiency, confirming DP's value.

Material and methods

We validated digital sign-out by following CAP, RCPath, and BDP guidelines. A two-phase approach was used: In the training phase, pathologists reviewed 15 cases digitally after conventional sign-out, providing feedback on workflow. In the validation phase, they reviewed 60 retrospective cases digitally, blinded to original reports. Discrepancies were classified as none, minor, or major by comparing digital and original diagnoses.

Results and discussion

In the training phase, 14 pathologists reviewed 210 cases over three months, providing feedback on digital sign-out. Four noted diagnostic challenges, including H. Pylori detection (n=2), polarization need (n=1), and melanin oversaturation (n=1). Other comments addressed navigation speed and magnification transitions. In the validation phase, seven pathologists reviewed 420 cases (2,928 slides). 91.4% showed no discrepancies, 7.4% had minor discrepancies, and 1.2% had major discrepancies affecting diagnosis. HER2 borderline misclassification (n=1) and missed inflammation (n=1) were reported. Two scans were blurry but unaffected diagnoses. Agreement between digital and analog review was 98.8%, with a median of 100% and a minimum of 95%

Conclusion

We have successfully integrated digital pathology into routine diagnostics, enhancing efficiency and flexibility. Pathologists can now work remotely, and our fully digitized Laboratory Information System streamlines data management, improving accessibility and workflow optimization.

Key words: Digital Pathology, Validation, Transition

P113 Alignment of consecutive multi-modal whole-tissue slides using image features

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Introduction

Spatial omics technologies enable the study of cellular and molecular activity within its native spatial context, providing insights into complex biological processes. Recent advances have extended spatial analysis beyond transcriptomics to include proteomics, metabolomics, and chromatin accessibility, paving the way for integrative multi-modal studies. While multi-modal samples could be derived from the same tissue slide, they are commonly taken from consecutive tissue sections. However, aligning consecutive tissue sections remains challenging due to artifacts and deformations introduced during slicing.

Material and methods

We introduce a method for aligning consecutive multimodal tissue sections using image-derived features obtained from stained tissue images. The method involves three steps: (1) Feature Extraction, where 16x16 pixel patches are generated from the images, and their features are extracted using a Vision Transformer pre-trained on ImageNet (DINO), producing 384 feature vectors per patch; (2) Graph-Based Alignment, where CAST, a unimodal alignment tools, is applied to learn a graph representation for spot locations and align image patches based on vector similarity; and (3) Spot Matching, where query spots are matched to reference spots based on proximity in the aligned space, creating a multi-modal matrix of combined features.

Results and discussion

Our results are applied to both uni-modal (spatial transcriptomics, immunofluorescence) and multi-modal (consecutive slide spatial transcriptomics and metabolomics) datasets, benchmarked against established alignment tools. Additionally, we present a use case on a multi-modal dataset featuring a bilateral ischemia-reperfusion mouse model.

Conclusion

Our method effectively aligns both uni-modal and multi-modal tissues, achieving performance comparable to existing, well-established tools. Additionally, it successfully generates a multi-modal matrix suitable for various downstream tasks.

Key words: multimodal, vision transformer, tissue alignment

P114 Enhancing Quantification of Interstitial Fibrosis in Non-Neoplastic Kidney Disease through Structural Segmentation

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Introduction

Accurate quantification of interstitial fibrosis (IF) is critical for chronic kidney disease prognosis and treatment. Traditional IF assessments rely on subjective visual evaluations by pathologists. Both digital image analysis (DIA) and deep learning (DL) methods have been proposed as alternatives but often lack workflows optimized for Sirius Red (SR)—a stain highly specific for collagen and showing high correlations with IF markers. Fully DL-based approaches also tend to rely on indirect IF annotations, given the difficulty of manually segmenting interstitial fibrotic regions for model training.

Material and methods

This study introduces a novel digital workflow to segment and measure interstitial fibrosis in SR-stained whole slide images (WSIs) by refining DIA algorithms with structural segmentation and consequent removal of non-interstitial structures. Sixteen WSIs with varying pathologist-graded fibrosis were evaluated using two color analysis techniques—red-green filtering (RG-f) and stain deconvolution (StDeconv)—compared against point counting. Fibrosis was measured as the ratio of fibrotic tissue to cortex area.

Results and discussion

Red-green filtering, combined with structural segmentation, achieved a Spearman correlation (rs) of 0.96 and a 2.5% mean absolute error, an improvement of 12.5% compared to the absence of structural segmentation. Both RG-f and StDeconv, after structural segmentation, performed similarly, though RG-f showed a slightly better correlation with the ground truth (rs: 0.96 vs. 0.92).

Conclusion

Removing non-interstitial structures significantly improved DIA performance with SR. Further refinement through SR-specialized DL morphological segmentation could automate this workflow, increasing its clinical usability. Additionally, masks generated by the proposed methods could support downstream DL training, addressing annotation challenges and fully automating IF quantification.

Key words: Interstitial fibrosis, Sirius red staining, Chronic kidney disease, Automatic quantification, Color analysis, Kidney structural segmentation

P115 Next-generation image compression for digital pathology: JPEG XL optimises storage, speed, and clinical workflow efficiency

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Introduction

The rapid adoption of digital pathology (DP) has introduced challenges in standardising whole-slide imaging (WSI) and managing large dataset efficiently. As many DP platforms are shifting toward browser-based viewers and cloud storages, advanced compression techniques are needed to handle massive data sizes. JPEG-XL, a next-generation format, offers superior compression efficiency over JPEG 2000 with minimal quality loss and lower computational complexity. Despite its adoption in DICOM, few studies have evaluated JPEG-XL's ability to preserve diagnostically critical details and its cost efficiency.

Material and methods

To assess the feasibility of JPEG-XL for web-based WSI distribution, we developed a system that converts proprietary WSI formats into tiled JPEG-XL images, displaying them in an in-house, browser-based WSI viewer. WebAssembly was implemented to enable JPEG-XL display on both client and server applications. A total of 10TB WSIs (.isyntax, .svs, .ndpi) were collected.

Results and discussion

JPEG-XL reduced WSI file size to ~30% of the original while maintaining diagnostic quality, validated by pathologists' visual assessment. Compression ratios for JPEG-XL and JPEG 2000 were comparable under the same PSNR metric. However, JPEG-XL showed significantly faster computational performance: JPEG 2000 required ~40 minutes for a 500MB biopsy sample while preserving perceptual quality (masked-SSIM), whereas JPEG-XL achieved similar results in just two minutes using a standard laptop CPU (Core i7, 32GB RAM) when optimized for speed.

Conclusion

Our findings demonstrate that JPEG-XL optimises storage, reduces network bandwidth, and lowers CPU resource demands, making it scalable for modern DP workflows. Further evaluation is needed for scanner and viewer compatibility, as well as broader industry standardisation.

Key words: JPEG XL, DICOM, whole-slide image, WSI, image compression, digital pathology

P116 Modelling of spatial association and disease stage within the coregistered fluorescent stained tumor microenvironment data in mice

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Introduction

Cyclic immunofluorescent staining is an antigen staining method that allows for the visualization of a large amount of antigens to be detected on the same tissue. As a result, a more complex array of relationships between antigen types can be analyzed using digitization through artificial intelligence (AI). The aim of this paper is to model the spatial association of tumor cells with cancer-associated fibroblasts, blood vessels etc. within lung tumor sections of mice.

Material and methods

Lung tumor sections of nine mice at three different disease stages were taken and cyclically stained in three cycles for nine antigens (Ck5, Ck7, CD34, etc.). AxioScan. Z1 was used to digitize the tissue slides. For each cycle, an AI cell segmentation technique and a subsequent in-house cell coregistration algorithm were performed. Cell location as well as antigen intensity were consequently saved per cell. Positivity for each antigen per cell was assessed by comparing cell intensity versus fluorescent background intensity. Each tissue was divided into a hexagonal grid and antigen specific information such as counts were saved per grid cell. R package INLA was used to perform Poisson regression models with spatial random effects in a Bayesian framework.

Results and discussion

Spatial relationships between tumor cells and its environment showed important variation within and between mice at different disease stages.

Conclusion

Sophisticated statistical modelling using AI processed data allows to quantify multiple spatial relationships in the tumor microenvironment that are not directly visually apparent at once, which could have important implications for the move towards personalized therapy.

Key words: cyclic staining, coregistration, cell detection, spatial modelling, tumor microenvironment, immunofluorescence

P117 Lobular breast cancer: A challenging subtype for artificial intelligence (AI) pathology tools

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Introduction

Tumoral heterogeneity is an important factor when diagnosing cancer. Among the most challenging diagnostic pathology patters, even for expert pathologists, one is lobular cancer, an invasive breast cancer subtype characterised by a noncohesive pattern of cells arranged in individual lines or as individual cells. The aim of this study was to analyse the diagnostic performance of AI for oestrogen quantification in lobular breast cancer patients

Material and methods

We retrospectively analysed 60 lobular breast cancer patients diagnosed in our Pathology Department in 2023, using the AI algorithm ER-PR workflow of Visiopharm to automatically quantify oestrogen staining

Results and discussion

The patient-based analysis showed that the typical lobular breast cancer pathology (noncohesive pattern of cells arranged in lines or individually) was not detected in the most of the cases. The range of non-detected tumoral tissue was 2%-100%. Patients were classified in 2 groups based on the percentage of non-detected tumour tissue in the biopsies, <50% (n=29; 48.3%) and >50% (n=31; 51.7%). Moreover, AI detected hormonal receptors staining for in situ carcinoma in 3 patients. Despite the low tumoral detection rate there was correlation between pathologist's diagnoses and AI in 27 patients (45%)

Conclusion

AI tools for automatic quantification require specific training in lobular breast cancer, in order to improve tumoral detection, as it is key for biomarker quantification. If better detection rates are achieved in the future, AI tools may be used for automatic quantification of lobular breast cancer biomarkers (hormonal receptors, proliferation index, Her2) in pathology departments.

Key words: Breast cancer, Lobular, VISIOPHARM

P118 Evaluating iterative deep learning as a labeling-efficient strategy for tubular segmentation in digital nephropathology

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Introduction

A fundamental step in assessing damage in chronic kidney disease is identifying and classifying kidney structures. While deep learning-based glomerular segmentation has advanced, fewer approaches exist for tubular segmentation, despite tubules being the most abundant kidney structure. Developing supervised deep learning models for segmentation requires large annotated datasets, which can be time-consuming to create. This challenge can be mitigated through iterative deep learning.

Material and methods

This study evaluates Quick Annotator (Miao, 2021), an open-source iterative deep-learning model for annotation in terms of applicability, efficiency, and performance on PAS-stained whole-slide images (WSIs) from non-neoplastic kidney biopsies at Haukeland University Hospital. By integrating deep learning and active learning, the tool enables users to iteratively refine segmentation predictions, potentially reducing annotation time. Three study settings for tubular annotation were evaluated using different annotation time intervals over 20 iterations. Efficiency improvement was measured as the ratio of final to initial annotation speed. Performance was compared to publicly available segmentation models and a manually annotated ground truth.

Results and discussion

The annotation model trained with 5-minute annotation intervals lacked sufficient data for meaningful predictions, showing no speed improvement. The 10-minute model improved annotation speed 1.5× by iteration 10 and 4.5× by iteration 18 , whereas the 20-minute model achieved similar results by iterations 6 and 10. The best iterative method surpassed manual methods after an annotation time of 180 minutes, equivalent to approximately 1,400 annotations.

Conclusion

This study demonstrates that iterative deep learning improves annotation efficiency, minimizing manual workload by accelerating tubule segmentation with few corrections, facilitating refinement of existing segmentation models.

Key words: Iterative Deep Learning , Tubule segmentation , Annotation efficiancy enhancement

P119 Inter-rater Disagreement In Digital Pathology

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Introduction

The field of pathology heavily relies on the expertise of trained pathologists, whose decisions directly impact patient treatment and, more recently, the development of machine learning models. However, a significant challenge here is the inherent uncertainty in expert annotations. Pathologists frequently disagree on the observed tissue features, often requiring peer consultation to reach a consensus.

Material and methods

We collected annotations of Gleason scores for 10 prostate tissue slides from six expert and two novice pathologists. We observed both agreements and disagreements in annotation areas, labels, and other features. To assess existing rater evaluation methods, we reviewed both simple (e.g. IoU) and more advanced techniques (e.g. Robust Bayesian Fusion). Our analysis revealed a lack of suitable methods specifically designed for comparing pathology annotations.

Results and discussion

We have identified several key challenges. Pathology images are large, limiting the efficient application of complex algorithms. Rater disagreement occurs across multiple dimensions, including spatial regions, shapes, and categorical or quantitative labels. There might not be clearly defined objects to look for. Labels may be context-dependent, influenced by tissue-specific characteristics. Annotator expertise is variable. Practical challenges add another layer of complexity, including variations in annotation tool precision, shape representation, zoom levels, and viewport limitations during the annotation process.

Conclusion

Given that machine learning models are predominantly trained on expert-labeled data, establishing a robust framework for annotation standardization and annotator performance evaluation is essential. We aim to design a framework for systematic performance assessment of raters.

Key words: inter-rater, disagreement, annotation, uncertainty

P120 A novel approach to the assessment of mismatch repair protein immunohistochemistry utilizing digital cytometric analysis

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Introduction

Mismatch repair protein (MMR) immunohistochemistry (IHC) is a commonly performed test, resulting in significant workload for pathologists. Clonal populations with abnormal MMR staining may have clinical significance but can be challenging to identify. Digital pathology enables the use of automated image analysis tools to assess IHC expression; these tools hold promise to increase efficiency and accuracy of reporting markers such as MMR.

Material and methods

67 endometrial carcinoma cases were digitized using a Hamatsu S360 slide scanner. A semi-automated QuPath pipeline was developed with a two-class object classifier, producing optical density measurements for analysis in RStudio. A digital cytometric analysis (DCA) for tumour and stroma was generated based on MMR IHC optical density. Cases were assessed using this approach followed by glass slide review.

Results and discussion

DCA demonstrated 100% sensitivity and a specificity of 97.9% over 264 slides, which was comparable to glass review that had 100% sensitivity and 96.3% specificity. In 1.9% of cases, the pathologist deferred interpretation of the DCA to glass slides. The reduced specificity is due to small clonal populations MMR deficiency that were not identified when initially reported and subsequent review of the glass slides confirmed clonal loss. There was a significant reduction in average review time with digital cytometric analysis (DCA 12.3 seconds, glass 53.7 seconds, p = 1.679e-12).

Conclusion

Digital cytometric analysis is a time-efficient, highly sensitive method for determining mismatch repair status including clonal loss. While glass slides remain necessary, this offers potential to enhance biomarker evaluation and streamline diagnostic workflows.

Key words: Digital Cytometric Analysis, Digital Pathology, Mismatch Repair, Biomarker Assessment, Digital Analysis, Clonal Populations

P121 Let's UNITE in Transatlantic Health Data Use: Introducing the "Understanding through Networked International Transatlantic Exploration" Project

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Introduction

Transatlantic health data sharing for clinical research faces significant challenges, highlighted during the COVID-19 pandemic when it was impossible to share highly relevant virus genome data, as samples could contain human DNA. Conceptualized during the Data for Health Conferences in 2023, the UNITE project aims to develop a model for transatlantic research collaborations by identifying regulatory hurdles when exchanging biomedical data between institutions inside and outside of the EU.

Material and methods

Using multimodal data from a cohort of ~700 prostate cancer patients as a proof-of-concept, UNITE proposed a framework to share data with transatlantic partners. Specifically, we aimed to identify technical safeguards and address ethical and regulatory challenges when working with patient data where consent cannot be obtained, balancing the importance of globally pooled research data for the public interest with individual rights.

Results and discussion

The framework integrates approaches ranging from statistical analyses to federated learning, covering interdisciplinary challenges. Federated learning, for instance, seeks to balance legal and ethical considerations, yet the potential reconstructability of training data undermines its promises. To address legal concerns regarding privacy-preserving federated learning modes, a legal assessment was obtained.

Conclusion

The framework comprises interfaces for data extraction, standardization and exchange. Global data pooling enhances real-world datasets by increasing the number of cases, diversity, and heterogeneity - essential for optimizing therapy and improving diagnostic methods. We believe that transatlantic, multinational data exchange is the key to advancing future research and ultimately enhancing patient care.

Key words: Transatlantic Health Data Exchange, Regulatory Framework, Ethics, GDPR, Federated Learning

P122 AI-Driven Cancer-Agnostic Histological Features to Improve TP53 Mutation Prediction in Prostate Cancer

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Introduction

Prostate cancer (PCa) is a leading cause of cancer-related mortality and morbidity worldwide. TP53 mutations are key drivers of PCa progression, influencing tumor aggressiveness, treatment resistance, and patient prognosis. However, these mutations remain undetectable through conventional histopathology, necessitating costly molecular profiling. Recent advances in AI suggest that certain molecular alterations, including TP53 mutations, may manifest as shared morphological patterns across different cancer types, a concept known as cancer-agnostic histomorphology. This study investigates whether TP53-driven histological features generalize beyond PCa and whether integrating multi-cancer histology data improves TP53 mutation prediction in PCa.

Material and methods

We employed foundational models trained on whole-slide images (WSIs) to extract feature embeddings, which were subsequently classified using Attention-Based Multiple Instance Learning (ABMIL) to capture subtle yet predictive morphological patterns. To assess the impact of cross-cancer histology, we conducted two experimental setups: (1) training and testing exclusively on PCa (TCGA-PRAD) and (2) training on a combined dataset of prostate (TCGA-PRAD), breast (TCGA-BRCA), and bladder cancer (TCGA-BLCA), while testing only on PCa.

Results and discussion

Our results demonstrate that leveraging cancer-agnostic TP53 histological features significantly improves predictive performance in prostate cancer, increasing AUC from 0.71 (trained on PCa-only) to 0.77 (trained on cross-cancer data).

Conclusion

These findings support the potential of cross-cancer AI-driven approaches in uncovering shared tumor morphologies, providing a scalable and cost-effective alternative for molecular profiling. Future work will focus on enhancing the explainability of these features, aiming to uncover the biological mechanisms underlying TP53-associated histological patterns and their impact on tumor progression across diverse cancer types.

Key words: Molecular profiling, Precision oncology, foundational model

P123 Multimodal AI for Atypical Hyperplasia Diagnosis: A Comparative Study of CNNs, GNNs, and Hybrid Models

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Introduction

The diagnosis of atypical hyperplasia in endometrial aspirates is complex due to morphological variations across the menstrual cycle, often leading to interobserver variability. This study explores the use of artificial intelligence to enhance diagnostic accuracy by developing an AI-assisted framework to improve reproducibility and clinical decision-making in gynecological pathology.

Material and methods

Twenty endometrial aspirates diagnosed with atypical endometrial hyperplasia were selected and routinely stained with hematoxylin and eosin (H&E). The slides were then digitally scanned using a 3D Histech P1000 scanner. Image annotation was performed with QuPath v0.4, identifying regions of atypical hyperplasia and normal tissue as controls. For each tile, cell detection and classification were conducted using CellDETR. Tile pathological classification (hyperplasia or normal) was performed pathological was performed using three different AI-based approaches: a convolutional neural network (CNN) with ResNet50, a graph neural network (GNN) based on a Graph Isomorphism Network (GIN), and a hybrid model integrating both architectures through a cross-attention mechanism.

Results and discussion

All models obtained promising results when classifying tissue patches but the hybrid model was the outstanding ones in global, achieving AUC values over 0.98 compared with CNN model which obtained 0.95 and GIN 0.82.

Conclusion

The integration of AI approaches combining spatial relationships and convolutional feature extraction enhances patch-level pathological classification. Our results show that the hybrid model, leveraging CNN-based feature extraction and GNN-based structural analysis through cross-attention, outperforms individual models, achieving an AUC over 0.98. This suggests that incorporating local histological patterns and global spatial context provides a more robust diagnostic framework, reducing variability and improving reproducibility in gynecological pathology.

Key words: Gynecological Pathology, Graphs and GNN, CNN

P124 AI model for Ki-67 index prediction for breast cancer trained purely on existing diagnostic data

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Introduction

The Ki67 proliferation index is a crucial biomarker used in breast cancer diagnosis to assess tumor growth and predict patient outcomes. However, manual counting of Ki67-positive cells is labor-intensive and prone to variability, making it inefficient for large-scale clinical use. To address this, artificial intelligence (AI) offers a powerful solution for automating and standardizing the process. We developed an AI model that accurately quantifies the Ki67 index while requiring minimal labeled data, significantly reducing annotation effort.

Material and methods

Our dataset consists of snapshots from whole-slide images (WSI) stained with hematoxylin and DAB, collected during routine breast cancer diagnosis at Masaryk Memorial Cancer Institute, eliminating additional workload for pathologists. Each image is labeled solely with the Ki67 proliferation index, without explicit epithelial region annotations or cell labels. We trained a convolutional neural network to estimate the Ki67 index directly from these images, leveraging weak supervision.

Results and discussion

Our model achieved a mean absolute error of 3.49 and a Pearson correlation coefficient of 0.9624 ($p < 0.001$) against ground truth Ki67 indices. We demonstrate that the model effectively learns key histological features, including nuclei count, nuclear positivity, and tumor epithelium structures. Despite being trained on snapshots from WSI, the model generalizes to full WSIs, accurately identifying hotspots and predicting Ki67 for both hotspots and entire WSIs.

Conclusion

We developed an effective solution to automate a common pathology task, reducing pathologists' workload. Requiring no specific labeling, it allows easy domain adaptation. Surprisingly, even with weak supervision and simple architecture, the model accurately detects complex morphological structures like tumor epithelium.

Key words: breast cancer, Ki-67 index, deep learning, weak supervision

P125 Evaluation of Digital Pathology Imaging in Punch Biopsy: Quality, Processing Time, Workflow, and Diagnostic Usability

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Introduction

Digital pathology has revolutionized histopathological diagnostics by enabling high-resolution imaging, remote access, and AI-assisted analysis. This study evaluates the image quality, scanning time, digital workflow efficiency, and diagnostic usability of digital pathology in punch biopsy cases.

Material and methods

Twenty punch biopsy samples were digitized using two routine scanners and one research scanner. Image quality was assessed based on resolution, color accuracy, and artifacts, rated as good, moderate, or poor. Pathologists reviewed digital slides for diagnostic adequacy. Workflow efficiency was analyzed, including image loading times and failures using a single viewer. Scanning and review times were recorded, and file sizes were considered in storage and accessibility.

Results and discussion

Image quality varied among scanners, with differences in resolution and color fidelity. Some scanners showed minor artifacts, while others provided superior clarity. The mean scanning time was 2.5 minutes per slide. Pathologists noted differences in diagnostic ease due to image clarity and color accuracy. The average file size per image was 1 GB, with color brightness rated as good and artifact levels as moderate. Workflow inefficiencies were observed due to inconsistent image loading times.

Conclusion

Digital pathology offers high-quality imaging, though performance varies by system. Workflow efficiency is affected by scanning speed, image loading reliability, and file size constraints. Optimal digital pathology solutions must balance image quality, speed, and usability. Future research should explore AI integration to enhance efficiency and image handling.

Key words: Image Quality , Scanning Efficiency , Diagnostic Usability , File Size, Digital Workflow, Punch Biopsy

P126 Disentangling Shared and Specific Information between Whole-Slide Images and Gene Expression for Interpretable Multimodal Cancer Survival Prediction

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Introduction

Combining whole-slide images and transcriptomics data offers a promising approach for cancer survival analysis, advancing integrated precision oncology. However, current models often entangle shared and specific information between whole-slide images and gene expression, limiting interpretability and potentially suppressing discriminative features.

Material and methods

We propose Disentangled and Interpretable Multimodal Attention Fusion (DIMAF), a survival prediction framework that separates intra- and inter-modal interactions between histology and transcriptomics to produce modality-specific and modality-shared representations, with disentanglement promoted through distance correlation. Additionally, we integrate Shapley Additive Explanations (SHAP) to assess the contributions of interpretable features within the modalities and the disentangled representations.

Results and discussion

We evaluated DIMAF on four TCGA data collections (for breast, bladder, lung, and kidney carcinomas), achieving a relative improvement of 1.85% in predictive performance and 23.7% in disentanglement over state-of-the-art multimodal models. SHAP values revealed the importance of modality-shared representations while confirming the contribution of modality-specific features to survival prediction. By combining SHAP values with attention, we gain a deeper understanding of the contributions and interactions of morphological and transcriptomic features. This approach reveals, for instance, that in high-risk breast cancer cases, the embedding representing gene expression of the E2F targets pathway (found and known to be associated with increased risk) exerts its influence primarily through cross-modal interactions with morphological features representing tumor cells.

Conclusion

Our approach enhanced predictive performance and disentanglement. Moreover, the combination of SHAP values with attention weights provides deeper insights into multimodal cancer biology, emphasizing the interpretable value of DIMAF in cancer survival prediction.

Key words: Cancer survival prediction, Multimodal fusion, Disentangled representation learning, Interpretability in AI, Histology, Transcriptomics

P127 Overdiagnosis in Digital Pathology: The Potential Role of Artificial Intelligence and the Global Challenge of Diagnostic Gaps

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Introduction

Overdiagnosis is a significant issue in medical imaging, seen in lung cancer screening, mammography, and prostate cancer screening, where advanced detection leads to overtreatment, patient anxiety, and rising healthcare costs. As Digital Pathology (DP) evolves, similar concerns arise. AI-driven tools, while not yet FDA-approved for primary diagnosis, are considered a potential solution to the global pathologist shortage. However, in low-resource regions, infrastructure and funding limitations hinder high-quality DP adoption, creating a unique form of overdiagnosis—accurate diagnoses are made, but necessary therapeutic interventions are lacking. In contrast, high-resource regions may experience increased detection of clinically irrelevant findings, leading to unnecessary treatments and additional costs. This study examines AI's role in DP, balancing diagnostic accuracy with overdiagnosis risks.

Material and methods

This study employs a literature review, conceptual modeling, and theoretical analysis to investigate AI-driven overdiagnosis in DP. By drawing parallels from overdiagnosis in other medical imaging fields, it highlights similar risks that may arise as AI becomes more integrated into DP workflows.

Results and discussion

The analysis emphasizes the need for balanced, context-specific AI implementation in DP. Developing regulatory frameworks and clinical guidelines will be essential to ensuring AI-augmented DP supports diagnostic accuracy while mitigating overdiagnosis risks.

Conclusion

AI can revolutionize DP, but its integration must address global disparities. The benefits of enhanced diagnostic accuracy must be weighed against the risks of overdiagnosis, ensuring responsible AI deployment that leads to meaningful, actionable diagnoses, particularly in low-resource regions where infrastructure is insufficient.

Key words: Overdiagnosis, Digital Pathology, Artificial Intelligence, low-resource regions, global pathologist shortage

P128 Gradient boosting to predict individual cell types from nuclei segmentations

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Introduction

Assessing the tumor microenvironment in H&E stained images is key to the discovery of new biomarkers in the fight against cancer. Recently, some tissue and cell segmentation and classification techniques using deep learning techniques have emerged to great success. This process can also be broken up into two steps. A class-agnostic segmentation approach followed by a machine learning approach using gradient boosting can provide more insights into which features contribute most to the classification of cells.

Material and methods

Nuclei were segmented using a pre-trained model from StarDist, which provided a label for every nucleus from which morphological, color-related and location-based features were extracted. Ten large in-house annotated regions of lung cancer tissue were used to distribute cells into clinically relevant classes, such as tumor, necrosis, fibrosis, lymphocytes, etc. The data was split into training, test and validation sets and a gradient boosting model was trained for multiclass prediction using XGBoost in R. Feature importances for the model were extracted.

Results and discussion

On the validation set, the multiclass misclassification error was ~11%. Variable importance showed that the average distance between the nearest neighboring nuclei was most important, followed by the nucleus size and the color values of the surrounding area of the nucleus.

Conclusion

Prediction of the cell type can be performed given an image and a segmentation label, where information on the neighboring cells also showed importance. This observation shows the need to implement more spatial features into the model.

Key words: Machine Learning, Tumor microenvironment, Cell typing, Feature importance, Gradient boosting

P129 Accelerating Routine Pathology Workflow with Digital Image Registration

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Introduction

Pathology faces increasing case numbers handled by fewer pathologists while time-consuming diagnostic tasks, e.g., with multiple slides, increase. Workflow automation is critical to address this gap. Diagnosing cancer, such as breast or prostate, requires H&E and immunohistochemistry (IHC) stains. IHC preparation takes about 2-6 days, after which the diagnosis is resumed. Comparing structures across slides is necessary, but locating previously identified positions on new slides is time-consuming and tiring.

Material and methods

We developed an automatic workflow and software prototype that: a) enables bookmarking suspect regions during initial H&E review in a browser-based viewer, b) identifies slide stacks in real-world digitized sections, thereby distinguishing on-slide controls from samples, c) automatically registers stacks using HistokatFusion[1], aligning each image to its transformed predecessor in the stack, d) displays aligned sections on top of the original H&E, starting at the bookmarks.

Results and discussion

A retrospective pilot study at University Hospital Erlangen involving 8 cases showed registration workflow to reduce diagnosis time from 540 to 478 seconds per case (11% acceleration) compared to a digital workflow, and from 579 to 478 seconds (17% acceleration) compared to an analog workflow. A video of the software prototype is available at https://s.fhg.de/ecdp-mevis-2025.

Conclusion

Image registration, already established in other medical fields, also accelerates diagnostic workflows in pathology. An extended study is planned, and further acceleration is possible by caching, parallelization, and further user training. These results represent the first real-time multimodal registration directly integrated into the pathological workflow, reducing cognitive load as well as an increasing effectiveness up to the final report.

Key words: browser-based viewer, automatically registered stacks , HistokatFusion, bookmarking, automatic workflow

P130 An AI-enabled and Automated Workflow for Tissue Macrodissection in Molecular Pathology

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Introduction

The morphological and molecular worlds are advancing at pace. While correlating molecular biomarkers with morphology is gaining interest, there is a more immediate gain by applying computational pathology to molecular diagnostics. A minimum tumour content in a sample is required for a reliable and sensitive molecular result. Currently, the selection of the region of interest, assessment of tumour content, and subsequent dissection are done manually, leading to a subjective and imprecise workflow. Digital computational pathology integrated with robotic dissection enables a quantifiable and standardised fully digital workflow. This has numerous advantages. Complex samples can be annotated with high precision and confidence and dissected precisely and with full traceability. In this joint effort the potential quality gains of such an automated and digital workflow are investigated.

Material and methods

A fully digital and AI-assisted tissue dissection workflow is implemented, comprising digital annotation and tumour content quantification using Indica Labs' Lung Macrodissect AI, followed by the automatic transfer of the annotation from the H&E reference slide to the dissection slide images and robotic dissection by the Xyall Tissector instrument. Pre- and post-dissection images are captured to determine the accuracy of the dissection. NGS results of the collected tissue specimens are compared to those of the manual workflow.

Results and discussion

The digital workflow yielded higher tumor content samples thereby increasing the number of cases eligible for large panel sequencing.

Conclusion

Integrating AI-based digital, computational pathology in tissue sample selection for genomic tumor profiling improves sample quality and contributes significantly to the quality of care.

Key words: Artificial intelligence, molecular pathology, tumor cell percentage, automatic tissue dissection, region of interest selection, digital pathology

P131 Automated Segmentation of Unstained Kidney Biopsies: The Feasibility and Challenges

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Introduction

Despite advances in computational pathology, automated segmentation of unstained kidney biopsy samples remains an unmet challenge. Addressing this gap would significantly contribute to enhancing kidney disease diagnostics by enabling faster, more objective tissue analysis while preserving samples for further molecular testing. Automation would also reduce reliance on staining protocols, minimizing inconsistencies and streamlining the diagnostic workflow. In this study, we investigated the feasibility of segmenting unstained kidney biopsy brightfield images to identify different renal structures – glomerulli, tubulli, vessels, and interstitium – using different image segmentation techniques.

Material and methods

Unstained, brightfield images of formalin-fixated paraffin-embedded kidney biopsy tissue were segmented using conventional methods and the Segment Anything Model (Kirillov et al., 2023). The results obtained were evaluated by both objective metrics and visual comparison with the same images previously segmented manually using QuPath software and confirmed by a pathologist's evaluation.

Results and discussion

Results showed that the employed methods failed to accurately segment the different renal structures. This is mainly due to the similarity in texture among different structures and the significant shape irregularities within the same class. For instance, the tested methods struggled to define the borders of glomeruli and to distinguish tubulli from the interstitium due to the lack of strong edges.

Conclusion

The applied segmentation models were insufficient for the task. The low contrast and structural complexity of the unstained brightfield images demand further pre- and post-processing, as well as the development of specialized deep learning models. Overcoming these challenges could enable fully automated kidney biopsy analysis, improving Chronic Kidney Disease insights and clinical decisions.

Key words: automatic segmentation, machine learning, kidney, unstained biopsies, Chronic Kidney Disease

P132 Colorectal Adenocarcinoma Segmentation Model – Validation of a Deep Learning Model on In-House Colorectal Biopsies

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Introduction

Colorectal cancer (CRC) is third most common cancer in males and second in females in developed countries. Deep learning-based segmentation models have shown promise in improving diagnostic precision. This study aims to validate a pre-trained CRC resection segmentation model for tumor detection in in-house colorectal biopsy specimens.

Material and methods

The Unet++ ResNet34 architecture was used for model training with a batch size of 64. The learning rate started at 5 x 10^-5 for the first 500 iterations and then reduced to 10^-5 for fine-tuning. Batches were formed by ensuring an equal number of patches from each class, assuming balanced class representation. Data filtering was applied by excluding patches where the annotated area was less than 10% for specific classes. Around 780 patches were used for training. Tumor segmentation from TASK-1 was utilized, and tumor class probability was assigned based on the average segmentation mask in tissue regions.

Results and discussion

The segmentation model achieved 95% accuracy on the external resection dataset. For in-house dataset validation, 169 whole slide images of routine colorectal biopsies were analyzed across three histological classes: (1) Adenocarcinoma & Adenoma, (2) Other malignancies than adenocarcinoma, and (3) Benign histology. The model demonstrated a good precision value of 0.80 with a recall bias of 0.72. Classification performance remained strong, with an AUC exceeding 0.80 and a positive predictive value surpassing 75%.

Conclusion

This deep learning model shows high potential for automated CRC detection, enhancing diagnostic accuracy. Further optimization and validation on larger, diverse datasets are needed for broader clinical application.

Key words: colorectal cancer, adenocarcinoma, deep learning, segmentation model, biopsy, validation

P133 Prospective validation of image-based artificial intelligence for cervical cancer screening in a resource-limited setting

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Introduction

Implementation of image-based artificial intelligence (AI) for cervical cancer screening in resource-limited settings could be especially advantageous due to the shortage of experts. Cervical cancer is the second deadliest cancer for women in low- and middle-income countries and is deemed eradicable with screening- and HPV vaccination programs. We have previously shown that AI algorithms can detect atypical cells in digitized Papanicolaou (pap) stained conventional cervical smears on par with human experts in a primary healthcare setting. In the current study, we conducted a prospective validation of the AI-based system.

Material and methods

We deployed a previously developed deep learning-based system on a new set of pap smears (n=265) collected from HIV-positive women at a primary healthcare hospital in Kwale region, Kenya. The conventional pap smears were digitized with a portable whole-slide scanner (Ocus20x, Grundium) and analysed with the AI algorithm. The AI results were compared to conventional manual microscopy performed by a pathologist.

Results and discussion

The area under the receiver operating characteristic curve (AUC) was 0.95 for high-grade and 0.83 for low-grade squamous intraepithelial lesions (HSIL and LSIL), with no HSIL misclassified as non-atypia.

Conclusion

Our proposed minimal infrastructure AI-based digital pathology solution for cervical cancer screening achieved high sensitivity for HSIL, with a lower performance for LSIL in a prospectively collected independent validation series. A slight decrease in accuracy as compared to the original study could be explained by a domain shift since the personnel collecting and preparing samples, the staining reagents and the scanner were different in this validation series.

Key words: Artificial intelligence, Deep learning, Cervical cancer, Low-resource settings

P134 Validation of a AI driven sTIL quantification pipeline against pathologist assessments in Head Neck Squamous Cell Carcinoma

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Introduction

Assessment of stromal tumor-infiltrating lymphocytes (sTILs) is emerging as a valuable prognostic marker, in the era of immunotherapy, although limited by difficulties in implementation of guidelines and poor inter-observer concordance.

Material and methods

Manual sTIL percentage was estimated on a single representative resection WSI of 83 patients of HNSCC (69 males, 14 females) independently by two pathologists (msTIL1 & msTIL2), as per the International immuno-oncology working group guidelines. Computational assessment (csTIL) was performed on two hotspots marked on each slide by 1 of the pathologist. The computational pipeline comprised of StarDist based nuclear segmentation and classification (epithelial, stromal and immune cells) pipeline trained on in-house datasets, using unsupervised clustering of handcrafted pathomic features, followed by segmentation of epithelial and stromal regions using Delaunay triangulation.

Results and discussion

The median (IQR) sTIL scores were 55 (40), 47.5 (36.2), 23.98 (16.3) for the 2 msTIL and csTIL assessments. The pairwise correlation between msTIL1/msTIL2 and csTIL was moderate (Pearson coefficient 0.48, 0.51 respectively) while the weighted kappa coefficient was poor (0.13 and 0.07). The correlation between both the pathologists was strong (Pearson coefficient 0.65, weighted kappa 0.49). Multi-rater weighted Cohen's kappa showed a weak (0.01) correlation. The current csTIL pipeline underestimated sTIL by a median of 25.5%.

Conclusion

Overall we found poor concordance between the manual sTIL scores from 2 expert pathologists and our initial computational sTIL scores based on various statistical measures. We intend to improve on this computational pipeline and present the complete evaluation of ~500 cases in due course for this meeting.

Key words: sTIL, Computational Pathology, AI, Digital Pathology, Clinical application of AI

P135 Diffusion Models for Morphology-Guided Transcriptomics: A Computational Framework

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Introduction

The emergence of foundation models in artificial intelligence presents unprecedented opportunities to understand complex biological systems. These models, capable of extracting discriminative representations from large datasets, pave the way for new multiscale and multimodal integration and prediction approaches. However, their application to digital pathology - considered as gold standard in medicine and the first visually structured omics expression of human tissue - remains largely unexplored. At the same time, spatial transcriptomics bridges the gap between tissue morphology and gene expression, offering a unique opportunity to capture spatial heterogeneity at the molecular level. The combined exploitation of these data could significantly enhance our understanding of underlying pathophysiological processes.

Material and methods

In this context, recent diffusion models provide a promising conceptual framework by capturing the intrinsic stochasticity of molecular expression, surpassing the deterministic mappings traditionally constructed. This conceptual approach also addresses the imbalance between histological patch size and gene expression vector size.

Results and discussion

To fully evaluate their potential for transcriptomic profile prediction, we propose an analytical framework that initially focuses on extracting transcriptomic profiles most correlated with morphological features. This requires a dedicated evaluation protocol that integrates both classical regression metrics and spatially-aware metrics, ensuring a biologically grounded and robust assessment of model performance. Our framework aims to standardize this evaluation by incorporating spatial coherence metrics, modality weighting strategies, and biologically relevant error quantification.

Conclusion

By establishing a rigorous methodological foundation, this work seeks to define a set of standards for multiscale analysis in digital pathology and transcriptomics.

Key words: Computational Pathology, Generative AI, Diffusion Model, Spatial transcriptomic

P136 Evaluation of Histopathology Foundation Models for General Purpose Task on head and Neck Cancer Tissue

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Introduction

Foundation models, primarily transformer-based architectures, have shown promise in histopathology image analysis. However, their large-scale nature raises concerns about computational cost and efficiency, especially for simpler histopathological tasks. We compare transformer-based foundation models with traditional convolutional neural networks (CNNs) to assess whether the resource-intensive training of foundation models is justified for fundamental histopathology tasks. By evaluating model performance, efficiency, and interpretability across various image analysis benchmarks, we aim to determine if the complexity of transformers provides a meaningful advantage over CNNs or if smaller, task-specific models suffice.

Material and methods

We evaluate deep learning models for histopathology by comparing their ability to extract and utilize information from foreground (tissue structures) and background (non-informative regions). Our analysis includes CNNs (ResNet50, ResNet34, DenseNet121, VGG16, VGG19), self-supervised models (MoCov2, SimCLR), and transformer-based models (UNI, UNI2, CONCH). We extract features from whole-slide image patches at 5X magnification (1.6 µm/pixel) and use K-means clustering to separate foreground from background, further subdividing the foreground into 15 clusters for detailed analysis.

Results and discussion

We analyzed the results from all model pairings for comparison. ResNet50 and CONCH showed the highest agreement, achieving a 99% IoU score, followed by ResNet34 and CONCH with 97% IoU. The weakest performance was observed in the SimCLR and UNI pairing with 80% IoU.

Conclusion

Our study highlights the need for caution when using transformer-based models in histopathology, as their effectiveness is problem-specific. CellViT struggles with single-nuclei segmentation, likely due to poor positional encoding, raising doubts about the necessity of large models when smaller, more efficient alternatives may suffice.

Key words: Foundation models, vision transformers, CNNs, UNI, ResNet

P137 Optimizing a Scanning Protocol for Liquid-Based Cervical Cytology on Whole Slide Images Using Z-Stack

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Introduction

In the field of gynecological cytology whole-slide imaging without using Z-stack to focus on 3-dimensional (3D) cell groups is limited. Z-Stack has many options for layer selection. We aimed to optimize a protocol with small file size and fast scan time using Z-stack by comparing different layers to increase confidence of pathologists' diagnosis on 3D clusters on WSIs.

Material and methods

Sixteen PAP smear cases diagnosed AIS(n=1), HSIL(n=2), LSIL(n=2), AGC (n=1) and NILM(n=10) were selected for our study. All glass slides were scanned with NanoZoomer S360 used at ×40 magnification with a pixel resolution of 0.23 µm. Four different protocols (13 layers with 0,6 µm distance (A), 7 layers with 1 µm distance (B), 5 layers with 1,5 µm distance (C), and 3 layers with 2 µm distance (D)) were created. All protocols were evaluated by two pathologists and compared by their scanning time, file size, quality (1-poor to 5-excellent) regarding pathologists' confidence

Results and discussion

No significant differences were seen between the protocols, concordance rates were all good to near perfect. Protocol A, B, C, D took 341, 209, 132, and 77 minutes respectively and file sizes followed this order. In addition, the quality score for A, B, C and D protocols were 4.1, 3.9, 3.3, and 3.3 respectively.

Conclusion

Protocol A is best for pathologists' confidence. However, when considering all results the optimized protocol for routine scanning has been shown to be Protocol B. Our next step is to use this protocol on more cases by involving more pathologists to get additional data such as diagnosis time.

Key words: Cytology, Scan protocol, Z-Stack, PAP smear

P138 Survival Modelling using whole slide images in Head Neck Squamous cell carcinoma achieves good predictive value

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Introduction
Disease-free survival modeling and outcome prediction is a complex, multi-faceted task often limited by complex relationships between variables and limited accuracy. The current published SOTA WSI-based modeling algorithms have shown, at best, moderate discriminatory power.

Material and methods
We trained and validated an Attention-MIL model using custom loss functions(paired index loss and mean squared error) on a cohort of locally advanced head-neck squamous cell carcinoma undergoing R0 resection of the primary tumor and neck nodes, followed by either adjuvant RT or CTRT, treated with curative intent. A single representative WSI from the primary tumor was selected per patient for training, with a rough tumor boundary drawn by a pathologist. We further tested the model performance on unseen slides.

Results and discussion
The mean(SD) age of the cohort was 45.09±9.8 years with M:F ratio of 6.134. All patients completed treatment. Disease progression occurred in 229/462 patients with a median follow-up of 95.9 months. There was no difference in survival between the treatment arms (Adjuvant RT vs CTRT) based on conventional clinicopathologic variables. The attention-MIL model achieved a c-index of 0.7544 on the training dataset and 0.6486 on the unseen dataset.

Conclusion
Semi-supervised modeling on a representative WSI of the primary tumor was able to achieve a good discriminatory power in an unseen dataset. We intend to present a more detailed analysis of an improved version of the model, combined into a fully automated pipeline, trained on multiple slides of the same patients and its additive value over a model trained on only conventional clinicopathological variables.

Key words: Attention MIL, Survival Modelling, Whole slide Image, Computational Pathology, AI driven predictive pipeline

P139 Efficient training of state-of-the-art pathology foundation models on orders of magnitude fewer WSIs

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Introduction

Recent advancements in computational pathology have been largely propelled by the development of modern vision foundation models (FMs) trained on vast collections of pathology images. Studies indicate that increasing the scale of training data and the model complexity often enhances FM's performance on downstream tasks.

Material and methods

In this work, we apply several changes to the standard workflow for training FMs on pathology images. Additionally, we implement a post-training technique for fine-tuning the FM on high-resolution images after training to enhance the embeddings by effectively increasing the number of tokens generated from every image.

Results and discussion

We demonstrate that high-performing pathology FMs can be trained with significantly fewer whole slide images (WSIs) than one may previously have thought necessary. We present several novel pathology FMs trained on up to two orders of magnitude fewer WSIs than those used for other state-of-the-art FMs while achieving comparable or superior performance. Even our model trained just on 12k TCGA WSIs, which we make publicly available, outperforms most existing FMs published to date.

Conclusion

The results presented in our work suggest that there still remains a significant potential for further improving the models and algorithms used to train pathology FMs to take full advantage of the vast available data. As pathology AI continues to evolve, we believe our work makes a solid contribution to the collective efforts of devising better pathology FMs. It brings us another step closer to achieving real impact in clinics, lowering the burden on pathologists, and ultimately improving the quality of provided healthcare.

Key words: Foundation models, Computational pathology, Whole Slide Images

P140 Super Vision Without Supervision: Multimodal Knowledge Distillation for Enhanced Representation Learning from Biomedical Imaging

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Introduction

Clinicians and medical researchers can rarely access state-of-the-art imaging methods for newly obtained patient samples, such as super-resolution microscopy, spatial -omics, or multiplex immunofluorescence. Researchers therefore usually only train machine learning models for routine imaging modalities and stains, such as H&E, as this enables new, unseen samples to be routinely processed by these models. However, this approach prevents models from learning from state-of-the-art modalities or incorporating prior knowledge. Existing multimodal approaches can lead to poorer results than unimodal training by neglecting useful features which would be learned by conventional approaches.

Material and methods

We present a new self-supervised knowledge distillation method, TriDeNT, which dynamically distils features from additional data sources to H&E during pre-training. We distil immunohistochemistry, immunofluorescence, spatial transcriptomics, and segmentation masks, and evaluate TriDeNT on a variety of clinically relevant tasks.

Results and discussion

TriDeNT achieves state-of-the-art performance, and learns measurably different, more biologically meaningful features. This makes TriDeNT more robust to distribution shift and few-shot learning, while retaining the desirable features of unimodal encoders, such as adversarial robustness, and prevents harmful or irrelevant paired data deteriorating the quality of learned representations. We find that knowledge distillation with TriDeNT improves performance on all 11 investigated tasks, with performance gains determined by the relevance of the paired data to the task.

Conclusion

We show TriDeNT is an exciting avenue for both improving clinically-relevant downstream task performance, and for biological hypothesis generation and biomarker discovery. TriDeNT leverages both state-of-the-art and routine data to create better models for discovery in the lab, and more personalised treatment for patients in the clinic.

Key words: Self supervised learning, Knowledge distillation, Histopathology, Multimodal data integration, Spatial Transcriptomics, Biomarker Discovery

P141 Metadata Quality Assurance Using Deep Learning Based Automated Stain Detection

Maximilian C. Koeller[1], Christoph Stroblberger[1], Christopher Kaltenecker[1], Maximilian Gletthofer[1], Renate Kain[1]

[1]Department of Pathology, Medical University of Vienna, Austria

Introduction

Staining information represents vital Whole Slide Image (WSI) metadata. Especially in the context of retrospective high throughput scanning of archived non-barcoded slides with handwritten labels, this information might be missing. Hence, it was investigated, if this problem can be solved using deep learning.

Material and methods

2994 WSIs of kidney biopsies uniformly distributed across six stain classes (HE, AFOG, PAS, Methenamine Silver, EVG, and "other", mostly IHC) were collected (499 WSIs/class). Per WSI approx. 47 tiles (512x512 px, ~0.5 um/px, >20% tissue) were randomly sampled, yielding 138,354 tiles. Tiles were split at WSI level into pretrain and test set (80:20). A ResNet50 (pretrained on ImageNet) was trained using 3-fold cross validation, standard ResNet normalization and no color augmentation. Stains were assigned at WSI-level by means of majority voting on 40 randomly sampled tiles.

Results and discussion

Initially an accuracy of 0.957 (± 0.004) was achieved at WSI level on the test set. Subsequently, misclassified WSIs were manually reviewed revealing that 86 WSIs were incorrectly labeled. Errors occurred either due to wrong data entry (2.61 %) or incorrect slide labels (0.26 %) constituting a total error rate of 2.86 % (CI 95%: 2.3 – 3.5). After correcting the wrong labels, the stain classifier exhibited an accuracy of 0.986 (± 0.004).

Conclusion

Stain detection can be readily solved using deep learning with high accuracy, even outperforming human annotators. Due to the low computational cost of the presented pipeline, it constitutes an ideal tool for either automated metadata generation or performing quality assurance on already existing metadata, thereby, improving metadata quality.

Key words: Stain Detection, Metadata, Quality Assurance, Deep Learning, Whole Slide Imaging

P142 Predicting molecular subtypes of muscle-invasive urothelial carcinoma using Histopathology Foundation Models

Christian Matek[1, 2, 3], Julian Main[1, 4], Daniel Firmbach[1], Miriam Angeloni[1], Fulvia Ferrazzi[1], Arndt Hartmann[1, 2, 3], Markus Eckstein[1, 2, 3]

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[2] Comprehensive Cancer Center EMN, University Hospital Erlangen, DE
[3] Bavarian Cancer Research Center (BZKF), University Hospital Erlangen, DE
[4] Georg-Simon-Ohm, Technische Hochschule Nürnberg, DE

Introduction

Several molecular classification schemes for muscle-invasive bladder cancer (MIBC) have been developed over the past few years, culminating in the consensus molecular classifier published by Kamoun et al. in 2020. It is the aim of these classifiers to provide a better patient stratification for novel therapeutic strategies in MIBC. Predicting these molecular classes from routine H&E slides thus meets an increasingly relevant clinical need.

Material and methods

We collected a local cohort of 235 MIBC cases (110 basal/squamous, 73 stroma-rich, 23 luminal unstable, 16 luminal papillary, 4 luminal unspecified, 9 neuroendocrine-like) as well as publically available MIBC data (TCGA). After exclusion of rare neuroendocrine-like cases, and combination of luminal cases into one category, we trained trained and evaluated several WSI-level subtype prediction classifiers using current histopathology foundation models.

Results and discussion

Algorithms allow molecular subtype prediction with a fair degree of accuracy, and tend to provide a histomorphologically reasonable attention distribution, although many current foundation models contain only little organ-specific training samples. Ablation studies suggest that classifier performance is still in the data-limited regime. It might be used to inform molecular downstream testing or augment the current workflow of molecular subtype determination.

Conclusion

Molecular subtypes of MIBC can be predicted using current foundation models with a fair degree of accuracy. Algorithm predictions may inform further downstream testing for patient stratification.

Key words: Urothelial Cancer, Foundation models, molecular subtype prediction

P143 Mapping the tumor microenvironment combining cyclic multiplex immunofluorescence with standard Hematoxylin-Eosin staining for whole slide imaging

Kim Nijsten[1], Sandrina Martens[1], Pascal Gervois[1, 3], Melvin Geubbelmans[2], Jari Claes[2], Dirk Valkenborg[2], Christel Faes[2], Michiel Thomeer[3, 4], Esther Wolfs[1]

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[2] Data Science Institute (DSI), UHasselt - Hasselt University, Belgium
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Introduction

The complexity and heterogeneity of the tumor microenvironment (TME) is a driving factor in disease progression and therapy resistance which poses a significant challenge to develop personalized cancer treatments. Visualizing the tumor and its microenvironment using standard histology and immunofluorescence staining allows for a comprehensive understanding of morphological and cell-specific features. Integrating these techniques with digital pathology approaches offers opportunities to analyze cellular and spatial heterogeneity. This study aims to develop a method that combines cyclic multiplex immunofluorescence (mIF) with Hematoxylin-Eosin (HE) staining on a single slide, followed by whole slide scanning to enhance understanding of TME cellular diversity.

Material and methods

Cyclic mIF was manually performed on mouse lung tumor tissue with various markers for the tumor, its microenvironment, and immune component. Antibody removal was obtained via a harsh stripping technique. Subsequently, HE was performed on the same tissue slide. Whole slide images were acquired using the AxioScan.Z1 digital slide scanner.

Results and discussion

The study successfully demonstrated sequential HE staining following mIF on one slide, and morphological characteristics observed in HE matched mIF findings. In the cyclic staining approach, we achieved a loss of signal through harsh antibody stripping in between each cycle.

Conclusion

Our innovative approach enabled the combination and digitization of mIF staining and standard HE on a single slide, providing insights into morphological and cell-specific features within the tumor microenvironment. Moreover, the acquired whole-slide images serve as a valuable resource for AI algorithm development, facilitating the identification of whole-slide spatial TME heterogeneity in future research crucial for developing precise diagnostics and personalized treatment strategies.

Key words: Tumor microenvironment , Heterogeneity, Cyclic multiplex immunofluorescence, Hematoxylin-Eosin staining, Whole slide imaging

P144 One Pixel to Many Objects Mapping for Nuclear Segmentation and Marker Evaluation in Spatial Biology

Calum MacAulay[1, 2], Shunsuke Ishige[1, 2], Puneet Arora[1], Paul Gallagher[1], Martial Guillaud[1, 2]

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[2] Integrative Oncology Program, University of British Columbia, Canada

Introduction

In tissue sections one is trying to delineate overlapping semi-transparent objects of random sizes and shapes, a technically demanding task that even human annotators find challenging to do repeatably.

Material and methods

A robust solution to this challenge can be achieved by using sequential UNets (SUNet). One UNet to identify nuclei centers and a second UNet to segment only the nuclei at every identified center and additional ones to segment cytoplasm, etc. This enables the correct delineation of every nucleus and cell even in areas with complex clusters of overlapping nuclei. This approach requires that one pixel can be mapped to multiple nuclei, a mapping ability which has multiple benefits. Using this approach on a Thionin (DNA specific) stained NSCLC TMA set of over 400 cases we demonstrated how unsupervised learning on just nuclei morphology and DNA distribution within a nuclei can define specific cell types that associated with clinical patient characteristics such as cancer type and stage, size, metastatic spread, genetic alteration status, patient sex and outcome.

Results and discussion

We demonstrate how the one-to-many mapping improves our ability to classify nuclei into distinct types or groups. We show that features calculated based on allowing one pixel to belong to multiple cell cytoplasm's can enhance our ability to quantify a cell's protein expression level and protein spatial distribution by enabling marker expression compensation based upon the amount and location of the observed cell overlap.

Conclusion

We demonstrate how a one pixel to multiple objects (nuclei/cells) mapping improves the quantification of nuclei features and protein marker expression.

Key words: Nuclei / Cell Segementation, Deep Learning, Lung Cancer, Spatial Biology

P145 Digital Network for Pathology within SISCAT: Strategy and Key Points for Transformation

Reixach Elisenda[1], Padial Alicia[2], Vives Marc[3], López Alex[4], Badia Daniel[5], Ferreres Joan Carles[6], Méndez Inma[7], Sant Francesc[8], Temprana Jordi[9]

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[2] CCF Center for Telecommunications and Information Technologies Espanya
[3] CIMD UDIAT Centre Diagnòstic Espanya
[4] Pathology Department Consorci Hospitalari de Vic Espanya
[5] Pathology Department Parc Taulí Hospital Universitari nstitut d'Investigació i Innovació Parc Taulí (I3PT-CERCA), Universitat Autònoma de Barcelona Espanya
[6] Pathology Department Althaia Xarxa Assistencial Universitària de Manresa Espanya
[7] Pathology Department Vall Hebron University Hospital Espanya

Introduction

The Catalan Health Service (CatSalut) is committed to support the digitalization of Pathology Departments across Catalonia's public healthcare hospitals, with full implementation set to be by 2025.

Material and methods

One of the first building block deployed was the Pat-SIMDCAT platform. Serving as the central repository, Pat-SIMDCAT stores and distributes using the DICOM standard (Supplement 145), high-resolution Whole Slide Images which can be retrieved by any connected hospital. Since 2022, Pat-SIMDCAT is safeguarding all bright-field, routine histopathology, histochemistry, immunohistochemistry, direct immunofluorescence, ISH, and FISH activity of eight hospitals of the Catalan Health Institute (ICS)2 resulting in an accumulated volume of 2.7 petabytes. In addition, seven more centres are currently connecting their digital pathology solution to Pat-SIMDCAT, and their full integration will be finished by the first quarter of 2025. By securing funds from the Spanish Recovery, Transformation and Resilience Plan and NextGeneration EU, CatSalut, with the help of a pathologist-working group, has soon tendered a centralized public procurement process to provide a digital pathology solution for the remaining Pathology Departments of the Catalan public healthcare system, all of which will also be integrated into the Pat-SIMDCAT.

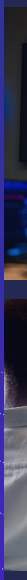
Results and discussion

All those building blocks will make possible a unique Digital Pathology Network in Catalonia promoting territorial equity and enabling collaborative work between pathologists from different institutions while addressing the future challenges of this specialty in the healthcare sector

Conclusion

All those building blocks will make possible a unique Digital Pathology Network in Catalonia promoting territorial equity and enabling collaborative work between pathologists from different institutions

Key words: Digital Pathology Network, DICOM standard, Tender



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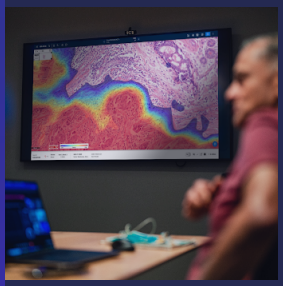



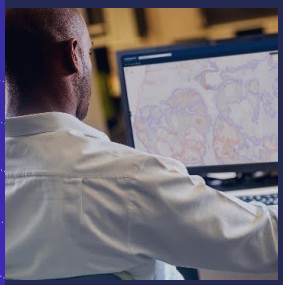
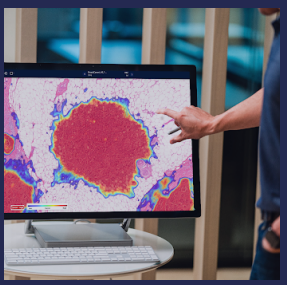

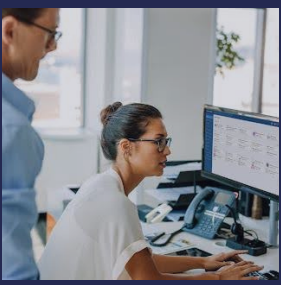

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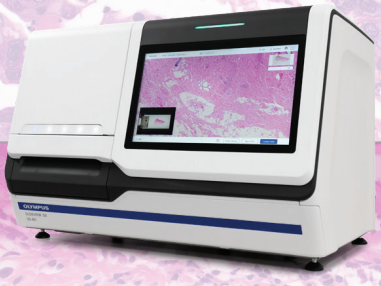

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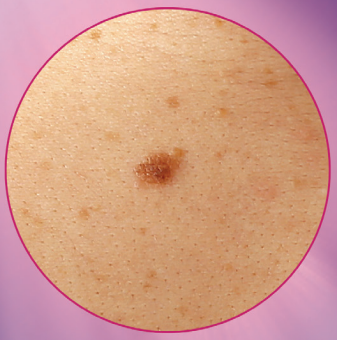

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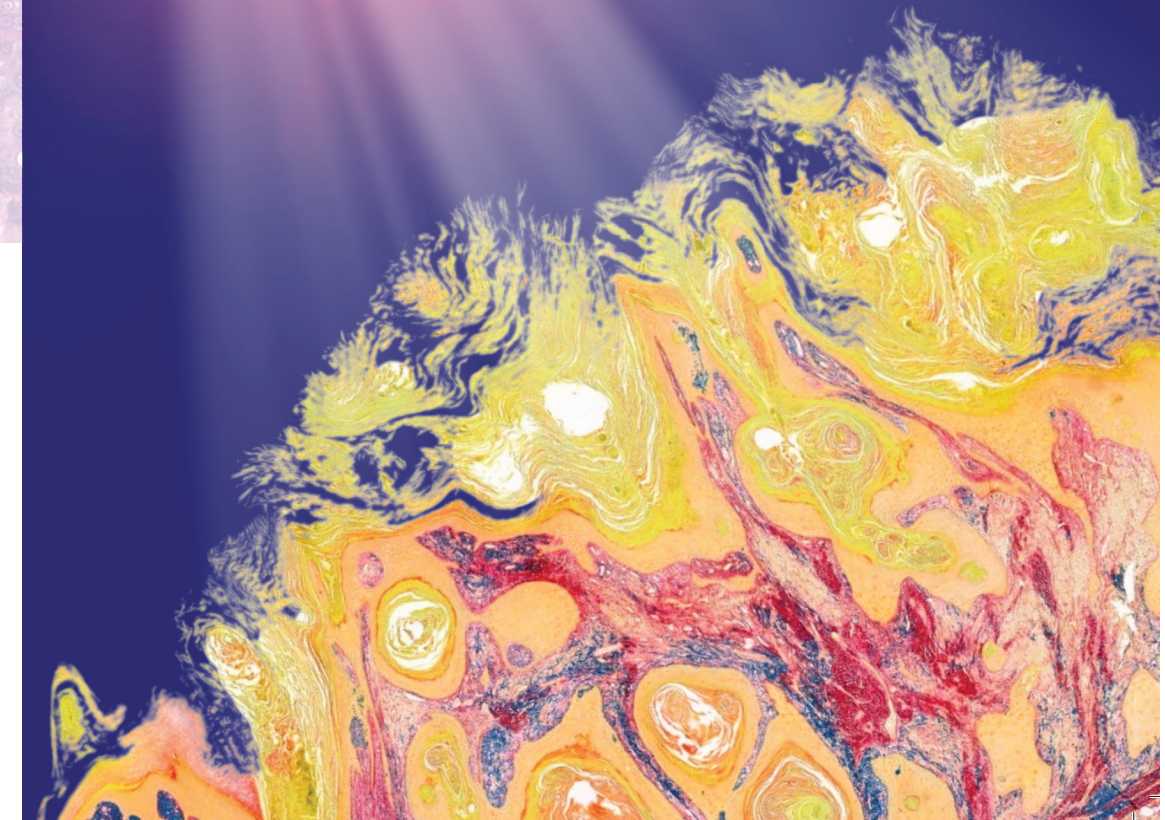

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26th June 2025

AUDITORIUM

13:00 – 13:45 Transforming Pathology: Achieving Digital Excellence in Cytology and Multi-Site Integration

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27th June 2025

AUDITORIUM

13:00 – 13:45 Implementing Digital Pathology in Clinical Practice: Regional Strategies and Hospital-Based Innovations

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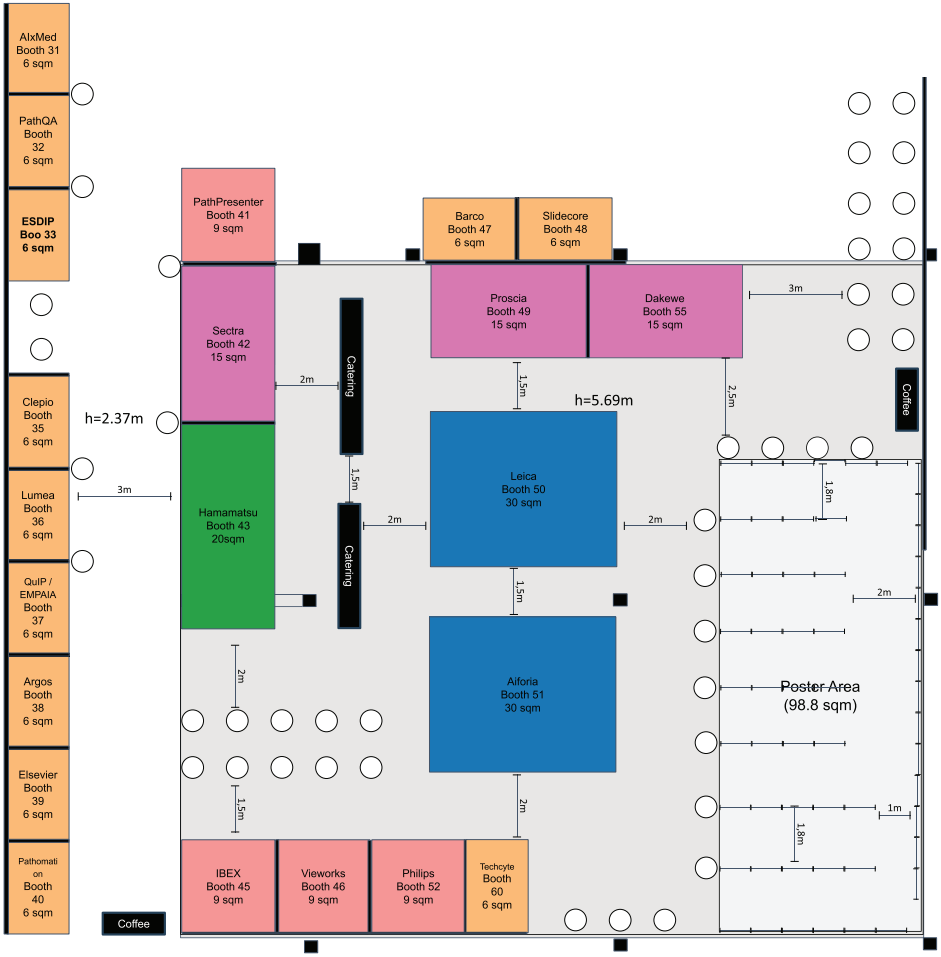
INDUSTRY EXHIBITION

EXHIBITION AREA RIGHT

INDUSTRY EXHIBITION

EXHIBITION AREA LEFT



LOCATION

The industry exhibition is located in the Conference Center.

OPENING HOURS

Thursday 26/06/2025
09:00 – 21:00
18:30 – 21:00
Poster Reception and
Get Together

Friday 27/06/2025
08:15 – 19:00

Saturday 28/06/2025
08:00 – 14:00

Booth number	Company	Booth number	Company
B03	Histofy	B31	aIx Med
B04	PathAI	B32	PathQA
B05	O3 Entreprise	B35	Clepio
B06	Qritive	B36	Lumea
B07	Paige	B37	QuIP / EMPAIA
B08	Infinitt	B38	Argos
B09	Fraunhofer	B39	Elsevier
B10	Aurora mScope	B40	Pathomation
B14	Evident	B41	PathPresenter
B15	Motic	B42	Sectra
B16	Epredia	B43	Hamamatsu
B17	KFBIO & Huawei	B45	IBEX
B18	3DHISTECH	B46	Vieworks
B19	Indica Labs	B47	Barco
B20	Optra Scan	B48	Slidescore
B21	Roche	B49	Proscia
B22	AetherAI	B50	Leica
B23	Celerato	B51	Aiforia
B24	UK Neqas	B52	Philips
B25	Mindpeak	B55	Dakewe
B26	Primaa	B60	Techcyte
B27	NTP		

PRE-CONGRESS WORKSHOPS

24th June 2025

09:00 - 18:00 | Room 8	IHE PaLM WG
09:00 - 19:45 | Room 5	Scanner Benchmark

25th June 2025

09:00 - 13:00 | Room 8	IHE PaLM WG
09:00 - 12:00 | Room 4	DICOM WG-26
09:00 - 19:45 | Room 5	Scanner Benchmark
12:00 - 14:00 | Room 7	ISO/AWI 24051-2 Drafting Group Meeting
13:00 - 14:00 | Room 6	Building Trust Through Ethical Innovation and Patient Partnership
13:00 - 15:30 | Room 4	DICOM WG-26
14:00 - 15:30 | Room 8	IHE PaLM WG
14:15 - 15:15 | Room 6	Cross-Continental Collaboration: Accelerating Digital Pathology Adoption Through Shared Knowledge
15:00 - 16:00 | Room 7	Regulatory Interaction Platform Stakeholder Engagement Meeting
15:30 - 17:00 | Room 6	Image Management Simplified: PathPresenter IMS for Clinical Care, Research, Education, & AI
16:00 - 18:00 | Room 4	IHE PaLM WG & DICOM WG-26 Joint Meeting
17:15 - 18:15 | Room 6	JSDP Companion Meeting

26th June 2025

13:50 | VIP Area	**SOCIAL MEDIA GET TOGETHER**

SOCIAL EVENT

All congress delegates, speakers, and exhibitors are invited to the ECDP2025 social event, which will take place on the evening of Friday, June 27th.

This year, the Social Event will be held at Can Magí, a historic estate located in the heart of Barcelona. Originally built in the 19th century, Can Magí is known for its stunning architecture, lush gardens, and elegant event spaces that provide a perfect blend of tradition and modernity.

Guests will enjoy a seated dinner accompanied by live music in a beautiful setting!

Please note that prior registration for the event is required (available via the registration page). The ticket price is 50€+VAT/person. Participation is on a first-come, first-served basis (max. 400 guests).

Shuttle buses to and from Can Magí are included.
Meeting point: outside the venue, in front of the entrance.

VENUE: Can Magí **ADDRESS:** Avinguda Can Magi, 5 Sant Cugat del Vallès

CONGRESS INFORMATION

ACT OF GOD
It is mutually agreed that in the event of total or partial cancellation of the Congress due to fire, strike, natural disaster (either threatened or actual), government regulations, or incidents not caused by the organizer, which would prevent its scheduled opening or continuance, the congress may be partially postponed or terminated as a whole. In this case, participants are not entitled to reclaim refunds on no account. Participants are obliged to have civil liability insurance.

CERTIFICATE OF ATTENDANCE
All participants will receive a certificate of attendance by email after the congress.

CONTINUING MEDICAL EDUCATION (CME) CREDITS
A CME application was submitted to the European Association Council for Continuing Medical Education (EACCME), which provides credits for attendance at the scientific sessions of the core program.

CONGRESS HOMEPAGE
www.ecdp2025.org

CONGRESS LANGUAGE
The official language of the congress will be English. Simultaneous translation will not be provided.

CONGRESS VENUE
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DATA PROTECTION
The protection of your data is important to us. All presentation files provided will be deleted immediately after the end of the congress.

GASTRONOMY
During the official coffee and lunch breaks participants will be offered snacks and beverages in the industry exhibition.

GET TOGETHER
The Get Together will take place on June 26th, 2025, from 18:30 to 21:00 in the Conference Center.

INDUSTRY EXHIBITION
The industry exhibition is located in the Conference Center.

CONGRESS INFORMATION

Opening Hours
Thursday (26/06/2025) 09:00 – 21:30
18:30 – 21:30 Poster Reception and Get Together
Friday (27/06/2025) 09:00 – 19:00
Saturday (08/06/2025) 08:30 – 15:00

INTERNET ACCESS
Free WIFI will be available at the congress venue. Login details will be provided on-site.

LIABILITY DISCLAIMER
The organizers cannot be held liable for any hindrance or disruption of congress proceedings arising from political, social, or economic events or any other unforeseen incidents beyond their control. The organizers will accept no liability for any personal injuries sustained or for loss or damage to property belonging to congress participants, either during or as a result of the congress or during all tours and events. Registration of a participant entails acceptance of these conditions.

LOST & FOUND
A Lost & Found box will be placed at the registration desk.

MEDIA CHECK
The media check is located in Tau Room. Speakers are kindly asked to hand over their presentation at the media check at your earliest convenience but not later than 1 hour before the session.

NAME BADGE
The name badge will be the official conference document and should be worn at all times in order to gain entry to the conference rooms and the exhibition hall. Admission to the conference will not be allowed without badge identification. In case of lost or forgotten badges, an administration fee of €10 will be charged.

PRE-CONGRESS WORKSHOPS
Pre-congress workshops will take place on Wednesday, June 25th, 2025

POSTER RECEPTION
The Poster Reception will take place on Thursday, June 6th, 2024 from 17:30 until 20:30.

CONGRESS INFORMATION

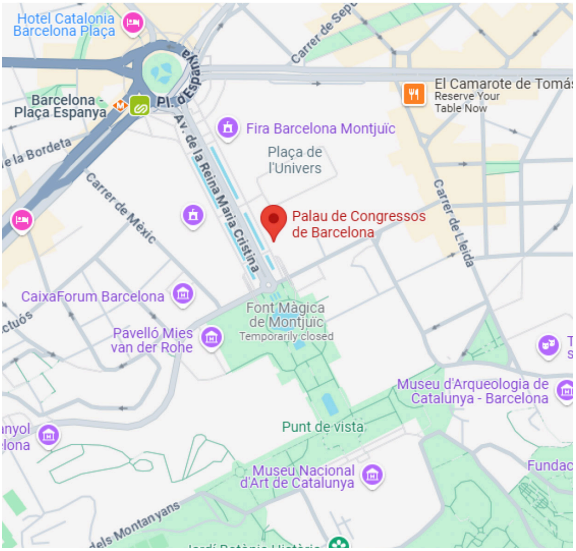
PROGRAM CHANGES
The organizer reserves the right to make changes if necessary. No full or partial refunds are made to the attendees in the event of cancellations or other changes in the program.

REGISTRATION DESK
The registration desk is located in the Exhibition Area. Registration is only valid if the complete payment of the congress fee as well as of other services booked has been made. Registration on-site is possible during the entire congress within the opening hours of the registration desk.

SOCIAL EVENT
Congress dinner
All congress delegates, speakers, and exhibitors are invited to the ECDP2025 social event which will take place on the evening of Friday, June 27th. Please see page 285 for details.

SMOKING
Smoking is strictly prohibited in the conference venue by law.

MAP



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CONGRESS INFORMATION

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Time of Printing June 13, 2025.
All information regarding speakers and times is subject to change.