ESDIP
EUROPEAN SOCIETY OF DIGITAL AND INTEGRATIVE PATHOLOGY

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ECDP2024

20th EUROPEAN CONGRESS ON DIGITAL PATHOLOGY

5th · 8th June 2024
Vilnius, Lithuania

PROGRAM

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WELCOME MESSAGE

Dear friends,
Dear colleagues,

We welcome you to the **20th European Congress on Digital Pathology 2024** in beautiful Vilnius, Lithuania!

We are thrilled to gather leading experts, researchers, and industry professionals in this vibrant city to explore the forefront of digital pathology. This congress promises an exceptional platform for knowledge exchange, innovative ideas, and collaborative networking.

Vilnius, with its rich history, stunning architecture, and warm hospitality, provides an inspiring backdrop for this event.

Together, let us embrace the power of digital pathology to revolutionize healthcare and improve patient outcomes. Prepare for insightful discussions, exciting breakthroughs, and a memorable congress experience.

Welcome to Vilnius, where the future of pathology awaits!

Arvydas Laurinavičius,

Congress President, ECDP2024

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Location
Radisson Blu Hotel
Lietuva Konstitucijos av. 20
LT-09308 Vilnius, Lithuania

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SCIENTIFIC PROGRAM OVERVIEW

	Thursday 06.06.2024		Friday 07.06.2024		Saturday 08.06.2024
Time	Alpha	Lambda	Alpha		Alpha
08:00 - 08:15			Breakfast Symposium (Alpha)		Best Poster Presentations
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08:30 - 08:45					
08:45 - 09:00			Alpha	Lambda	
09:00 - 09:05	Opening		Impact and Sustainability of Digital Pathology and AI	Multiplex Imaging and Spatial Technologies	Keynote Talk II
09:05 - 09:20					
09:20 - 09:30	Keynote Talk I				
09:30 - 09:50			The Odd Couple		Machine Learning & AI Algorithm Development II
09:50 - 10:00				Advancements in Digital Cyto-pathology	
10:00 - 10:20	Integrative, Molecular and Spatial Pathology				
10:20 - 10:30					
10:30 - 10:45			Coffee Break		
10:45 - 11:00	Coffee Break				
11:00 - 11:15					Coffee Break
11:15 - 11:30	Machine Learning & AI Clinical Application I		Machine Learning & AI Clinical Application II	Oral Free Pre-sentations II	What's in it for me as a researcher/ patient? How to leverage existing European Networks?
11:30 - 11:50					
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12:30 - 12:45	Lunch Break		Lunch Break		
12:45 - 13:00					Closing
13:00 - 13:15	Lunch Symposium (Alpha)		Lunch Symposium (Alpha)		Lunch Break
13:15 - 13:30					
13:30 - 13:45					
13:45 - 14:00					
14:00 - 14:20	Machine Learning & AI Algorithm Development I	Oral Free Presentations I	Digital Pathology Neighborhood	Oral Free Presenta-tions III	
14:20 - 14:40					
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15:30 - 15:40			Coffee Break		
15:40 - 16:00					
16:00 - 16:10	Coffee Break				
16:10 - 16:30				Virtual Pathology in Education	
16:30 - 16:50	Datasharing and Application of AI	Data Annotation, Preprocess-ing & Quality Control	Technical and Semantic Interoperability		
16:50 - 17:00					
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17:10 - 17:20					
17:20 - 17:30					
17:30 - 17:45		Poster Reception and Get Together (Exhibition)	IHE PaLM & DICOM WG 26		
17:45 - 18:00	ESDIP Annual General Meeting				
18:00 - 18:15					
18:15 - 18:30					
18:30 - 19:00			Social Event		
19:00 - 20:30					
20:30 - 22:00					

SCIENTIFIC PROGRAM JUNE 6 | Alpha Room

09:00 - 09:20 **OPENING**

09:00 **Arvydas Laurinavičius** Lithuania
Welcome words from the Congress President

09:05 **Norman Zerbe** Germany
Welcome words from the ESDIP President

09:10 **Olegas Niaksu** Lithuania
Digital transformation of healthcare – a national perspective from the Ministry of Health

09:20 - 09:50 **KEYNOTE TALK I**

CHAIR
Arvydas Laurinavičius Lithuania

INVITED SPEAKER
09:20 **Richard Levenson** United States of America
The next step (?): From whole-slide imaging to no-slide imaging

09:50 - 10:45 **INTEGRATIVE, MOLECULAR AND SPATIAL PATHOLOGY**

CHAIR
Inti Zlobec Switzerland

INVITED SPEAKER
09:50 **Hannah Williams** Switzerland
Resolving the transcriptional landscape of colorectal cancer through spatial transcriptomics

ABSTRACTS
10:10 **Spyridon Bakas** United States of America A42
Detecting Histologic & Clinical Glioblastoma Patterns of Prognostic Relevance

10:20 **Elaine Chan** Malaysia A33
Spatially Resolved Transciptomic Profilling Of Formalin-Fixed Colorectal Cancer (CRC) Tissues Between Well & Poorly Differentiated Tissue Areas

10:30 **Leander Van Eekelen** The Netherlands A66
Immunotherapy response prediction for non-small cell lung cancer is improved by using cell-graphs of the tumor microenvironment

11:15 - 12:30 Machine Learning & AI Clinical Application I

CHAIRS
Kurt Zatloukal Austria
Tom Bisson Germany

INVITED SPEAKER
11:15 **Naoko Tsuyama** Japan
Bridging the gap: enhancing pathologists' interpretability of AI via feature visualisation

ABSTRACTS
11:35 **Bart Sturm** The Netherlands A05
Deep learning predicts the effect of neo-adjuvant chemotherapy for patients with triple negative breast cancer

11:45 **Elaine Chan** Malaysia A34
Pancreatic Cancer Classification Using Deep Convolutional Neural Network to Aid The Analysis of Fine Needle Aspirates for Pancreatic Cancer Diagnosis

11:55 **Anthony Manet** Norway A67
Predicting prostate cancer outcome from histopathology section images using deep learning

12:05 **Waleed Ahmad** Germany A80
Computational pathology platform for lung cancer: development and validation of diagnostic and prognostic algorithms

12:15 **Farbod Khoraminia** The Netherlands A59
Deep Learning Unveils Molecular Footprints in Histology: Predicting Molecular Subtypes from Bladder Cancer Histology Slides

14:00 - 16:00 MACHINE LEARNING AND AI ALGORITHM DEVELOPMENT I

CHAIR
Mircea Serbanescu Romania
Nadieh Khalili The Netherlands

INVITED SPEAKER
14:00 **Daniel Racoceanu** France
Virtual staining using trustworthy and scalable pipeline

ABSTRACTS

14:20 **Kastytis Sidlauskas** United Kingdom A83
Predictive Morphological Markers for Ductal Carcinoma In Situ: A Computational Approach to Risk Stratification

14:30 **Adam Shephard** United Kingdom A04
ODYN: An Artificial Intelligence-based Pipeline for the Prediction of Malignant Transformation in Oral Epithelial Dysplasia

14:40 **Ana Leni Frei** Switzerland A60
Using tumor topology to predict patient survival after neoadjuvant chemoradiotherapy in rectal cancer

14:50 **Jingsong Liu** Germany A63
Diff-ST: Staining Translation between HE and IHC by Diffusion Models

15:00 **Mark Eastwood** United Kingdom A64
Multi-task GNN Prediction in Breast Cancer using Deep Features and Cellular Composition Statistics

15:10 **Dominique Van Midden** The Netherlands A57
Deep learning-based segmentation of peritubular capillaries in kidney transplant biopsies

15:20 **Emilio Madrigal** United States of America A48
The FHIR Standard and Digital Pathology: Accelerating Workflow Evolution

15:30 **Ujjwal Baid** United States of America A43
Federated Learning for the Classification of Tumor Infiltrating Lymphocytes: One DL model for 12 cancer types

15:40 **Kesi Xu** United Kingdom A77
Is Segment Anything Model Generalisable for Histology Images?

15:50 **Alboukadel Kassambara** France A68
Attentive Deep-Learning model for predicting Immunoscore in TNBC from MyProbe RHU H&E images: histological interpretability and clinical outcomes

16:30 - 17:30 **DATASHARING AND APPLICATION OF AI**

PANELISTS
Naoko Tsuyama Japan
Inti Zlobec Switzerland
Michael Quick United States of America
Junya Fukuoka Japan
Norman Zerbe Germany

SCIENTIFIC PROGRAM JUNE 6 | Lambda Room

14:00 - 16:00 **ORAL FREE PRESENTATIONS I**

CHAIRS
Luca Cima Italy
Allan Rasmusson Lithuania

ABSTRACTS

14:00 **Shireen Padayachy** United Kingdom A14
Optimising the cellular pathology laboratory workflow during the digital pathology transition: film vs. glass

14:10 **Emil Plesea** Romania A39
Sex related differences between fibrillary morphological profile of aortic tunica media

14:20 **Hrafn Weishaupt** Norway A65
Clustering of glomerular image patches identifies clinically relevant lesion categories

14:30 **Renaldas Augulis** Lithuania A73
Computational pathology model to assess acute and chronic transformations of the tubulointerstitial compartment in renal allograft biopsies

14:40 **Daniel Firmbach** Germany A20
Quantification of Crypt Branching in the Colon Mucosa using Machine Learning: A Shape-based Approach

14:50 **Leana Ducor** Switzerland A58
Quantitative Analysis of Bile Duct Morphology and Spatial Distribution in Nonalcoholic Steatohepatitis (NASH) Liver Biopsies Across Disease Stages

15:00 **Marek Wodzinski** Switzerland A07
Improving Quality Control of Whole Slide Images by Explicit Artifact Augmentation

15:10 **Johanna Palacios** Spain A51
What to look for when choosing a slide scanner for your laboratory

15:20 **Nimisha Tiwari** India A76
Deep Learning models to differentiate Non-invasive Follicular Thyroid Neoplasm with Papillary-like nuclear features (NIFTP) from other thyroid lesions

15:30 **Mauro Gwerder** Switzerland A40
Quantification of EMT transition and stromal infiltrative growth patterns using molecular and morphological feature extraction in colorectal cancer

15:40 **Adrien Navaggioli** France A30
Computer-Aided Diagnosis in Digital Dermatopathology: Automatic Detection of Malignant Lesions

15:50 **Talat Zehra** Pakistan A25
Model for detecting metastatic deposits in lymph nodes of colorectal carcinoma on digital/ Non WSI images

16:30 - 17:30 DATA ANNOTATION, PREPROCESSING & QUALITY CONTROL

CHAIRS
Vincenzo L'Imperio Italy
Sara Oliveira The Netherlands

INVITED SPEAKER

16:30 **Adam Shephard** United Kingdom
OMTscoring: a fully automated pipeline for the prediction of malignant transformation in oral epithelial dysplasia

ABSTRACTS

16:50 **Zhilong Weng** Germany A72
GrandQC tool: A radical solution for quality control problem in digital pathology

17:00 **John Weldon** Ireland A21
Leveraging a Colorectal AI Model for Quality Assurance in a Digital Pathology Diagnostic Platform

17:10 **Marina D'Amato** The Netherlands A56
Automated Quality Control in Histopathology through Artifact Segmentation

17:20 **Yujie Xiang** Sweden A47
How do unsharp areas of histopathology whole slide images impact deep learning model performance and how can the problem be reduced?

SCIENTIFIC PROGRAM JUNE 7 | Alpha Room

09:00 - 09:30 **IMPACT AND SUSTAINABILITY OF DIGITAL PATHOLOGY AND AI**

CHAIRS
Emily Clarke United Kingdom
Milda Poceviciute Sweden

INVITED SPEAKER
09:00 **Peter Boor** Germany
Ecologically Sustainable AI for Pathology

ABSTRACT
09:20 **Stavros Pantelakos** Greece A03
Old tools for new uses: AABACUS as a task-specific model approach to monetizing outcomes of pathology AI solutions

09:30 - 10:30 **THE ODD COUPLE**

CHAIRS
Arvydas Laurinavicius Lithuania
Vincenzo Della Mea Italy

INVITED SPEAKER
09:30 **Diana Montezuma** Portugal
Sara Oliveira The Netherlands
Ink to insight: a perspective on annotation approaches for Computational Pathology

ABSTRACTS
09:50 **Niklas Prenissl** Germany
Jonas Dippel Germany A19
AI-based Anomaly Detection for Clinical-Grade Histopathological Diagnostics

10:00 **Glenn Broeckx** Belgium A41
A Multi-Feature AI Solution for Diagnosis Support of Breast Excisions: A Clinical Validation Study

10:10 **Allan Rasmusson** Lithuania
Dovile Zilenaite-Petrulaitiene Lithuania A52
Hexagonal Grid-based Methods for Pathology: An Overlooked Approach for Spatial Analytics

10:20 **Anders Blilie** Norway
Nita Mulliqi Sweden A23
Artificial Intelligence Assisted Prostate Cancer Diagnosis for Reduced Use of Immunohistochemistry

11:00 - 12:30 MACHINE LEARNING AND AI CLINICAL APPLICATION II

CHAIRS
Adam Shephard United Kingdom
Yuri Tolkach Germany

INVITED SPEAKER
11:00 **Emily Clarke** United Kingdom
Generating objective prognostic biomarkers in whole slide images of melanoma using artificial intelligence

ABSTRACTS
11:20 **Leslie Tessier** The Netherlands A08
Large-scale validation of AI-assisted mitosis counting in breast cancer

11:30 **Shubham Innani** United States of America A44
Self-supervised determination of glioma IDH mutation status from H&E-stained whole slide images

11:40 **Huong Quynh Nguyen** Germany A26
Automatic Detection of Esophageal Cancer in Whole Slide Images

11:50 **Emil Plesea** Romania A29
Relationship between abrasion and dentin morphology in occlusal dysfunction

12:00 **Yannis Schumann** Germany A35
Predicting Epigenetic Ependymoma Types from Histological Whole-Slide Images Using Deep Neural Networks

12:10 **Eltjona Mane** Italy A62
Deep learning algorithm on H&E whole slide images to characterize TP53 alterations frequency and spatial distribution in breast cancer

12:20 **Mostafa Jahanifar** United Kingdom A75
Exploring the Clinical Utility of Artificial Intelligence in Mitosis Scoring for Breast Cancer

14:00 - 15:30 **DIGITAL PATHOLOGY NEIGHBORHOOD**

CHAIRS
Norman Zerbe Germany
Johan Lundin Finland

INVITED SPEAKERS

14:00 **Riyad El-Khoury** Lebanon
Beyond the microscope: challenges in digital pathology implementation at AUBMC

14:15 **Abdulaziz Alajlan** Saudi Arabia
Future of digital pathology directions: the untold story

14:30 **Hicham El Attar** Morocco
Digital pathology in Africa: how the dream becomes true

14:45 **Sangeeta Desai** India
The agony and ecstasy of digital transformation

16:00 - 17:30 **TECHNICAL AND SEMANTIC INTEROPERABILITY**

CHAIRS
Peter Hufnagl Germany
Riki Merrick United States of America

INVITED SPEAKERS

16:00 **Paul Seegers** The Netherlands
An Introduction to Standardized Structured Reporting and Future Perspectives

16:20 **Sabine Leh** Norway
Building bridges in pathology: Integrating systems for better diagnostics

ABSTRACTS

16:40 **Cleo-Aron Weis** Germany A31
What to learn by Pokémon in the field of nephropathology: About generating diagnostic decision trees based on knowledge graphs.

16:50 **Christoph Jansen** Germany A32
Bridging AI apps and DICOMweb systems via the EMPAIA platform

17:00 **Tom Bisson** Germany A37
Publishing Pathology Routine Data for Research Use: Technical and Legal Challenges

17:10 **Francesca Vanzo** Italy A46
Digital Pathology Aid for Telemedicine

17:20 **Moses Yook** Republic of Korea A28
Procedures for Building a Digital Pathology Data Set for the CODiPAI Project

17:30 - 18:00 **IHE PALM & DICOM WG 26**

INVITED SPEAKERS

17:15 **Kevin Sharp** United States of America

17:30 **Riki Merrick** United States of America

SCIENTIFIC PROGRAM JUNE 7 | Lambda Room

09:00 - 10:00 **MULTIPLEX IMAGING AND SPATIAL TECHNOLOGIES**

CHAIRS
Rasmus Kiehl Germany
Dovile Zilenaite-Petrulaitiene Lithuania

INVITED SPEAKERS

09:00 **Niclas Blessin** Germany
The use of BLEACH&STAIN multiplex fluorescence immunohistochemistry and artificial intelligence facilitates the identification of spatial immune prognosis markers in muscle-invasive urothelial cancer

09:20 **Virginijus Barzda** Canada
Multiphoton digital histopathology

ABSTRACTS

09:40 **Julius Drachneris** Lithuania A61
Prognostic significance of the spatial distribution of tumor infiltrating immune cells in of non-muscle-invasive papillary urothelial carcinoma

09:50 **Sonja Koivukoski** Finland A69
Unstained tissue imaging and virtual HE staining of whole slide images: towards clinical tumor assessment

10:00 - 10:30 **ADVANCEMENTS IN DIGITAL CYTOPATHOLOGY**

CHAIRS
Jordi Temprana Spain
Petr Holub Czechia

INVITED SPEAKER

10:00 **Liron Pantanowitz** United States of America
Recommendations from the American Society of Cytopathology for AI Use in Cytology

ABSTRACT

10:20 **Xiaorong Sun** China A02
AI Cervical Cancer Screening Diagnosis Quality Control

11:00 - 12:30 **ORAL FREE PRESENTATIONS II**

CHAIRS
Rita Carvalho Germany
David Ameisen France

ABSTRACTS

11:00 **Waleed Ahmad** Germany A82
Development and clinical validation of a prognostic algorithm for stroma-tumor ratio quantification in non-small cell lung cancer

11:10 **Volker Bruns** Germany A15
Interactive generic analysis of H&E slides using a combination of multiple AIs

11:20 **Shubham Innani** United States of America A45
Deep Learning Subtyping of Multi-institutional Renal Oncocytic Neoplasms from H&E-stained Whole Slide Images

11:30 **Johanna Palacios** Spain A49
Digital Pathology implementation Journey in a network of 14 hospitals in Spain.

11:40 **Volodymyr Chapman** United Kingdom A22
Nuclear distribution clusters associate with mutation profile in Follicular Lymphoma

11:50 **Patrick Stunkel** Norway A70
Real-time Pathology Dashboards for Lab Worker Motivation: An Experience Report

12:00 **Marek Wodzinski** Switzerland A06
DeeperHistReg: Robust Whole Slide Images Registration Framework

12:10 **Giorgio Cazzaniga** Italy A36
Enhancing Pathology Report Coding with Advanced NLP Models: A Comparative Study

12:20 **Amjad Khan** Switzerland A38
Deep Learning-Based Detection of Lymph Node Metastases of Upper Gastrointestinal Tract Adenocarcinoma

14:00 - 15:30 **ORAL FREE PRESENTATIONS III**

CHAIRS
Junya Fukuoka Japan
Linas Petkevičius Lithuania

ABSTRACTS

14:00 **Rokas Stulpinas** Lithuania A11
Predicting Survival of HCC Patients after Liver Resection by AI-Driven Fiberomics and Hexagonal Grid Analytics

14:10 **Volker Bruns** Germany A16
IHC Cell Analysis – More than just Cell Counting: A proposed Workflow

14:20 **Elias Baumann** Switzerland A09
HoVer-NeXt: A Next Generation Whole Slide Image Nuclei Segmentation and Classification Pipeline

14:30 **Rita Sarkis** Switzerland A10
MegaQuant: Fully Integrated Deep-Learning Workflow in QuPath - Application to the Detection of Megakaryocytes in Human Bone Marrow

14:40 **Ozben Yalcin** Turkey A13
Ki-67 Decision Support Algorithm for Pathology Residents

14:50 **Daan Schouten** The Netherlands A54
Full Resolution Three-Dimensional Reconstruction of Non-Serial Prostate Whole-Mounts: Pilot Validation and Initial Results

15:00 **Maximilian Fischer** Germany A53
Semi-supervised automated Gleason Grading on WSI

15:10 **Elena Osteikaitė** Lithuania A18
Non-linear microscopy for cervical cancer diagnostics

15:20 **Yasemin Topuz** Turkey A27
Epidermis Segmentation Based on U-Net Variations in Melanoma Whole Slide Images

16:00 - 17:00 **VIRTUAL PATHOLOGY IN EDUCATION**

CHAIRS
Nasir Rajpoot United Kingdom
Sangeeta Desai India

INVITED SPEAKER

16:00 **Luca Cima** Italy
Digital Teaching and Learning: Enhancing Pathology Education Through Technology

ABSTRACTS

16:20 **Ilknur Turkmen** Turkey A50
Histopathology Atlas: An open-source Whole Slide Image (WSI) collection for educational purposes

16:30 **Thiyaphat Laohawetwanit** Thailand A17
Preparing for pathology boards with ChatGPT: AI-assisted digestive system exam creation for residents

16:40 **Su Young Kim** Republic of Korea A01
Building online digital pathology library for education using conventional mirrorless cameras.

16:50 **Xiaoyi Ji** Sweden A24
The impact of temporal variation in digital pathology scanners on diagnostic artificial intelligence models

SCIENTIFIC PROGRAM JUNE 8 | Alpha Room

08:00 - 09:00 **BEST POSTER PRESENTATIONS**

CHAIRS
Julius Drachneris Lithuania
Vincenzo L'Imperio Italy

09:00 - 09:30 **KEYNOTE TALK II**

CHAIR
Norman Zerbe Germany

INVITED SPEAKER
09:00 **Faisal Mahmood** United States of America
Multimodal generative AI for pathology

09:30 - 11:00 **MACHINE LEARNING & AI ALGORITHM DEVELOPMENT II**

CHAIRS
Diana Montezuma Portugal
Jeroen van der Laak The Netherlands

INVITED SPEAKER
09:30 **Milda Poceviciute** Sweden
Foundation models - the end of generalisation challenges in computational pathology?

ABSTRACTS
09:50 **Mikaël Simard** United Kingdom A12
An attention-based multiple instance learning framework for predicting soft tissue tumour diagnosis

10:00 **Shi Pan** United Kingdom A55
HistoMIL: A Python package for training multiple instance learning models on histopathology slides

10:10 **Ajey Pai** The Netherlands A71
Reliable comparisons between AI models and human experts in computational pathology

10:20 **Stefan Reinhard** Switzerland A81
Bringing data science to AI supported tissue diagnostics

10:30 **João D. Nunes** Portugal A78
Weakly Supervised Domain Adaptation for Robust Colorectal Pathology Classification

10:40 **Michelle Stegeman** The Netherlands A79
Vision Language Foundation Models for Scoring Tumor-Infiltrating Lymphocytes in Breast Cancer through Text Prompting

10:50 **Neda Zamanitajeddin** United Kingdom A74
Benchmarking Domain Generalization Algorithms in Computational Pathology

11:30 - 12:45 **WHAT'S IN IT FOR ME AS A RESEARCHER/PATIENT? HOW TO LEVERAGE EXISTING EUROPEAN NETWORKS?**

CHAIRS
Sabine Leh Norway
Daniel Racoceanu France

INVITED SPEAKERS

11:30 **Jeroen van der Laak** The Netherlands
Building the AI repository for Europe: the Bigpicture project

11:45 **Peter Hufnagl** Germany
How to use EMPAIA for my research projects?

12:00 **Petr Holub** Czechia
Leveraging BBMRI-ERIC for XAI research in digital pathology

12:45 - 13:00 **CLOSING**

PANELISTS
Arvydas Laurinavicius Lithuania
Norman Zerbe Germany
Jordi Temprana Spain

ORAL PRESENTATIONS

A01

Building online digital pathology library for education using conventional mirrorless cameras.

Su Young Kim[1]

[1] Department of Pathology, the Catholic University of Korea, College of Medicine, Republic of Korea

Introduction

In conventional digital pathology, we need a dedicated scanner and a viewer. Usually, the scanner is expensive, and the viewer need to be installed in user computer. Technology of mirrorless digital camera has evolved. Sensors are getting bigger, and more pixels are crowded in the same area. In addition, lenses showing better resolution and magnification are continuously introduced in the market. With the help of this new technology, we may not need a microscope to explore microscopic world of tis-sue samples. Mirrorless cameras with high resolution sensors and high magnification lenses may replace micro-scope in the field of digital pathology.

Material and methods

In this project, I tested several mirrorless camera bodies and macro lenses for digital pathology. Products from the 5 camera manufacturers and 7 lens manufacturers were tested. The scanned files were in png format and delivered to the medical students in real pathology class using conventional online image service platforms.

Results and discussion

Some of the camera bodies and lenses that I tested produced images with acceptable quality. The best practice workflow was established to build large image library. The images were uploaded to conventional image service platform and structured based on human organ systems. With web browser and Internet connection, the students were able to access the image library at any time.

Conclusion

Conventional mirrorless cameras and macro lenses can be used to build digital pathology library. They are useful alternatives where dedicated digital pathology facility is not established.

Key words: mirrorless camera, macro, digital pathology, online library

A02

AI Cervical Cancer Screening Diagnosis Quality Control

Xiarong Sun[1], Baochuan Pang[1], Wei Zhang[1], Hua Li[1]

[1] Cytology, Landing Med, China

Introduction

This article explores how to perform quality control for AI cervical cancer screening.

Material and methods

From October to November 2022, 528,040 women in China's Hubei Province participated in cervical cancer screening. Cervical samples were obtained through liquid-based thin-layer cytology and stained with Papanicolaou (Pap) method. Subsequently, cervical images were scanned and uploaded to the Landing Med Cloud Platform for AI analysis. The analyzed images underwent primary screening by cytotechnologists and were categorized into positive and negative groups. Cytopathologists examined 100% of positive samples and randomly selected 10% of negative samples for grading diagnosis according to The Bethesda System standards.

Results and discussion

Among 528,040 women, cervical samples were diagnosed as 498,836 cases (94.47%) NILM, 19,504 cases (3.69%) ASCUS, 5,566 cases (1.05%) LSIL, 2,628 cases (0.50%) ASC-H, 795 cases (0.15%) HSIL, and 403 cases (0.08%) AGC. The ASC/SIL ratio was 3.48, and the A-H/A+A-H ratio was 11.87%. Among these screened women, 6,298 underwent cervical biopsy, revealing 3,408 cases of cervical inflammation, 2,135 cases of CIN I, 327 cases of CIN II, 377 cases of CIN II, and 51 cases of invasive cancer through histopathological diagnosis. Comparing the concordance rates between cytology and histology, the agreement rates for diagnosing CIN II+ in ASCUS, LSIL, ASC-H, HSIL, and AGC were 4.22%, 12.01%, 26.88%, 60.09%, and 6.56%, respectively.

Conclusion

1.Compared to conventional cytology, AI cervical cancer screening has slightly increased the diagnostic rate of ASCUS. 2.Implementing quality control for AI cervical cancer screening can achieve a level comparable to manual cervical cancer screening. 3.AI screening technology is applicable for large-scale population-based cervical cancer screening.

Key words: Artificial Intelligence, Cytopathology, Cervical Cancer, ASCUS, Cytology, Quality Control

A03

Old tools for new uses: AABACUS as a task-specific model approach to monetizing outcomes of pathology AI solutions

Stavros Pantelakos[1, 2], Martha Nifora[3, 4]

[1] Department of Cytology, Evaggelismos General Hostital of Athens, Greece
[2] Department of Medicine, School of Health Sciences, National and Kapodistrean University of Athens, Greece
[3] Istomedica Private Pathology Lab, Greece
[4] Department of Biomedical Sciences, School of Health and Care Sciences, University of West Attica, Greece

Introduction

Cost-containment policies affect decision-taking in healthcare. In this context, the need for monetization of digital health interventions has been recently stressed out. Previous studies have attempted to extrapolate cost-containment in conjunction with the impementation of digital pathology solutions mostly on the basis of operational cost savings or diagnostic error reduction. However, no study has attempted to link specific tasks performed by AI algorithms to financial figures. Herein, we make use of a workload measurement tool for the purpose of monetizing particular outcomes from the implementation of a pathology AI solution.

Material and methods

~130 prostate core biopsies were encoded using the Automatable Activity-Based Approach to Complexity Unit Scoring (AABACUS). Then, assuming full clinical deployment of the prostate cancer screening tool developed by Campanella et al., avoided workload, FTE gains and respective cost-savings were calculated.

Results and discussion

Total avoided workload was estimated at 1314 complexity units (CU). FTE gains were calculated at 0.077, whereas projected cost savings were as high as €1617/year.

Conclusion

AABACUS appears to be a suitable economic evaluation tool regarding the possible implementation of different task-specific AI solutions in a given histopathology laboratory, considering it is a task-specific workload measurement tool per design.

Key words: AI solutions, Impact, Sustainability, Workload, Monetization, Cost-savings

A04

ODYN: An Artificial Intelligence-based Pipeline for the Prediction of Malignant Transformation in Oral Epithelial Dysplasia

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Introduction

Oral epithelial dysplasia (OED) is a premalignant histopathological diagnosis given to lesions of the oral cavity that have an increased risk of progression to malignancy. The grading of OED encounters substantial inter/intra-rater variability, offering limited prognostic reliability and potentially leading to suboptimal treatment decisions. To address this, we developed an artificial intelligence (AI) pipeline for OED segmentation, classification and transformation prediction with haematoxylin and eosin (H&E) stained whole slide images (WSIs).

Material and methods

Our innovative Transformer-based pipeline, named ODYN, proficiently classifies OED and assigns a predictive score (ODYN-score) quantifying the risk of malignant transformation. Employing a shallow neural network, we determine slide-level ODYN-scores based on nuclear features within dysplastic tissue patches. The model was trained on a large digital dataset utilising three different scanners (Sheffield, 292 OED WSIs, 96 control WSIs) and undergoes external validation across three independent centres (Birmingham and Belfast, UK, and São Paulo, Brazil; 108 OED WSIs).

Results and discussion

Model testing gained an F1-score of 0.71 for OED segmentation, and 0.96 for dysplastic vs non-dysplastic tissue classification. Our AI pipeline achieved an AUROC of 0.74 for malignancy prediction, surpassing other state-of-the-art methods and demonstrating comparable results to clinical grading systems.

Conclusion

We present a new Transformer-based model for the semantic segmentation and classification of OED using the largest multi-centric OED dataset to date (400 WSIs). This is the first study to use Transformers for semantic segmentation in oral histology WSIs, demonstrating reliable and promising results for enhancing OED diagnosis and prognosis prediction.

Key words: Oral Epithelial Dysplasia, ODYN, Transformer, Dysplasia Segmentation, Malignancy Transformation, Computational Pathology

A05

Deep learning predicts the effect of neo-adjuvant chemotherapy for patients with triple negative breast cancer

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Introduction

Triple negative breast cancer (TNBC) is an aggressive subcategory of breast cancer with poor prognosis and high risk of recurrence. Systemic chemotherapy is offered prior to surgery, so called neo-adjuvant chemotherapy (NAC), to downstage the disease. This study aims to predict the outcome of NAC with deep learning technology based on the microscopic morphological characteristics in whole slide images from the tumor biopsy prior to therapy.

Material and methods

A convolutional neural network was trained on 221 H&E stained biopsies of carcinoma of no special type from 205 patients. Cases were divided in three cohorts, with a good, moderate or bad response to NAC, defined as residual tumor < 10%, 10-50% and > 50% respectively. Manual segmentation of the tumor area was performed comprising invasive carcinoma. The model was tested on 52 new biopsies of 50 patients. Because of the relative low number of moderate and bad responder cases, and in order to achieve a better discrimination for potential visual biomarkers, the moderate and bad response cohorts were merged.

Results and discussion

The predictive performance of the model was calculated by means of the area under the receiver operator curve (AUC ROC). 95% Confidence intervals (CI) were calculated for better understanding of the range of values. In the test set the AUC ROC performance score was 0.696 with a CI of 0.532 – 0.861.

Conclusion

This proof-of-concept study shows that H&E pre-operative biopsies from TNBC, by means of deep learning technology, contain valuable information having predictive value for the outcome of NAC resulting in an AUC value of 0.696.

Key words: Deep learning, Artificial intelligence, WSI, Breast carcinoma, Chemotherapy, Prediction

A06

DeeperHistReg: Robust Whole Slide Images Registration Framework

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Introduction

The automatic registration of differently stained whole slide images (WSIs) is crucial for improving diagnosis and prognosis by fusing complementary information emerging from different visible structures. It is also useful to quickly transfer annotations between consecutive or restained slides, thus significantly reducing the annotation time and associated costs. Nevertheless, the slide preparation is different for each stain and the tissue undergoes complex deformations. Therefore, a robust, efficient, and accurate registration method is highly desired by the scientific community and hospitals specializing in digital pathology.

Material and methods

We propose a ready to-use open source software that enables the users to easily perform automatic registration of WSIs. The proposed framework consists of novel deep learning-based and classical iterative algorithms. The framework allows the user to directly register the WSIs, transform them at any desired magnification level, and transfer the annotations to the target slide. The framework is available in an associated repository: https://github.com/MWod/DeeperHistReg

Results and discussion

We evaluated the proposed framework using three open datasets: ANHIR, ACROBAT, and HyReCo in terms of the target registration error. The algorithms incorporated into the framework are among the best performing ones worldwide. They have won the ACROBAT challenge, provide the most accurate registration results for the HyReCo dataset, and are among the best-performing ones for the ANHIR dataset.

Conclusion

The proposed framework is robust and does not require fine-tuning to any particular dataset. The framework can be directly used in practical applications, thus allowing the practitioners to easily perform WSIs registration that may be useful for other downstream tasks in digital pathology.

Key words: WSI Registration, Image Registration, Artificial Intelligence, Deep Learning, Digital Pathology

A07

Improving Quality Control of Whole Slide Images by Explicit Artifact Augmentation

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Introduction

The problem of artifacts in WSI acquisition, prevalent in both clinical workflows and research-oriented settings, often necessitates human intervention and rescanning. Overcoming this challenge requires developing quality control algorithms, that are hindered by the limited availability of relevant annotated data in histopathology. The manual annotation of ground-truth for artifact detection methods is expensive and time-consuming. This work addresses the issue by proposing a method dedicated to augmenting whole slide images with artifacts.

Material and methods

We propose a method that seamlessly generates and blends artifacts from an external library to a given histopathology dataset. The augmented datasets are then utilized to train artifact classification methods. Such an approach artificially increases the heterogeneity of the training sets dedicated to quality control. Since the lack of annotated artifacts is one of the most difficult challenges in the automatic artifact detection, the work is a significant contribution to overcoming this challenge. The framework, model, weights, and ground-truth annotations are freely released to facilitate open science and reproducible research.

Results and discussion

The impact of augmentation is evaluated in the context of artifact classification. We quantitatively compare the influence of the augmentation and show an improvement from 0.10 to 0.01 AUROC depending on the artifact type. The method is evaluated on several open datasets, as well as using closed clinical cases.

Conclusion

The proposed method can be used to improve the generalizability of artifact detection methods to previously unseen cases. The robustness of quality control is crucial for the following downstream tasks like WSI classification or segmentation.

Key words: Deep Learning, Artificial Intelligence, Quality Control, Artifacts, Data Augmentation, Digital Pathology

A08

Large-scale validation of AI-assisted mitosis counting in breast cancer

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Introduction

Expectations surrounding artificial intelligence (AI) in pathology are high. In contrast, little is known about the impact of AI on clinical practice, especially in tedious tasks such as mitotic activity scoring in breast cancer. Mitotic activity is a critical feature in the Nottingham grading system. Despite its high prognostic value, mitosis scoring suffers from interobserver variability and is often considered time-consuming, making it a good candidate to benefit from AI support. In this large-scale international validation study, we measured the impact of an AI algorithm (Aiosyn Mitosis Breast) aimed at detecting mitoses in breast cancer slides on mitotic scoring. The effect of AI was evaluated on time consumption, accuracy (compared to a panel of 3 experts), and interobserver variability.

Material and methods

The study involved 28 pathologists from 9 countries. A total of 210 whole slide images (WSIs) of biopsies and resections stained with H&E and originating from 8 international centers were selected. Participants were divided into 2 groups following a split-plot, each reading 105 WSIs twice in a randomized order: once with AI and once without in two sessions separated by a washout period of 3 weeks.

Results and discussion

We observed a time gain of 10.4% with AI ($p < 0.001$), a 15.5% increase in productivity on resections, and a decrease in interobserver variability ($p < 0.001$). Accuracy did not decrease with AI ($p < 0.001$, non-inferiority).

Conclusion

Our study suggests that readily available AI can play a significant role in pathology globally by decreasing time consumption and improving interobserver reproducibility and, therefore, patient care.

Key words: AI, Breast cancer, Mitosis, Validation study

A09

HoVer-NeXt: A Next Generation Whole Slide Image Nuclei Segmentation and Classification Pipeline

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Introduction

Cancer progression and patient outcomes depend on a variety of cell types, their density, and spatial organization in tissues. On hematoxylin & eosin (H&E) stained whole slide images (WSI), cell nuclei are easily identifiable and previous work has shown that deep learning models can accurately detect, segment, and classify them in a reproducible way. The publicly available Lizard colorectal cancer nuclei segmentation and classification dataset covers multiple cell types, but crucially lacks cells undergoing mitosis. Moreover, long inference times of current models makes large scale investigations time-consuming and expensive.

Material and methods

In this work, we propose HoVer-NeXt, a highly scalable pipeline for accurate nuclei segmentation and classification. We optimize our model for WSI inference and make it easy to use. We extend the Lizard dataset with a mitosis class using an additional mitosis dataset and a self-training routine. Furthermore, we validate the model on additionally created mitosis and eosinophil datasets. For comparison with other methods, we also train HoVer-NeXt on the PanNuke pan-cancer dataset.

Results and discussion

HoVer-NeXt runs inference at 1.8s/mm2 at 0.5mpp, 3.2s/mm2 at 0.25mpp and, trained on Lizard-Mitosis, achieves 0.84 binary detection F1-score and 0.758 mean balanced accuracy on 7 classes. On PanNuke, HoVer-NeXt performs competitively with 47.7 mPQTiss (+3% on HoVer-Net), 0.782 mean balanced accuracy, and runs 6x faster than CellViT and 17x faster than HoVer-Net.

Conclusion

HoVer-NeXt paves the way towards extensive single-cell information directly from H&E slides, leading towards quantitative WSI investigations even on large cohorts. Code, model weights as well as all datasets are publicly available on github.

Key words: Panoptic segmentation, Nuclei segmentation and classification, Deep learning, Whole slide inference

A10

MegaQuant: Fully Integrated Deep-Learning Workflow in QuPath - Application to the Detection of Megakaryocytes in Human Bone Marrow

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Introduction

Megakaryocytes (MKs), precursors of platelets, can be altered by clinical conditions and their assessment is of diagnostic value. When evaluated on H&E images, they are challenging to segment due to their complex shape. Here, we propose a fully integrated workflow implemented within QuPath, leveraging existing deep-learning tools to segment and quantify MKs.

Material and methods

First, we rely on the image management platform Omero to organize our datasets and annotations with seamless access in QuPath by multiple users. QuPath facilitates the annotation of ground truth data, which was done both manually and using a foundation model, Segment Anything Model (SAM). This ground truth annotation (n=984 SAM annotated MKs used for the training, and n=483 for CellPose validation) was validated by a pathologist and used to train a customized Cellpose model, with iterative refinement between annotations and detections. Subsequently, StarDist was adapted to detect nuclear regions within the Cellpose-detected MK regions.

Results and discussion

The CellPose model detects MKs of different morphological features. Applied to 37-H&E trephine images with 2 training and 1 validation tile each, it provides morphometric parameters for every MK. SAM significantly accelerated annotation. Our workflow provided insights into the morphological heterogeneity, characteristics, and spatial distribution of MKs based solely on H&E images.

Conclusion

We believe that this fully integrated workflow within one platform, QuPath, could facilitate the adoption of MegaQuant in a clinical context and enable integration of MK quantitative information within diagnostic pathology reports. Moreover, it paves the way for a public MK-specific CellPose model for broader use in QuPath and Python applications.

Key words: Computational Pathology, Hematology, QuPath, CellPose, Omero, StarDist

A11

Predicting Survival of HCC Patients after Liver Resection by AI-Driven Fiberomics and Hexagonal Grid Analytics

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Introduction

The disruption of normal liver fiber framework is a key element in the evolution of hepatocellular carcinoma (HCC). Our study aimed to utilize artificial intelligence for identifying clinically relevant fiber morphometrics in HCC and the surrounding liver parenchyma.

Material and methods

In 105 HCC whole slide images (WSI) obtained after liver resection, a convolutional neural network extracted collagen (PicroSirius Red-positive) and reticulin (silver-impregnated) fiber masks. Furthermore, the slides were divided into neoplastic and peritumoral liver areas using manual annotations. HALO-AI was utilized to segment the tissue into epithelial, stromal, and background classes. A hexagonal grid was superimposed and the tissue areas and fiber features were sampled from each hexagon. Classifying hexagons by tissue content and ranking them by their distance to the closest epithelial edge enabled analysis of fiber features in the tissue interfaces. Cox regression with LASSO regularization was used to assess the impact on overall survival, with factor analysis (FA) aiding interpretation.

Results and discussion

The regression models where every variable exhibited a p-value <0.05 were comprised of 30 unique components, which were subsequently subjected to FA, that identified six factors, explaining 85.12% of the variance. In particular, two models had a C-index >0.7 and both contained patient age, HCC multifocality, one reticulin-derived feature at the tumor edge, and one collagen-derived feature at the epithelial edge of peritumoral liver.

Conclusion

Our study showed prognostic value at the tumor compartment derived from reticulin structure properties, while at the peritumoral liver, collagen characteristics were significant. The study underscores the importance of precise tissue zoning for extracting prognostic information from WSIs.

Key words: HCC, CNN, artificial intelligence, fiberomics, hexagonal grid, predicting survival

A12

An attention-based multiple instance learning framework for predicting soft tissue tumour diagnoses

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Introduction

Diagnosing soft tissue tumours (STT) is challenging due to their rarity, large number (>100) of subtypes and overlapping morphological features. This often requires multiple costly and time-consuming supplementary tests. The aim of this work is to develop a deep learning framework to improve diagnostic accuracy of STT and their mimics in a time and cost-efficient manner, something not previously reported.

Material and methods

3988 digital whole slide images (WSI) representing 23 STT subtypes, characterised by molecular features, comprising in-house and cases referred from different institutions, were used as a training set. The framework has two steps: first a model was trained using pathologists' annotations to identify tumour tiles. Secondly, WSI are classified into one of the 23 subtypes using 125 randomly sampled tumour tiles at 3 zoom levels, which are then fed into an attention-based multiple instance learning framework. Training was done with 5 different seeds to generate an ensemble model for prediction.

Results and discussion

The framework was tested on a set of 80 WSI, stained with H&E in 28 institutions, comprising 16 diagnoses. We obtained an accuracy of 72%. However, the top 3 predicted diagnoses generated the correct diagnosis in 95% of WSIs.

Conclusion

The STT deep learning classifier has potential to reduce time and cost in reaching accurate STT diagnoses. Future work includes increasing the numbers of diagnoses and evaluation of model performance in a real-world setting. As a step towards interpretability, attention maps generated during the process will be used to identify key areas on which diagnoses are made.

Key words: soft tissue tumours, multiple instance learning, sarcoma, attention maps, deep learning, computer vision

A13

Ki-67 Decision Support Algorithm for Pathology Residents

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Introduction

Ki-67 scoring is of essential importance in the evaluation of breast cancer. We evaluated a Ki-67 algorithm as a decision support tool to improve accuracy for pathologist residence.

Material and methods

We retrospectively evaluated Ki-67 scores on whole slide images (WSI) obtained from 156 consecutive breast cancer patients. Two senior pathologists determined the 2.1mm2 hotspot to be evaluated. Ki-67 scores from senior pathologists were compared with results generated by the algorithm; results from 10 pathology residents; and results from pathology residents with the assistance of the algorithm. In addition to numerical results from the algorithm, residents were also presented with a visual representation of nuclei that were counted and excluded. Statistical analysis was performed using Wilcoxon and intra-class correlation (ICC) tests.

Results and discussion

The mean Ki-67 scores from senior pathologists and the algorithm were 23±18 and 24±18, respectively (ICC: 0.98). Ki-67 scores from the residents were 19±16 and 22±16, without and with input from the algorithm, respectively. With input from the algorithm, residents' scores were significantly closer to those obtained by senior pathologists (p=0.008). Residents modified their scores in 53.8% of the cases where 74% of the better scores were characterized by an increase in the original scores.

Conclusion

The results obtained by the Ki-67 algorithm were highly correlated with those assessed by senior pathologists. We demonstrated that the algorithm may serve as a decision support tool for residents to align their results with those of senior pathologists.

Key words: ki-67, algorithm, decision support

A14

Optimising the cellular pathology laboratory workflow during the digital pathology transition: film vs. glass

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Introduction

Digital pathology is rapidly being introduced within cellular pathology departments UK-wide. The laboratory workflow is being critically analysed to ensure that whole slide image (WSI) production is to a diagnostic standard and not impacting turnaround times. Resin-coated plastic film coverslipping has been proposed to save time and reduce the file size of WSI at a minimally increased cost compared to glass. This study tested the feasibility of Sakura Tissue-Tek® Coverslipping film in our laboratory and evaluated the quality of the WSI produced compared to our standard workflow.

Material and methods

Two sections from 26 representative formalin-fixed paraffin-embedded tissue blocks were cut. One was processed using the film coverslip and the other with glass. The digital WSI were blindly analysed by three consultant histopathologists and nine scientists.

Results and discussion

The film coverslip workflow was feasible in our laboratory. The workflow was quicker and had fewer steps. Both methods produced 100% diagnostic quality WSI. Film coverslipping produced higher quality WSI compared to glass in 61.5% and 57.7% of cases analysed by scientists and pathologists respectively. Air bubbles were more common with glass coverslips compared to film - 11.5% vs. 0%.

Conclusion

Film coverslipping is feasible in our laboratory and produces diagnostic-quality WSI. These results suggest that the image quality may be improved when using film coverslips compared to glass consistent with emerging data from other centres. The realised time savings, estimated at 9 days per year for our laboratory, and reduction in data storage requirements will be the scope of future analysis.

Key words: Histopathology, Digital pathology, Scanning, Coverslip, Laboratory workflow

A15

Interactive generic analysis of H&E slides using a combination of multiple AIs

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Introduction

The quantitative analysis of H&E-stained tissue specimens is complex. Many known biomarkers involve the measurement of density or abundance of certain cell types in a ROI such intra- vs. peritumoral. Other biomarkers require evaluation of spatial cell neighborhoods. Here, we present an interactive workflow comprising multiple AI tools that can be combined realize such tasks.

Material and methods

Proposed tool chain: (1) a tissue detection distinguishes foreground from background; (2) a fast and user-trainable tissue classifier based on Few Shot Learning, to identify and coarsely outline tissues such areas tumor, mucosa, etc.; (3), Optionally, a specialized segmentation of macro-structures such as glands within the mucosa; (4) masking the (tumor) microenvironment by computing concentric inwards and outwards margins; (5) a cell recognition AI outlines and classifies typical cell types such as tumor cells, benign epithelial cells, various immune cells, etc., and groups them by the ROIs detected in 2-4); and (6) a spatial analysis that regards cells as nodes in a graph (Delauney triangulation) and computes statistics on cell neighborhoods.

Results and discussion

The tools listed above have been integrated into an interactive software (MIKAIA) that can be used by pathologists without programming to execute complex analyses such as tumor-infiltrating-lymphocytes (TILs), cancer-associated-fibroblasts (CAFs), lymphocytes in crypts (Cryptitis), chronic vs. acute inflammation, to name a few examples.

Conclusion

By enabling users to combine multiple AI models freely in conjunction with additional auxiliary processing steps, a multitude of tasks can be realized. Based on the exported quantitative results, new biomarkers can be mined in these human-interpretable histological features.

Key words: biomarker, TILs, workflow, H&E

A16

IHC Cell Analysis – More than just Cell Counting: A proposed Workflow

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Introduction

In (pre-)clinical research, the quantitative analysis of immunohistochemical (IHC) stains is a frequent task. Automatic image analysis can increase both objectivity and throughput. At the core, it comprises the counting of IHC-stained cells. Here, we propose an automatic workflow and focus on pre- and post-processing steps.

Material and methods

This workflow has emerged over the course of a multitude of IHC analyses we have conducted in cooperation with other research groups: (1) Division of slide into distinct scan areas to support multiple specimen per slide; (2) Automatic tissue segmentation; (3) Subdivision of specimens into ROIs (e.g., "metastasis") in order to collect separate cell statistics; (4) Automatic creation of concentric ROI-distance-zones; (5) Cell detection and assignment to distinct ROIs and scan areas; (6) Cell qualification: computation of morphometric and color attributes; (7) False positive filtering; (8) Hotspots location using a dynamic hotspot-definition; (9) spatial clustering of cells using a dynamic cluster definition; (10) visualization using interactive markup and heatmaps; (11) export of results to CSV for downstream statistical analysis; (12) export of markup files, experiment settings, etc., for documentation and repeatability.

Results and discussion

The workflow has been realized in an interactive software (MIKAIA) that can be used directly by pathologists.

Conclusion

We propose a generic IHC analysis workflow that has been successfully employed in multiple studies of different organs. (AI) Cell detection is the central part but must be flanked by various pre- and postprocessing steps in order to yield meaningful endpoints, including cell abundance, cell density, hotspots and spatial clustering, all reported individually per ROI and scan area.

Key words: IHC, Cell Detection, workflow, preclinical

A17

Preparing for pathology boards with ChatGPT: AI-assisted digestive system exam creation for residents

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Introduction

Previous studies have investigated generative AI's ability to develop multiple-choice questions (MCQs) for undergraduate medical education. However, little is known about ChatGPT's effectiveness in crafting board exam-like assessments. This research aims to evaluate the effectiveness of customized ChatGPT 4 in generating MCQs with explanations for pathology board examinations, specifically for digestive system pathology.

Material and methods

A customized ChatGPT model was developed to generate MCQs and explanations, with its content evaluated for accuracy and relevance by expert pathologists. These MCQs were later administered to pathology residents, and an analysis was conducted to assess question difficulty, accuracy, item discrimination, and internal consistency.

Results and discussion

ChatGPT produced 80 MCQs on digestive pathology, receiving moderate to high marks for accuracy, relevance, and quality. Challenges in cognitive level and distractor quality were noted. The MCQs, tested by 9 residents with a median experience of 1 year (range = 6-30 months), resulted in an average score of 57.4 (71.8%). Significant performance differences were seen between second and third-year residents ($p < 0.01$), with no variation across topics. The test analysis showed moderate difficulty (average correct answers per question = 6.38 out of 9), effective discrimination (index = 0.15), and good consistency (Cronbach's alpha = 0.74).

Conclusion

ChatGPT 4 showed considerable promise as an additional resource in pathology education, particularly in creating MCQs and explanations akin to those found in board exams. Although the content produced by AI was of high quality, it required further refinement and review by experts.

Key words: artificial intelligence, examination, histopathology, diagnosis

A18

Non-linear microscopy for cervical cancer diagnostics

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Introduction

Non-linear microscopy could potentially serve as a diagnostic tool for cervical cancer and other cancer types. The extracellular matrix collagen molecules produce a second harmonic generation (SHG) signal, which shows the ultrastructure and the orientation of collagen fibers. A third harmonic generation (THG) signal allows to observe the nuclei of cells. By analysing the non-linear responses at the tumor margin, changes in the collagen structure are observed between the cancerous and normal tissue. The analysis of changes in the collagen organization can potentially be used as a diagnostic tool in clinical histopathology.

Material and methods

The investigation method includes the SHG microscopy imaging of collagen with different polarization states using the Double Stokes-Mueller Polarimetry (DSMP) and Polarization–in, Polarization–out (PIPO) methods. The distribution maps of C ratio (the orientation of fibers out of the image plane) and R ratio (the description of the structural organization of the collagen fibers in the focal volume) were generated from the recorded signals. The maps of collagen fibers can be colocalized and compared with the nuclei of cancer cells visualized with THG imaging.

Results and discussion

The results present SHG and THG images, C and R ratio distribution maps, which show areas of the tissue near the tumor and further away from it. The images show enlarged nuclei of cancerous cells, and an increase of R ratio values indicating a larger structural disorder of collagen at the tumor margin.

Conclusion

The multimodal non-linear microscopy provides additional structural information, and can be incorporated in the work flow of H&E tissue histopathology.

Key words: Microscopy, Non-linear, Second Harmonic Generation, Polarization, Collagen

A19

AI-based Anomaly Detection for Clinical-Grade Histopathological Diagnostics

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Introduction

A major unsolved challenge for the broad implementation of AI in histopathological diagnostics lies in the highly heterogeneous frequencies of diseases. As most current AI models in histopathology follow the paradigm of supervised learning, they perform well only on common diseases with ample amounts of available training data. Less frequent diseases (which show, collectively, a sizeable number), however, need to be taken into account whenever a diagnosis is rendered and may cause severe misclassifications in models trained by supervised learning. An effective technique for detecting infrequent (i.e. anomalous) diseases from long-tail disease distributions is needed.

Material and methods

We collected a large real-world dataset of GI biopsies, which are prototypical of the problem, from two large university hospitals. We adapted different state-of-the-art deep anomaly detection (AD) methods to our setting, namely AD based on self supervised learning and Outlier Exposure. Further, we generated explainatory heatmaps to guide pathologists' view to anamalous tissue areas.

Results and discussion

Our best-performing approach, which only requires training data from common findings and is based on Outlier Exposure, reached over 95% (stomach) and 91% (colon) AUROC in detecting anomalous findings with a wide range of different morphological patterns. It provides interpretable heatmaps locating the anomalous tissue and generalizes across hospitals and scanners.

Conclusion

This study establishes the first effective clinical application of AI-based AD in histopathology that can facilitate case prioritization and reduce the amount of missed diagnoses. Further, when combined with supervised classification of common findings, AI-AD could eliminate the risk of overlooking less frequent and potentially severe diseases, thereby driving automation in routine diagnostics.

Key words: Artificial Intelligence (AI), Computational Pathology, Anomaly Detection (AD), Image Analysis

A20

Quantification of Crypt Branching in the Colon Mucosa using Machine Learning: A Shape-based Approach

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Introduction

Branching of colon crypts is a histological hallmark of inflammatory bowel diseases (IBDs). Specifically, symmetric and asymmetric crypt branching have been suggested as two distinct reaction patterns of the colon mucosa. Hence, classification of those two patterns might lead to a better differentiability of IBD subtypes.

Material and methods

Our data consists of whole slide images of patients with colitis ulcerosa (n=100), Crohn's disease (n=100), infective colitis (n=50), and colitis ulcerosa with low-grade intraepithelial neoplasia alio loco (n=50). First, we segmented crypts using an epithelial segmentation model. We then classified the segmented crypts based on classic ensemble and deep-learning strategies. As a basis of our classification, we only provide shape-based information on the tissue architecture, either in the form of hand-crafted features based on the segmented crypt polygon or the mask of the segmented polygon.

Results and discussion

Our best performing classic ensemble models achieve a mean balanced accuracy of about 0.80, while our best-performing deep-learning model achieves a mean balanced accuracy of 0.78.

Conclusion

Our models are able to classify branching crypts based on shape-based information alone, corroborating a previous, qualitative morphological observation. Combined with the interpretability of classic ensemble models and hand-crafted features, this allows tracking the decision process for an individual crypt and discerning the important characteristics for classification in general.

Key words: Crypt Branching, Inflammatory Bowel Disease, Machine Learning

A21

Leveraging a Colorectal AI Model for Quality Assurance in a Digital Pathology Diagnostic Platform

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Introduction

Incorrect diagnosis of colorectal disorders can lead to higher morbidity and mortality rates, particularly in advanced polyps. Implementing AI-driven quality assurance as a safety read on clinical colorectal cases gives a second pair of eyes to each case, and has the potential to greatly reduce the incidence of misdiagnosis.

Material and methods

A proprietary classifier utilising weakly supervised learning was developed for slide-level classification of colorectal biopsies. The model underwent training using a dataset of over 25,000 whole slide images (WSI) of H&E colon biopsies collected from two distinct institutions, one in Ireland and the other in the USA, all captured at 20x magnification. This comprehensive training dataset encompassed a total of 32 different biopsy diagnoses. This classifier was used to make predictions on cases after they have been authorised by pathologists, and so any diagnostic discordance can potentially be addressed in a timely fashion.

Results and discussion

The system was evaluated on 1,000 clinical cases. Of these, ~10% were flagged as discordant. Of the flagged cases, ~33% were confirmed to be borderline cases where pathologists were unlikely to form a clear consensus. ~50% were AI overcalls due to artefact in the WSI. ~10% were genuine pathologist undercalls, where our in-house pathologists would upgrade the original diagnosis severity to match the AI prediction.

Conclusion

With its high level of sensitivity, and acceptable specificity, the colorectal AI model can serve as a valuable tool within a digital pathology diagnostic platform. This may provide hospitals, pathologists and patients with increased peace of mind that the chance of diagnostic error is greatly reduced

Key words: Screening, Colorectal, AI, Quality, Assurance, Clinical

A22

Nuclear distribution clusters associate with mutation profile in Follicular Lymphoma

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Introduction

Previous efforts in Follicular Lymphoma (FL) have not bridged the gap between mutation profile, cellular composition, and survival. We address this using unsupervised clustering of patients' cell distributions. We further characterise clusters using mutation profile, labelled nuclei, and overall survival.

Material and methods

236 cases from the Hematological Malignancy Research Network dataset were used, with random partitioning of FFPE H&E images into discovery (144) validation (92) datasets. Nuclear features describing morphology, texture and intensity were measured in unlabelled nuclei, followed by balanced sampling to create a 1 dimensional UMAP embedding. Pairwise comparison of nuclear distributions using the Anderson-Darling statistic and subsequent agglomerative clustering grouped patients by nuclear distribution. Cluster number was determined using maximum Calinski-Harabasz score that maintained cluster membership above 20 patients. Welch's t was used for statistical testing; Cohen's d for effect size and Cox Proportional Hazards for survival analyses.

Results and discussion

3 nuclear distribution groups were identified. Group A was enriched for the previously reported 'FL_Com' mutation profile (d: 1.20; $p < 0.0001$), had high proportions of mature lymphocytes and 5-year overall survival (OS) of 0.87 across treatment groups. Group C had high proportions of centroblasts, reduced OS risk in Watch & Wait patients (5-year OS: 0.96, HR vs. non group C = 0.52; 95% CI: 0.27 – 0.98; $p = 0.045$) and low 5-year OS in chemotherapy patients (0.67). Group B represented a heterogeneous group between A and C.

Conclusion

These results evidence existence of nuclear phenotype groups in FL, some of which appear to have starkly different survival between treatment groups.

Key words: Unsupervised learning, Mutation profiles, Treatment response

A23

Artificial Intelligence Assisted Prostate Cancer Diagnosis for Reduced Use of Immunohistochemistry

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Introduction

Pathologists often use immunohistochemistry (IHC) staining to confirm cancer in prostate biopsies, but this process is costly and time-consuming. Artificial intelligence (AI) holds promise for assisting prostate cancer diagnosis and may decrease reliance on IHC. We propose an AI model to minimize IHC staining during biopsy assessment.

Material and methods

We collected data from prostate cancer patients (n=888) diagnosed routinely at the Stavanger University Hospital between 2016 and 2018. Slides (n=5810) were digitized on a Hamamatsu S60 scanner and used to train and validate a deep multiple-instance learning algorithm for prostate cancer detection. Looking only at slides where pathologists ordered IHC in the primary diagnostic workup (n=1071), we evaluated AI-performance in detecting malignant slides based only on Hematoxylin and Eosin stained tissue.

Results and discussion

We evaluated a scenario where IHC is ordered only for cases deemed uncertain by pathologists and having an AI-predicted probability of malignancy exceeding 1%. This results in very few false negatives (Sensitivity=0.95), whilst at the same time forgoing IHC for all negative AI-predictions. This would avoid IHC for 378/1071 (35.3%) slides, while resulting in a false negative diagnosis for 20/1071 (1.2%) slides. We are in the process of conducting additional validation analyses on fully external cohorts.

Conclusion

Incorporating an AI model in prostate cancer diagnosis workflow can decrease reliance on IHC staining, thereby streamlining the diagnostic process and reducing costs. This approach could save both money and laboratory resources while reducing time to patient diagnosis.

Key words: Artificial intelligence, Immunohistochemistry, Prostate cancer, Core needle biopsy

A24

The impact of temporal variation in digital pathology scanners on diagnostic artificial intelligence models

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Introduction

Concerns have been raised over 'AI aging' — the decline in AI performance over time — but it is unknown whether variations in scanners lead to this phenomenon in digital pathology. Here, we explore variation in scanner characteristics over time, assess its potential impact on diagnostic AI models, and evaluate whether this problem can be mitigated with physical color calibration.

Material and methods

We utilized 119 prostate core needle biopsy slides from Stavanger University Hospital, Norway, with a balanced ISUP grade distribution, plus a Sierra calibration slide. Two consecutive baseline scannings were performed on a Hamamatsu NanoZoomer S60 scanner to assess reproducibility in the absence of any temporal variation, and will be followed by repeated scanning every 14 days for one year. The impact of scanner-induced temporal variance on AI model performance will be evaluated on an in-development deep multiple instance learning model trained on over 46,000 whole slide images for prostate cancer diagnosis. We will compare model performance across the time points, both with and without physical color calibration.

Results and discussion

Preliminary results support the AI aging hypothesis. Upon finishing data collection, we will quantify changes in diagnostic performance metrics (sensitivity and specificity, Cohen's kappa) over time. Additionally, pathologists will evaluate the slides with discrepant AI results to provide insights into the potential causes of variation.

Conclusion

This study pioneers the investigation of temporal variance in digital pathology scanners and its potential impact on AI models, and introduces a real-time quality assurance approach for ensuring stable performance of scanners and AI over time.

Key words: artificial intelligence, scanner variation, quality assurance

A25

Model for detecting metastatic deposits in lymph nodes of colorectal carcinoma on digital/ Non WSI images

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Introduction

Colorectal cancer (CRC) constitutes around 10% of global cancer. Routine pathology labs face an immense diagnostic workload due to the increased occurrence of CRC. In most cases, examining lymph node metastasis histologically in CRC patients can be arduous, prompting consideration for an artificial intelligence (AI)-supported workflow due to the growing number of slides to be examined, demanding heightened precision and effort. In this study, an existing deep learning model was applied to digital images to identify metastatic deposits in lymph nodes of previously diagnosed cases of colorectal carcinoma.

Material and methods

This was a retrospective cross sectional study which included digital images of glass slides containing sections of lymph nodes obtained from radical resection of primary CRC. 60 previously diagnosed cases of colorectal cancer were selected from Agha Khan University Hospital. The images were prepared at 10X through a camera connected to Nikon microscope. Both positive and negative tumor regions in a lymph node were photographed. The images were then uploaded into an open source software, Q path by a computational pathologist and deep learning model Ensemble was applied for the identification of tumor deposits in lymph node.

Results and discussion

In our study, sensitivity was 84% and specificity 67.9%. The P-value was highly significant and it was <0.05 (<0.0001). Out of the 36 positive lymph nodes detected by AI, 27(75%) were true positive and 9(25%) were false positive.

Conclusion

Though it was a small study but its results were really appreciating. We used a software which was meant for whole slide images and also for different set of population but the performance of software was highly commendable.

Key words: digital pathology, mtastsis, lymph nodes

A26

Automatic Detection of Esophageal Cancer in Whole Slide Images

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Introduction

Esophageal adenocarcinoma (EAC) is one of the most rapidly increasing cancers in the world, and a known precursor is Barrett's Esophagus. In this project, we explore the ability of Artificial Intelligence (AI) to detect EAC in Whole Slide Images (WSIs) of Barrett biopsies.

Material and methods

BarrettNet is a clinical cohort collected in Germany at 25 different institutions to follow and record the progression of Barrett patients from 2013 to 2023. We utilize 1294 labeled WSIs of 500 distinct cases from this cohort to develop our classifier. Our model is based on Multiple Instance Learning (MIL), where only slide-level annotation is required; thus, the annotation time is effectively minimized. Our approach is inspired by "Clustering-constrained Attention Multiple Instance Learning" (CLAM) and therefore adopts an attention-based mechanism that facilitates slide-level aggregation from patch-level representations. During pre-processing, we incorporate Otsu thresholding for tissue segmentation, and tissue patches of 256×256 pixels are generated. A pre-trained ResNet50 is then used for feature extraction, followed by an inference step, where patch-level binary clustering happens and predictions are constructed. To prevent overfitting, a dropout of P=0.25 is applied during training. For validation, we employed 10-fold Monte Carlo cross-validation, with 80% of slides for training, and 10% each for validation and testing.

Results and discussion

Our model achieves an average Area Under the Curve (AUC) of 0.87 with an accuracy of 0.91, which outperforms other MIL-based methods.

Conclusion

Based on these outcomes, it is evident that our model exhibits significant proficiency in the case of esophageal cancer.

Key words: Barrett Esophagus, Esophageal Cancer, Multiple Instance Learning, BarrettNET, Cancer Detection

A27

Epidermis Segmentation Based on U-Net Variations in Melanoma Whole Slide Images

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Introduction

Skin cancer is one of the most common types of cancer worldwide and its incidence rate is increasing day by day. Melanoma, a type of skin cancer, accounts for 21% of all skin cancers but it is responsible for 47% of deaths due to skin cancer-related deaths. Depth of invasion is the most important parameter to determine the tumor stage in melanoma and It is measured from the top of the granular layer of the epidermis, to the deepest part of the tumor. The main motivation of the research is to performs the epidermis segmentation, one of the most important steps to make tumor staging computer-aided, by using customized form of the UNet architecture.

Material and methods

This study was performed on 23.437 patches extracted from 41 melanoma whole slide image samples from the TCGA-SKCM dataset. Traditional segmentation architectures use maxpooling and deconvolution for down/up sampling. In this study, strided convolution was used instead of maxpooling for downsampling and its performance was analyzed on basic UNet, UNet++ and UNet3+ architectures. The results were improved using a postprocessing method developed using the epidermis position.

Results and discussion

According to results, it was found that the highest success ratio in WSI test samples was achieved in the UNet3+ architecture with strided convolution for downsampling and deconvolution for upsampling a with Dice Coefficient Score of 0.879.

Conclusion

This study investigated four different up/down sampling methods and three different UNet model performances in epidermis segmentation. It was shown UNet3+ with strided convolution and deconvolution can give more successful results for epidermis segmentation task.

Key words: Epidermis Segmentation, Melanoma, UNet, Strided Deconvolution

A28

Procedures for Building a Digital Pathology Data Set for the CODiPAI Project

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Introduction

The Collaborative Open Digital Pathology Artificial Intelligence (CODiPAI) project is a large-scale digital pathology data construction and artificial intelligence software development work that started in second quarter of 2021 with support from the Korean government. We designed several procedures to build a complete data set with clinical information and image annotation.

Material and methods

The whole slide image (WSI) that has been de-identified and given a CODiPAI ID is converted to the CODiPAI standard format and uploaded to the cloud platform. Then, it will be able to check the images using CODiPAI ID in CODiPAI project management system (PMS). After that, researcher can enter either clinical information or annotation information in any order. Once the clinical information has been entered by the first researcher, the second researcher can confirm and complete it. Also, once the first researcher completes the input of annotation information, the second researcher verifies it. The third researcher of the annotation information can terminate the procedure only when all clinical information and annotation information have been entered, and when terminated, a complete data set is created.

Results and discussion

As of 27 February 2024, 125,590 WSIs have been loaded onto the cloud platform, of which 83,397 (66.4%) data sets have been completed by more than 70 active researchers. And this number continues to increase.

Conclusion

The results demonstrate a large data set created through procedures with a multiple verification can secure an appropriate level of quality for producing artificial intelligence algorithms and software.

Key words: Digital Pathology, Cloud Platform, Big Data, Data Set, Procedures, Whole Slide Image

A29

Relationship between abrasion and dentin morphology in occlusal dysfunction

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Introduction

Occlusal dysfunction may generate abrasion of occlusal surface which, further may determine dentinal morphological changes in all tooth's regions. The authors aimed to assess the possible influence of abrasion on dentin morphology using artificial intelligence tools.

Material and methods

69 decalcified teeth of all types with abrasion were included in paraffin and sectioned in the long axis. Samples were stained with Haematoxilin-Eosin. The morphological parameters were: dentinal-tubule-wall percentage (DT_W%) and dentinal-tubule-space percentage (DT_S%). They were automatically measured using an "in house" designed, dedicated software, on digital slides, in crown's occlusal area-COA, under abrasion area. Average values were compared and assessed with Pearson's test and Student test.

Results and discussion

DT_W% and DT_S% revealed a strong inverse correlation (Pearson's test "p" value < 0.0001) in all types of teeth meaning that if one was increasing the other was decreasing. In COA, DT_W% had a decreasing oscillating trend from incisors to molars on upper arch, with a spike on canines and a collapse in premolars. Its values were higher than those of corresponding mandibular teeth, excepting the premolars. On mandible, DT_W% had an oscillating but stable trend. In turn, DT_W% had an oscillating decreasing trend on both dental arches but always with higher values in mandibular teeth. It presented a spike at the level of mandibular canines and lowest values at the level of maxillary molars.

Conclusion

The abrasion caused by occlusal dysfunction determines further morphological changes in the underlying dentin depending on tooth type and dental arch.

Key words: Occlusal dysfunction, Abrasion, Dentin, Image analysis, Morphometry

A30

Computer-Aided Diagnosis in Digital Dermatopathology: Automatic Detection of Malignant Lesions

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Introduction

The majority of malignant lesions in dermatopathology are basal cell carcinomas (BCC), squamous cell carcinomas (SCC), or melanomas. The automatic detection of such lesions, along with automated measurement of lesion thickness and margins, could assist pathologists in establishing faster and more accurate diagnoses.

Material and methods

We gathered and annotated 1795 WSI containing both malignant and benign lesions, as well as healthy tissues. We used a method based on Deep Feature Learning to train a classifier on patches at a 20x zoom level to identify melanoma, BCC, or SCC. Computer vision-based methods are then used to automatically measure the thickness of the lesion and the lateral and deep surgical margins.

Results and discussion

The test dataset includes 392 WSI of the most common malignant lesions, as well as 500 WSI of healthy tissue or benign lesions. The F1-score of our classification model for detecting malignant lesions is 0.892. The balanced accuracy of our model in predicting the diagnosis of melanoma, BCC, or SCC is 0.965. At the patch-level, it can detect a malignant lesion with a precision-recall area under the curve (AUC) of 0.946. Lesions and sample measurements are consistent with medical practice, and a clinical validation study is currently ongoing.

Conclusion

We propose the first algorithm capable of locating and identifying cutaneous malignant lesions in histopathological WSI, while also automatically measuring the thickness and margins. Ongoing developments are expected to further improve the results. The detection of benign lesions, the classification of subtypes of malignant lesions, and the automatic detection and counting of mitosis are also subjects of research.

Key words: Dermatopathology, AI, automated lesion measurements, automated surgical margins, lesion classification, lesion detection

A31

What to learn by Pokémon in the field of nephropathology: About generating diagnostic decision trees based on knowledge graphs

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Introduction

How useful would be diagnostic algorithms that map the plethora of clearly defined entities and help to distinguish them from the relevant, potentially mimicking differential diagnoses. However, such checklists are scarce due to the limited number of experts and their time constraints. In this project, we demonstrate how decision trees can be constructed using comprehensive knowledge graphs, exploring how graph quality and topology impact tree generation. Using a assumable near perfect Pokémon graph as an illustrative example, derived from extensive fan work, we investigate this phenomenon.

Material and methods

Utilizing the "Graph them all Pokémon" graph and the published Pokémon tree of life, we construct a large graph. We employ the MINDWALC algorithm, adapting it to subgraphs with flat, hierarchical, or combined topologies, and experiment with three novel walking strategies.

Results and discussion

Employing Pokémon datasets as a toy model, we observe that as edges are gradually removed, resulting in graph deterioration, the complexity of decision trees increases. We also find that different graph topologies, such as flat and hierarchical, akin to medical ontologies like SNOMEDCT or KBC, influence decision tree generation. Additionally, we enhance the MINDWALC algorithm's walking strategies.

Conclusion

Utilizing an almost-perfect Pokémon knowledge graph allows the establishment of a new decision-tree-generating method, which can subsequently be applied to real datasets, such as those in nephropathology, irrespective of graph quality.

Key words: Decision Tree, Computer Lingustics, Nephropathology

A32

Bridging AI apps and DICOMweb systems via the EMPAIA platform

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Introduction

Whole Slide Images (WSI) are stored in vendor-proprietary formats or in standard DICOM. Picture Archiving and Communications Systems (PACS) provide capabilities for viewing and communicating medical images. The web-based EMPAIA platform defines a public interface specification for integration of Artificial Intelligence (AI) applications that serves as a vendor-agnostic abstraction layer on top of various formats and clinical systems. Here, we present an adapter bridging EMPAIA to a DICOMweb PACS.

Material and methods

The EMPAIA interface and DICOMweb both support JSON representation. The adapter is implemented as a proxy service between an AI and a PACS. It makes DICOMweb Study and Series metadata requests to a PACS, transforms the responses into EMPAIA Case and Image objects and returns the result to the AI client. It uses the existing open-source Python libraries dicomweb-client (metadata) and wsidicom (image data).

Results and discussion

The implementation is a functional prototype. Standard compatibility was tested against the open-source dcm4chee PACS. We experienced challenges dealing with object sorting and pagination in DICOMweb. We found unique identifier incompatibility between the EMPAIA object ID and its DICOM equivalent, requiring an additional matcher.

Conclusion

Our efforts suggest ways to improve compatibility with DICOM, e.g., removal of identifier format restrictions in future EMPAIA specification upgrades, and improvements in the DICOMweb standard and respective libraries. We aim to demonstrate interoperability of open protocols, to accelerate AI adoption and to endorse DICOMweb as a standard.

Key words: dicomweb, dicom, standards, interoperability, open protocols, artificial intelligence

A33

Spatially Resolved Transciptomic Profilling Of Formalin-Fixed Colorectal Cancer (CRC) Tissues Between Well & Poorly Differentiated Tissue Areas

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Introduction

The prevention and detection of colorectal cancer at an early stage had been a challenge mainly due to the limited availability and specificity of biomarkers. This study aimed to utilize gene expression profile in spatially defined metastatic colorectal cancer to identify biomarkers associated with colorectal cancer cells between well differentiated (low grade) and poorly differentiated (high grade) tumour areas.

Material and methods

Formalin fixed paraffin embedded block were obtained from Hospital Selayang and the RNA quality of the tissue was assessed by calculating DV200 of RNA extracted from freshly tissue sections. A spatial transcriptomic workflow was carried out using the 10x Visium CytAssist FFPE Spatial Gene Expression kit. The constructed library was sequenced, and the gene expression data was then analysed and visualized using Space Ranger and Loupe Browser software. Subsequently, secondary analysis such as PANTHER and STRING were used to further analyse the overall biological function as well as the pathway involved.

Results and discussion

FN, SFRP2, ITGB, ACTA and SPARC were identified as the differentially expressed gene between well differentiated (low grade) and poorly differentiated (high grade) tumour areas. These differential expressed genes (DEGs) were mostly upregulated in the binding process, expressed in the cellular process and involved in the integrin signalling pathway. Integrin functions as both signalling molecules and integral components of the cellular migration machinery.

Conclusion

FN, SFRP2, ITGB, ACTA and SPARC were identified as the differentially expressed genes between high and low grade tumour areas. These genes could be potential biomarkers that aid in early detection of colorectal cancer.

Key words: colorectal cancer, spatial transcriptomic, cancer grading

A34

Pancreatic Cancer Classification Using Deep Convolutional Neural Network to Aid The Analysis of Fine Needle Aspirates for Pancreatic Cancer Diagnosis

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Introduction

The poor survival rate of pancreatic cancer is likely due to its aggressive nature and its challenges to detect early. The current diagnosis of pancreatic cancer is done by pathologists by manually examining tissue biopsy under the microscope. This method is time consuming and often results in late or deferred treatment. This study develop a classification model for pancreatic cancer from whole slides images.

Material and methods

The collected slides (pap and cell blocks) were digitised for the development of the deep learning algorithms for recognition of normal and cancerous pancreatic cells. Image data augmentation was implemented to increase the training set. Metrics such as accuracy, loss, precision, recall, f1-score and the confusion matrix were used to quantify the model's performance. The training history, showcasing accuracy and loss over epochs, was visualised to understand the model's learning progression.

Results and discussion

1294 single cell images (1058 cancerous cells and 236 normal cells) were classified into the training set whilst 1124 single cell images (888 cancerous cells and 236 normal cells) are grouped into the Test set. The CNN model developed to detect cancer cells from pap and cell blocks have an accuracy of 98% and sensitivity and precision of more than 85%.

Conclusion

This paper presents the development of a deep learning model aimed at detecting pancreatic cancer cells in whole slide images. The training process utilised a dataset consisting of single cell images of pancreatic cells. To enhance the model's performance, image data augmentation techniques were employed to increase the number of training samples, resulting in improved validation accuracies.

Key words: Pancreatic Cancer, deep learning model, Cell Block

A35

Predicting Epigenetic Ependymoma Types from Histological Whole-Slide Images Using Deep Neural Networks

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Introduction

Ependymomas are neuroepithelial neoplasms of the central nervous system and are divided into 10 clinically distinct types based on epigenetic (DNA methylation) profiles. For their diagnosis, the current standard practice is to integrate epigenetic information with histological assessment of slide images. However, recent studies have detected regular mismatch between those two methods for a fraction of ependymoma cases and it is unclear how to resolve these constellations in diagnostics.

Material and methods

We collected sample-matched epigenetic profiles and whole-slide images (Hematoxylin- and Eosin stain) of 356 ependymomas from different anatomical compartments. Attention-based classification models (CLAM, PMID: 33649564) were trained to predict the epigenetic ependymoma types from the slide images and the models were compared the results from histological annotations by neuropathologists for a fraction of cases.

Results and discussion

With 98% average accuracy for major spinal cord ependymoma types (80% average balanced accuracy for different anatomical compartments), our approach yielded reliable predictions of the epigenetic types. Self-supervised encoder training was crucial for classification performance. The classifiers improved over board-certified neuropathologists and its attentions scores were leveraged to correlate epigenetic and morphological ependymoma characteristics. Image normalization and augmentation facilitated domain adaptation towards whole-slide images from other medical facilities and brightfield microscopy images.

Conclusion

We established an interpretable method to reliably predict epigenetic ependymoma types from histological whole-slide images. Our approach provides a fast and inexpensive way for first assessment of molecular ependymoma classification, provides morphological interpretability and may prospectively enable rapid decisions on patient-specific treatment in the upcoming era of digital pathology.

Key words: Neuropathology, Cancer, Multiple Instance Learning, Self-Supervised Learning, Attention

A36

Enhancing Pathology Report Coding with Advanced NLP Models: A Comparative Study

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Introduction

The integration of Standardized Structured Reports (SSR) with SNOMED-CT is crucial for advancing data interoperability and analysis in digital pathology. However, the prevalent use of narrative reports complicates efficient data management and analysis. This study introduces a novel approach leveraging Natural Language Processing (NLP) and Large Language Models (LLMs) to automate the mapping of SNOMED-CT codes to narrative reports.

Material and methods

Our methodology expands on traditional NLP models by incorporating encoder-only and causal autoregressive frameworks, including multilingual variants of BERT and T5 models, fine-tuned on domain-specific corpora. We introduced continual learning with the BERT multilingual base variant and a fine-tuned QLora adaptation of the LLama and Mistral models, aiming to improve coding accuracy and F1 scores. Experimentations were carried out on about 400000 pathology reports in italian language.

Results and discussion

The application of these advanced NLP techniques resulted in metric improvements, with both the BERT multilingual base variant and the QLora adapted models achieving accuracy and F1 scores of 0.86, surpassing previous benchmarks of 0.84. This demonstrates the potential of advanced NLP techniques in accurately encoding pathology reports.

Conclusion

This study highlights the effectiveness of employing advanced NLP and LLMs in the automatic SNOMED-CT coding of narrative pathology reports, achieving state-of-the-art performance. Future research will address current limitations in training instance volume and quality and aim to enhance model explainability through saliency maps, NLP explanations, and contrastive learning for multi-code scenarios.

Key words: SNOMED-CT Coding, NLP, LLM

A37

Publishing Pathology Routine Data for Research Use: Technical and Legal Challenges

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Introduction

Healthcare institutions acquire and store large amounts of data from routine clinical care, such as images, lab test results, and other data. These resources are highly valuable for research. However, GDPR mandated restrictions (e.g. de-identification, data protection impact assessments) need to be considered.

Material and methods

The PROSurvival project (https://www.prosurvival.org/) aims at compiling and publishing a curated multi-center cohort of 1000 prostate cancer cases from patients who underwent radical prostatectomy. In addition to WSIs, clinical data (e.g., pTNM, PSA, Gleason Score, recurrence-free survival, clinical trajectory) are collected from university hospitals in Berlin and Frankfurt. Federated learning is used to train a deep learning model on this dataset without exchanging data directly. The requirements for publishing this dataset are discussed with data protection authorities.

Results and discussion

Significant challenges have surfaced during this process. The WSIs need to be converted to DICOM as a standard format without degrading image quality. A standard-based format for the clinical data is needed. A suitable research data repository in the EU must be found. Finally, the requirements of the GDPR are interpreted differently in the federal states of Germany and, therefore, need to be considered individually.

Conclusion

Challenges remain for the publication of medical routine data for research, even though efforts are underway to reduce hurdles and to change the mentality of retaining data within healthcare institutions. Ultimately, guidelines are needed to enable hospitals to share their data under FAIR conditions, legally and efficiently for research without requiring a research project in each individual case.

Key words: Research data, whole-slide images, de-identification, DICOM, GDPR, FAIR

A38

Deep Learning-Based Detection of Lymph Node Metastases of Upper Gastrointestinal Tract Adenocarcinoma

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Introduction

We recently developed and implemented "MetAssist", a deep learning model for colorectal cancer lymph node metastasis detection into our routine diagnostic workflow. We now updated MetAssist with a new state-of-the-art segmentation model, Mask2Former, to adapt it to upper gastrointestinal adenocarcinoma (UGA) lymph node metastases without UGA-specific training. We compared the scores predicted by the model at the slide level with a pathologist's diagnosis.

Material and methods

One hundred and fourteen whole slide images of UGA lymph node metastases were analyzed by the updated MetAssist algorithm, which automatically segments the lymph node tissue, detects metastases in each segmented tissue and calculates the slide-level score. All false-negative cases were re-evaluated by the pathologist using the predicted overlays to thoroughly assess the performance of the model.

Results and discussion

Updated MetAssist achieved an accuracy of 85% on UGA cases. Seventeen cases were detected as false negatives by the model. In these cases, poor quality stains, signet ring cell phenotypes, micropapillary growth patterns, and very few cells of adenocarcinoma were challenging for the model. The model was still able to indicate adenocarcinoma regions in falsely predicted cases, however, the optimal threshold still needs to be explored.

Conclusion

Our results show that updated MetAssist was able to detect the metastases in most cases. We are extending our study to further evaluate the adaptability of the model for UGA cases on a larger cohort.

Key words: Deep learning, Digital pathology, Lymph node metastases , Upper Gastrointestinal Tract , Adenocarcinoma

A39

Sex related differences between fibrillary morphological profile of aortic tunica media

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Introduction

There are many morphological differences at tissue level between men and women. The authors aimed to compare the densities-D variations fi the aortic tunica media-AO_TM main fibrillary components (Elastic fibers–FE, Collagen fibers-FCOL, smooth muscle fibers-FM) along the aortic regions between men and women.

Material and methods

Four aortic rings (base-01_B, arch-02_C, thoracic-03_Th, abdominal-04_Ab) were taken from 90 cases (55 men and 35 women) during necropsies. Samples were processed using the classical HP technique and stained with Orcein (for FE), and Goldner's trichrome (for FCOL and FM) and transformed in virtual slides. Quantitative measurements of different fibers densities were made using a custom-made software developed in Matlab (Mathworks, USA). Average values-AV were compared with "t" test and Pearson's test.

Results and discussion

FE_D had a general decreasing trend along the aortic length, with a significant spike in 02_C in women whereas FCOL_D and FM_D had general slightly increasing trends along the aortic length, with collapses of FCOL_D in women and FM_D in men, both in 02_C. AVs of FE_D and FM_D were higher in men than in women whereas AVs of FCOL_D were higher in women than in men along almost the entire vascular length. In all types of fibers, the reversal of the ratio occurred in the aortic arch area.

Conclusion

The remodelling process of the AO_TM fibrillar composition along its length is following somehow parallel paths but with different fluctuations from one sex to another.

Key words: Aorta, media layer, morphology, fibrillar component, image analysis, morphometry

A40

Quantification of EMT transition and stromal infiltrative growth patterns using molecular and morphological feature extraction in colorectal cancer

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Introduction

The metastatic progression of adenocarcinoma is hypothesized to be associated with epithelial-mesenchymal transition (EMT). We have previously shown that EMT correlates with the size of epithelial compartments (cluster size) and stromal infiltrative growth patterns. Here, we quantitatively analyze EMT processes and their correlation with cluster size and infiltrative growth patterns.

Material and methods

Images were generated using sequential Immunofluorescence (COMET, Lunaphore Technologies) on two cohorts: five CRC whole slide images (WSI) and a Tissue Microarray (TMA) cohort of 162 pre-treatment rectal cancer biopsies. After epithelium segmentation and cluster size assessment, we calculated an EMT score per tumor cell using expression profiles of six epithelial markers. Furthermore, we quantified fibroblasts within 20µm of each cancer cell to create the interaction score. High values correspond to increased tumor micro-environment (TME) interaction, as seen in infiltrative stromal invasion.

Results and discussion

We observed increased EMT scores in smaller epithelial compartments ($p<0.001$). Similarly, we found strong correlations ($p<0.001$) between EMT score and interaction score for WSI cases showing dominance of infiltrative growth patterns ($r=0.72$) compared to cases showing a dominance of pushing invasion patterns ($r=0.23$). In our biopsy TMA cohort, the correlation of EMT score with either interaction score or cluster size similarly indicates worse response to neoadjuvant treatment ($p=0.051$ and 0.014 respectively).

Conclusion

The metastatic process encapsulates a complex interplay between gradual molecular and morphological transitions within cancer, which we identified quantitatively on a whole-slide level and a large neoadjuvant treated rectal cohort. We hereby show the power of adding a spatial component to expression patterns to drive biomarker discovery.

Key words: Sequential immunofluorescence, Image analysis, Spatial analysis, Molecular feature extraction, Epithelial-mesenchymal transition

A41

A Multi-Feature AI Solution for Diagnosis Support of Breast Excisions: A Clinical Validation Study

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Introduction

This study aimed to clinically validate the performance of an artificial intelligence (AI)-based solution for detection of invasive and in-situ carcinomas in breast excisions compared to a robust ground truth (GT) established by multiple expert pathologists.

Material and methods

An AI algorithm, previously validated on biopsies, was tested in a standalone performance study on an external cohort comprising 248 retrospectively collected breast excisions. AI results on invasive and in-situ carcinoma were compared with GT diagnosis that was reached by concordance between two blinded pathologists who reviewed the slides. Discrepancies were adjudicated by a third expert pathologist.

Results and discussion

The AI-algorithm demonstrated a high performance compared to the GT with an AUC of 0.986 (95% CI: 0.973-0.998) for the detection of invasive carcinoma (specificity 96.3%, sensitivity 89.9%) and an AUC of 0.994 (95% CI: 0.987-1) for the detection of DCIS (sensitivity 95.6%, specificity 95%). The AI differentiated well between subtypes of invasive and grades of in-situ cancers with an AUC of 0.963 (95% CI: 0.922-1) for IDC vs. ILC and an AUC of 0.970 (95% CI: 0.931-1) for DCIS high grade vs. low grade. For the exploratory endpoints, the AI was able to predict the presence of TILs (sensitivity 91.4%, specificity 100%) and the presence of lymphatic invasion (sensitivity 72.2%, specificity 86.4%).

Conclusion

This study reports the successful clinical validation of an AI-based solution in the detection of clinically relevant diagnostic parameters regarding invasive and in situ breast carcinoma in resection specimen, offering an important tool for computer-aided diagnosis in routine pathology practice.

Key words: Breast cancer, Artificial intelligence, Validation

A42

Detecting Histologic & Clinical Glioblastoma Patterns of Prognostic Relevance

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Introduction

Glioblastoma is the most common and aggressive primary adult brain tumor, without substantial prognostic improvements observed since 2005 due to limited disease understanding. Utilizing interpretable computational methods for prognostic stratification integrating whole slide images (WSI) and clinical features (CF) could contribute to improved clinical decision-making.

Material and methods

TCGA-GBM and TCGA-LGG data were reclassified following the 2021 WHO classification criteria, identifying 188 glioblastoma (IDH-wt,Gr.4) and stratified as short- (<9months) and long-survivors (>13months). H&E-stained WSI underwent comprehensive curation, and weakly-supervised attention-based multiple-instance-learning facilitated interpretation of predictions by generating attention heatmaps. The prognostic relevance of 14 CF was assessed independently and integratively using XGBoost and SHapely Additive exPlanations (SHAP). Late fusion averaged the output probabilities of these two models for final decision-making. Quantitative evaluation was based on 10-fold monte-carlo cross-validation, using training(80%), validation(10%), and unseen-test(10%) splits.

Results and discussion

Analysis of i) imaging ii) CF and iii) their integration demonstrated AUC_Test of 0.68, 0.74, and 0.76 respectively. Interpretation of attention heatmaps revealed long-survivors to be associated with histologically malignant areas of necrosis, hypercellularity, and atypia, while short survivors indicated more aggressive infiltrative features including leptomeningeal involvement. The top contributing CF (based on SHAP analysis) for patient prognostic stratification were age, Karnofsky performance score, Percent aneuploidy, and Mutation count.

Conclusion

Integrating imaging and CF yields superior prognostic stratification performance, when compared with each of them independently. Our study also supports interpretation of algorithmic decisions towards enhancing understanding of GBM by identifying underlying morphological and clinical patterns of prognostic relevance.

Key words: GBM, Prognostic stratification, Whole slide image, XGBoost, Multimodal, Interpretability

A43

Federated Learning for the Classification of Tumor Infiltrating Lymphocytes: One DL model for 12 cancer types

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Introduction

Tumor-infiltrating lymphocytes (TIL) patterns in whole slide images (WSIs) provide salient information about immune response in the tumor microenvironment and are correlated with clinical outcomes in early-stage cancers. Deep learning (DL) is commonly used in WSI analysis. However, the accumulation of large, centralized training datasets is challenging due to privacy, ownership, and regulatory concerns. Federated learning (FL) offers a promising strategy for obviating multi-institutional data-sharing for model training.

Material and methods

662 WSIs from 12 cancer types in The Cancer Genome Atlas repository were grouped according to cancer type to create a FL setup . A classification model with the VGG network architecture was trained using FL, to distinguish between TIL-positive and TIL-negative 50x50um image patches in WSIs and create spatial maps of TILs. Model performance was quantitatively evaluated per cancer type (cross-validation leaving one cancer type out).

Results and discussion

The FL model achieved an 89% average balanced accuracy (ABA) across sites , while the models trained with a centralized dataset and datasets at individual sites had ABACL=88% and ABAIND=76-87%, respectively. Qualitative evaluation of resulting TIL maps indicated that TIL density predictions of the FL consensus model were comparable to those using centralized learning (CL).

Conclusion

FL has comparable performance to CL in developing a single TIL classification model for 12 cancer types, while mitigating the challenges of data sharing and centralized data collection due to privacy and regulatory concerns. FL further enables sites without a large-scale oncology database to contribute towards DL model development, thus enhancing collaborative research across diverse datasets.

Key words: Federated Learning, Classification, Histopathology, Digital Pathology, Tumor-infiltrating-lymphocytes, Artificial Intelligence

A44

Self-supervised determination of glioma IDH mutation status from H&E-stained whole slide images

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Introduction

Infiltrating gliomas are the predominant primary adult brain tumors. Isocitrate-dehydrogenase (IDH) mutational status is diagnostically critical, with prognostic and therapeutic implications, but only determined after molecular analysis. Here we seek an interpretable computational predictor of IDH status from H&E-stained whole slide images (WSI).

Material and methods

We identified 1,534 WSI (756 IDH-wildtype, 778 IDH-mutant) from TCGA-LGG/TCGA-GBM, and 114 WSI (82 IDH-wildtype, 32 IDH-mutant) from the University of Pennsylvania (UPenn). 20X magnification WSI underwent comprehensive curation and tiling into 256x256 patches. Features were extracted using pre-trained i) ImageNet weights as baseline, and ii) self-supervised vision transformer(SSL-ViT). A weakly-supervised attention-based multiple-instance-learning framework distinguished WSI between IDH-wildtype/IDH-mutant, while generating attention heatmaps for visual interpretation. Performance was initially evaluated as 10-fold cross-validation (CV) across TCGA data partitioned in training (80%), validation (10%), and test (10%) sets. Independent evaluation conducted on the unseen hold-out UPenn data.

Results and discussion

Evaluation on TCGA and UPenn data yielded accuracy of 88.8% (AUC-cv=0.955) and 92.6% (AUC-hold-out=0.976), respectively, with high sensitivity, i.e., confidence in predicting IDH-mutant. The SSL-ViT model on hold-out data demonstrated superior accuracy and AUC to the baseline, by 6.7% and 10.8% improvements, respectively. Heatmap assessment indicated IDH-wildtype tumors exhibit distinct regions of significant pleomorphism and microvascular proliferation, while IDH-mutant tumors exhibit dense nodular cell concentrations, microcystic architecture, uniform gemistocytic cells, and fibrillary background areas.

Conclusion

Our accurate H&E-based computational determination of glioma IDH status, with interpretations aligned with human-identifiable features, can obviate the need for molecular analysis and enable expedited diagnosis even in community settings.

Key words: Self-supervised learning, IDH, gliomas, Whole Slide Images, interpretation, AUC

A45

Deep Learning Subtyping of Multi-institutional Renal Oncocytic Neoplasms from H&E-stained Whole Slide Images

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Introduction

Renal oncocytic neoplasms describe the well-established entities of renal oncocytoma (RO) and chromophobe renal cell carcinoma (ChRCC), as well as a subset of tumors sharing features of both, including a new entity termed low-grade oncocytic tumor (LOT). Morphological similarities between the two tumors make their accurate diagnosis feasible only through a combination of immunophenotyping and molecular testing. Here we introduce a novel generalizable subtype classification approach for RO, ChRCC, and LOT based solely on H&E-stained whole slide images (WSI) and weakly-supervised deep learning (DL).

Material and methods

DL training and evaluation relied on 381 WSI of 156 cases, from 6 institutions, with renal oncocytic tumors (140 RO, 171 ChRCC, and 70 LOT). 72 independent hold-out WSI from 20 cases were used for generalizability assessment (29, 32, and 11, from 8 RO, 9 ChRCC, and 3 LOT, respectively). Comprehensive patch-based (256x256) pre-processing at 20x magnification eliminated artifacts on each WSI before feature extraction. Our weakly-supervised attention-based multiple-instance-learning DL model was quantitatively evaluated through 10-fold cross-validation with case-level stratification, and subsequently validated independently on the hold-out data.

Results and discussion

Our DL model yields generalizable performance, with a 10-fold average accuracy of 80% (AUC=0.93), aligning with the hold-out accuracy of 82% (AUC=0.93).

Conclusion

Our proposed approach contributes to a comprehensive solution for addressing commonly encountered renal oncocytic neoplasms, encompassing well-established entities like RO and ChRCC, along with the challenging "gray zone" LOT, thereby proving relevant in contemporary clinical settings. It further holds potential to revolutionize renal tumors' clinical management by prioritizing organ preservation.

Key words: Deep Learning, Renal Cell Carcinoma, Chromophobe, Oncocytoma

A46

Digital Pathology Aid for Telemedicine

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Introduction

The exchange of digital pathology images is becoming increasingly in demand among different settings. Due to the high level of specialization required, not many anatomic pathologists are able to report every type of biopsies (i.e. specific types of kidney biopsies). This leads to an increased number of preventable treatments such as dialysis and transplants, causing potential worsening of patient quality of life and high costs for health organizations and public administrations.

Material and methods

The proposed approach firstly takes into consideration profiles and guidelines of IHE PaLM. Additionally, the XRR, XDS-I.b and XDS profiles are useful for reporting and sharing images/documents, along with Supplements from the DICOM Working group 26 which include the DICOM Pathology data model referenced in the IHE PaLM DPIA profile. Furthermore, the SWF (Scheduled Workflow) profile from IHE Radiology Domain facilitates registration, ordering, scheduling, imaging acquisition, storage and viewing transactions (for features not covered by IHE PaLM profiles).

Results and discussion

This method for addressing the image exchange of digital pathology slides allows to engage interoperability in procurement strategy for a telemedicine scenario by summarizing and exploring various IHE profiles in the interoperability and imaging domains extending their application to the specific context of digital pathology.

Conclusion

The fact that most of the actors and the transactions taken into account are drawn from established IHE profiles, allows the conclusion that risks are minimized. The time is now ripe to take this step forward.

Key words: interoperability, telemedicine, workflow

A47

How do unsharp areas of histopathology whole slide images impact deep learning model performance and how can the problem be reduced?

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Introduction

AI-based analysis of histopathology whole slide images (WSIs) is central in computational pathology. However, image quality can impact model performance. Here, we investigate to what extent image sharpness impacts deep convolutional neural network classification performance. We propose a multi-model approach for reducing the problem as well.

Material and methods

This study includes 916 hematoxylin and eosin (H&E)-stained WSIs from Swedish breast cancer patients (one WSI per patient). We evaluate the binary classification of Nottingham Histologic Grade 1 vs. 3 using ResNet18. Taking a simulation approach, Gaussian blur at varying levels was added to tiles, and classification performance was evaluated. Also, we propose a multi-model approach. Three models were trained on data with variable amounts of Gaussian blur, and at prediction time, tiles were allocated to each model based on estimated blurriness. Performance was evaluated over 5-fold cross-validation.

Results and discussion

The classification performance for the model trained and evaluated on original image tiles had an AUC=0.89 (base model). A model trained with mildly blurred tiles (sigma=0.5) improved performance over the base model when moderate to high blur was added to validation WSIs. Using the multi-model approach, the base model could be outperformed by the multi-model approach in two scenarios: 1) moderate blur across all tiles (AUC: 0.76 vs. 0.71); 2) a mix of slight, moderate, and high blur across the tiles (AUC: 0.82 vs. 0.79).

Conclusion

Unsharp image tiles (local blurriness) can reduce model performance. The proposed multi-model approach improved performance under some conditions, which could improve quality in both research and clinical settings.

Key words: breast cancer, WSI analysis, artificial intelligence, deep learning, quality control

A48

The FHIR Standard and Digital Pathology: Accelerating Workflow Evolution

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Introduction

The adoption and understanding of digital pathology are rising, yet implementation remains challenging. One major hurdle is the lack of cohesive solutions to facilitate the seamless transition to digital workflows. In response to this challenge, we developed a novel web-based solution leveraging the Fast Healthcare Interoperability Resources (FHIR) standard to optimize our digitization workflows by effectively managing all critical stages: request, fulfillment, and delivery.

Material and methods

Utilizing FHIR workflow and diagnostic medicine modules, we developed relational data models and custom request forms in TypeScript to address various digitization needs. API endpoints were set up for our anatomic pathology laboratory information system, enriching requests with metadata. These requests populate worklists for our scanning personnel, facilitating a smooth transition from physical assets to digital files with provisions for quality control documentation. Digitized slides are accessible in our custom viewer only upon validation of a corresponding request. Furthermore, finalized requests prompt automated email notifications in batches to designated pathologists.

Results and discussion

Our new system successfully modernized our digitization operation, reducing manual intervention and embracing automated processes. Over eight months, 65 users have generated 32,242 requests for educational (51%), clinical (45%), and research (4%) purposes, resulting in 26.4 terabytes of whole slide imaging files.

Conclusion

A key aspect of digital pathology's transformative potential lies in the coordination between hardware and software components. Despite the FHIR standard's initial structure not being inherently optimized for laboratory transactional data exchanges, our system showcases that a relational representation of the standard can enhance workflow efficiency and facilitate better data management for subsequent analytics and process enhancement.

Key words: FHIR, digital pathology, workflow management

A49

Digital Pathology implementation Journey in a network of 14 hospitals in Spain.

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Introduction

Digitalization of pathology laboratories has been a growing trend for over a decade. It has the potential to revolutionize the way clinical diagnosis are made while improving safety and quality. In the Spanish National Health System there are few laboratories that have deployed digital pathology platforms. Castille & Leon's pathology digitalization project begun in early 2022 when a focus group of 6 pathologist was created and started working along with the Regional Health Department with the main goal to introduce whole slide images for diagnosis.

Material and methods

A definition of needs was stablished, and meticulously planned the essentials, taking into account all functional and technological requisites, and started the process of our public procurement, which was built on four different public tenders. One decentralized tender for scanners for each hospital, and three centralized tenders for PACS (Picture Archiving and Communications Systems), Workstations and Technology infrastructure-data storage.

Results and discussion

In this complicated timeline, 5 of our 14 hospitals have already finished their procurement on acquiring scanners, and Pannoramic®1000 and Pannoramic®480 scanners (3DHISTECH Ltd®) were chosen. There are still 9 hospitals to be decided. On the PACS/VNA and AI solution side, we are currently on an open procurement on the evaluating fase of the 4 offers submitted, right on the verge of finalizing the process and soon to have an awardee.

Conclusion

Even though we are an ongoing process with still much ahead, are model of digital workflow implementation at SACYL, demonstrates that with careful planning and adoption of simple measures, and addressing key barriers, it can be done.

Key words: implementation, tender, procurement, pathology

A50

Histopathology Atlas: An open-source Whole Slide Image (WSI) collection for educational purposes

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Introduction

WSI for medical school and resident education became popular recently. Storage and sharing WSI via web has challenges. We are developing a modular, free, open-source WSI collection for educational purposes.

Material and methods

Slides are scanned with Leica Aperio AT2 or GT450 at 40x and anonymised. Regions are cropped from svs images using ImageScope. The svs files are converted into dzi using VIPS software. The files are modified with OpenSeadragon and plugins, then uploaded to GitHub servers. The website is built with Quarto and hosted on GitHub pages, rendered into Turkish and English websites via GitHub actions, with monthly pdf, epub releases. Collections from different institutions (with youtube videos) and images with artificial reality features are being added.

Results and discussion

The Histopathology Atlas is available via https://www.histopathologyatlas.com/ and https://www.patolojiatlasi.com/ also as ebook and pdf. The codes are available https://github.com/pathologyatlas/ and https://github.com/patolojiatlasi/. Being dependent only on static website features it is possible to publish from various servers without database structure. The images are divided into small tiles which makes the storage and sharing of images easier. Templates are used, thus rendering of different formats are easier.

Conclusion

The Histopathology Atlas is an ongoing initiative with regular updates and open to contributions. Having a modular structure it is easy to restructure and create different versions for different courses. Since the WSI are converted merely into a website format, they can be downloaded, carried and presented without additional software. Although Openseadragon has long been used for research and pathology images, with the availability of digital pathology we are using it to expand the educational use.

Key words: atlas, education, opensource, wsi, histopathology

A51

What to look for when choosing a slide scanner for your laboratory.

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Introduction

Purchasing a digital slide scanner is a serious financial decision that should not be taken lightly. Castilla & Leon Health system is currently conducting DP implementation in a network of 14 hospitals in Spain.

Material and methods

Since our region's demographic and hospitals are so diverse with different needs and technological requisites, we performed a technical analysis on 5 prechosen brands of scanners and travel around different hospitals in Spain, with 20 slides selected meticulously with a variety of difficulties to test the performance and error management, as well as gather information on technical and personal experience of the technicians.

Results and discussion

Detail reports on each test and a comparative table with scanning time, scanning mode, image quality, occurrence of errors, management and repercussions of those errors, need for manual or automatic rescanning and capacity were made. All the questions regarding on how we intend to use the scanners now and in the future, capability of scanning the daily workload of our hospitals, space needed, overnight scanning, simplicity for our technicians, interoperability, and how to cover each of our hospitals needs were answer.

Conclusion

With the results on our tests, we wrote two different public tenders for scanners, one for our bigger hospitals and the other for our smaller hospitals. As now, five of our hospitals have already awarded their public tender for scanners, and at the moment we have an open procurement for PACS / VNA and AI solution, in the hope of having our departments completely digitalized by the end of this year.

Key words: whole slide image, slide scanner, technical analysis, pathology

A52

Hexagonal Grid-based Methods for Pathology: An Overlooked Approach for Spatial Analytics

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Introduction

As pathology has developed over the past decades, the search for biomarkers has evolved from eye-balling global estimates like cellular counts and hotspots per histological section to analyzing intricate spatial relationships between different cell types. This evolution is crucial for quantification of intratumoral heterogeneity and distributions of cells within the tumor microenvironment. In between methods for global quantity estimation and local point-based methods (e.g., clustering, distance fields, k-nearest neighbor) lies a set of methods for spatial subsampling by regular grids, such as hexagonal grids (honeycombs). So far, these have been underutilized in pathology.

Material and methods

In this talk we outline how to exploit hexagonal grids - "honeycomb analytics" - for computing spatial pathology features by first considering some technical data extraction challenges and guidelines for how to correctly dichotomize the data by the grid. We then cover how the grids offer alternative ways of defining and analyzing several important concepts and quantities for the application as biomarkers in pathology, such as proliferation hotspots and spatial distributions of cells.

Results and discussion

Lastly, we give examples of how hexagonal grids have been utilized for assessment of intratumoral heterogeneity and immune cell density profiles across tissue interface zones (ImmunoGradient).

Conclusion

We conclude that hexagonal grid-based computational methods offer unique advantages for advancing spatial analysis in pathology.

Key words: Spatial Analysis, Regular Grids, Tumor Microenvironment, Heterogeneity, Hotspots, Haralick's Entropy

A53

Semi-supervised automated Gleason Grading on WSI

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Introduction

The Gleason grading system, which distinguishes between distinct forms of prostate cancer, continues to be the most effective predictive tool for patients with prostate cancer despite having relatively significant inter-observer variability compared to other recognized tumor grading schemes. This variability poses a major challenge for the development of reliable automated Gleason Grading Systems. To address this problem, we propose a novel deep-learning based automated Gleason Grading system, that was developed during the AGGC challenge. It is specifically optimized for clinical challenges and generalizes across issues such as handling different biopsy types (whole mount or needle core) and various scanner types.

Material and methods

We utilize a noisy student approach with five-fold cross-validation and exhaustive RandAugment for data augmentation. This method addresses partial annotations in our dataset, where correct predictions may occur without thorough annotation. We tackle high class imbalances using weighted point-based sampling (per class) and 20% random sampling for the teacher model in background-predicted scenarios. During inference, we aggregate predictions from five folds with 50% overlap, employing a Gaussian weighted kernel for inference patches and Test Time augmentation via flipping. To refine predicted class boundaries, we apply erosion and dilation in postprocessing.

Results and discussion

On the final Leaderboard of the challenge, the proposed method achieved an accuracy of 73.46% on the whole mount slides, 66.86% on needle core biopsies and 69.31 on the scanner generalization task, which results in the weighted final score of 71.31%. As reference: first and second ranked teams achieved 76.20% and 74.13% respectively.

Conclusion

Our approach yields improved Gleason Grading and is publically available.

Key words: Digital Pathology, Noisy Student, Automated Gleason Grading

A54

Full Resolution Three-Dimensional Reconstruction of Non-Serial Prostate Whole-Mounts: Pilot Validation and Initial Results

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Introduction

Three-dimensional reconstruction in histopathology can be achieved by the co-registration of consecutive digitized whole-slide images to reconstruct an anatomical volume of interest. These 3D reconstructions greatly enhance the pathologist's ability to inspect and relate tumour growth patterns to pre-operative 3D imaging and pave the way for automated specimen analysis. Although several algorithms have been proposed for this task, these either require additional input (i.e. ex vivo MRI), are limited to low-resolution versions of the slide or expect serial slicing rather than the more common sparse sampling of a specimen, which severely limits clinical applicability. In this work, we present a deep-learning based algorithm which addresses all of the aforementioned limitations and demonstrate its effectiveness on 20 prostatectomy samples with 4-9 slides each.

Material and methods

We tune and validate our algorithm on a cohort of respectively 30 and 20 prostatectomy specimens with routine sparse sampling with a four mm distance between slices, prepared as whole-mount sections and stained with H&E. The algorithm is powered by a transformer (LightGlue) for feature extraction and matching and was evaluated using median target registration error (TRE) between automatically detected landmarks and a normalized Dice coefficient to assess shape congruency.

Results and discussion

The proposed algorithm achieved a correct reconstruction in 16/20 (80%) cases and obtained a mean TRE of 1.53 ± 0.71 vs 7.75 ± 1.83 mm and normalized Dice of 0.95 ± 0.03 vs. 0.84 ± 0.04 compared to the baseline method of aligning slides by centerpoint.

Conclusion

We present a novel algorithm for automated full-resolution 3D reconstruction from sparsely sampled prostatectomy specimens.

Key words: prostate cancer, 3d image reconstruction, image registration, whole-slide imaging

A55

HistoMIL: A Python package for training multiple instance learning models on histopathology slides

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Introduction

Digital pathology Whole Slide Image(WSI) datasets consist of large images scanned from original diagnostic tissue slides stained with Hematoxylin and Eosin(H&E),often containing gigapixel in single file. Although transfer learning(TL) was initially used for WSI classification tasks,recent research has introduced multiple instance learning (MIL) as an alternative protocol. However, applying MIL methods in computational biology and clinical settings remains challenging. This complexity arises from the need for intricate data preprocessing to reconcile the incompatibility between raw data types and modern deep learning frameworks,the cumbersome process of model deployment,and the computationally expensive steps involved in self-supervised learning.

Material and methods

In response to the critical need for advancing the integration of MIL algorithms within the field of computational pathology,we present HistoMIL,an innovative Python package meticulously designed to facilitate the application,training,and deployment of MIL algorithms by computational pathologists and researchers. HistoMIL offers a self-supervised module specifically developed for the training of feature encoders in the pathology domain, thereby enhancing model performance. It provides a comprehensive toolkit that encompasses TL and introduces three MIL algorithms: ABMIL, DSMIL and TransMIL, each designed to address distinct challenges in the analysis of histopathological data.

Results and discussion

HistoMIL facilitates seamless customization and new algorithm integration. We demonstrate HistoMIL's capability in predicting the expression of 2,487 cancer hallmark genes across breast cancer histology slides from TCGA,with AUROC scores reaching 85%. Notably,the package excels in identifying cell proliferation,highlighting both the potential and limitations of deploying deep learning in gene expression analysis.

Conclusion

HistoMIL is presented as a user-friendly tool,aiming to demystify deep learning applications for the research community.

Key words: deep learning, Whole Slide Image, multiple instance learning

A56

Automated Quality Control in Histopathology through Artifact Segmentation

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Introduction

Whole-slide imaging (WSI) has revolutionized histopathology, enabling the digitalization of glass slides and computational analysis through deep learning (DL). However, the presence of artifacts during slide preparation and digitization poses significant challenges for both pathologists and AI systems, hindering accurate diagnoses. In this study, we propose a DL-based model for artifact segmentation and quality control in WSI.

Material and methods

Our training dataset consists of 100 slides with diverse tissue and stain types, digitized across seven scanners to capture real-world variability. The DL model, based on DeepLabV3+ with EfficientNet-B2 encoder, is trained to segment six common artifacts: tissue folds, pen marker, ink, air bubbles, dust, and out-of-focus areas. Validation involves 500 additional cases, including preclinical tissue from rats and dogs, as well as an extended range of human organs and tissues.

Results and discussion

The model demonstrates efficacy in artifact segmentation, with a pixel-level average Dice score of 0.83 and 94% accuracy in binary classification of artifact versus non-artifact tissues. At the slide-level, an AUC of 0.95 is achieved in categorizing slides into poor or good quality based on the proportion of tissue covered by artifacts.

Conclusion

Our study highlights the potential of DL-based artifact detection in WSI to streamline the quality control process in histopathology. By prescreening slide quality, our method offers a promising solution to reduce the burden of quality control processes in clinics, ultimately ensuring more efficient and accurate diagnoses. Future work will focus on further refining the model's performance and exploring its implementation in clinical practice.

Key words: quality control, artifact segmentation, deep learning

A57

Deep learning-based segmentation of peritubular capillaries in kidney transplant biopsies.

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Introduction

The Banff classification system is used for diagnosis and classification of kidney transplant biopsies. An important feature of antibody-mediated rejection (ABMR) is peritubular capillaritis (ptc), defined as the presence of inflammation in peritubular capillaries (PTCs). However, assessing the extent of peritubular capillaritis suffers from interobserver variability and is time-consuming. Automated assessment would offer great benefits.

Material and methods

Kidney transplant biopsies (n=67) were stained with periodic-acid Schiff (PAS) and scanned with a P1000 (3DHISTECH, Hungary) whole slide image (WSI) scanner (0.24 µm/pixel). To obtain reliable annotations, the PAS-stained WSI were re-stained using anti-CD34-antibody. Guided by the restaining, a pathologist manually annotated over 20,000 PTCs on the PAS-stained WSI. For PTCs versus non-PTCs segmentation, we trained a U-Net model (ImageNet pre-trained ResNet50 backbone) with 160,000 patches (512 x 512 pixels, 0.24 µm/pixel) per epoch.

Results and discussion

A Dice score of 67.9% and 98.3%, and a Jaccard Index of 52.3% and 96.6%, for the PTCs versus non-PTCs regions, respectively was achieved. While there was a satisfactory performance in most cases, we observed less accuracy in cases with prominent interstitial changes, such as atrophic tubules and interstitial matrix deposition, which make PTCs less recognizable.

Conclusion

We developed a segmentation model for PTCs in PAS-stained kidney transplant biopsies, which in contrast to healthy tissue also include areas of inflammation and chronic damage. This is a first step towards a more accurate, reproducible scoring of peritubular capillaritis. Our next goal is to develop an algorithm for inflammatory cell detection, as this is necessary for automated ptc scoring.

Key words: Deep learning, Kidney, Transplant, Peritubular capillaritis, Segmentation

A58

Quantitative Analysis of Bile Duct Morphology and Spatial Distribution in Nonalcoholic Steatohepatitis (NASH) Liver Biopsies Across Disease Stages.

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Introduction

Non-alcoholic fatty liver disease progresses from simple fat accumulation to inflammation and fibrosis, leading to severe liver damage. Diagnosis relies on liver biopsies, which confirm the disease's presence and identify its stage and progression factors, highlighting the need for enhanced characterisation and understanding. Central to its progression are hepatic progenitor cells and ductular reactions—key indicators of liver regeneration in response to damage, critical for assessing the risk of disease advancement. This study introduces an automated tool for detecting these indicators in liver biopsies, aiming to improve the stratification of progression risk in liver disease by quantifying the presence and distribution of hepatic progenitor cells and ductular reactions.

Material and methods

Liver biopsies from 40 patients diagnosed with NAFLD/NASH were then digitised with HE, Trichrome, and Cytokeratin 7 stains. Bile ducts and isolated CK7-expressing cells were segmented, and their morphological characteristics and CK7 staining textures were extracted. These features classified the stained objects into main bile ducts, ductular reactions, and isolated CK7-positive cells, and fed into a graph neural network along with the objects' location.

Results and discussion

More than 8000 CK7 positive objects were detected. Their morphological and densitometric characteristics, spatial distribution, and embeddings in the graph neural networks were inserted into a high-dimensional data mining pipeline. Pathologically relevant signatures were identified and compared to NASH pathological scoring.

Conclusion

This approach algorithmically distinguished main bile ducts, proliferating ductules and possible hepatic progenitor cells to study their characteristics and complex distribution in liver biopsies, possibly leading the path to the discovery of digital biomarkers of disease progression.

Key words: Computational Pathology, Instance Segmentation, Spatial Biology, Graph-Neural Networks, Semantic Representation, Digital Biomarkers

A59

Deep Learning Unveils Molecular Footprints in Histology: Predicting Molecular Subtypes from Bladder Cancer Histology Slides

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Introduction

Transurethral tumor resection followed by intravesical bacillus Calmette-Guerin (BCG) is standard care for high-risk non-muscle-invasive bladder cancer (HR-NMIBC) patients. However, ≈20% progress to advanced stages despite BCG. Molecular profiling identified BCG response subtypes (BRS 1/2/3); BRS3 correlates with worse outcome. Traditional methods for subtype differentiation, are costly and resource-intensive. We used deep learning (DL) to predict BRS1/2 versus BRS3 molecular subtypes from digitized histology slides, emphasizing BRS3 as a cost- and time-effective method.

Material and methods

H&E-stained slides were digitized, excluding blurry images. Areas from which RNA was extracted were annotated pixel-wise by, using QuPath. Image tiles of 512x512 pixels at 10X/20X/40X magnifications were extracted with 25% overlap. BRS1 and BRS2 images were classified together, separate from BRS3 images. Post-normalization, patients were split 80/20 for training/validation, with 5-fold cross-validation. DL models (DenseNet, Inception, ShuffleNet, ResNet) classified tiles into BRS3 and BRS1/2. Patient-level classification used majority voting. Model efficacy was gauged by AUC.

Results and discussion

Of 245 H&E slides, 45 were discarded for quality. From 200 patients the distribution was 70:30 between BRS1&2 and BRS3. DenseNet best identified BRS subtypes at 10x with 0.65 AUC and 0.03 standard deviation for tile-level, and 0.80 AUC and 0.05 standard deviation for patient-level predictions.

Conclusion

Our study demonstrates that DL can identify BRS3 vs. BRS1/2 subtypes from H&E slides. This method can identify BRS3 HR-NMIBC patients who may benefit from alternative treatments than BCG in a cost and time-efficient manner. Future goals are evaluating model performance on an independent test cohort and predicting additional molecular markers for fine-tuning.

Key words: Artificial Intelligence, Bladder Cancer, Deep Learning, Molecular Subtype

A60

Using tumor topology to predict patient survival after neoadjuvant chemoradiotherapy in rectal cancer

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Introduction

Tumor regression grading (TRG) is used to evaluate tumor response after neoadjuvant chemoradiotherapy (nCRT) and predict patient outcome in advanced rectal cancer (RC). However, this TRG often fails to accurately predict patient overall survival (OS), especially for those with intermediate response to nCRT. We propose here a new patient stratification based on residual tumor topology.

Material and methods

On a cohort of 74 RC neoadjuvantly treated patients (1071 slides), Cerberus and an epithelial graph-based classification models were applied to detect tumor cells, which were then clustered based on a distance threshold of 25 µm, forming supernodes. The average number of epithelial cells per supernode, the area spanned by the supernodes as well as the density and number of supernodes were aggregated over all slides and averaged to obtain patient-level observations. Using Cox proportional hazard models these measures were compared with clinical variables (age, sex, ypTNM, Dworak/Becker TRGs) to predict patient OS.

Results and discussion

Tumor area and supernode size were both prognostic. Combining these two measures, the cohort was stratified into 3 groups: a good prognosis group showing big clusters (>80 cells/supernode) over a small area (<650 mm2), an intermediate group having small clusters over a small area and a bad group with large area. This stratification was significantly better ($p<0.005$) at predicting patient OS than Dworak/Becker TRGs and ypTNM for both the whole cohort and intermediate responders.

Conclusion

The topology of residual tumor cells in the tissue post nCRT predicts patient outcome more accurately than standard TRG. These results are currently being validated on an external cohort.

Key words: rectal cancer, neoadjuvant treatment, cell detection, cell clustering, supernode, tumor topology

A61

Prognostic significance of the spatial distribution of tumor infiltrating immune cells in of non-muscle-invasive papillary urothelial carcinoma

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Introduction

Non-muscle-invasive papillary urothelial carcinoma (NMIPUC) is the most common type of bladder cancer with a highly variable clinical course. The importance of the tumor microenvironment is well established in predicting the response to immunotherapy. We evaluated the impact of the spatial distribution of tumor-associated macrophages and tumor-infiltrating lymphocytes on relapse-free survival (RFS) of the patients treated with BCG immunotherapy.

Material and methods

Whole slide images of CD8, CD20, ICOS, CD163, and CD11c immunohistochemical stains underwent artifact exclusion, stromal epithelial classification, cell identification, and distribution assessment using HALO® AI software. Additionally, CD20 staining was used for tertiary lymphoid structure (TLS) identification. We assessed absolute densities in the interface zone, immunodrop (ID, ratio between the cell densities infiltrating epithelial and stromal aspects of the interface), and presence of TLS using univariate Cox regression to select the features for multivariate Cox regression and Kaplan Meier survival analysis.

Results and discussion

By univariate Cox regression ID of CD8, CD11c, and ICOS, together with tumor stage and anamnesis of positive reTUR showed significant association with patients RFS ($p < 0.05$). By multivariate Cox regression, the best-performing models included a combination of CD11c ID and history of positive reTUR, a combination of CD11c ID and tumor stage (concordances index 0.7427 and 0.703 respectively).

Conclusion

The spatial density profiles of CD8, CD11c, and ICOS positive cells across the tumor-stroma interface are significant predictors of RFS in these patients, while absolute densities of the cells are of lower prognostic value.

Key words: Tumor infiltrating lymphocytes, Tumor associated macrophages, Immunogradient

A62

Deep learning algorithm on H&E whole slide images to characterize TP53 alterations frequency and spatial distribution in breast cancer

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Introduction

The application of deep learning (DL) algorithms to hematoxylin and eosin (H&E) whole slide images (WSIs) holds significant promise for predicting crucial molecular features in breast cancer (BC), such as gBRCA alterations. These methodologies represent potential tools for pre-screening patients for actionable molecular alterations. Here, we have developed a H&E-based DL framework to characterize TP53 status in BC, addressing intra-tumor heterogeneity.

Material and methods

After pseudo-anonymization, H&E and p53 immunohistochemistry (IHC)-stained slides from a case of hormone receptor (HR)-negative BC with a TP53 mutation were digitized. The SVS H&E WSIs were analyzed using a proprietary PyTorch-based pipeline on a GPU-enhanced virtual machine. Both pre-processing and model inference phases were executed. The presence of tumor tissue and p53 expression levels were quantified using a classifier with a Dice probability threshold of >0.75. Independent assessment and scoring were also performed by a breast pathologist (BP).

Results and discussion

The DL pipeline and the BP provided closely matched estimations for the total tissue area (2.6 cm^2 vs. 2.7 cm^2, respectively). Concordant measurements were obtained for the tumor tissue area (1.0 cm^2 for both DL and BP). The DL analysis revealed that p53 was aberrantly overexpressed in 92% of the tumor area with an overall Dice coefficient of 0.82, closely aligning with the BP's assessment of 90%.

Conclusion

This proof-of-concept study underscores the potential clinical applicability of our DL framework for evaluating TP53 status on H&E WSIs in HR-negative BC. The findings suggest that our approach can serve as a valuable tool in identifying hallmark alterations in BC.

Key words: breast cancer, artificial intelligence, deep learning, TP53, heterogeneity

A63

Diff-ST: Staining Translation between HE and IHC by Diffusion Models

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Introduction

Histopathological examinations often use hematoxylin and eosin (HE) staining to visualize tissue structures and immunohistochemistry (IHC) to detect specific protein expression, like HER2 in breast and gastric cancers [BCI]. However, IHC is costly and time-consuming. Moreover, adjacent slices for HE and IHC may represent different tissue states or even miss tumor areas. Finally, cutting multiple slices reduces tissue material, which can be critical for small biopsies. Virtual IHC staining without cutting new slices is therefore favorable.

Material and methods

To address these challenges, we propose Diff-ST, a Denoising Diffusion Probabilistic Models (DDPM) based method to generate IHC images given HE images. The synthetic IHC images provide high-resolved, detailed, and structurally reserved information for clinical decisions. In contrast to Generative Adversarial Network (GAN) based approaches, the diffusion models introduce stochasticity into staining translation, yielding more diverse generated samples. However, a notable drawback of DDPM lies in the color deviation induced by domain bias. We enhance the loss function design to address this inherent issue by incorporating an additional similarity-based component alongside the common mean squared error (MSE) loss.

Results and discussion

Empirical study shows that incorporating this structural constraint accelerates the model training and improves the overall efficiency. Consequently, the proposed Diff-ST method achieves comparable or even better performance to state-of-the-art (SOTA) GAN-based approaches, iincluding BCI-Stainer, Pixel2Pixel, CutMix, etc., when assessed using quantitative evaluation metrics such as Structural Similarity (SSIM) and Peak Signal-to-Noise Ratio (PSNR).

Conclusion

Overall, Diff-ST presents promising prospects for advancing clinical virtual staining and further facilitating histological diagnosis.

Key words: Virtual Staining, Image Translation, Brease cancer, Deep Learning, Diffusion Model

A64

Multi-task GNN Prediction in Breast Cancer using Deep Features and Cellular Composition Statistics

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Introduction

When faced with limited training data, a multi-task approach can be beneficial. While learning the prediction task, the training signal for separate but related tasks can help learn features that are relevant to multiple tasks when a multi-task model architecture with a common encoder is used.

Material and methods

We introduce a multi-task Graph Neural Network architecture to solve 7 prediction tasks on 3000 breast cancer WSIs. We predict ER, PR and HER2 status, presence of Ductal Carcinoma in Situ (DCIS), presence of Lobular Neoplasia (LN), Grade, and lymph node metastasis. This is the first such highly multi-task model to our knowledge. Each WSI is represented as a network of nodes, where each node is an image patch with feature vector consisting of deep features from the CTransPath foundation model (a self-supervised model trained on a large dataset of WSIs across multiple tissue types) combined with cellular composition features from HoVer-Net cell segmentation in each patch. These features include cell type counts, and statistics describing cellular morphology in each patch (distributions of cell area and circularity).

Results and discussion

Results (AUROC, 5-fold cross validation) on the above tasks are 0.93, 0.83 and 0.85 for ER, PR and HER2 Status, 0.86 on Grade, 0.73 on DCIS, 0.81 on LN 0.71, and 0.70 for metastasis prediction. Attention-based pooling provides interpretability, allowing visualization of the most important areas of the WSI for each task.

Conclusion

Our multi-task architecture can efficiently and accurately perform a range of prediction tasks on Breast Cancer WSIs, performing competitively with state-of-the-art and particularly well on PR Status prediction.

Key words: Breast Cancer, Graph Neural Networks, Multi-task architecture, Deep learning, Receptor Status Prediction

A65

Clustering of glomerular image patches identifies clinically relevant lesion categories

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Introduction

In nephropathology, the classification of glomerular lesions is one of the tasks most extensively studied using artificial intelligence. However, the supervised training of deep learning models is hampered by a lack of large-scale labeled image datasets. The current study investigated whether clustering can automatically detect clinically relevant groups of glomeruli, thus reducing the demand for manual labeling and potentially enabling unsupervised deep learning opportunities.

Material and methods

To address this question, the project gathered over 130000 glomeruli by applying automatic segmentation on more than 1000 WSIs from publicly available repositories. Using this dataset, a large number of deep learning models for feature extraction and different clustering strategies were then investigated with respect to their ability to automatically distinguish various classes of glomerular lesions.

Results and discussion

Evaluating different deep learning-based feature extraction strategies, the project demonstrated a consistent separation of glomeruli into at least the two most prominent lesion categories, globally sclerosed and non-globally sclerosed. Subsequently, clustering enabled an automatic detection of these classes, reaching accuracies over 95%. In addition, more advanced/recent feature extraction methods appeared to even enable a further sub-clustering of the non-globally sclerosed glomeruli into more fine-grained lesion categories.

Conclusion

The project demonstrates unsupervised strategies for detecting at least two classes of lesions among glomerular images and illustrates that more advanced clustering strategies might even achieve the separation into more than just two classes. Building on these results it might be possible to design semi-automatic labeling approaches or even fully unsupervised learning strategies when training glomerular classification models.

Key words: nephropathology, glomeruli, global glomerulosclerosis, unsupervised learning, clustering

A66

Immunotherapy response prediction for non-small cell lung cancer is improved by using cell-graphs of the tumor microenvironment

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Introduction

Immunotherapy has made a substantial impact on the treatment of non-small cell lung cancer (NSCLC) patients, but few treated patients show durable clinical benefit. There is a need for a biomarker capable of selecting potential responders with greater predictive power than the current clinical standard, the tumor proportion score. We investigated graph neural networks (GNNs) for predicting immunotherapy response based on the tumor micro-environment (TME) in H&E whole slide images of NSCLC patients.

Material and methods

We processed 93 retrospectively collected NSCLC H&E biopsies or resections by i) detecting tumor and immune cells within the tissue using HoVerNet, ii) finding the densest region of tumor cells, iii) taking a 500 micrometer crop around this hotspot, hypothesizing that it is representative of the TME, iv) building a cell-graph of the hotspot using cell coordinates/type as node features. We trained three GNN architectures (GCN, GraphSage and GIN) on the graphs using five-fold cross-validation on two binary endpoints: 1-year overall survival (OS) and progression-free survival (PFS), measured from treatment start to radiological progression, death or loss to follow-up.

Results and discussion

Median follow-up was 11 months. The mean C-index (using the model's softmax as risk score) across five folds for all endpoints was consistently highest for the GIN model (OS: 0.727 ± 0.067, PFS: 0.599 ± 0.113), as compared to using the TPS thresholded at 1% (OS: 0.511, PFS: 0.512).

Conclusion

GNN assessment of H&E slides holds promise for better identifying responders to immunotherapy in NSCLC. Further studies on using GNNs, which describe relationships between cell types in the TME, are necessary.

Key words: Immunotherapy, Non-small cell lung cancer, Deep learning

A67

Predicting prostate cancer outcome from histopathology section images using deep learning

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Introduction

Prostate cancer (PCa) ranks as the second most common cancer in men worldwide, with over 1.4 million new cases annually. New biomarkers can enhance our understanding of carcinogenesis and ability to identify aggressive tumors both before and after surgical treatment. Using deep learning, we aimed to develop a biomarker capable of predicting patient outcomes directly from images of hematoxylin and eosin (H&E)-stained slides of radical prostatectomy specimens.

Material and methods

A previously defined deep learning network, DoMore-v1, was trained and tuned using 917 PCa patients (2037 slides) from three cohorts to create the new biomarker, DoMore-v1-PCa, which classifies each patient as good, uncertain, or poor prognosis based solely on images of H&E-stained slides. An external dataset consisting of 258 patients (774 slides) was used for testing with biochemical recurrence as primary endpoint, defined as a single PSA ≥ 0.4 ng/ml.

Results and discussion

The biomarker classified 128 (49.6%) patients as good prognosis, 95 (36.8%) as poor prognosis, and the remaining patients as uncertain prognosis. The hazard ratio between poor and good prognosis was 9.04 (95% CI 4.59-17.80; $p<0.0001$) in univariable analysis and 3.36 (95% CI 1.52-7.44; $p=0.0027$) in multivariable analysis incorporating standard clinicopathological parameters. The biomarker was significant in Gleason grade group 2 ($p=0.0011$) which consisted of 152 (58.9%) of the 258 test patients.

Conclusion

External testing suggests that the DoMore-v1-PCa biomarker can potentially improve risk stratification after radical prostatectomy and inform subsequent follow-up and treatment. Future work will be directed towards adapting this biomarker for use in diagnostic biopsies, aiming to enhance existing active surveillance protocols.

Key words: deep learning, image analysis, prostate cancer, histopathology, risk prediction, prognosis

A68

Attentive Deep-Learning model for predicting Immunoscore in TNBC from MyProbe RHU H&E images: histological interpretability and clinical outcomes

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Introduction

Early triple-negative breast cancer (TNBC) stratification is crucial to avoid over-treatment and evaluate current therapeutic strategy efficiency. In this context, immune infiltration is associated with a better prognosis in this patient population and could be assessed with Immunoscore®, a standardized prognostic immunohistochemistry test. Additionally, H&E material are a common source of knowledge in clinical environment. Here, we propose to leverage H&E information with an Artificial Intelligence-based model to predict Immunoscore in TNBC and associated interpretability.

Material and methods

H&E-stained tumor slides from 262 TNBC patients from MyProbe RHU clinical cohorts (PACS-01/-04/-05/CLB/IGR) were digitized. Slides were first processed in preanalytical steps, comprising of quality control, batch effect balancing and automatic artefact removal. In a second step, slides underwent postanalytics feature extraction with two deep-learning models (Imagenet and MOCO architectures). An attention-based deep-learning classifier was then applied to predict a two-class Immunoscore-AI and provide morphological interpretation based on common histological characteristics. Clinical association to Immunoscore-AI was then assessed.

Results and discussion

Out of the 20 cross-validated models from Imagenet and MOCO, the two best performing models achieved AUC/F1/Accuracy performances of respectively [0.98; 0.87; 0.92] and [0.98; 0.90; 0.95]. We show that the predictions are consistent with Immunoscore principles. The Immunoscore-AI prediction is characterized by an immune infiltration guided towards the tumor region and its surroundings in the microenvironment. The progression-free survival was significantly different between predicted Immunoscore-AI classes.

Conclusion

We present the first interpretable deep-learning model for predicting Immunoscore in TNBC patients based on H&E slides. It allows the prediction of immune infiltration with high performance, biological confidence and clinical relevance.

Key words: Artificial intelligence, Digital Pathology, H&E, Attentive Deep-Learning models, Immuno-oncology, TNBC

A69

Unstained tissue imaging and virtual HE staining of whole slide images: towards clinical tumor assessment

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Introduction

Hematoxylin and eosin (HE) is the standard stain for histology and it is by far the most used stain in the clinics by pathologists. Histological stainings make tissues visible to the human eye by highlighting certain cellular and tissue structures. This chemical technique, however, is irreversible, making the tissue unusable for other methodologies and subsequent measurements. Here, we evaluate techniques to perform HE staining computationally from clinical whole slide images (WSIs) acquired with brightfield microscopy.

Material and methods

Our sample set consisted of clinical invasive breast cancer samples of varying ER, PR and HER2 statuses. We first imaged the slides as unstained, then chemically stained the samples with HE and imaged the samples again. We then virtually stained the samples utilizing a supervised deep learning approach, Pix2Pix. Finally, we thoroughly analyzed the results by comparing the histology of the virtually stained tissues to ground truth HE from WSI to nuclear level.

Results and discussion

We found that the structure of cancerous regions is very distinguishable. The different structures found in the samples such as stroma, inflammatory cells, and cancer tissue are distinct, although the heterogeneity of the sample set caused some structures to perform sub-optimally. However, in well performing areas we can achieve even sub-cellular resolution, proving that there is great promise in the method.

Conclusion

Our findings highlight the potential of virtual HE staining of brightfield WSIs for both research and clinical histopathology while simultaneously opening possibilities for histological staining to become more sustainable and streamlined.

Key words: computational histology, digital pathology, HE staining, histology, virtual staining, whole slide image (WSI)

A70

Real-time Pathology Dashboards for Lab Worker Motivation: An Experience Report

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Introduction

In this presentation we continue our previously introduced line of research into using event logs from laboratory information systems to improve workflows. Specifically, we introduce a dashboard, called "LiveView", that presents key performance indicators relating to daily throughput rates in the laboratory, such as grossed specimen, sectioned blocks, and stained slides, in near real-time.

Material and methods

The software solution was created using a design science approach. Feedback on the final product was gathered through a questionnaire administered to a small cohort of lab technicians (n=25) and open-ended interviews. A statistical analysis was conducted on the results of the questionnaire to analyze trends in the perception of the dashboard by the lab workers before and after the introduction of the dashboard.

Results and discussion

Our investigation indicates that the lab workers are cautiously optimistic about the dashboard. Some see potential for enhancing motivation through acknowledgment of realistic goals achieved, as opposed to a demotivating constant influx of patient specimens. While it is too early to definitively assess the dashboard's impact on productivity quantitively, we plan to monitor and compare key performance data with historical records continuously.

Conclusion

There is limited literature evidence about dashboard applications in the field of pathology. To our knowledge, the other existing solutions all show a lower update frequency than our solution. Also, they lack the notion of a goal-aligned motivation mechanism. This study provides a concrete example of how previously untapped event data can be utilized for process improvement by building “home-grown” products.

Key words: Dashboards, Process Monitoring, Event Data, User Involvement

A71

Reliable comparisons between AI models and human experts in computational pathology

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Introduction

n digital pathology, obtaining unambiguous labels for AI model development is challenging since experts disagree frequently. While concordance statistics measure AI-human agreement levels, it is hard to determine if AI outperforms human scoring due to ambiguous labels. In this work, we evaluate human experts, an AI model and compare them in determining the intra tumoral stroma percentage (ITSP) from H&E-stained whole slide images (WSIs) using the discrepancy ratio (DR). We argue that this metric provides more value for AI model evaluation than traditional AI-to-human concordance metrics as it accounts for interrater variability.

Material and methods

An AI model was trained to segment tumor and stromal compartments on WSIs of breast resections obtained from TCGA (n=172). Two pathologists scored the ITSP on circular representative areas of 3.1mm2 on the WSIs marked by a third expert. The ITSP from the AI model were quantified and compared with those obtained from human experts.

Results and discussion

While determining the ITSP on unseen data (n=212), the average disagreement between human experts was 15.44%. Whereas the average disagreement between AI model and individual human experts was 16.98%. The AI model was found to be at par with the average human expert at determining the ITSP (DR=1.09).

Conclusion

We apply the discrepancy ratio to compare the performance of an AI model with human experts at determining the ITSP in WSIs of breast resections. Our results indicate that the AI model performs similarly to the average human expert. Reliable comparisons between AI and humans is essential for future research in bio marker discovery.

Key words: AI safety, Breast Cancer, Quantitative biomarkers, Computational pathology, Digital pathology, Oncology

A72

GrandQC tool: A radical solution for quality control problem in digital pathology

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Introduction

The main hurdle for clinical implementation of digital pathology AI tools is numerous artifacts related to tissue section preparation and digitization, that can critically affect the performance in downstream tasks. The study aimed to develop a powerful quality control (QC) tool for processing the H&E-stained slides.

Material and methods

A large, multi-organ, multi-institute cohort (whole slide images/WSI n=357) was precisely annotated for tissue/background regions, and 7 artifact types (folds, "dark spots", foreign objects, pen markings, glass edges, air bubbles, out-of-focus) and artifact-free tissue. Two algorithms were trained: 1) tissue-vs-background segmentation, 2) artifact segmentation (three different magnifications). One large independent test cohort was manually annotated (WSI n=318) for formal validation. Multiple independent cohorts scanned by 7 most common scanning systems were further analyzed.

Results and discussion

Formal validation showed very high precision of tissue detection and artifact segmentation (average Dice score for 10x/7x/5x: 0.824/0.808/0.785, respectively). Multiple (>20) cohorts were used to analyze international, inter-institutional, inter-scanner, and internal variabilities of quality showing very high levels of heterogeneity among departments. Two human analysts quantitatively graded the tool's performance in five cohorts resulting in high scores for both tasks.

Conclusion

GrandQC tool is a quick and precise tool for the QC and is a radical solution for the artifact problem during downstream tasks. It will be open-sourced together with parts of the test dataset. The evaluation of international case cohorts represents an objective blueprint for inter-department comparison. GrandQC can be effectively used for audit and targeted improvements in tissue section quality.

Key words: artifacts, digital pathology, segmentation, quality control, tissue detection

A73

Computational pathology model to assess acute and chronic transformations of the tubulointerstitial compartment in renal allograft biopsies

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Introduction

Managing patients with kidney allografts largely depends on biopsy diagnosis which is based on semiquantitative assessments of rejection features and extent of acute and chronic changes within the renal parenchyma. These conventional methods often suffer from a lack of reproducibility. To address this, we developed a computational methodology for automated and quantitative analysis of histopathological changes in the tubulointerstitial compartment of the renal cortex from whole slide images of Picrosirius red-stained biopsy slides

Material and methods

A total of 852 biopsies were used for model training, with validation performed on internal (n=172) and external (n=94) test datasets. Deep learning techniques were employed for segmentation followed by morphometric feature extraction from renal tubules, interstitium, and peritubular capillaries. Seven morphometric indicators were extracted to assess interrelated spatial transformations within the compartment.

Results and discussion

Our analysis revealed quantifiable features correlating with Banff scores, identifying distinct morphometric patterns associated with acute rejection and renal function post-biopsy. Notably, acute and chronic injuries were differentiated, highlighting morphometric indicators' clinical relevance.

Conclusion

In conclusion, multivariate analysis of tubulointerstitial morphometry data effectively discriminated and quantified acute and chronic injury components. The proposed method, tailored for renal allograft biopsies, promises a more standardized and reproducible approach to pathology assessment, with potential applicability across a wider spectrum of kidney pathologies.

Key words: digital image analysis, machine learning, deep learning, morphometry, multivariate analysis, kidney

A74

Benchmarking Domain Generalization Algorithms in Computational Pathology

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Introduction

In Computational Pathology (CPath), deep learning models excel in analysing multi-gigapixel histology images. However, domain shift (DS) caused by out-of-distribution data from disparate imaging devices hampers model generalization. Addressing the challenge of DS in CPath, this study benchmarks 28 state-of-the-art (SOTA) domain generalization (DG). The focus is on evaluating their effectiveness in mitigating DS challenges across diverse datasets.

Material and methods

Our investigation adopts a systematic approach, utilizing a ResNet50 model within the well-structured experimental design of the "DomainBed" toolbox. We explore in-domain model selection scenarios and employ Stain Augmentation as a modality-specific algorithm, alongside 27 SOTA DG algorithms, to comprehensively benchmark DG methodologies. These methods are investigated on large-scale Camelyon17, MIDOG22, and HISTOPANTUM datasets for metastasis, mitosis, and tumour detection tasks across multiple centres and cancers, respectively.

Results and discussion

In 3526 cross-validation experiments, Stain Augmentation consistently outperforms other methods in terms of F1 score and accuracy (86.2% and 87.1%), especially in datasets with complex domain shifts. Interestingly, the baseline Empirical Risk Minimization algorithm with standard augmentation demonstrates comparable or superior performance to sophisticated DG algorithms, challenging the conventional belief in their necessity for CPath tasks.

Conclusion

Our findings underscore the efficacy of simpler methods like ERM with basic augmentation and Stain Augmentation in addressing DS challenges in computational pathology. The study advocates for careful experimental design and extensive augmentation, highlighting their pivotal role in training robust classifiers. This work contributes practical insights into the selection and effectiveness of DG algorithms, emphasizing the importance of DG and addressing DS challenges.

Key words: Domain Generalization, Benchmarking, Computational Pathology, DomainBed, Stain Augmentation

A75

Exploring the Clinical Utility of Artificial Intelligence in Mitosis Scoring for Breast Cancer

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Introduction

The recent advancements in artificial intelligence (AI) have shown remarkable capabilities in identifying and quantifying mitotic figures. However, the practical application of AI in clinical settings, particularly in comparison to existing methodologies, remains to be thoroughly evaluated. This research aims to explore the most effective way to utilize AI for scoring mitotic figures in breast cancer (BC).

Material and methods

We employed whole slide images from a substantial BC cohort with extended follow-up, which included a discovery set (n=1715) and a validation set (n=859) from the Nottingham University Hospitals. An external test set (n=757) was also used from the breast cancer cohort of The Cancer Genome Atlas (TCGA-BRCA). Three different methods were used to assess the mitotic count using automated detection: the mitotic count per tumor area (MCT), the mitotic index (MI), and the mitotic activity index (MAI).

Results and discussion

All three automated metrics (MCT, MI, and MAI) showed significant correlations with clinicopathologic characteristics and patient survival. However, the mitotic counts and the derived cutoffs varied significantly between the three methods. MAI and MCT were positively correlated with the gold standard visual scoring method used in the Nottingham grading system and Ki67 scores. In multivariate Cox regression analysis, MAI emerged as the only independent predictor of survival.

Conclusion

For clinical applications, the optimal method of scoring mitosis using AI needs careful consideration. Among the methods evaluated, MAI appears to provide reliable and reproducible results, accurately quantifying mitotic figures in BC.

Key words: mitosis score, breast cancer, patient outcome, clinical application, artificial intelligence

A76

Deep Learning models to differentiate Non-invasive Follicular Thyroid Neoplasm with Papillary-like nuclear features (NIFTP) from other thyroid lesions

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Introduction

NIFTP is a low-risk thyroid neoplasm with a follicular growth pattern and papillary thyroid carcinoma (PTC)-like nuclear features. It is well-circumscribed/ encapsulated and non-invasive. NIFTP's accurate diagnosis is challenging due to interobserver variability and ill-developed nuclear and histological features that overlap with the other thyroid lesions.

Material and methods

In this study we have incorporated more than 93 slides from 93 patients to develop and validate a deep learning-based image classification model to differentiate NIFTP from the other thyroid lesions, i.e., Adenomatous Goiter (AG), Hyperplastic thyroid nodule (HTN), Follicular Adenoma (FA), Follicular Variant of Papillary Thyroid Carcinoma (FVPTC), and classical Papillary Thyroid Carcinoma (cPTC) using histopathological whole slide images (WSI) using 75 slides in the training cohort and 18 slides in the test cohort. We built a classification model using a hierarchical transfer learning approach focusing on the architectural pattern and nuclear features of the lesions. Additionally, an in-house tool was developed to preprocess the WSI into image tiles.

Results and discussion

The hierarchical classification model classified NIFTP accurately at stage two with an overall accuracy of more than 80% in the test dataset and a similar accuracy on the external validation dataset. The sensitivity and specificity ranged between 70% to 95%, respectively.

Conclusion

This study reports a successful development of a three staged hierarchical image classification model to validate NIFTP. Overall our research demonstrates the potential of deep learning algorithms to increase the precision and efficiency of thyroid lesion diagnosis, contributing an enhancement in the patient care and management.

Key words: Histopathology, Deep learning, Hierarchical Transfer Learning, Artificial Intelligence, Thyroid, NIFTP

A77

Is Segment Anything Model Generalisable for Histology Images?

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Introduction

We propose using a nuclei detection model to provide bounding boxes or central points of nuclei as visual prompts for segment anything model (SAM) in generating nuclear instance masks from histology images, to reduce the manual input. In this work, we evaluate SAM for the task of nuclear instance segmentation performance with zero-shot learning and finetuning. We compare SAM with other representative methods in nuclear instance segmentation.

Material and methods

First, the finetuned YOLOv8 model is employed to detect the nuclei in the H&E image. The resulting detection output is transformed into positive and negative point prompt as the input of SAM, for the initial nuclei mask predictions. Post-processing removes extra objects from the mask and aggregates patches into the tile size nuclei instance prediction map. Only the mask decoder of SAM model is fine-tuned, while the image and prompt encoders are frozen.

Results and discussion

With ground truth nuclei bounding boxes as the prompt, zero-shot SAM shows the best result, better than the fine-tuned interactive segmentation model, NuClick in 6.03% in PQ score and 4.90% in Dice score. The proposed method achieved 0.569 in PQ score, outperforming HoVer-Net where the PQ score for HoverNet is 0.514, on a large colon tissue dataset, Lizard dataset, with 495,179 nuclei annotations. The method can accurately segment the smallest cells in crowded areas where HoVer-Net fails.

Conclusion

The finetuned SAM using nuclear central point as prompt, shows better generalisability than HoVer-Net on Lizard dataset. After fine-tuning, SAM has the potential to become a foundation model in CPath due to its good generalisability.

Key words: Foundation Model, Nuclei Segmentation, Nuclear Detection

A78

Weakly Supervised Domain Adaptation for Robust Colorectal Pathology Classification

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Introduction

Generalizing deep learning (DL) models for Whole Slide Image (WSI) analysis from a source distribution to samples from other laboratories and clinical sites is still difficult, due to the high variability of WSIs. To tackle this, we designed a domain adaptation (DA) strategy to generalize a colorectal grading (Non-neoplastic, Low-grade, and High-grade lesions) system (deep tile encoder followed by TransMIL tile aggregator) to a target domain.

Material and methods

We use the partially public CRS10K dataset as source domain and the private BernCRC dataset as target domain. We evaluate three alternatives: a) baseline, where the full model is designed with source domain data only; b) Unsupervised Domain Adaptation (UDA), where the target data is also used in the training of the encoder using FixMatch; c) Semi-supervised Domain Adaptation (SSDA), where the target data is used to optimize the aggregator.

Results and discussion

UDA achieves a quadratic weighted kappa (QWK) of 56.36% and accuracy (Acc) of 66.59%, representing an increase of, respectively, +15.33% and +8.59% when compared with the baseline. In turn, SSDA results in a QWK: 71.60% and Acc of 84.11%, when compared with a QWK of 69.69% and Acc of 81.54 % for the baseline. Overall, FixMatch is an effective feature learning strategy for DA in digital pathology.

Conclusion

In this work, we show that the use of unlabeled data from the target domain allows learning more stable features and increases model robustness, thus leading to more reliable systems that can assist the work of pathologists.

Key words: Unsupervised Domain Adaptation, Semi-supervised Domain Adaptation, Digital Pathology, Colorectal Cancer, Whole Slide Images

A79

Vision Language Foundation Models for Scoring Tumor-Infiltrating Lymphocytes in Breast Cancer through Text Prompting

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Introduction

We explored the potential of the PLIP generalist vision-language AI model to quantify tumor-infiltrating lymphocytes (TILs) in breast cancer via text prompting. Contrary to task-specific deep learning models, trained with manual annotations for tasks such as tissue segmentation or cell detection, we used textual prompts to tailor a single model to assess multiple morphological features.

Material and methods

We prompted PLIP with strings "An HE image containing tumor associated stroma" and "An HE image containing high amount of lymphocytes" and used the cosine similarity between text embeddings and embeddings of non-overlapping patches to obtain likelihood maps for these features. Cosine similarity for lymphocytes was used as a surrogate for TIL density, assessed only in patches in which the tumor associated stroma likelihood exceeded a threshold (computed using the validation set) We used two datasets with slide-level TILs assessed by a pathologist. We optimized using 82 biopsies and resections from the WSITILS training subset of the TIGERchallenge, and evaluated on 56 external biopsies from the Verona hospital. Also, a comparison was performed with the TIGER submission scoring highest on segmentation and detection.

Results and discussion

Our approach yielded TILs scores with a Pearson correlation of 0.57 compared to the pathologists' assessment on external biopsies, on which the tiger algorithm achieved a Pearson correlation of 0.74.

Conclusion

While our approach showed a lower Pearson correlation than the tiger algorithm, which was specifically tuned for this problem, we demonstrated a viable strategy that circumvents the need for extensive data, annotations, and training specific deep-learning models for individual tasks.

Key words: vision language foundation models, tumor-infiltrating lymphocytes, breast cancer, text prompting, histopathology

A80

Computational pathology platform for lung cancer: development and validation of diagnostic and prognostic algorithms

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Introduction

Non-small cell lung cancer (NSCLC) is one of the most common malignant tumors. ranks as a leading cause of cancer-related deaths globally. Despite the digital revolution in pathology, a significant gap exists in the availability of potent, clinical-grade tools specifically for NSCLC. The study aimed to develop a clinically useful computational pathology platform for NSCLC that can be a foundation for multiple downstream applications and provide immediate value for patient care optimization and individualization.

Material and methods

We trained the primary multi-class tissue segmentation algorithm on a substantial, high-quality, manually annotated dataset of whole slide images (WSI) with lung adenocarcinoma (LUAD) and lung squamous cell carcinomas (LUSC). Two downstream applications are investigated. NSCLC subtyping algorithm is trained and validated using a large, multi-institutional (n=6), multi-scanner (n=5), international cohort of NSCLC cases (slides/patients 4097/1527). Five expert pathologists were included in the validation. Four new, AI-derived, fully explainable, quantitative, prognostic parameters (based on tertiary lymphoid structure and necrosis assessment) are developed and validated for different clinical endpoints.

Results and discussion

The computational platform we developed enables the high-precision, quantitative analysis of H&E-stained slides. The downstream subtyping algorithm allows for high-accuracy classification into LUSC and LUAD (including mucinous) subtypes. The newly developed prognostic parameters facilitate robust and independent risk stratification of patients with LUAD and LUSC.

Conclusion

We developed a comprehensive computational pathology platform specifically for NSCLC. It could be immediately leveraged to optimize diagnostics and patient care. We also introduced four novel, independent prognostic parameters with significant potential for patient stratification.

Key words: lung cancer, AI, diagnostics, prognosis, validation

A81

Bringing data science to AI supported tissue diagnostics

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Introduction

In digital pathology, the knowledge gap between AI developers in research and domain experts (pathologists) presents an important challenge . To ease interaction and foster more accurate feedback loops from the pathologist, an automated pipeline is required to establish support not only for the end user, but also for other parties involved in scanning, analysis, data visualization, and downstream data analysis. We propose a scalable framework with a toolkit for flexible and effortless integration.

Material and methods

The framework consists of two integrated components. The first is an automated workflow that picks, identifies, and organizes the slides. This process also includes managing the jobs on the High-Performance Cluster (HPC) and fetching the results. The second component is a full-stack web app that presents the outcomes to pathologists and collects feedback for validation and further improvements.

Results and discussion

The proof-of-concept (POC) successfully demonstrated the integration of the first AI model in 2023. Valuable input from pathologists enabled the development of a highly personalized solution tailored to their and the researchers' needs. In addition to the main components, there is currently a customized HPC connector to run containerized AI modules and a connector to a Lab Information System (LIS) with ongoing refinement for future modules.

Conclusion

The proposed framework is not intended to replace any existing system. Instead, its aim is to provide framework. Its widespread acceptance among laboratory staff, pathologists, and scientists represents a significant step towards the intersection of digital pathology and AI. A public release is expected in 2024.

Key words: Integration, Framework, AI

A82

Development and clinical validation of a prognostic algorithm for stroma-tumor ratio quantification in non-small cell lung cancer

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Introduction

Lung cancer, a leading cause of mortality worldwide, necessitates advancements in diagnostics and treatment. The study aims to develop a digital pathology algorithm for the quantification of stroma/tumor-ratio (STR) from H&E-stained images in non-small cell lung cancer (NSCLC) patients that provides clinically meaningful prognostic stratification.

Material and methods

The developed STR algorithm consists of two modules: a powerful lung cancer segmentation algorithm and a downstream algorithm for STR quantification from segmented tissue masks. One retrospective cohort for exploration (n=902) and three validation cohorts (n=789) with lung adenocarcinoma (LUAD), squamous cell lung carcinoma (LUSC) and available follow-up information were included to identify and validate optimal prognostic cut-offs.

Results and discussion

During exploration, the best cutoff for LUAD allowed for the identification of a high-risk patient group with a multivariate assessment hazard ratio (HR) of 2.12 ($p<0.001$) for OS, HR of 2.35 ($p<0.001$) for CSS, and HR of 1.50 ($p=0.038$) for PFS endpoints. Similarly, in the merged validation cohort, multivariate HR was 1.62 ($p<0.001$), 1.66 ($p=0.002$), and 2.15 ($p=0.012$) for OS, CSS, and PFS, correspondingly. The STR analysis in LUSC allows for the identification of a relatively small subset of patients with unfavorable prognosis, meaning less prognostic significance compared to LUAD.

Conclusion

The quantification of STR with a developed fully automatized algorithm demonstrates substantial independent prognostic value in LUAD. Conversely, in LUSC, the results indicate only limited prognostic role of STR for a small subset of patients, implying that prognostic stratification in LUSC patients should include other parameters.

Key words: Stroma/tumor-ratio (STR), Segmentation-algorithm, Image analysis, Non-small cell lung cancer (NSCLC)

A83

Predictive Morphological Markers for Ductal Carcinoma In Situ: A Computational Approach to Risk Stratification

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Introduction

Ductal Carcinoma in situ (DCIS) is a pre-invasive breast cancer that may or may not progress to invasive cancer. Despite this uncertainty, all women diagnosed with DCIS undergo surgical excision and additional therapy. This study distinguishes morphological features across various nuclear types, aiming to lay the groundwork for predictive models.

Material and methods

We utilised HoVer-Net, fine-tuned with 50,000 manually annotated nuclei, for nuclear segmentation/classification in whole slide images. Additionally, the DeepLab model with a ResNet backbone facilitated nine-class region segmentation, distinguishing benign ducts, DCIS, stroma, among others. Using selected regions from 321 cases of the UK/ANZ DCIS trial, we assessed nuclear morphology and applied logistic regression and random forest models to identify prognostic features for DCIS progression.

Results and discussion

The DeepLab model, enhanced with a ResNet backbone, achieved a Dice score of 0.87, while the fine-tuned HoVer-Net exhibited an F1 score of 0.81 for nuclear classification. Our analysis discerned 17 morphological distinctions with statistical significance ($p<0.05$) between progressors and non-progressors, particularly in cellular orientation, eccentricity and solidity of lymphocytes and nuclear radii, perimeter and orientation within neoplastic nuclei. The logistic regression and random forest findings were consistent, underlining the importance of these features in predicting DCIS behaviour.

Conclusion

We have successfully developed a 9-class region segmentation model and enhanced HoVer-Net for nuclear classification, identifying critical morphological features that may serve as prognostic markers for DCIS progression risk. The next phase of our research will integrate these features into a validated, interpretable computational model, aiming to improve predictions of DCIS progression.

Key words: DCIS, breast cancer, morphometrics, machine learning

POSTER PRESENTATIONS

P01

Use of a novel deep learning model for detection of LD bodies and granulomas in cases of cutaneous leishmaniasis- A neglected tropical disease of the developing world

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Introduction

The ever-increasing use of digitalization and artificial intelligence has left its impact on every field of life. With the aid of Artificial intelligence, the work of pathologists can become much easier, as these techniques can quantify accurately, measure and pick up small pathologies which can be missed by pathologists if they are overworked. The aim of the study was to validate LD bodies and granuloma identification by artificial intelligent software verses manual diagnosis

Material and methods

A Cross sectional study carried out at Aga Khan university hospital from previously diagnosed cases of cutaneous leishmaniasis. Whole slide images (WSIs) were prepared through Huron digital pathology scanner. WSIs were uploaded into the software of Aiforia and trained for granuloma and LD bodies identification

Results and discussion

By applying Kolmogorov-Smirnov test, the area and count for Granuloma as well as for Leishmaniasis were found non-normally distributed (P-value < 0.05wa). The overall diagnostic accuracy was the diagnostic accuracy of AI in identification of granuloma in terms of counts. For leishmaniasis, the diagnostic accuracy in terms of count was 78.33%.91

Conclusion

Artificial intelligence (AI) algorithms have an important role to play to lower the burden on already-constrained physicians. Large validation studies are required before using it as pathologist-assisted tool. This was our small study but its results were highly encouraging and we hope that further validation studies like this will be conducted in future to harness the power of AI as pathologist assisted tool in identification of LD bodies and granuloma in cutaneous leishmaniasis and other granulomatous diseases.

Key words: Leishmaniasis, artificial inteligence, automated detection

P02

Quantifying Enhanced Sensitivity in HER2-Low Spectrum: Comparing HercepTest and 4B5 Utilizing the Visiopharm HER2 APP

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Introduction

Human Epidermal Growth Factor Receptor 2 (HER2) status is pivotal in breast cancer diagnosis and therapeutic decision-making. Recent findings by Rüschoff et al. (2022) highlight increased sensitivity of HercepTest on the HER2-low spectrum compared to 4B5. This work explores the potential of using AI in quantifying this enhanced sensitivity, evaluating its utility in reflex testing, and establishing its complementarity with the Agilent HercepTest.

Material and methods

Utilizing digital pathology tools, we employed the Visiopharm HER2 APP to quantify the heightened sensitivity of HercepTest in detecting HER2-low cases compared to 4B5. A focus was placed on evaluating the potential compensation for the increased incidence of 2+ cases for reflex testing. Further comparisons with Fluorescence In Situ Hybridization (FISH) were performed to validate the utility of the Visiopharm HER2 APP in overcoming potential drawbacks.

Results and discussion

Our findings confirm Rüschoff et al.'s observations, demonstrating the use of HER2 AI's ability to precisely quantify the increased sensitivity of HercepTest on the HER2-low spectrum compared to 4B5. Preliminary results suggest that HER2 AI can compensate for the higher incidence of 2+ cases in reflex testing. Notably, the Agilent HercepTest and HER2 AI exhibit complementary characteristics.

Conclusion

The HER2 AI emerges as a valuable tool for quantifying the increased sensitivity of HercepTest on the HER2-low spectrum. While potentially compensating for the drawbacks of reflex testing. The complementary nature of the Agilent HercepTest and HER2 AI opens avenues for a comprehensive approach to HER2 status determination in breast cancer.

Key words: HER2, Breast cancer, AI, Herceptest, 4B5, Sensitivity

P03

Establishing a digital pathology repository for h & e stained slides & ffpes stored at the pathology department since 1942

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Introduction

The Department of Pathology at the College of Health Sciences, Makerere University is host to a precious historical archive of haematoxylin and eosin (H&E) stained pathology slides and corresponding formalin fixed, paraffin-wax embedded (FFPE) tissue blocks since 1942. This—from incisional, aspirational, and excisional biopsies as well as postmortem tissue cut-up, fixing and staining of human pathologies seen in Uganda and its neighboring countries. In the recent years, storage and management of this resource has been un financed neglected; risking loss of its integrity to oblivion. The overall goal of this proposal is to establish a digital pathology repository for this resource.

Material and methods

A mixed method design

Results and discussion

i) memorandum of understanding between Makerere University, IARC, and the sponsor (Government of France), (ii) administrative & scientific core to manage and oversee the project, (iii) viability report on H & E stained slides and their matched FFPE tissue blocks in the archive, (iv) a state of the art digital pathology facility , (v) special staining, immunohistochemistry and molecular typing of the same, (vi) Adjudicated consensus diagnosis from review of historical notes, (vii) digitized high resolution images of the slides & clinical diagnostic notes, and (viii) trained Ugandan technicians and pathologists on the capture, storage, and retrieval of digital pathology slides.

Conclusion

This project will preserve and avail a precious historical resource of histopathology for Uganda and the world at large. This will form basis for training and the development of assisted digital pathology diagnosis in Uganda and Africa at large.

Key words: H & E slides , FFPEs, Digital Pathology, Repository, Uganda, Africa

P04

Enhancing Prostate Cancer Diagnosis: AI-Driven Virtual Biopsy for Optimal Targeted Biopsy Approach and Gleason Grading Strategy

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Introduction

The optimal approach to magnetic resonance imaging (MRI) fusion targeted prostate biopsy (PB) remains unclear. We developed a precise segmentation AI algorithm for tumor detection and Gleason grading (GG) and an algorithm for virtual prostate biopsy that are used together to systematically investigate and find an optimal approach to targeted PB.

Material and methods

AI algorithms were developed using a manually annotated dataset (slides n=442). A virtual biopsy algorithm was developed that can perform randomised biopsies from tumor regions in whole-mount whole-slide images. A cohort of 115 radical prostatectomy (RPE) patient cases with MRI-visible tumors (n=121) was used for our systematic studies. Three expert genitourinary (GU) pathologists participated in the validation.

Results and discussion

The tumor detection algorithm (aware version sensitivity/specificity 0.99/0.90, balanced version 0.97/0.97) and GG algorithm (quadratic kappa range vs pathologists 0.77-0.78) perform on par with expert GU pathologists. In total, 65.340 virtual biopsies were performed with the following results: 1) four biopsy cores is the optimal number for a targeted PB, 2) cumulative GG strategy is better than using maximal Gleason score, 3) regularization of inter-core distance does not improve the predictive accuracy for RPE Gleason score, 4) AI algorithm (based on cumulative GG strategy) predicted the RPE Gleason score of the tumor better than 2 of 3 expert GU pathologists.

Conclusion

In this study, using an original approach of virtual prostate biopsy on the real cohort of patient cases, we find the optimal approach to targeted PB. We publicly release two large datasets with associated expert pathologists' GG and our virtual biopsy algorithm.

Key words: Prostate cancer, AI, Targeted biopsy, MRI, Optimal Approach

P05

A Comparative Study of Artificial Intelligence Integration in Bladder Cancer Screening: Enhancing Accuracy and Efficiency

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Introduction

This study evaluates a software screening system that incorporates an artificial intelligence (AI)-assisted platform (AIxURO) aimed at improving bladder cancer screening using urine cytology. The adoption of this system within the clinical workflow holds the potential to significantly boost both the efficacy and efficiency of urine cytological reporting.

Material and methods

AIxURO, designed to quantify candidate cells in whole-slide images (WSIs) of urine cytology following The Paris System (TPS) guidelines, has been validated in prior independent clinical studies. A three-armed study design was conducted to compare the diagnostic results of 200 slides and their corresponding WSIs using three screening modalities: microscopy, WSI only, and AIxURO. Each sample set was assessed by one cytopathologist and two cytotechnologists, who evaluated the sets across all modalities, providing diagnoses that aligned with TPS criteria. Screening times were recorded. Performance metrics and efficiency were comparatively analyzed to determine AIxURO's impact on the standard cytopathology workflow.

Results and discussion

AIxURO reclassified certain ground-truth diagnoses from high-grade urothelial carcinoma (HGUC) or suspicious for HGUC (SHGUC) to atypical urothelial cell (AUC) or negative for HGUC (NHGUC). Of 100 positive (HGUC/SHGUC/AUC) and 100 negative (NHGUC) cases, AIxURO and microscopy outperformed WSI only in sensitivity (66.0-87.0% and 86.0-89.0% versus 66.0-73.0%) and specificity (89.0-95.0% and 83.0-94.0% versus 81.0-88.0%). While AIxURO demonstrated slightly lower sensitivity than microscopy, it exhibited higher specificity and significantly reduced the average screening time per case by 25.8%-58.7% ($P<0.05$).

Conclusion

This study highlights AIxURO's potential to significantly enhance the efficiency of urine cytology reporting without compromising diagnostic accuracy, emphasizing the clinical benefits of incorporating AI into digital cytopathology.

Key words: Artificial Intelligence, Urine Cytology, Bladder Cancer, Whole Slide Image, Digital Cytopathology, Computer-aided Diagnosis

P06

AI-based stroma-tumor ratio quantification algorithm: evaluation of prognostic role in primary colorectal cancer

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Introduction

Stroma-tumor ratio (STR) quantification in primary colorectal cancer is a prognostic parameter. Earlier studies involved relevant region selection and STR quantification by human analysts, prone to interobserver variability. The aim of the current study was to develop an automatized, quantitative algorithm for STR analysis based on precise segmentation of H&E-stained histological tissue sections.

Material and methods

STR quantification algorithm was developed based on a segmentation backbone, allowing accurate pixel-wise mapping of all relevant tissue classes (n=12). Two well characterized cohorts of patients with stage I-IV primary colorectal cancer and available digital H&E histological slides were included (n=548 and n=231). Three sizes of analytical "window" for STR analysis were tested (1.0, 1.5, and 2.0 mm). The maximal STR value per case was used for prognostic analysis involving different clinical endpoints.

Results and discussion

Regional heterogeneity of STR was high in most tumors, with the algorithm effectively finding the most relevant region for analysis. Maximal case-level STR values depend on the size of the analytical "window", which also influences the prognostic performance of STR and must be standardized. In Cox survival analysis, an analytical "window" size of 1 mm allowed best performance, with an independent prognostic role retained in the context of other pathological variables for overall survival endpoint.

Conclusion

An automatized, quantitative tool for STR assessment in primary colorectal cancer was developed. STR might be of limited value in patients with MSI tumors, with most prognostic benefits of analysis in patients with MSS tumors. Standardization of STR quantification is important given that analytical parameters can substantially influence the prognostic performance.

Key words: Stroma-tumor ratio, colorectal cancer, prognosis, digital pathology, AI algorithm

P07

Non-diagnostic time in digital pathology: An empirical study over ten-year period

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Introduction

Our previous study showed a shorter digital diagnostic time, compared to microscopy. In this study we have observed multiple tasks affecting a non-diagnostic time, over ten-year period.

Material and methods

Slide handling, image adjustments, magnification exchange, slide annotations/measurements, report preparation, medical coding and sign off were non-diagnostic tasks observed between microscopy (Nikon Eclipse i80) and digital pathology platforms (SymPathy/Unilab LIMS integrated with Aperio/Sectra on 14'' laptops) by two senior pathologists. An increased productivity (number of cases reported per hour) was a measure of potential savings in a digital non-diagnostic time. Workload data were retrieved from our LIMS.

Results and discussion

Slide handling related tasks were all consolidated or faster in digital pathology. Image adjustments, magnification exchange and slide annotations/measurements were faster in digital pathology. Report preparation, coding and sign off were consolidated and/or faster in digital pathology, supported by canned reports. Synchronized viewings of multiple images and double click for zero to 80x zoom functionalities in Sectra were crucial to faster diagnostics, as not available on the microscope. The one-step login access to our digital platform contributed to faster operation of all tasks. Workload data showed an increase in productivity by 30%, compared to microscopy, for both pathologists.

Conclusion

Consolidations of multiple tasks in digital pathology and system innovations exclusive to digital pathology have led to a considerable decrease in non-diagnostic time. In our experience, shorter diagnostic and non-diagnostic digital time together amounted to an increased productivity by 40%, compared to microscopy.

Key words: digital pathology, non-diagnostic time, increased productivity

P08

A Deep Learning Framework Deploying 'Segment Anything' to Detect Mitotic Figures from Haematoxylin and Eosin-Stained Slides for Multiple Tumour Types

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Introduction

Mitotic activity is essential for grading various types of tumours. Quantifying it by counting mitotic figures from 10 high-power fields is time-consuming and prone to inter-observer variation. We propose a deep-learning framework deploying "segment anything" (SAM), an advanced segmentation model trained using billions of real-world objects, to detect mitotic figures in haematoxylin and eosin (H&E)-stained slides.

Material and methods

Our framework was developed using five open-source databases (ICPR, TUPAC, CCMCT, CMC, MIDOG++), comprising 68,687 mitotic figures from eight different scanners and eight types of human and canine tumours. SAM was deployed to generate the masks of the figures annotated using bounding boxes. These masks were manually reviewed and integrated with H&E patches within a pre-trained ResNet18 model to classify mitotic figures. The framework was tested on the MIDOG++ testing set and the F1 scores were compared to those reported by the MIDOG++ challenge.

Results and discussion

The framework yields testing F1 scores of 0.807±0.02 (MIDOG++: 0.71±0.02), 0.830±0.01 (MIDOG++: 0.81±0.01), 0.749±0.01 (MIDOG++: 0.69±0.01) and 0.620±0.02 (MIDOG++: 0.59±0.01) in detecting mitotic figures from breast carcinoma, melanoma, soft tissue sarcoma and neuroendocrine tumour, respectively. The detection accuracy was significantly enhanced ($p<0.001$) by incorporating revised SAM masks during training. A web application was developed to facilitate rapid and accessible mitosis detection on research H&E slides.

Conclusion

We developed a novel deep-learning framework incorporating the SAM mask generator for mitosis detection. It achieved state-of-the-art performance in detecting mitotic figures from various types of human tumours. Future work includes applying the framework to external clinical cases to compare the computer-identified mitotic index against pathologist assessments.

Key words: Mitosis Detection, Digital Pathology, Deep Learning, Segment Anything, Computer Vision

P09

Standardizing Reporting of Core Needle Biopsy Tortuosity: BiopTort - A Computer Aided Protocol for Grading Tortuosity in Clinical Workflows

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Introduction

Core needle biopsies (CNB) are among the most common biopsy procedures, yielding long, thin cores which are prone to deformation (e.g., stretching, compressing, twisting). Resulting tortuosity creates challenges in tissue processing/embedding, with even absence of diagnostically relevant tissue after paraffin block sectioning. Despite the clinical need to minimize tortuosity, there is no existing protocol to report its presence systematically. Here we (a) established an actionable protocol for grading core biopsy tortuosity, (b) built BiopTort, a software tool which assigns CNB images interpretable, discrete grades based on extracted tortuosity features consistent with the protocol, and (c) investigated the impact of (a) and (b) on inter-pathologist agreement and grading time.

Material and methods

Using a held-out CNB dataset (N=167), 3 pathologists graded tortuosity in 3 stages: (1) Baseline: a three-tier scale (low, medium, high) based on prior experience, (2) Protocol: after a washout period, regraded using our four-tier tortuosity grading protocol, (3) BiopTort-Aided: after another washout period, regraded with the protocol along with BiopTort. Inter-rater agreement for each stage using Fleiss' kappa was then computed.

Results and discussion

Fleiss' kappa (0.19±0.07, 0.42±0.06, 0.63±0.06) and average time per slide (8.0s, 24.2s 13.3s), respectively for baseline/protocol/BiopTort-aided stages, suggest that our protocol lessens inter-pathologist variability, with BiopTort even further reducing variability while also improving grading protocol employment time-cost.

Conclusion

Our results suggest that when our protocol and BiopTort are deployed together in CNB workflows for routine quality control tracking, they will fulfill the latent need for standardized, efficient and actionable reporting of CNB tortuosity. BiopTort is released open-source for community usage (bioptort.com).

Key words: Core needle biopsy, inter-rater agreement, tortuosity, quality assurance, image analysis

P10

Prospective Technical Deployment of Artificial Intelligence Pathology Platform to Three UK Hospitals for Real-time Use in Patient Pathways

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Introduction
Artificial intelligence (AI) technologies in digital pathology are often assessed offline or as a standalone modality, rather than in live clinical pathways. This is due to, among many factors, the complexity of integrating the AI systems into existing health information systems, and the technical performance requirements for real-time delivery of AI outputs.

Material and methods
To deliver a multicenter health economics study program, three UK trusts with distinct digital pathology infrastructure required prospective, live deployment of AI software that helps pathologists in diagnosing and grading prostate cancer core needle biopsy specimens. Metadata and process requirements for image transfer to a cloud computing infrastructure were determined. Then, a test environment was created and validated prior to end user acceptance testing, followed by live use.

Results and discussion
Three distinct solutions were architected adhering to local hospital and pathology department requirements. The final solutions involved: (1) direct laboratory information management system (LIMS) integration; (2) specimen tracking system integration with local image file export to dedicated server; and (3) image management system (IMS) daily export with direct cloud upload and scheduled scripted ingestion.

Conclusion
Deploying AI in pathology to real-time patient pathways requires local system integration, sourcing images and associating the corresponding metadata. The three deployments required close multidisciplinary discussion at each site including biomedical scientists, information technology (IT) teams, pathologists, and the industry partner. Secure cloud computing allows timely delivery of AI results for real-time clinical use.

Key words: artificial intelligence, integration, prospective, cloud computing

P11

Deep pathomics in locally advanced Non-Small Cell Lung Cancer: a digital tool for predicting response to chemoradiotherapy

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Introduction

Despite the advantages offered by personalized treatments, there is presently no way to predict response to chemoradiotherapy in patients with non-small cell lung cancer. In this exploratory study, we investigated the application of deep learning techniques to histological tissue slides, with the aim of predicting the response to therapy in stage III NSCLC.

Material and methods

We evaluated 35 digitalized tissue slides (biopsies or surgical specimens) obtained from patients with stage IIIA-IIIB NSCLC. Patients were classified as responders or non-responders based on the target volume reduction shown on weekly CT scans performed during chemoradiation treatment. Digital tissue slides were tested by five pre-trained convolutional neural networks (CNNs)-AlexNet, VGG, MobileNet, GoogLeNet, and ResNet-using a leave-two patient-out cross validation approach, and we evaluated the networks' performances.

Results and discussion

GoogLeNet was globally found to be the best CNN, correctly classifying 8/12 responders and 10/11 non-responders. Moreover, Deep-Pathomics was found to be highly specific (TNr: 90.1) and quite sensitive (TPr: 0.75) in predicting response to chemoradiation.

Conclusion

Our data showed that AI could surpass the capabilities of all presently available diagnostic systems, supplying additional information beyond that currently obtainable in clinical practice. The ability to predict a patient's response to treatment could guide the development of new and more effective therapeutic AI-based approaches and could therefore be considered an effective and innovative step forward in personalised medicine.

Key words: Lung Cancer, AI, Deep Learning, Pathomics, Prediction, Chemoradiotherapy

P12

Automated AI-assisted assessment of NAS and fibrosis stage in biopsy-confirmed rodent models of MASH

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Introduction

NAFLD Activity Scoring (NAS) and fibrosis staging is widely used in clinical trials and preclinical studies for metabolic dysfunction-associated steatohepatitis (MASH). The present study aimed to develop and validate an automated deep learning-assisted digital imaging analysis pipeline, termed GHOST (Gubra Histopathological Objective Scoring Technology) for objective assessment of NAS and fibrosis stage in rodent models of MASH.

Material and methods

Liver biopsies were obtained from GAN DIO-MASH mice and CDAA-HFD rats. GHOST was applied to HE and PSR stained sections for the assessment of NAS (n=338 mice) and fibrosis stage (Kleiner classification, n=537 mice). GHOST was extended to perform fibrosis scoring (Ishak classification) on PSR-stained sections from CDAA-HFD rats (n=86). All GHOST data were validated against manual scoring performed by expert histopathologists.

Results and discussion

GHOST detected central veins and portal areas, enabling segmentation of zones for scoring. All relevant cell types, including hepatocytes, inflammatory cells and ballooned hepatocytes, were identified in HE sections. PSR-stained fibers were localized in the sinusoidal and periportal space. There was a high concordance between automated and expert histopathologist manual scores for NAS (K = 0.72), fibrosis (K = 0.84) in GAN DIO-NASH mice as well as for Ishak fibrosis scores (K =0.82) in CDAA-HFD rats.

Conclusion

GHOST-based whole-section NAS and fibrosis scores in the two rodent models of MASH were in strong agreement with manual scoring by expert histopathologists. GHOST facilitates fast, accurate and reproducible scoring of liver disease severity in mouse and rat models of MASH, being highly instrumental to assess histological effects of preclinical drug candidates.

Key words: AI , MASH, Fibrosis

P13

AI-powered analysis of tissue slides to reveal the cellular composition and the spatial organization of the tumor microenvironment

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Introduction

Digital pathology and artificial intelligence (AI) applied to histopathological images are gaining interest in immune-oncology, since they allow to streamline and ameliorate diagnostic and prognostic processes. The aim of this work was the development of a pipeline for the computational analysis of cancer tissues stained by H&E to find cell- or tissue-level features that could have a clinical relevance.

Material and methods

The pipeline includes the adoption of machine and deep learning algorithms for what concerns cell segmentation, cell classification, tissue segmentation and spatial analysis. Specifically, open source platforms such as QuPath and RStudio were adopted to segment cells, classify them in a supervised manner, and perform spatial analyses.

Results and discussion

On H&E images, we trained a machine learning classifier to detect tumor cells within the tumor region and then analyse their spatial clustering by exploiting the Ripley's K function. Accordingly, patients were classified as "highly clustered", "poorly clustered" or "uniformly distributed". Then, another classifier was trained to distinguish lymphocytes from other cells, and their density was computed within and outside the tumor bed. According to this score, samples were classified as "immune desert", "immune excluded" and "inflamed". The combination of these two AI-based classifications significantly correlated with the prognosis.

Conclusion

AI-powered H&E allowed us to classify samples based on quantitative data and the combination of the tumor and immune predictors generated clinical relevant results. These tools, once validated, may contribute to discover novel tumor and immune classifiers and human interpretable features.

Key words: tumor microenvironment, digital pathology, artificial intelligence, imaging mass cytometry

P14

White matter hyperintensities and the surrounding normal appearing white matter are associated with water channel disruption in the aged human brain

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Introduction

Age-related MRI T2 white matter hyperintensities (WMH) are common and associated with neurological decline. We investigated histopathological underpinnings of MRI WMH and surrounding normal appearing white matter (NAWM), with a focus on astroglial phenotypes.

Material and methods

Brain samples from 51 oldest-old Oregon Alzheimer's Disease Research Center participants who came to autopsy underwent post-mortem (PM) 7 tesla MRI with targeted histopathological sampling of WMH and NAWM. Stained slides were digitized and quantified. Mixed effects models determined differences in molecular characteristics between WMH and the NAWM and across NAWM.

Results and discussion

PM MRI-targeted WMHs are characterized by demyelination, microglial activation, and prominent astrocytic alterations, including disrupted aquaporin expression. Similar changes occur within the surrounding NAWM in a pattern of decreasing severity with increased distance from WMHs.

Conclusion

Decreased aquaporin expression within WMH and proximal NAWM suggest an overwhelmed system wherein water homeostasis is no longer maintained, contributing to WM damage in older individuals.

Key words: Brain, Aging, Aquaporin, Imaging, Hyperintensities, Histopathology

P15

Digital pathology and AI-based approaches characterizing the interactions between tumor microenvironment components and their spatial distribution

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Introduction

Digital pathology coupled with artificial intelligence (AI)-based approaches is receiving great attention in the field of oncoimmunology, as this can improve current diagnostic workflows and potentiate the analytic outputs. The aim of this work consists of combining different histopathological approaches and high-throughput computational imaging tools to analyse and dissect the tumor microenvironment (TME).

Material and methods

Firstly, we focused on tumor tissue and structure, by computational analysis of H&E-stained slides. So, we trained a deep learning algorithm to identify tumor cells and we explored their spatial distribution by deploying the Ripley's K-function.

Results and discussion

The resulting K-score value classifies each tumor spot as diffuse, poorly or highly clustered. To better understand the complex interactions between TME cellular components and their spatial distribution, we performed a deeper investigation of the immune contexture, taking advantage of the HyperionTM Imaging System. By preserving tissue architecture and cell morphology information, it allows the simultaneous investigation of 23 protein markers related to tumor cells, tissue architecture and immune cells. We made multiparametric computational analysis of the IMC images to firstly distinguish between tumor and stromal tissues, and then to evaluate the frequency of immune cell populations in the tumor nests versus fibrotic stroma. Finally, in poorly and highly clustered samples, we investigated the tumor heterogeneity in terms of interactions between immune cells and tumor cell distribution within the tissue.

Conclusion

The results of our analysis expected to provide the opportunity to investigate spatial patterns and cell interactions at single-cell level, leading to the identification of tumor patient profiles with clinical relevance.

Key words: Digital pathology, artificial inteligence , tumor microenvironment, immunohistochemistry, H&E, imaging mass cytometry

P16

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

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Introduction

HER2 constitutes a significant prognostic biomarker for breast carcinoma and for HER2-targeted therapy. The recent emphasis on HER2-low-expressing tumors stresses the necessity for more standardized scoring. This study aimed to show that artificial intelligence (AI)-based solution (Galen Breast HER2) may improve pathologists' standardization and accuracy.

Material and methods

This two-arm reader study on 197 retrospective breast biopsies and excisions retrieved from the Ziekenhuis Netwerk Antwerpenhospital (Belgium), compared HER2 scoring performance of two reader pathologists using digital review alone, or supported by AI, which detects the invasive tumor area, classifies tumor cells based on their staining pattern and derives a slide-level HER2 score. Both arms were compared to ground truth (GT) established by a consensus of two breast sub-specialists, according to ASCO/CAP 2018 guidelines.

Results and discussion

The overall inter-observer agreement among GT pathologists was 88.83%. The reader pathologists supported by AI showed significant improvement in overall accuracy of 7.5% in comparison to the non-AI arm, and 5.9% accuracy improvement for HER2 low relevant- cutoff (0 vs. 1+/2+/3+) . Similarly, pathologists supported by the AI demonstrated higher overall inter-observer agreement (96.94% vs 84.56% without AI), as well as higher agreement for 0 vs 1+/2+/3+ (96.94% vs 84.56) and 0/1+ vs 2+/3+ (96.94% vs 91.75%) cutoffs. The AI overall accuracy for HER2 scoring was 86.3%. For HER2 0 vs 1+/2+/3+ and 0/1+ vs 2+/3+ cut-offs, AI accuracy was 95.4% and 92.9%, respectively.

Conclusion

This study demonstrated that the use of Galen Breast HER2 solution may improve pathologists' reproducibility and accuracy of HER2 scoring, particularly for identifying HER2 Low.

Key words: Artificial Intelligence , Breast Cancer, HER2 , Image Analysis, Deep Learning

P17

Machine learning algorithm for the detection of Reed-Sternberg cells from classical Hodgkin Lymphoma

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Introduction

10-20% of treated patients with classical Hodgkin lymphoma (cHL) are refractory to treatment or end up suffering a relapse. Currently, the risk stratification parameters in patients with cHL are clinical, analytical and radiological. However, more and more studies show the importance of tools based on digital quantification for the correct typing of these patients.

Material and methods

Twenty-nine cases of cHL were studied in formalin-fixed, paraffin-embedded diagnostic lymph node biopsies. The scanning was performed using the Pannoramic® Midi model (3DHistech Ltd., Budapest, Hungary), for the complete preparation and with a resolution of 0.25 µm per pixel. Digital image analysis for detection of Hodgkin-Reed Sterneberg (HRS) cells and cell quantification have been carried out using the free access software QuPath (https:/qupath.github.io/).

Results and discussion

A principal component analysis (PCA) selected the most representative cellular features. The test set identified 71.4% of the HRS cells, 89.9% of the stromal cells and 96.9% of the tumor microenvironment cells. The validation set identified 26.2% of the HRS cells, 66% of the stromal cells and 97.1% of the tumor microenvironment cells.

Conclusion

It is necessary to increase the number of annotations made to achieve a more precise algorithm, eliminating as much noise as possible from the dataset. This study contributes to a more precise classification of the patient with cHL, allowing future immunohistochemical quantification studies to be carried out based on the results obtained.

Key words: Hodgkin lymphoma, digital pathology, QuPath, machine learning

P18

Deep Learning Enabled End-to-end Pipeline for Automatic Grading of HER2 in Breast Cancer

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Introduction

The histopathological evaluation of invasive carcinoma breast samples involves assessing the expression of HER2, critical in breast cancer diagnosis and treatment planning. However, accurately determining HER2 expression can be challenging, leading to variability among pathologists.

Material and methods

We introduce a deep learning-based pipeline to assist pathologists in classifying HER2 expression in WSIs of breast tissue samples. This pipeline incorporates automated carcinoma detection, removing the need for manual input. Additionally, it features a patch-based algorithm trained with 5000 annotated patches to classify HER2 expression. Patch-level classifications are aggregated to derive a comprehensive slide score. To evaluate performance, four pathologists independently assess 167 WSIs with varying HER2 expression levels. Ground truth scores were determined as the majority or mean score assigned among pathologists, for classification and regression respectively. We explored various approaches for patch aggregation at slide-level, employing predefined rules for both classification and regression, as well as a learned regressor based on the number of patches in each score for a slide.

Results and discussion

We observed a weak inter-observer agreement, with a mean Cohen's Kappa coefficient of 0.44 (±0.1), mainly between classes 0 and 1+ (k=0.62 when merging 0 and 1+). For the classification task into three grades (0-1+, 2+, and 3+), our pipeline achieved an accuracy of 90.3%. In the regression task, our manual regressor achieved an R^2 value of 0.53, while our learned regressor significantly improved performance to R^2=0.7.

Conclusion

Our work shows our complete pipeline effectively determines HER2 slide scores, aligning well with pathologists' assessments. This underscores its potential as a valuable tool for pathological data analysis.

Key words: her2, deep-learning, automatic, reproducibility

P19

ActiveVisium: An AI-Based Assistant for Rapid Visium Spot Annotation

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Introduction

Spatial transcriptomics technologies such as 10x Visium enable studying gene expressions within tissue context. A crucial step in the validation of experimental and computational analysis methods includes cross-referencing the findings with spot-level pathologist annotations. With typical experiments comprising numerous tissue samples containing 5,000 to 11,000 spots each, manual annotation quickly becomes impractical. To address this challenge, we introduce ActiveVisium - an AI-based assistant for rapid Visium spot annotation.

Material and methods

ActiveVisium leverages foundation models in digital pathology combined with active learning methods to facilitate spot annotations. Starting from a small fraction of annotated spots, ActiveVisium predicts annotations for remaining unannotated spots. The model is iteratively refined by the pathologist's feedback and annotations that are provided for the most informative unannotated spots identified via active learning strategies.

Results and discussion

ActiveVisium is validated on FFPE breast and FF colorectal cancer samples, demonstrating its effectiveness in complex and heterogeneous tumour environments. By annotating around 10% of all spots in the breast cancer sample, the model achieves high predictive performance, with an average f-score exceeding 0.8. In the case of colorectal cancer samples, the model demonstrates strong annotation transfer capabilities across replicates and donors: an f-score over 0.7 is achieved for tumour spots without any prior annotations.

Conclusion

As an AI assistant, ActiveVisium facilitates the annotation process, enabling pathologists for the first time to annotate previously prohibitively large ST datasets and to focus on refining annotations. This greatly facilitates ST data analysis and development and validation of novel computational approaches, e.g. prediction of transcriptomic signatures from HE images.

Key words: spatial transcriptomics, active learning, digital pathology

P20

Developing an Artificial Intelligence-based Logistic Model for Automated Bladder Cancer Screening in Digital Urine Cytology

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Introduction

This study develops a bladder cancer screening tool in digital urine cytology using AIxURO, an artificial intelligence (AI)-powered software system. The receiver operating characteristic (ROC) curve was utilized to assess the logistic model's accuracy, and Youden's index was used to determine the optimal cut-off value for AI-identified target cells, enabling AIxURO to accurately predict cancer.

Material and methods

In alignment with The Paris System (TPS) criteria, AIxURO was developed to quantify suspicious cancer cells (categorized as "suspicious for high-grade urothelial carcinoma" or higher in TPS) and atypical cells ("atypical urothelial cells" according to TPS) in cytology images. AIxURO analyzed 1,856 cases, comprising 390 positive and 1,466 negative cases, as the training set. Additionally, a separate validation set of 169 cases (81 positive and 88 negative cases) was evaluated. Logistic regression was conducted to predict cancer status, utilizing variables including the total number of suspicious cancer cells, atypical cells, and their logarithmic transformations. The model's predictive accuracy was determined by evaluating its sensitivity and specificity.

Results and discussion

The logistic model, based on the logarithmic number of atypical cells, demonstrated optimal performance in the training set, achieving 75.9% sensitivity and 73.0% specificity, with cut-off values set at 10 cells for Cytospin and 49 cells for SurePath slides. Upon application to the validation set, the model sustained its high efficacy, achieving 75.3% sensitivity and 87.5% specificity.

Conclusion

The logistic model and its optimal cut-off value for AIxURO have been successfully established and validated. These findings indicate that AIxURO holds promising potential for automating bladder cancer screening within routine urine cytology practices.

Key words: Artificial Intelligence, Bladder Cancer Prediction, Digital Urine Cytology, Receiver Operating Characteristic Curve, Logistic Regression, Youden's Index

P21

Explaining a Deep U-Net Trained for Tumor Detection in Histological Whole Slide Images

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Introduction

In this work, we investigate the behavior of a deep learning model trained to detect 40+ skin diseases in histological whole slide images. We use explainable AI techniques to visualize important features and compare them with features used for diagnosis by pathologists.

Material and methods

We apply two methods to hidden layers of the deep learning model, to gain insight into its behavior: 1. Synthesize an input image that maximally activates a given neuron of the model. This provides information about what the model is generally looking for. 2. Explain the prediction of the model for a given input image using four features (e.g. pigments or high-level edge of basal cell carcinoma would be a feature). Those features are automatically extracted from the model, they are not predefined.

Results and discussion

We observe that the model arrives at its prediction by increasingly extracting high-level structures from the data the deeper the information progresses into the model. At the beginning, individual cell nuclei are extracted. This is followed by structures formed from cell nuclei, such as palisading cells arranged in a row. The deeper into the model, the more differentiation is made by disease, i.e. earlier layers recognize palisading cells in general, while deeper layers of the model are more strongly differentiating between palisading cells belonging to basal cell carcinoma or other types of lesions.

Conclusion

We investigated the behavior of an AI model and observed that the structures it extracts and bases its prediction on are human-understandable, and similar to the features used by pathologists for diagnosis.

Key words: Deep Learning, Explainable AI, Computer Vision

P22

The next generation of open standards for scalable Digital Pathology visualization and analysis

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Introduction

As Digital Pathology imaging has advanced in scale, visualization and analysis workflows of brightfield (RGB) whole slide image (WSI) datasets are challenged to rely on efficient and scalable technologies for data storage and retrieval. Numerous image file formats are proprietary and rely on local storage. The Open Microscopy Environment's (OME) Next-Generation File Format (OME-NGFF) is a novel image data concept for cloud-native implementations in bioimaging. OME-NGFF's critical advantage is that single image tiles within a larger dataset can be accessed without the need to seek through the entire file, regardless of the storage modality. Image data can therefore be accessed directly from the cloud rather than downloading locally.

Material and methods

We implemented the NGFF concept on a widely adopted open standard, OME-TIFF, to enable arbitrary access of data subsets while maintaining support for popular lossy and lossless compression options. This involves the generation of an index file which describes offsets within the OME-TIFF.

Results and discussion

Indexed OME-TIFF enabled the retrieval of WSI data from object storage such as Amazon's S3 at speeds comparable to original file formats on network file storage at a tenth of the cost.

Conclusion

The application of NGFF concepts to OME-TIFF for Digital Pathology data enables cloud-first visualization and analysis implementations in this domain for the first time. Future work will apply these same concepts to additional modalities, such as fluorescence, and other formats common to Digital Pathology workflows, such as DICOM.

Key words: cloud, open source, file formats, OME-NGFF, OME-TIFF

P23

Histopathology classifier for high risk Diffuse Large B-Cell Lymphoma

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Introduction

Diffuse Large B-Cell Lymphoma is a common cancer with ~400,000 annual diagnoses, globally. Subgrouping into cell of origin expression profiles has clinical utility, with significantly better outcome in Germinal Centre B-Cell (GCB). We present a classifier trained on histopathology data to predict GCB expression, with secondary utility in stratifying high risk GCB patients.

Material and methods

273 DLBCL cases from the population-based Hematological Malignancy Research Network dataset, with associated FFPE H&E (272) and / or immunohistochemistry data (IHC; 67) were used. Image features were extracted using Owkin's Phikon vision transformer at 20x magnification. Multiple instance learning models were trained to classify GCB expression on image features for each staining modality. A histogram boosting classification tree was used to make final predictions, allowing operation despite missing data for any modality. Models were evaluated against true expression with AUC-ROC. Survival analyses were conducted on predicted groups with Cox proportional hazards models.

Results and discussion

CD10 and BCL6 IHC models achieved AUC-ROCs of 0.73 and 0.69, respectively, on 14/72 test cases with IHC data. Poor H&E classifier performance of 0.51 led to final model AUC-ROC of 0.54 on test data. Among true GCB cases, those predicted to be positive by our model had higher overall survival risk (HR vs. predicted negative: 1.85; 95% CI: 1.00 – 3.40; p = 0.05).

Conclusion

Despite poor performance in prediction of GCB expression profile, our model appears to predict high risk among true GCB cases. Future work will focus on interpreting the model, to understand histopathological indicators of high risk in GCB DLBCL.

Key words: Expression profiles, Weakly-supervised learning, Survival groups

P24

Aiforia Clinical Suite for Prostate Cancer: A Holistic Assistive Tool for Prostate Cancer Management

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Introduction

Prostate cancer is the second most common occurring cancer among men, and the high incidence rates cause significant burden to healthcare. Analysis of biopsies is time-consuming and prone to interobserver variability. Aiforia® Clinical Suite for Prostate Cancer is a software product consisting of viewer and AI-trained image analysis algorithms. It produces automated analysis detecting tumor epithelium, Gleason patterns, length measures and adverse findings from WSIs. The performance was investigated with a broad set of clinical samples and several clinical laboratories.

Material and methods

WSIs of HE-stained slides from 111 prostate cancer patients were digitized. The images were analyzed in two independent rounds: with and without the assistance of the product, and a variety of statistical characteristics were calculated. 7 slides were also analyzed by 141 pathologists in 15 countries, and the consensus was compared to the product's result.

Results and discussion

The model can predict positive observations with 96.8 % recall ratio (range 93-100%) and 89.8% precision (86.9-93.9%). Overall accuracy (F1) was 93.2% (89.8-96.6%). The reliability of agreement between with/without the assitance was 0.846 (Cohen's weighed kappa, 0.788-0.878). Time spent for Gleason pattern analysis/slide was significantly reduced (34.1%) with the assistance of the product. The Gleason grading was in a good agreement with the consensus expert opinions.

Conclusion

The use of WSI and automated image analysis in the assessment of prostate biopsies is accurate and timesaving. Furthermore, the use of AI-aided tumor grading seems to reduce interobserver variability. These observations warrant further studies, including the reliability of the length measurement and accuracy of the adverse findings.

Key words: Prostate cancer management, AI/ML, Whole slide imaging, Automated image analysis

P25

Digital pathology and artificial intelligence in developing countries: a scoping review

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Introduction

Transformation of the practice of pathology with digital pathology and artificial intelligence is expanding. The extent of implementation and the impact of this change in developing countries is unclear. This study aimed to determine the current landscape on the applications of digital pathology and/or artificial intelligence in low resource settings.

Material and methods

For this scoping review, a PubMed database search was conducted for the following keywords: digital pathology; artificial intelligence; global south; resource limited; resource constrained; low resource; low middle income; resource poor; and developing country. Articles were analyzed qualitatively for themes in relation to applications of digital pathology and/or artificial intelligence in resource constrained settings.

Results and discussion

The electronic database search identified 746 results. After the removal of duplicates, the number was reduced to 420. The literature review identified 40 articles published between July 2008 and December 2023 after eligibility screening. Of the 40 articles, 9 (22.5%) were published in 2023; 13 focused on telepathology (32.5%), 10 focused on teaching-research-education (25%), 6 focused on low-cost/affordable/economical solutions (15%), and 3 focused on adoption (7.5%).

Conclusion

This study indicates that there is awareness and interest combined with an upward trend in research on the topic in low middle income countries. This review also shows that; currently, the technology is mostly utilized for learning, and research centers around open sources and local low-cost solutions.

Key words: digital pathology, artificial intelligence, scoping review, developing country

P26

An Institutional Experience Analyzing Amendments to Cut Error Rates in Surgical Pathology

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Introduction

Amended surgical pathology reports, can serve as a telescopic view of the entire surgical pathology workflow. Measuring the rate at which surgical pathology reports are amended can be used to ensure quality control. A detailed study of amended reports can improve the quality of reporting in surgical pathology in at least 2 ways: (1) tracking amendment frequencies and the distributions of amendment types across different organ systems reveals pertinent aspects of quality in surgical pathology (2) this type of tracking can help in measuring the effects of efforts to improve surgical pathology reports

Material and methods

This study was conducted at a tertiary care oncology center. The duration of this study was from January 2016 through December 2020(five years). The following were looked for in amended reports: misidentification, specimen defects, misinterpretation, and report defects. The information thus gathered was utilized to sort case-by-case root cause analysis of amendments and to evaluate the clinical implications of such amendments, if any.Results: A total of 57381 surgical pathology cases were signed out during the 5 years. Of these, amendments were issued on 80 cases (0.14 %). About one-third of the amendments were due to misinterpretation.

Results and discussion

A total of 57381 surgical pathology cases were signed out during the 5 years. Of these, amendments were issued on 80 cases (0.14 %).

Conclusion

A surgical pathology report is the final outcome of all the processes. Amendments can be a reliable tool for a record loss of information or introduction of misinformation during the workflow process in a histopathology

Key words: Workflow, Amendements, Surgical pathology, Staging , Misinterpretation , Specimen

P27

Turn around time as a metric of quality control in surgical pathology departmentv

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Introduction

A crucial metric in surgical pathology laboratories is the turnaround time (TAT), essential for timely diagnoses. This study aimed to analyze TATs and identify contributing factors for 695 diagnostic surgical biopsies at a tertiary cancer center.

Material and methods

Cases were categorized as routine (hematoxylin-eosin staining only) or complex (requiring ancillary tests like immunohistochemistry, special staining, etc.). Kaplan-Meier plots were employed to visualize the fraction of case completion against time.Specimens from all organizations systems were included .

Results and discussion

The overall mean TAT was 3.7±2 days, with routine cases at 3±2 days and complex cases at 5±2 days .Survival analysis revealed prolonged TAT for complex cases and those involving immunohistochemistry. Organ-specific analysis highlighted variations in TAT, with brain biopsies presenting the highest complexity and longest TAT. Surprisingly, malignant cases demonstrated slightly shorter TATs compared to benign cases ($p = 0.026$). Other factors for delays included absence of clinical information, decalcification time and slide volume.

Conclusion

This study underscores the need for standardized TAT expectations based on case complexity, efficient clinical data , laboratory management, etc. to enhance diagnostic reporting and offers a foundation for improved TAT practices.

Key words: Kaplan mier , Turn around time , Surgical pathology, Diagnosis , Immunohistochemistry , Laboratory management

P28

Attention-based Multiple Instance Learning to Estimate Risk of Prostate Cancer from Whole Slide Images

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Introduction

Novel automated Gleason grading algorithms are limited by the variability of the grading system. Ideally, an automated algorithm should also be able to estimate the risk of cancer progression. Motivated by this, we have developed a model, based on the principles of attention-based multiple instance learning aimed at predicting the need for intervention, without explicit Gleason grading.

Material and methods

Two cohorts were used, collected at four hospitals within Region Skåne, Sweden. The Gleason cohort comprises 652 WSIs with patch-level Gleason grade annotations. The Prostate Cancer Research International Active Surveillance (PRIAS) cohort includes 147 patients with over 4000 biopsies and corresponding pathology reports. Our framework consists of a feature extractor trained on the Gleason cohort in a supervised fashion to separate malignant from benign patches, followed by a predictor trained on the PRIAS cohort. The output is the intervention risk based on all WSIs from a specific visit, with the ground truth label indicating whether the patient remained on active surveillance or received treatment.

Results and discussion

Our framework achieved an average AUC of 0.83 (±0.05) in cross-validation. Replacing the original feature extractor with one pre-trained on ImageNet gave an average AUC of 0.83 (±0.05). On the test set, they score 0.84 and 0.67 respectively. As a comparison, applying our Gleason grade network to the test data, and classifying according to protocol gives an AUC of 0.58.

Conclusion

This is a work in progress with the final goal to develop an algorithm that can accurately forecast prostate cancer progression, at multiple future time-steps. Encouragingly, our framework shows promising results.

Key words: Prostate Cancer, Deep Learning , Whole Slide Images, Risk estimation, Multiple Instance Learning

P29

Multicenter digital pathology user experience survey of 54 Finnish pathologists

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Introduction

Fimlab Laboratories and Turku University Hospital implemented digital pathology (DP) simultaneously but with different strategies. At Fimlab, all histological slides were scanned starting from the first go-live date, allowing individual pathologists to determine when to cease the distribution of glass slides. In contrast, Turku initiated slide scanning and screen diagnostics gradually focusing on anatomical subspecialties.

Material and methods

A comprehensive user experience survey was completed by 54/66 (81.8%) pathologists after one year of digital diagnostics. Statistical differences between Fimlab and Turku were performed using SPSS version 29.

Results and discussion

The median utility grade of DP was 9 in both sites (mode 10, mean 8.5, range 1-10)($p=0.50$). DP was adopted in ≤ 1 month for 75.9% of the pathologists ($p=0.30$). The vast majority (86.8%) of the pathologists signed out 90-100% of the cases digitally ($p=0.56$), and most had analyzed over 2,000 cases using DP ($p=0.02$). Considering DP as a whole, 62.3% reported DP was faster whereas 17% preferred LM ($p=0.07$). Remote working was convenient for 96.8% at Fimlab and 62.5% at Turku ($p=0.01$). In the self-assessment questions, 90.6% were able to share screens in consultation, and 77.8% felt like fluent users.

Conclusion

Both strategies led to widespread use of DP in less than 10 months. The median utility of digital transition was excellent and most pathologists adapted to the screen rapidly. After one year, the vast majority of the cases were reported digitally only, which we consider sufficient for workflow gains. Almost no statistical differences were seen after one year of implementation, suggesting that both strategies are viable.

Key words: digital pathology, implementation strategy, user experience, remote diagnostics

P30

Deep learning models for predicting lymph node metastasis in thyroid cancer core needle biopsy samples

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Introduction

Preoperatively predicting lymph node metastasis (LNM) in patients with thyroid cancer is important for selecting appropriate treatment options. We aimed to develop a deep learning model using whole slide images (WSIs) of thyroid core needle biopsy (CNB) to predict LNM in patients undergoing thyroid surgery.

Material and methods

The study used 600 WSIs of CNB specimens with pathology diagnoses and confirmed LNM status after surgery. CNB diagnoses included follicular neoplasm (n=102) and malignancy (n=498), of which 294 (49%) were found to have LNM. Two state-of-the-art multiple instance learning (MIL) models were trained using 383 WSIs, and their performance was tested on 96 WSIs during the training phase. We then evaluated the models with the best performance on a separate set of 121 WSIs.

Results and discussion

One MIL model assumed that instances in a bag were independently and identically distributed, while the other model considered them to be correlated. Attention maps were generated to analyze the outcomes of these deep-learning models. These maps effectively highlighted significant regions within a WSI that are crucial for diagnosis, providing insights into the decision-making process of the model. Both MIL models achieved similar accuracy on the test dataset, with an Area Under the Curve of 71% and an F1 score of 65.

Conclusion

The results demonstrate the potential of deep learning in predicting LNM and suggest that improved results can be achieved with larger datasets.

Key words: Thyroid tumor, Lymph node metastasis, Core needle biopsy, Multiple instance learning , Deep-learning, Prediction

P31

Cancer cell state determines tumor-stroma interaction dynamics and patient survival in head and neck cancer

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Introduction

Epithelial tumors are characterized by high levels of inter- and intra-tumor heterogeneity, which complicates diagnostics and results in variable responses to treatment. The contribution of dynamic cancer-stroma interactions to this heterogeneity is poorly understood. Here we report a computational analysis paradigm to quantify phenotypic diversity of tumor and stroma in head and neck squamous cell carcinoma (HNSCC) patient biopsies with single cell resolution.

Material and methods

We analyze 600+ HNSCC biopsies stained with multiplexed immunofluorescence using a computational algorithm combining cell state markers with cell- and tissue-scale morphological features to identify phenotypic signatures that correlate with clinical outcomes. We then perform spatial transcriptomics on patient biopsies and employ in vitro studies of 3D cancer spheroids to investigate tumor-stroma dynamics and signalling.

Results and discussion

By combining cell state markers with cell- and tissue-scale morphological features, we identify phenotypic signatures that correlate with disease-relevant features, including metastasis and recurrence. By combining the tumor phenotypes with stromal signatures, we observe that partial epithelial-mesenchymal transition (pEMT) renders tumors sensitive to the stromal composition, generating a strong prognostic and predictive signature. Using spatial transcriptomics of patient biopsies and analysis of 3D cancer spheroid dynamics, we identify the fibrotic stroma–pEMT axis as a major hub for intercompartment signaling that reprograms cancer cells to generate a dynamic, invasive interface at the tumor stroma boundary.

Conclusion

Taken together, we describe a quantification paradigm to identify and classify clinically relevant tumor phenotypes, and discover a cell state-dependent interplay between stromal and epithelial compartments that drives cancer aggression.

Key words: Multiplexed immunofluorescence, Spatial phenotyping, HNSCC, Epithelial mesenchymal transition, Tumor-stroma interactions

P32

Validation of an AI-based solution for breast cancer risk stratification using routine digital histopathology images

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Introduction

Stratipath Breast is a CE-IVD marked AI-based solution for prognostic risk stratification of breast cancer patients into high- and low-risk groups, using haematoxylin and eosin (H&E)-stained histopathology whole slide images (WSIs). In this retrospective validation study, we assess the prognostic performance of Stratipath Breast.

Material and methods

The study included patients (N=2719) diagnosed with primary breast cancer at two healthcare locations in Sweden. The patients were stratified into low- and high-risk groups by Stratipath Breast using H&E stained WSIs from the surgically resected tumours. The prognostic performance was evaluated using time-to-event analysis by multivariable Cox Proportional Hazards analysis with progression-free survival (PFS) as the primary endpoint.

Results and discussion

In the clinically relevant ER+/HER2- subgroup, the estimated Hazard Ratio (HR) associated with PFS between low- and high-risk groups was 2.76 (95% CI:1.63-4.66, p-value<0.001) after adjusting for established risk factors. In the ER+/HER2- Nottingham Histological Grade (NHG) 2 (intermediate risk) subgroup, the HR was 2.20 (95% CI:1.22-3.98, p-value=0.009) between low- and high-risk groups.

Conclusion

The results indicate an independent prognostic value of Stratipath Breast in both the clinically relevant ER+/HER2- and NHG2/ER+/HER2- subgroups. Improved image-based risk stratification of intermediate-risk ER+/HER2- breast cancers provides information relevant for treatment decisions of adjuvant chemotherapy and has the potential to reduce both under and over-treatment, shorten lead times, and reduce costs compared to molecular diagnostics.

Key words: Artificial intelligence, computational pathology, prognostics, breast cancer, histopathology

P33

Machine Learning-Based Tumor-Infiltrating Lymphocytes Analysis in Colorectal Cancer: Techniques, Performance Metrics, and Clinical Outcomes

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Introduction
Tumor-infiltrating lymphocytes (TIL) can have a crucial impact on diagnosis or decision-making for treating patients with colorectal cancer (CRC), but the inter-observer agreement for quantifying TILs is not perfect. We aimed to systematically review the machine learning (ML) techniques applied for TIL identification on CRC histopathological images to investigate their performance, patient outcomes, and clinical aspects.

Material and methods
Original publications from 2000 to 2022 on PubMed and Scopus databases were retrieved. 722 articles were screened based on inclusion and exclusion criteria. Finally, clinical and technical data extraction was done in ten studies. Subsequently, the association of TIL levels with patient outcomes was investigated.

Results and discussion
Deep learning and traditional ML models are promising in TILs segmentation, classification, detection, quantification and spatial distribution. Deep learning models achieved higher performance for identifying TILs in different locations in whole tumor regions. Most studies have been done to identify specific subtypes of TILs, such as CD3 and CD8 cells. Stromal or intraepithelial-TILs were identified in a few studies. However, few studies identified TILs in the tumor margins. There is an association between automated TILs level and improved outcomes. Due to lack of standard threshold for categorizing TIL densities, some studies have tried different cut-off points to determine the association of TIL levels with patients' outcomes.

Conclusion
Despite some differences in methodology, pipelines, and datasets, most studies have shown a significant positive association between the higher level of TILs and favorable outcomes in CRC. However, a large multi-institutional CRC dataset with a diverse and multi-ethnic population must validate and generalize ML methods.

Key words: Tumor-infiltrating lymphocytes, Colorectal cancer, Machine learning, Deep learning, Biomarker

P34

Spatial Transcriptomic Analysis of Colorectal Cancer: Identification Of Biomarkers Linked To Muscle Invasion

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Introduction

Colorectal cancer is Malaysia's third leading cause of cancer-related mortality. Spatial transcriptomics provides a comprehensive roadmap of transcriptional activity within intact tissue sections. This study aimed to use spatial transcriptomic to identify genes enriched in muscular areas within colorectal cancer tissue and investigate their association with tumor invasion.

Material and methods

Sections of FFPE colorectal cancer samples (5 um) were mounted on Visium Gene Expression slides, followed by staining and imaging. After hybridization with a human transcriptome, the tissues were de-crosslinked and the probes were captured. The resultant cDNA library was RT-PCR amplified and then sequenced on the Illumina NovaSeq 6000. The reads obtained were aligned and superimposed onto H&E-stained tissue images, enabling analysis of gene expression with morphological context. Data visualisation was performed on the Loupe Browser v.6.5.0 software, followed by bioinformatic analysis with DAVID, STRING, and PANTHER.

Results and discussion

A total of 1,382 differentially expressed genes mapped back to the Muscularis Propria region were identified. The top 50 upregulated genes were enriched in "PI3K-Akt signaling pathway", “protein digestion and absorption”, “focal adhesion”, “ECM-receptor interaction”, and “MicroRNAs in cancer” . The differential expressed genes identified were COL1A1, COL1A2, COL3A1, COL5A2, MMP14, and PECAM1.

Conclusion

The PI3K-Akt signaling pathway, platelet activation, and collagen-platelet adhesion play an important role in tumour muscular invasion of CRC. The genes identified in this study (COL1A1, COL1A2, COL3A1, COL5A2, MMP14, and PECAM1) could have potential for biomarker development for colorectal cancer treatment and management.

Key words: colorectal cancer , spatial transcriptomics profiling, tumour muscular invasion

P35

Morphometric analysis of aortic diameter and wall layers depending on sex

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Introduction

Genetic differences between men and women determine the prevalence, manifestations and response to treatment of diseases. The authors aimed to compare the variations of aortic diameter and wall layers' thicknesses along the aortic regions between men and women.

Material and methods

Four aortic tissue rings (base-01_B, arch-02_C, thoracic-03_Th, abdominal-04_Ab) were taken during autopsies from 90 cases (55 men and 35 women). Aortic diameter-AO_D was determined with an "in-house" dedicated software on calibrated photos of the above mentioned tissue rings fixed in buffered formalin. Intimal and media thicknesses (IN_Th and MED_Th) were manually measured on digital slides stained with Orcein in four different points without wall lesion for each ring. Average values-AV were compared using Pearson's test.

Results and discussion

AO_D and MED_Th had a decreasing treand whereas IN_Th had an increasing trend along the aortic length in both sexes. AV values of AO_D and IN_Th were higher in men than in women in all topographic aortic regions, whereas AV values of MED_Th were higher in women than in men excepting 03_Th where they were slightly higher in men than in women (Pearson's test "p" value < 0.0001).

Conclusion

This remodelling process of the aortic wall along its length is following the same pattern in both sexes, generally with higher AV values of investigated parameters in men than in women.

Key words: Aorta, morphology, image analysis, morphometry

P36

Virtual Microscopy for Academic Pathology Education at the Medical University of Vienna

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Introduction

Digitalisation in education is an emerging concept that has been emphasized especially by the COVID 19 pandemic. Furthermore, Virtual Microscopy (VM) is ideally suited to translate conventional state of the art teaching into the digital space. Consequently, our department established a VM environment to fulfill these needs.

Material and methods

Cytomine an open-source solution was set up in 2021 and, after an initial testing phase, was used in elected courses during 2022 and 2023. Initially during remote teaching, later as on-site and self-education tool. In 2022 a semi-structured survey was performed to evaluate the effectiveness of and demands of students on the solution. Furthermore, students' usage statistics were analyzed in both years.

Results and discussion

147 students voluntarily participated in the survey. 95.2% of students were satisfied with the solution, 66,7% were very satisfied. A positive impact on content comprehension was experienced by 95.6% of students, 70.7% experienced a strong positive impact. The main advantage of the solution was the »discussion of histological structures on an instance level in an interactive way with peers, student assistants and educators alike by the means of dedicated annotations«. 3459 image consultations and 2997 annotation creations were observed in 2022. In 2023 during which self-education was encouraged, a total of 18.130 image consultations and 67.991 annotation selections were observed.

Conclusion

VM is highly demanded by students, greatly improves their perceived content comprehension and is ideally suited as a self-education tool that is readily adopted. Furthermore, student annotation capability seems paramount for successful VM.

Key words: virtual microscopy, digital education, remote learning

P37

Vision Transformers for Breast Cancer Classification

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Introduction

In this abstract we propose a self-attention Vision Transformer (ViT) model tailored for breast cancer histology image classification. The image set used for training is part of the ICIAR 2018 Grand Challenge on BreAst Cancer Histology images (BACH), for which both baselines and state-of-the-art are available.

Material and methods

In this research, the ViT model serves as the foundational architecture for all our experiments, owing to its established success in diverse computer vision tasks, especially image classification. We examine various training strategies and configurations, including pretraining, dimension resizing, data augmentation strategies, patch overlap and patch size configurations, in order to evaluate their impact on the effectiveness of the histology image classification. The developed models were trained and validated on BACH, and then tested also on two further datasets (BRACS and AIDPATH) to study generalizability capabilities.

Results and discussion

The achieved accuracy of 0.91 surpasses the top results of the BACH challenge (accuracy: 0.87), albeit marginally trailing behind the best post-challenge performance (accuracy: 0.92). On BRACS, accuracy is 0.85 for normal tissue, 0.88 for in situ and invasive carcinomas, but only 0.36 for benign diseases. However, benign cases were the least accurately recognized in BACH too. Identification of invasive carcinoma on the weakly annotated AIDPATH dataset reached 0.92 accuracy.

Conclusion

Our results confirm that pretraining on large-scale general datasets is advantageous. We also show the potential benefits of using domain-specific pretraining datasets, to further improve the model's performance. Additionally, we provide evidence for the increase in effectiveness gathered trough geometric and color data augmentation techniques.

Key words: breast cancer, vision transformers, normalization

P38

Investigating the effect of resolution differences on segmentation using Whole Slide Images

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Introduction

The analysis of tissue architectures via convolutional neural networks aims to correctly identify image features belonging to a morphological pattern. An important aspect of Whole Slide Imaging (WSI) and microscopy in general is the resolution of the input image, impacting features learned using deep learning techniques and therefore influencing the decisions made by the algorithm. Hence, exploring the effects of image resolution on segmentation of WSI is valuable.

Material and methods

Cancer WSI were generated at a 40x magnification, resulting in a pyramidal image structure. Annotated tumor and immune regions were defined and sectioned into 2000x2000 tiles. Nucleus segmentation using a pre-trained model was performed on 200 tiles with resolutions of 0.11 and 0.44 µm per pixel. After location-wise matching, a hierarchical list of high-resolution within low-resolution detections was generated, with a percentage of 'coverage' of low-resolution nuclei. Distributions of the coverages between immune and tumor tissue regions were compared via a Kolmogorov-Smirnov (KGS) test.

Results and discussion

The hierarchical dataset showed significant differences between the number of detections on high-and low-resolution images, especially in tumor regions, where nucleoli were incorrectly detected as separate nuclei in high-resolution images. Coverages are significantly different between tumor and immune regions based on the KGS test and can be used as a new feature for classification.

Conclusion

Based on these results, it is imperative that resolution effects are checked when implementing deep learning models, as input images are not checked for resolution. Multiple resolutions can be used to classify tumor against immune regions in cancer tissue.

Key words: Whole Slide Imaging, Segmentation, Image resolution, Digital Pathology

P39

An educational annotation platform to improve knowledge retention for histopathology

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Introduction

Digital pathology is adopted increasingly in research and is slowly becoming more widespread in the clinic. Therefore, educational courses should also follow this shift, allowing students to familiarize themselves with digital pathology before using it on a daily basis as either researchers or clinical pathologists. For optimal knowledge retention, an interactive platform is desired, without increasing the workload for teaching staff.

Material and methods

The platform was built on the current research platform from Aspect Analytics. Slides were uploaded to the inventory, and multiple cases were added to projects. Labels were created and from these labels, groups were made related to specific cases. Annotations used different tools, i.e. a polygon or a freeform. In each project, students could indicate whether they completed a case, or they could report a problem. Students were able to log in using their university account via an SSO system.

Results and discussion

We created four projects, each containing several cases. One of these projects was made mandatory for students. The created label sets ranged from four labels up to eighteen labels, each with a unique color. A solution key was also created, which was made visible on the platform after students completed their annotations. Teachers were able to see which students had completed specific projects, and the annotations could be exported as GeoJSONs.

Conclusion

We successfully created projects in which students annotated different structures. In the next years, this platform will be extended with automated analysis of the student's annotations using GeoJSON exported files and algorithms.

Key words: Annotations, Education, Digital pathology

P40

Novel volumetric scanning method with dynamic Z stacks yields high quality PAP smears at par with traditional microscope

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Introduction

Digital pathology use in cytopathology has been limited predominantly to research as 3D cell clusters are not in focus with routine best focus 2D imaging which gives suboptimal results. Volumetric scanning of cytopathology smears may provide a viable solution, by capturing all cellular features with Z depth perception similar to the traditional microscopy.

Material and methods

Volumetric scanning with dynamic Z stacks and single best-focus imaging was performed for thirty liquid based cytology (LBC) PAP smears using a Pramana HT scanner. Our novel method captures the dynamic Z stacks at every FOV and then fuses them unlike other methods of capturing single best focus image in the optimal Z plane. Both cohorts (best focus vs fused Z stacks) were evaluated by Pathologists. An inline slide quality analysis algorithm for focus and other errors was run to determine the effect of scanning techniques on algorithm performance.

Results and discussion

The overall image quality of all 30 PAP smears with volumetric scanning was found better than best focus imaging and comparable to traditional microscopy as determined by Pathologists. A focus detection algorithm yielded more than 99% in focus fields in PAP smears with Z stacking. The inline quality analysis algorithm facilitates inline rescanning of selected FOVs for optimal image quality. Besides, the dynamic Z stacks storage provides a visualization experience similar to the traditional microscope.

Conclusion

Volumetric imaging of PAP smears with dynamic Z stacks preserves cumulative cellular details distributed across the Z-stack layers, thus creating higher quality images at par with current standard of traditional microscopy for the cytopathology domain.

Key words: Volumetric scanning , Digital cytopathology, PAP smear, Z stacks , Slide quality, Inline algorithm

P41

A robust region of interest registration approach on breast histological whole slide images

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Introduction

Tumour infiltrating lymphocytes (TILs) have a prognostic value in breast cancer (BC) specimens, and their identification is performed in a specific region of interest (ROI) following Salgado's criteria. This study aims to automatise the detection of these ROIs across whole slide images (WSIs) of BC specimens based on a given ROI of a WSI selected by a pathologist.

Material and methods

We analysed 55 BC specimens, where a pathologist annotated the same ROI in three haematoxylin and eosin WSIs. Two registration approaches were compared: direct ROI prediction from the first WSI to the second and third WSIs (M1) and a chain approach where the third WSI's ROI is derived from the predicted ROI of the second WSI (M2). We investigated the preprocessing phase for the rigid registration of Virtual Alignment of pathoLogy Image Series (VALIS) to obtain a ROI proposal without failure, meaning there is no empty overlap with the ROI annotated by the pathologist.

Results and discussion

Our registration process is designed to be robust since it considers the potential for tissue flipping during the preparation. Additionally, by tuning the preprocessing phase, our method prevents M1 from failing on two ROI predictions of the third WSI. The dice score is 0.849 for the second WSI's ROI predictions. Neither of the two approaches shows a significant quantitative superiority over the other in the third WSI's ROI predictions since the dice score is 0.791 for M1 and 0.789 for M2.

Conclusion

Our proposed registration technique holds promise for improving ROI detection for TIL evaluation in breast cancer assessment.

Key words: Image Registration, Whole slide image, Region of interest, Robustness, Breast cancer, VALIS

P42

Automated detection of out-of-focus regions by SlideQC BF on the FocusPath dataset

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Introduction

Assessing image quality is crucial to identify artifacts that might negatively impact the diagnosis or performance of image analysis algorithms. Detecting out-of-focus regions by manual quality control is laborious and time-consuming, and out-of-focus regions are often only detected after in-depth review. Indica Labs' SlideQC BF, an AI-based image quality control tool, was developed to automatically detect and segment artifacts, including out-of-focus regions.

Material and methods

A DenseNet-based network was trained using 4915 annotations for artifacts such as air bubbles, dust/debris, folds, out-of-focus, and pen marker, along with a set of synthetically generated out-of-focus images sourced from 689 Haematoxylin and Eosin (H&E) and immunohistochemistry (IHC) stained whole-slide images. Out-of-focus detection by SlideQC was evaluated on an external test cohort, the "FocusPath" dataset, on 960 images obtained at 16 z-levels, captured across 30 regions.

Results and discussion

The expected out-of-focus pattern from z-stacking was reproduced, with the percent artifact area increasing as the z-level position distanced from the in-focus position. A binarization scheme was applied considering all patches with absolute z-level 0 and 1 as sharp and those equal to or larger than 2 as blurry. The median percent artifact was 6.1% for the sharp z-levels and 100% for the blurry z-levels.

Conclusion

Automated quality control tools such as SlideQC BF can be applied to identify out-of-focus regions, improving workflow efficiency by flagging slides that might require rescanning or excluding out-of-focus regions from downstream image analysis.

Key words: Out-of-focus , Quality control, Artifact detection , Deep learning

P43

Integration of slide quality parameters with WSI DICOM expands the outreach of digital pathology

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Introduction

Quality analysis of whole slide images (WSI) is needed to ensure suitability for pathological evaluation. Usually, quality assessments are performed after generation of the DICOM image, so these are not readily available for integration with DICOM images. Here we present our work of generating quality-related parameters in parallel with the scanning process, so that quality parameters are immediately available for integration with WSI DICOM file.

Material and methods

For this pilot one hundred slides were scanned using Pramana HT scanner. In parallel to scanning operation, all slides were evaluated for slide quality metrics (eg. focus error, stitching error, presence of bubbles, debris, and annotations) and slide attributes (faint and dark area percentage, stain type and scan statistics). Alongside scanning, slide quality parameters and related masks (i.e. visual representations overlaid on WSI) were analysed and embedded as private tags into the DICOM files. The enriched DICOM files with embedded quality parameters were evaluated by Pathologists for assessing slide suitability for clinical decision making.

Results and discussion

For all the slides, quality parameters and slide attributes were readily available as soon as scanning was completed facilitating its embedding into the WSI DICOM files. Enriched DICOM with embedded quality parameters promotes interoperability with other viewer solutions as these quality parameters are readily available for review as well as for secondary consultation.

Conclusion

Inline quality assessment of WSI facilitates embedding of quality parameters into DICOM files which paves the way for rapid clinical adoption of digital pathology by obviating the need of costly, time consuming and labor intensive manual quality analysis of WSI.

Key words: Enriched DICOM, Inline quality analysis, Interoperability, WSI , DICOM, Digital pathology

P44

Integrated deep learning and graph-based exploration of cellular dormancy in histopathology images of colon cancer

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Introduction

Tumour dormancy has been associated with resistance to chemotherapy, but predicting the risk of dormancy and emerging resistance in cancer remains a highly challenging problem. Here, we introduce an integrated deep learning and graph-based framework to identify and explore dormancy and its microenvironmental contexture in colorectal cancer using digital pathology slides and matched RNA-seq data from 456 patients available from the Cancer Genome Atlas (TCGA).

Material and methods

To assess the levels of dormancy within bulk tumours, we established RNA-seq derived scores reflecting the ratio of ERK/p38 activity, which determines the ability of cancer cells to enter dormancy. We then used these scores to categorise tumours as fast/moderately proliferating or dormant. Next, we trained a weakly supervised model based on the Inception v3 architecture to recognize these patterns of dormancy in matched H&E whole slide images (WSIs). To gain insight into the spatial organization of dormancy, we inferred the cellular composition of the tissue via nuclear segmentation using HoVer-Net and stored the inferred connections between tumour cells, stroma and lymphocytes in a Neo4J graph database, allowing us to efficiently and flexibly query large-scale interactions.

Results and discussion

Our H&E-based AI classifier achieved an average AUC of 83% in detecting patients with dormant tumours, who had a significantly shorter time to disease relapse after chemotherapy treatment. Our graph-based methods uncovered a protected local niche of dormancy that is enriched in stromal barriers impeding immune recognition.

Conclusion

Our study showcases the potential of combining deep learning and graph theory to gain new insights into therapeutically-relevant cancer cell states using digital pathology.

Key words: cancer dormancy, chemotherapy resistance, H&E stained slides, RNA-sequencing, graph theory, tumour microenvironment

P45

Informatics in Pathology: A Preliminary Study About the Pathologists from Türkiye

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Introduction

Information about the background of countries in digital pathology (DP) might give clues for development and allow comparison with different parts of the world.

Material and methods

A questionnaire prepared by two experienced digital pathologists was sent to Turkish pathologists with the help of Federations of Pathologists about their experience and opinions on informatics in pathology.

Results and discussion

Of the 157 participants (nearly 10% of Turkish pathologists), 35,1%, 36,9%, 28% were academicians, specialists & residents respectively. Pathologists working at laboratories with information systems (LIS) and fully/partially digitalized laboratory workflow were in 8.3% and 31,2% of the participants. 23.6% of the participants could ask for additional biomarkers through LIS. Virtual microscopy (VM) was available in 21% of the participants' labs. 15,2% were using VM for patient diagnosis and 8.3% used software during evaluation (Eg: ki67, cerbB2...). VM case set for educational purposes was prepared by 9.5% and annotated by 6,6% of participants. 28.4% of the participants shared cases at DP projects, 29% made annotations for the research projects, and 22,3% were participants. 6.4% performed in silico research. When the participants were asked about the future of VM in education/research and diagnostic facilities, 89.1% and 91.1% had high expectations, however only 21% thought replacement of VM was likely. 80% of the participants wanted more practical education activities in DP.

Conclusion

These results highlight the developing background and potential of DP in Türkiye Acknowledgment: Many thanks to the Turkish Pathology Federation, Turkish Bioinformatics Working Group, Prof Dr Aydın Sav, and participants.

Key words: Informatics in pathology, digital pathology,, virtual microscopy, Türkiye, questionnaire

P46

Automatic H.pylori detection on Warthin-Starry WSI with AI

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Introduction

One of the difficulties in digital pathology adaptation period is detecting H.pylori. Existing AI models utilise HE and Giemsa stains to aid diagnosis. We have observed that Warthin-Starry has better contrast on images and wanted to evaluate an AI model to see the possibility of H.pylori detection with minimal training.

Material and methods

Twelve Warthin-Starry stains, featuring diverse bacterial clusters annotated with discrete categories: +1 class signified a single bacterium, +2 represented two or more bacteria in discernible rows, +3 clustered three or more bacteria. A tissue detection algorithm was trained to recognize tissue edges, a critical aspect for identifying regions prone to bacterial migration. Augmentation transformations were implemented on all images, adjusting parameters by 10% from default values. The convolutional neural network (CNN) model was developed using Aiforia Create (version 5.7.1) by Aiforia Technologies Plc, training process spanned 3 hours and 22 minutes. For validation, 10 samples (2 negative,8 positive) were used.

Results and discussion

The model training yielded a robust outcome, with a minimal total area error of 0.02%. This model demonstrated effective generalisation when tested on a separate dataset. The application of this trained AI model to analyze a new Whole Slide Image (WSI) requires approximately 1 minute per WSI.

Conclusion

Detection and stratification of H.pylori was achieved successfully for the test set. With minimal training it was possible to evaluate H.pylori within minutes. This is the first time such an AI model predicting three categories of H.Pylori detection on Warthin-Starry has been developed. Expanding the dataset would further augment the model's capabilities and enhance its generalizability.

Key words: H.pylori, Warthin-Starry, CNN, WSI, gastric biopsy

P47

Extracting information from semi-structured Pathology Reports

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Introduction

Pathology reports are text files that contain information in various styles. Although synoptic/structured reports are becoming common, most reports are still written free text. We tried to extract information from semi-structured Turkish pathology reports using regular expressions and large language models.

Material and methods

Ninety-two renal tumor pathology reports were exported from the laboratory information system as unstructured text. They were anonymised and the diagnosis field was extracted. Target information were tumor localisation, size, stage, lymphovascular invasion, necrosis, rhabdoid morphology, sarcomatoid components, stage, surgical margins. These features were extracted using regular expressions in R-project, and the results were reevaluated by a pathologist to represent the ground truth. We used Python and OpenAI API for GPT models with Named Entity Recognition, using zero-shot, one-shot, few-shot examples and different temperature values. Precision recall, F1 metrics were used for evaluation. For NER a modified evaluation is used, not word order but the content. We used the labaled data to fine-tune BERT based models and tried open source modelsin HuggingFace including those fine-tuned for Turkish.

Results and discussion

We have found regular expressions and language models to be useful in information extraction from pathology reports. The best result was obtained with GPT-35-Turbo few-shot and GPT-4 few-shot models has 0.94 average F1 score.

Conclusion

Medical text in Turkish contains jargon that are not widely accepted and not follow general language rules. Report structures and content also vary among institutions. Although regular expressions can be used for certain type of tumor reports from certain institutions, a more generasible method is required to extract information from pathology reports.

Key words: text mining, pathology reports, large language models, regular expression, GPT, named entity recognition

P48

Detecting tumor regions in lung cancer tissue sections using Gaussian Process modelling of cell-specific features generated by artificial intelligence

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Introduction

In recent years, digital techniques have become an important complement in the field of pathology, often providing biological insight beyond the limits of human perception. Standard pathological practice can identify tumor regions within tissue microenvironments based on a set of visual identifiers. We aimed to construct a model for digitally detecting tumor regions and identify the cell-level aspects driving the detection.

Material and methods

Ten non-small cell lung cancer patient H&E stained samples were selected used in this study, which were subsequently scanned by the Zeiss Axio Scan Z1. Regions were independently annotated as tumoral or non-tumoral by two histologists to use for training and validation. Nucleus segmentation was performed and several features were generated per nucleus, including spatial coordinates. Each feature was aggregated at a regional level and modeled as a distinct spatial Gaussian process. The resulting information was then used as predictor for tumor or non-tumor regions in a logistic regression model.

Results and discussion

Prediction accuracy, sensitivity and specificity were calculated. The most suitable combinations of cell-level aspects - geometric, color-related and density-related - were shown to be predictive for detecting whether regions are tumoral.

Conclusion

Whereas many cell-level aspects that were important for identifying tumor regions were intuitive, some were less self-explanatory and could be important in clarifying identifiers that have a uniquely digital nature and would therefore be missed by the human eye.

Key words: region detection, artificial intelligence, cell detection, H&E staining, cell-level aspects

P49

Evaluation of Ki-67 in WSI subjected to compression

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Introduction

Whole Slide Images can be compressed to reduce size without losing details to human eye. Here we investigated a novel compression model to see if automatic Ki-67 proliferation index detection changes due to the compression.

Material and methods

Twenty breast tumor Ki-67 WSI are included. Images exported from Sectra in .svs and compressed into .tiff via OptiSize Technomind software. Paired images are anonymised, randomised and reimported into Sectra. Paired images are aligned and synchronized. Two corresponding areas (500 cell each) in each case measured using Sectra's built-in tool. An assessment is conducted on the mathematical analyses, specifically the Peak Signal-to-Noise Ratio(PSNR) and Structure Similarity Index Measure(SSIM), applied to both the original and compressed images.

Results and discussion

Original images were 9.13GB (min:138MB, max:1.34GB), compressed were 3.74GB in size (min:65MB, max:401MB), with an 59% reduction in total size. PSNR value 44.20dB (min:41.61dB, max:47.57dB). PSNR values exceeding 40dB are deemed highly favorable for assessing the similarity of two identical images. SSIM measured 0.975 (min:0.96,max:0.99), where 1 indicates perfect, 0 indicates no similarity. Median Ki-67 index was 17.9% in original images (min:0.1%,max:54.2%), and 18.2% in compressed (min:0.1%,max:55.1%) (p=0.07). Individual differences are detected without any predilection towards a group.

Conclusion

The mathematical verification of the image compression ratio performed a promising outcome. There were individual differences in cases. Some were due to the selection of exact location, detection of cells and also classification of detected same cell. The in-built tool of Sectra only allows a circular selection and does not differentiate tumor vs stroma. These points will be addressed using additional AI-based tools for Ki-67.

Key words: WSI, Compression, Ki-67, Breast

P50

Deep Learning-Based Classification of SOX2 Expression Levels in Breast Cancer Whole Slide Images

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Introduction

Breast cancer, the most common cancer in women, relies on biomarkers for diagnosis and prognosis of the disease. SOX2, a transcription factor associated with therapeutic resistance, is emerging as a promising prognostic biomarker.

Material and methods

This study presents a deep learning algorithm to classify SOX2 expression levels in whole slide images of breast cancer. The research evaluates the effectiveness of a multiple instance learning approach. A comparative analysis is performed between the manual selection of tiles by a pathologist and a fully automated method. The model is trained and evaluated using a 5-fold cross-validation technique on a dataset of 24 whole slide images.

Results and discussion

Slide-level classification results yielded an f1-score of 68% using tiles selected by a pathologist and 41% using a fully automated method.

Conclusion

Given breast cancer heterogeneity, accurate representation of whole slide images is essential for robust biomarker expression classification. Future work could explore the use of graph neural networks to ensure adequate information capture.

Key words: breast cancer, SOX2, deep learning, digital pathology, whole slide images, biomarker classification

P51

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

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Introduction

The Banff classification is the gold standard for histopathologic assessment of transplant kidney biopsies. It consists of 17 lesion scores, 10 of which focus on the presence and extent of inflammatory cells in different kidney compartments. As this scoring suffers from subjectivity and is very time consuming, development of automated biopsy assessment holds great potential to reduce pathologist's workload and increase scoring consistency.

Material and methods

The MONKEY challenge focuses on detection of inflammatory cells, specifically lymphocytes and monocytes, in PAS-stained kidney transplant biopsies. It is run on the Grand Challenge Platform (monkey.grand-challenge.org) with leaderboards for individual tasks. The dataset consists of annotated regions from a multi-centric cohort of 120 WSIs. To ensure reliable annotations, the slides are re-stained with antibodies against CD3, CD20, and PU.1 to identify lymphocytes and monocytes, respectively. Algorithm performance will be evaluated on a test set from a separate institution.

Results and discussion

The challenge is planned to open before summer 2024. It will result in a best performing algorithm to detect inflammatory cells in PAS-stained biopsies. This algorithm will be accessible for the research community and will be further incorporated in AI for automated Banff lesion scoring. The MONKEY dataset will remain publicly available for research purposes.

Conclusion

Several of our previous challenges (CAMELYON, PANDA and TIGER), where such wisdom-of-the-crowd approach was applied for urgent clinical applications, have produced highly successful algorithms, sometimes even surpassing experienced pathologists. The MONKEY challenge is highly ambitious as it aims to differentiate between lymphocytes and monocytes, bringing us a step closer to automated Banff lesion scoring.

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

P52

Streamlining Colon Biopsy Screening with Interpretable Machine Learning

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Introduction

The rising rates of screening for early detection of colon cancer are exacerbating the strain on histopathology resources globally. Machine learning methods offer a promising solution to alleviate this burden by effectively filtering out normal slides that do not require further intervention, thereby streamlining the diagnostic process for cancer screening.

Material and methods

We performed colon biopsy screening using both black-box and interpretable machine learning. For the black-box method, we performed pooling of a sequence of patch features extracted from a pre-trained Vision Transformer using a single Multi-Head Attention (MHA) Transformer layer. For the interpretable method, we extracted clinically relevant features from nuclei, stroma and gland components that were detected by a U-Net-based segmentation model. These features were then used as input to a predictive model.

Results and discussion

We assessed each approach using a dataset consisting of 7,181 endoscopic colon biopsy slides with 5-fold cross-validation, stratified across patients and labels. For normal, non-neoplastic, and neoplastic categories, MHA achieved AUC-ROC scores of 0.9725±0.0048, 0.9438±0.0137 and 0.9921±0.0033, respectively. Combining non-neoplastic and neoplastic (the abnormal category) achieved 0.8562±0.0522 specificity at 95% sensitivity. Regarding the interpretable approach, initial findings indicate performance on par with the MHA, albeit offering enhanced model transparency.

Conclusion

We introduced two competitive colon biopsy screening methods that show the potential to reduce the burden currently placed on pathologists worldwide. Specifically, our proposed interpretable approach can assist pathologists in making diagnostic decisions and enhance their trust in the algorithm, facilitating its eventual integration into clinical practice.

Key words: Interpretable AI, colon biopsy screening, computational pathology

P53

Towards Comprehensive Segmentation of Colorectal Histology Images: A Multi-Task Learning Approach

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Introduction

Segmentation of diverse objects within colorectal histology images is crucial for extracting interpretable features that provide insights for accurate diagnosis and prognosis. Traditional segmentation strategies, which typically handle tasks independently, are impractical in real-world clinical settings due to poor scalability.

Material and methods

We introduce a multi-task learning segmentation pipeline capable of concurrently addressing six segmentation tasks, including instance segmentation of glands, nuclei, and lumen; detection of goblet and signet ring cells; and semantic segmentation of more than ten classes within colorectal images. Our novel approach achieves inference several times faster than multiple separate models for each task without sacrificing performance. The model was developed using a dataset derived from 825 patients, encompassing over 830,000 histology objects, to ensure strong generalisability across unseen images.

Results and discussion

Comparative analysis reveals that our framework matches or surpasses the performance metrics (including Dice coefficient, F1 score, and panoptic quality) of traditional single-task models, while being around 6 times faster. This does not compromise the ability to discern and extract meaningful features from histology images, which are vital for accurate disease diagnosis and prognosis.

Conclusion

We show that efficiently processing data in a clinical setting can be achieved by performing multiple tasks simultaneously with a single model, which reduces inference times. Our multi-task learning pipeline is specifically designed to speed up inference by a factor of 6 while demonstrating that learning multiple tasks together is comparable to training several single-task models. This represents a significant advancement in operational efficiency and accuracy for the comprehensive analysis of colorectal histology images in real-world applications.

Key words: Multi-task learning, Segmentation, Colorectal histology images

P54

Leveraging AI-powered tools for a streamlined analysis of multiplex H&E and IHC images to characterize the tumor landscape

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Introduction

The combination of hematoxylin and eosin (H&E) staining and immunohistochemistry (IHC) allows for a precise assessment of the morphological and molecular characteristics of tumors. Digital pathology (DP) and artificial intelligence (AI) are revolutionizing immuno-oncology by enabling precise analysis of tumor tissues at the cellular level. These technologies facilitate the prediction of immune responses and identification of biomarkers, enabling more effective therapeutic strategies against cancer.

Material and methods

Here, we combined H&E and Brightplex®, a chromogenic multiplex-IHC staining allowing the detection of several biomarkers on a single FFPE tissue section. The section is repeatedly stained, first with H&E then with antibodies, digitized and destained, to detect various biomarkers. Whole slide images are fused to create a virtual multi-channels image where regions of interest and biomarkers are detected using AI-based algorithms.

Results and discussion

AI-models were trained on H&E, with IHC serving as a basis for establishing ground truth annotations. The integration of these models allowed us to partially automate the Brightplex®-DP-workflow. Other models were trained to replicate, using AI, the quality control of samples typically performed by pathologists.

Conclusion

The automation of the DP workflow has made image analysis faster, more efficient and reproducible. Furthermore, sample quality control being partially carried out with AI helps reduce the time required by the pathologists to review cases, allowing them to focus on more critical tasks. The use of IHC data was critical for generating models capable of classifying various stromal populations which are not visibly discernable by eye on H&E.

Key words: Artificial intelligence, Digital Pathology, H&E , IHC , Immuno-oncology, Whole Slide Image

P55

Deep Learning Solutions for Quality Control in Histopathology

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Introduction

In digital histopathology, ensuring the reliability of image analysis is paramount for accurate diagnosis. However, preparation and scanning artifacts might occur. Their presence on Whole Slide Images (WSIs) can significantly impact algorithms' performance and may impede the pathologist's workflow as artifacts reduce slide readability. In this study, we propose deep learning solutions for quality control in histopathology, with the dual objectives of improving image analysis quality and providing workflow decision support for slides with detected artifacts.

Material and methods

We curated a fully annotated WSIs dataset with 14 artifacts classes. Our approach leverages deep learning models, including the U-Net architecture, for semantic segmentation of artifacts that can be detected at low magnification, such as folds, air bubbles, foreign objects and out-of-focus regions. For smaller artifacts that require higher magnification such as small ink spots, we rely on patch-based predictions. Furthermore, we introduce a quality scoring mechanism that assesses the severity of detected artifacts and provides slides management recommendation based on artifacts' localization and quality score. Based on this recommendation, decisions can be made regarding whether actions such as re-slicing or re-staining are necessary.

Results and discussion

We demonstrate accurate detection for all these artifacts using our approach. Additionally, we compare a mitosis detection algorithm's performance with and without our artifacts detection framework to demonstrate error reduction. Finally, we evaluate our decision support pipeline against expert pathologist decisions.

Conclusion

Overall, our deep learning-based approach holds promise for enhancing image analysis quality and facilitating informed decision-making in histopathology practice.

Key words: Digital Pathology, Deep Learning, Quality Control, Quality Assessment , Artifacts Detection

P56

Differences in response to adjuvant chemotherapy between breast cancer risk groups defined by a prognostic AI-based risk stratification model

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Introduction
Adjuvant chemotherapy (aCT) improves breast cancer (BC) survival but also carries toxicity. In clinical routine, multiple factors contribute to treatment decision for aCT, among them, Nottingham histological grade (NHG), which is prognostic but suffers from high inter-rater variability. Stratipath Breast is a CE-IVD marked AI-based prognostic risk stratification model, providing an objective alternative for risk-stratification. In this retrospective observational cohort study, we assess different impact of aCT on progression-free survival (PFS) by Stratipath Breast risk groups.

Material and methods
We followed 2719 BC patients, categorized as either Stratipath Breast high- or low-risk, from 2008 and 2019. Clinicopathological information was obtained from the Swedish National Quality Register for Breast Cancer. Using Cox Proportional Hazards model, we calculated hazards ratios (HRs) and 95% confidence intervals (CIs) for aCT on PFS, considering both main effects and the interaction between aCT and Stratipath Breast risk group. We adjusted for potential confounding by age, estrogen-(ER), progesterone-, and HER2-receptors, tumor size, and node status.

Results and discussion
During follow-up, 1025 patients underwent aCT, and 121 experienced disease progression. The association between aCT and PFS differed by Stratipath Breast risk groups (HR=0.47, 95% CI=0.27-0.85 in the high-risk group; HR=1.79, 95% CI=0.77-4.16 in the low-risk group, p-for-interaction=0.005). A similar trend was observed among ER-positive HER2-negative patients, though the results were not statistically significant.

Conclusion
In this observational study we found that aCT improved survival (PFS) in the Stratipath-Breast high-risk group, but not in the low-risk group, suggesting Stratipath breast may provide additional insights into patient response to aCT.

Key words: Breast cancer, Histopathology, Adjuvant chemotherapy, Stratipath Breast, Deep learning

P57

Calculation of Ki-67-index in gastroenteropancreatic neuroendocrine tumors with open-source software QuPath

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[1] Faculty of Medicine, University of Bergen (UiB), Norway
[2] Department of Pathology, Haukeland University Hospital, Norway
[3] Department of Clinical Medicine, University of Bergen (UiB), Norway

Introduction

The histologic grading of gastroenteropancreatic neuroendocrine tumors (GEP-NETs) relies on the Ki67 index, traditionally assessed through manual counting, which is susceptible to inter- and intra-observer variation and consumes significant time and energy, raising concerns about their reliability and efficiency. This study investigates the utility of QuPath, an open-source software, in quantifying Ki67 positivity in GEP-NETs, aiming for performance comparable to commercial software applications.

Material and methods

Through a thorough literature review, we examined the current landscape of automated image analysis in research and clinical pathology, with a focus on QuPath's utility in Ki67 detection. Subsequently, we evaluated QuPath's performance in quantifying Ki67 positivity in whole slide images (WSI) of GEP-NETs with a Ki67 score of less than 5%, comparing it against manual counting, considered as the "ground truth" by pathologists. Using QuPath 0.4.0 and the StarDist plugin, we implemented two models (StarDist1 and StarDist2) for automated cell detection. Subsequently, the predicted cells from regions of interest in 28 WSIs were then manually labelled and used to train an object classifier, which was finally evaluated in a separate set of 10 WSIs with 80 regions of interest.

Results and discussion

Our results indicated strong performance of QuPath in tumour cell detection (ICC=0.91 and ICC=0.82, respectively) compared to manual counting. However, discrepancies arose in QuPath's ability for Ki67+ tumour cell detection (ICC=0.27 and ICC=0.17, respectively)

Conclusion

In conclusion, while QuPath holds promise in digital pathology, challenges persist in standardization and performance optimization. Despite limitations, QuPath's potential warrants further exploration and protocol refinement for enhanced assessment and clinical application.

Key words: QuPath, Ki67, GEP-NETs, StarDist, Digital Pathology

P58

Tissue Detection and Segmentation in Diverse Histopathology Images

Greta Markert[1], William Prew[1], Florian Markowetz[1]

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Introduction

With the rise of deep learning for histopathology images, the need for preprocessing the image to only focus on tissue and not other artefacts on slides increases. We introduce TissueTector, a fast, lightweight, and simple tissue detection pipeline for segmenting and patching tissue samples for training neural networks. This open-source algorithm outperforms the current preprocessing techniques across several quantitative and qualitative benchmarks on a diverse of challenges in a variety of common tissue stains used in the clinic, able to segment both H&E and IHC stains.

Material and methods

This is achieved using only efficient and simple tools including filtering techniques, separate channel filtering, and contrast enhancement. We use the HED color space to detect H&E slides and use the gray color space for IHC staining. For detecting pen markers as well as other artefacts, we filter the HSV color space.

Results and discussion

Without the use of machine learning models, our method can be easily implemented into current workflows with greatly reduced overhead and minimal parameter adjustment leaving greater processing power available for model training.

Conclusion

As such, the overall pipeline achieves greater speed and accuracy in comparison to other algorithms, while still able to perform on a range of more difficult cases including non-standard tissue samples, and ignore common artefacts, such as pen-marks, leaving only relevant data for training.

Key words: tissue detection, segmentation, histopathology, preprocessing

P59

Artificial Intelligence-enabled Nonlinear Multimodal Polarimetric Microscopy for Melanoma Diagnostics and Prognostics

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[8] Faculty of Mathematics and Informatics, Vilnius University, Lithuania
[9] Life Sciences Centre, Vilnius University, Lithuania
[10] Department of Medical Oncology, National Cancer Institute, Lithuania

Introduction

The processes of tumorigenesis and metastasis affect the extracellular matrix (ECM) as well as the cellular components of tissue. Collagen, being the primary constituent of the ECM, is also responsible for facilitating cell migration. Nonlinear multimodal polarimetric microscopy (NMPM) is a technique that integrates various imaging modalities such as second-harmonic generation (SHG), third-harmonic generation (THG) and multiphoton excitation fluorescence (MPEF) and enables a thorough investigation of cellular and extracellular components in hematoxylin and eosin-stained (H&E) and unstained histological slices. Previous studies have shown that polarimetric second-harmonic generation microscopy coupled with artificial intelligence can aid in diagnosis of breast and lung cancer.

Material and methods

In this research, histological slices of melanoma stained with H&E were examined. These samples represented various types and stages of melanoma. Analysis incorporated all three modalities each serving a specific purpose: MPEF revealed eosin-stained ECM, THG highlighted hematoxylin-stained cell nuclei and SHG exposed collagen, which due to its non-centrosymmetric nature is known to generate polarization-sensitive SHG signal. Analysis of the SHG signal was carried out in the context of double Stokes-Mueller polarimetry (DSMP) formalism and yielded information about the collagen ultrastructure.

Results and discussion

Data from all three channels was analyzed employing texture analysis, statistical methods, and a combination of supervised and unsupervised machine learning. Additionally, a segmentation algorithm was developed to detect cell nuclei and assess nuclear morphology.

Conclusion

The study demonstrated the versatility of this analysis for tasks such as delineating tumor margins, distinguishing between tumorous and inflammatory regions, identifying the type and stage of melanoma, and potentially recognizing rapidly advancing melanoma cases.

Key words: Stokes-Mueller polarimetry, Nonlinear Multimodal Microscopy, Texture Analysis, Segmentation, Machine Learning, Digital Histopathology

P60

Semantic segmentation combined with nuclei center detection for quantification of KI-67 histopathological images

David Anglada-Rotger[1], Sonia Rabanaque[1], Julia Sala[1], Philippe Salembier[1], Ferran Marques[1], Montse Pardas[1]

[1] Image Processing Group, Universitat Politècnica de Catalunya (UPC), Espanya

Introduction

In our study, we present an innovative approach to the automatic segmentation and classification of tumor cell nuclei within breast cancer histopathology slides. Leveraging a unique combination of dual Convolutional Neural Networks (CNNs) for semantic segmentation and for nuclei center detection, our methodology significantly enhances the precision of cell separation and classification.

Material and methods

We developed a robust methodology by creating a database from whole slide images. This includes a semantic segmentation network based on the U-Net architecture for identifying cell types and a cell center detection network, also U-Net based, that estimates the center of masses for each nucleus, which is represented as a Gaussian. This dual network strategy is designed to elevate the precision of cell segmentation and classification within histopathology slides.

Results and discussion

Our results demonstrate a substantial improvement in segmentation and classification accuracy, with a weighted F1-score of 0.7802 across different test folds, surpassing the capabilities of the state-of-the-art architecture, HoverNet, having an special improvement in detecting the non-epithelial cells. This performance underscores the effectiveness of our U-Net based models in accurately identifying and classifying tumor cell nuclei.

Conclusion

Concluding, our study highlights the potential of our method to aid pathologists by providing a more accurate and efficient diagnostic tool, particularly for evaluating cell proliferation rates. With a mean absolute error of 2.5688% in Ki-67 score predictions, our approach not only proves its clinical applicability but also sets a new standard in digital pathology, promising significant advancements in the accuracy of breast cancer histopathology analysis.

Key words: Deep Learning, Computer Vision, Ki-67 , Histopathology

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June 6

13:00 - 13:45 | Alpha Room
3DHISTECH LTD

June 7

08:00 - 08:45 | Alpha Room
LEICA BIOSYSTEMS

June 7

13:00 - 13:45 | Alpha Room
EPREDIA

INDUSTRY EXHIBITION

LOCATION

The industry exhibition is located in the Conference Center.

OPENING HOURS

Opening Hours

Thursday (06/06/2024)	09:00 – 20:00
	17:30 – 20:30 Poster Reception and Get Together
Friday (07/06/2024)	08:30 – 18:30
Saturday (08/06/2024)	08:30 – 15:00

Booth Number	Company
B02	JSHD
B05	BARCO NV
B06	Histofy Ltd
B07	SPOT Imaging
B08	EMPAIA International e. V.
B09	Pathomation
B10	ESDIP
B12	MOTIC EUROPE SLU
B13	Lumea
B14	Huawei
B15	Ibex Medical Analytics
B16	Hamamatsu Photonics
B17	Nikon Europe
B18	KFBIO
B19	Fraunhofer IIS
B20	WSK Medical
B21	Argos
B22	CYTOMINE CORPORATION SA
B23	Celerato
B24	Paige
B25	Roche Diagnostics International
B26	Aiforia Technologies Plc
B27	3DHISTECH LTD
B29	Histomography
B30	Winmedic
B31	Proscia
B32	Alxmed
B33	Evident Europe GmbH
B35	Sectra Imaging IT Solutions AB
B36	Indica Labs
B37	PathAI
B38	Aiosyn
B39	Leica Microsistemas Lda.
B40	Epredia
B36	Indica Labs
B37	PathAI
B38	Aiosyn
B39	Leica Microsistemas Lda.
B40	Epredia

PRE-CONGRESS WORKSHOPS

June 5

10:00 - 12:00 Room Epsilon
IHE PaLM

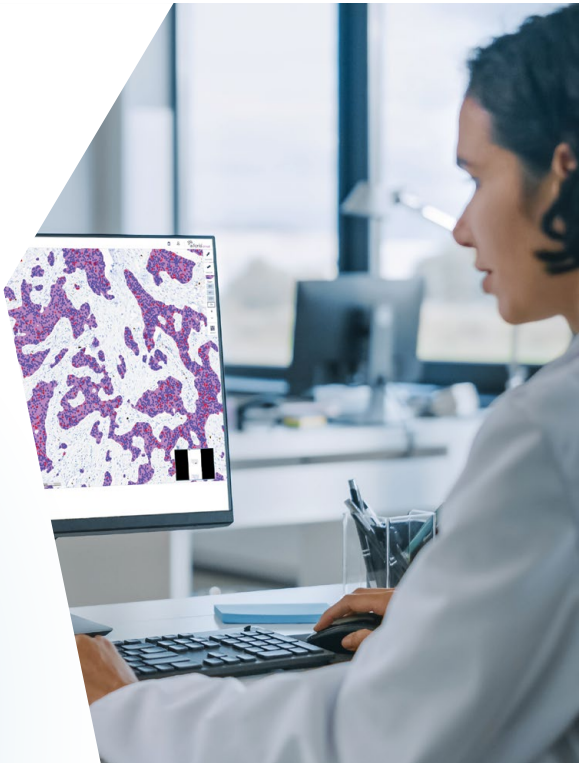
11:00 - 13:00 Room Lambda
EURASIA ACADEMY FOLLOW-UP

13:00 - 15:00 Room Epsilon
IHE PaLM

13:30 - 15:00 Room Lambda
3DHISTECH

15:00 - 19:00 Room Gamma
DICOM WG-26

15:30 - 17:00 Room Lambda
Hamamatsu



SOCIAL EVENT

All congress delegates, speakers, and exhibitors are invited to the ECDP2024 social event, which will take place on the evening of Friday, June 7th.

This year, the Social Event will take place in the courtyard of Vilnius Picture Gallery, a palace built in the early 17th century, that has been constantly expanded and reconstructed. In the 19th century, the palace became a characteristic building of the late classicism style. Today, it is one of the most interesting ensembles of this style in the city of Vilnius.

A seated dinner accompanied by live music awaits you!

Please note that a dedicated registration for the event is required in advance (available via the registration page). The ticket price is 50€/person. Participation is on a first-come, first-served basis (max. 400 guests).

Address: Didžioji g. 4, Vilnius, 01128 Vilniaus m. sav., Lithuania

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.ecdp2024.org

CONGRESS LANGUAGE
The official language of the congress will be English. Simultaneous translation will not be provided.

CONGRESS VENUE
Radisson Blu Hotel
Lietuva Konstitucijos av. 20
LT-09308 Vilnius, Lithuania

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 6th, 2024, from 17:30 to 20:30 in the Conference Center.

INDUSTRY EXHIBITION

The industry exhibition is located in the Conference Center.

Opening Hours

Thursday (06/06/2024)	09:00 – 20:00
	17:30 – 20:30 Poster Reception and Get Together
Friday (07/06/2024)	08:30 – 18:30
Saturday (08/06/2024)	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 5th, 2024.

POSTER RECEPTION
The Poster Reception will take place on Thursday, June 6th, 2024 from 17:30 until 20:30.

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.

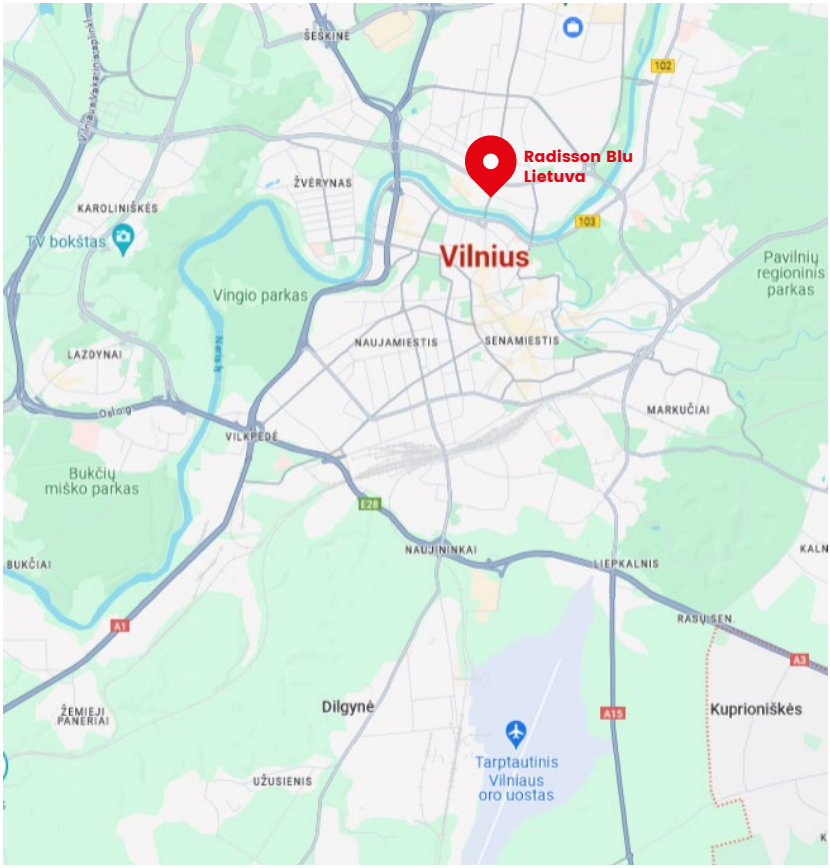
REGISTRATION DESK
The registration desk is located in the Exhibition Area. Registration is only valid if the complete payment of the congress fee as well as of other services booked has been made. Registration on-site is possible during the entire congress within the opening hours of the registration desk.

SOCIAL EVENT
Congress dinner
All congress delegates, speakers, and exhibitors are invited to the ECDP2024 social event which will take place on the evening of Friday, June 7th. Please see page 171 for details.

SMOKING
Smoking is strictly prohibited in the conference venue by law.

MAP

From Vilnius International Airport (LIT): distance: 9km; est. time: 10-12 minutes by car; taxi is approx., 15-20€. Public transit takes approx. 30-40 min., with several options, including buses and trains from the airport to the city center.



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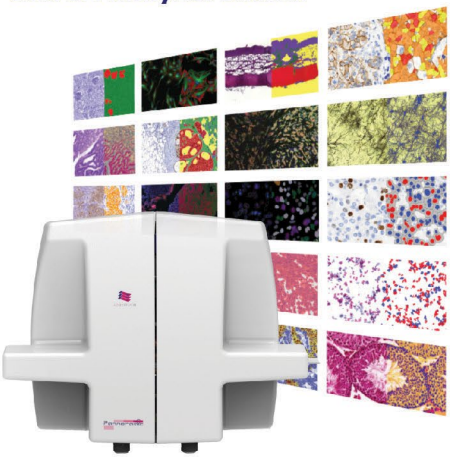

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Time of Printing
May 31, 2024.
All information regarding speakers and times is subject to change.

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