AFSDP
African society of digital pathology

SCIENTIFIC *Program*

28-30 APRIL 2026 | SOFITEL ROYAL BAY RESORT AGADIR, MOROCCO

MESSAGE FROM THE ORGANIZING COMMITTEE

The African Congress on Digital Pathology 2026 (AFCDP 2026) brings together pathologists, researchers, clinicians, and industry partners from across Africa and beyond, united by a shared commitment to advancing pathology through digital innovation.

Building on the success of its first edition, this congress reflects the growing momentum of digital pathology across the continent. As healthcare systems continue to evolve, digital tools are becoming essential to modern diagnostics, enabling improved accuracy, facilitating collaboration, and expanding access to specialized expertise.

Across Africa, these developments represent a meaningful opportunity to strengthen diagnostic capacity, support education and training, and promote research that addresses local priorities. AFCDP 2026 serves as a platform for scientific exchange, multidisciplinary dialogue, and the development of sustainable collaborations.

Through keynote lectures, scientific sessions, hands-on workshops, and industry engagement, this congress highlights current advances, addresses ongoing challenges, and explores future directions for digital pathology in Africa.

Welcome to the second edition of the African Congress on Digital Pathology 2026. We wish you a productive congress and an enjoyable experience.

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DAY 1 MORNING – WORKSHOPS, 28 APRIL 2026

Speaker / Orateur :
Soufiane Zakaria azdad

Session chair :
Achraf Miry

09:00-12:00

WORKSHOP A :
Preanalytical in Pathology: How can we use AI and Digital to improve the Workflow?

Mohammed VI University Hospital

Speaker / Orateur :
Camelia Radulescu

Session chair :
Hajar El Agouri

09:00-12:00

WORKSHOP B :
AI tools in breast cancer

UPSSA UNIVERSITY - PRIMAA

Speaker / Orateur :
Cecile Badoual

Session chair :
Hicham El Attar

09:00-12:00

WORKSHOP C :
HER2 AI Scoring

Sofitel Resort - AstraZeneca

Speaker / Orateur :
Julien Calderaro

Session chair :
Ferdaous Idlahcen

09:00-12:00

WORKSHOP D :
Introduction to computational pathology for pathologists and data scientists

UPSSA UNIVERSITY

Speaker / Orateur :
Aaron Han
Chhavi Chauhan

Session chair :
ANAS Belbachir

09:00-12:00

WORKSHOP E :
Quality Control in Digital Pathology

UPSSA UNIVERSITY

12:00-13:00

LUNCH

DAY 1 AFTERNOON - 28 APRIL 2026

13:00–14:00

REGISTRATION

SESSION A– Building the Foundations of Digital Pathology in Africa

Session Chairs: chakri Imad, Basma el sabaa, Rais Hanane

14:00–15:00

OPENING CEREMONY AND OPENING REMARKS

Speaker / Orateur :
Chege Joshua Kibera
Kenya

15:00–15:30

Keynote Lecture: The Future of Pathology in Africa

Speaker / Orateur :
Julien Calderaro
France

15:30 -16:00

AI in Pathology: Opportunities and Obstacles

Speaker / Orateur :
Essam Ezzat Ayad Ibrahim Doss
Egypt

16:00–16:30

Digital Pathology and AI In Africa: Egyptian Experience

Speaker / Orateur :
Bushra Mofadal
Sudan

16:30–17:00

Pathology Under Bombardment: Can Digital Pathology Sustain Diagnostic Services?

17:00–17:10

COFFEE BREAK

SESSION B– Building the Foundations of Digital Pathology in Africa

Session chairs: Israa laklouk, Dawit Solomon Demeke, Boujaheb Youssef

17:10–17:40

INDUSTRY SYMPOSIUM 1

HAMAMATSU

Speaker / Orateur :
Junya Fukuoka
Japan

17:40 -18:10

Global Trends In Digital Pathology: Lessons For Emerging Health Systems

Speaker / Orateur :
Norman Zerbe
Germany

18:10–18:40

Whole Slide Imaging Infrastructure & Readiness For Digital Transition: The Tutorial

Speakers / Orateurs :
Junya Fukuoka
El Attar Hicham
Norman Zerbe
Cecile Badoual

18:40 -19:10

Panel Discussion:
How Can Africa Leapfrog Into The Digital Pathology

19:10–19:50

INDUSTRY SYMPOSIUM 2

LEICA

DAY 2 - 29 APRIL 2026

SESSION C - Artificial Intelligence : from concept to clinical use

Session Chairs: Sanae abbaoui, Mehdi EL Faquiri, Imad Ziouziou

08: 00–08:30

Speaker / Orateur :
Joe Poh Sheng Yeong
Singapore

Plenary Lecture: Artificial Intelligence in Pathology:
From research to Clinical Impact

08:30–09:00

Speaker / Orateur :
Meriem Regragui
Morocco

Can Digital cytology and AI make thyroid cytology more accurate?

09:00–09:30

Speaker / Orateur :
Camelia Mihaela Radulescu
France

Digital cytology and AI in the field of bladder cancer diagnosis

09:30–10:00

Speaker / Orateur :
Andrey Bychkov
Japan

Cytology and AI
Overview of AI and Digital cytology for cervical cancer screening

10:00-10-15

COFFEE BREAK + POSTER SESSION

10:15–10:45

Speaker / Orateur :
Sabine Maria Leh
Norway

Applying Digital Pathology in Clinical Practice and Education: NonNeoplastic Disease as a Use Case

10:45-11:15

Speaker / Orateur :
Matthew G Hanna
USA

Digital pathology and AI as tool against infectious disease in Africa

SESSION D - Computational Pathology : How can we create an African movement

Session chairs: Karkouri Mehdi, Benhadda Hicham, Oqbani Kenza

11:15 -11:45

Speaker / Orateur :
Chhavi Chauhan
USA

Ethics in digital pathology and AI research

11:45 -12:15

Speaker / Orateur :
Nadieh Khalili
Netherlands

Computational Pathology: Benchmarks and community initiatives

12:15-12:45

INDUSTRY SYMPOSIUM 3

DIGIPATICS PROJECT: 5 MILLION SLIDES AND ARTIFICIAL INTELLIGENCE IN A NETWORK OF 8 HOSPITALS

By Jordi Temprana Salvador

3D HISTECH

12:45-13:00

COFFEE BREAK + POSTER SESSION

SESSION D - Computational Pathology : How can we create an African movement

Speaker / Orateur :
Hafsa Akebli
Morocco

13:00-13:30

Multimodal oncology Agents for clinical decision support

Speaker / Orateur :
Heather Couture
USA

13:00-13:30

Fondation model in pathology

13:30-14:00

INDUSTRY SYMPOSIUM 4

BREAKING BINARY: THE EVOLVING HER2 CLASSIFICATION AND REPORTING STANDARDS

ASTRAZENECA

14:30- 15:30

LUNCH BREAK

SESSION E - UNIFORMISATION and COLLABORATION IN THE DIGITAL PATHOLOGY FIELD AND AI

Session chairs: Zouhour Idder Fadoukhair, Ouadie Qamouss, Achraf Miry

15:30-16:00

INDUSTRY SYMPOSIUM 5

ANATOMOPATHOLOGIE AUTOUR DE L'INTELLIGENCE ARTIFICIELLE : RETOUR D'EXPÉRIENCE DE L'INSTITUT NATIONAL D'ONCOLOGIE DE RABAT»

By Khanoussi Basma

MASTERLAB

Speaker / Orateur :
Ekaterina Bazyleva
The Netherlandss

16:00–16:30

Interoperability in the Implementation of SSR In Pathology Practice International Approach

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Speaker / Orateur :
Paul Arnold Seegers
The Netherlandss

16:30–17:00

Introduction To ICCR Templates and SNOMED CT: An Inventory to Use

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Speaker / Orateur :
Matthew G Hanna
USA

17:00-17:30

Data Collection and Data Sharing as Global Project

Speaker / Orateur :
Fadaili Amal
Morocco

17:30–18:00

Synoptic reporting in oncopathology: morrocan experience

Speakers / Orateurs :
Norman Zerbe
Junya Fukuoka
Israa Laklouk
Joshua Kibera

18:00-18:30

Panel Discussion:
Digital Pathology Alliance:
a model of worldwide Collaboration

DAY 3 – 30 APRIL 2026

SESSION F : Education , GEN AI , and Future Vision

Session chairs: Bouchra amaoui, Khabal youssef, Mir Youssef

08:30-09:00

Speaker / Orateur :
İlknur Türkmen
Turkey

Apps development during live dp implementation - challenges and advantages

09:00-09:30

Speaker / Orateur :
Ehsan Ullah
New Zealand

Practical Guide for Pathologists to use Generative AI

09:30-09:45

COFFEE BREAK + POSTER SESSION

09:45-10:15

Speaker / Orateur :
Daniel Gomes Pinto
Portugal

Gen AI applications and Benchmarking in Pathology

DAY 3 – 30 APRIL 2026

SESSION F : Education , GEN AI , and Future Vision

Speakers / Orateurs :
Andrey Bichkov
Sanae Abbaoui
Nadya Layachi
Rémi Millant

10:15-10:45

Panel discussion:
Industry-Public-Private Partnerships and Funding Models for Digital Pathology in Africa

Speaker / Orateur :
Basma El Sabaa
Egypt

10:45-11:15

Closing Keynote:
Charting the Roadmap for Digital Pathology in Africa 2025–2030: recommendations of AFSDP

Speakers / Orateurs :
El Attar Hicham
Norman Zerbe
Junya Fukuoka

11:15-11:45

Closing Ceremony
PRIZE & MOU Signature
Certificate Distribution

Feasibility of a competency-based Artificial Intelligence in Medicine Elective Course integrating digital pathology tools: A Prospective two-cycle evaluation at an Egyptian Medical School

Khadiga Mohamed Ali1, Khaled Ahmed Hussein2, Gehad Ahmad Saleh3, Lojaen Shalabi2, Ahmed Negm4, and Mohammed H. El Fahar5
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2 Mansoura Manchester Program, Faculty of Medicine, Mansoura University, Mansoura, Egypt
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Abstract:

Background

Artificial intelligence (AI) is becoming more integrated into clinical diagnostics, especially in the fields of digital pathology and radiology. However, formal AI training in undergraduate medical education (UGME) is still rare worldwide and almost nonexistent in African medical curricula. Ongoing challenges to implementation include curricular overload, infrastructure limitations and faculty readiness, especially in low- and middle-income settings (LMIC). It is still unclear whether open-source digital pathology tools can be used to deliver and continuously enhance a structured competency-based AI elective in a resource-constrained environment.

Objectives

The aim is to evaluate the feasibility, student satisfaction and iterative curricular improvement of an AI in Medicine elective course that integrates digital pathology and radiology tools, offered to undergraduate medical students within Mansoura Manchester Program for Medical Education at Mansoura Faculty of Medicine, Egypt.

Methods

A prospective educational intervention study was conducted over two-cycle across consecutive academic years (2024, cohort 1, n=45 students and 2025, cohort 2 of 62 students). The 20-hour competency-based curriculum included lectures on AI fundamentals and ethics, along with practical workshops using open-source software including Motic (virtual microscopy), Sedeen and QuPath (whole slide image (WSI) annotation in pathology), and RadiAnt DICOM viewer (medical image segmentation in radiology). Group assignments were structured around WSI analysis in pathology and radiology image segmentation tasks. Student satisfaction and perceived learning outcomes were assessed through anonymous Likert-scale surveys (5 points scale) covering content relevance, practical applicability and instructor effectiveness. Between cohort satisfaction scores were compared using the Mann-Whitney U test. Qualitative feedback was collected through open-ended survey questions. Pass rates and assessment scores were recorded. Curricular modifications for cohort 2 were guided by cohort 1 feedback.

Results

Course completion rates were consistently high across both cohorts with cohort 1 achieving 97.8% (44/45) and cohort 2 reaching 98.4%, (61/62). Mean overall satisfaction scores improved significantly from 3.92 ± 1.14 in cohort 1 to 4.53 ± 0.75 in cohort 2. All seven survey domains demonstrated statistically significant improvement between cohorts (all $p < 0.001$), including teaching materials (3.95 ± 1.02 compared to 4.55 ± 0.67), course activities and assessment (4.03 ± 1.05 versus 4.64 ± 0.63), instructor effectiveness (4 ± 1.14 against 4.59 ± 0.73), course introduction (3.96 ± 1.1 versus 4.57 ± 0.6), online teaching (3.74 ± 1.34 compared to 4.31 ± 0.99) and overall evaluation (3.82 ± 1.2 versus 4.33 ± 0.91). Feedback from cohort 1 highlighted challenges some students faced in engaging during online sessions leading to curriculum adjustments that included more hands-on sessions for cohort 2 which was associated with the observed satisfaction gains.

Conclusion

A structured competency-based AI elective course that integrates open-source digital pathology and radiology tools can be effectively implemented and continuously refined in a resource-limited LMIC medical school setting, achieving high completion rates and increasing student satisfaction. This two-cycle experience offers a replicable model for institutions in Africa and other low-resource settings to incorporate foundational AI skills, including digital pathology literacy into UGME curricula. Prospective multicenter studies with validated AI competency assessments and longer-term outcome tracking are needed to confirm the educational effectiveness and generalizability of this approach.

Keywords: Artificial intelligence; Undergraduate medical students, Curriculum, Digital Pathology, competency-based education

A Deep Learning-Based Framework for Predicting Spatial Transcriptomic Clusters from Digital Histopathology in Glioblastoma

Anass Oukhdouch*, Sara El Attar, Basma Zinbi, Souad Sellami & Hanane Rais

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Anatomic Pathology Department, University Hospital Mohammed VI, Marrakech, Morocco.
Bio-Pathology unity, Clinical Research Centre (CRC), University Hospital Mohammed VI, Marrakech, Morocco.

Background

Glioblastoma (GBM) is the most aggressive primary brain tumor, characterized by profound intra-tumoral heterogeneity. Spatial transcriptomics enables high-resolution molecular profiling of cancer niches, but remains expensive. Whether routine hematoxylin and eosin (H&E) histopathology encodes sufficient morphological information (e.g necrosis, proliferation, MVP, mitosis.) to predict spatial molecular organization remains unknown.

Objective

To develop and proof-of-concept a deep learning-based framework capable of predicting spatial transcriptomic clusters from H&E whole-slide image (WSI) patches in glioblastoma, bridging routine digital pathology (DP) with molecular spatial data.

Methods

A human GBM Visium spatial transcriptomic dataset (Parent_Visium_Human_Glioblastoma) was processed using Scanpy. Following quality control (2,976 tissue spots retained), normalization, and selection of 3,000 highly variable genes (HVGs), spots were clustered using the Leiden algorithm (resolution=0.5), yielding 10 spatially coherent molecular clusters. For each tissue spot, a 224×224-pixel patch was extracted from the corresponding H&E image using spot pixel coordinates and hires scale factors (scale=0.150). A ResNet18 convolutional neural network (CNN) was fine-tuned to predict cluster identity from patch morphology. Training employed 5-fold stratified cross-validation with weighted cross-entropy loss to address class imbalance (cluster sizes: 66-656 spots). Model explainability was assessed using Gradient-weighted Class Activation Mapping (GradCAM) to identify histo-morphological features driving cluster predictions.

Results

The ResNet18 model achieved a mean weighted F1-score of 0.774 ± 0.009 and overall accuracy of 77.4% across 5-fold cross-validation, significantly exceeding chance-level performance. Across all folds, training and validation curves showed steady convergence without overfitting (range: 0.762-0.786), confirming robust generalization. Spatial reconstruction of ResNet18 predictions showed a remarkable agreement with transcriptomic clustering ground truth, with 2,362 of 2,976 spots (79.4%) correctly assigned. Prediction errors were predominantly localized to inter-cluster boundary zones, in line with transitional molecular gradients in GBM that are known to exist. Per-cluster analysis revealed heterogeneous predictability: clusters C7 and C9 achieved F1-scores of 0.97 and 0.95 respectively with prediction confidence of 1.00, indicating niches that are morphologically stereotyped. Transitional clusters (C2, C3: F1=0.61-0.62) showed reciprocal confusion, reflecting morphological overlap at molecular boundaries. Pathologically coherent attention patterns were confirmed by GradCAM explainability analysis: proliferative clusters emphasized dense nuclear areas, necrotic zones displayed attention on acellular regions, and high-performing clusters (C7, C9) displayed highly consistent stereotyped attention maps that might correspond to pseudopalisading necrosis.

Conclusion

This proof-of-concept study shows that deep learning applied to standard H&E coloration can accurately predict the spatial transcriptomic molecular organization in GBM (F1=0.774, accuracy=77.4%). GradCAM analysis confirmed that the model learned pathological and morphological features. These findings suggest that molecular spatial heterogeneity in GBM is partially encoded in histo-morphological features detectable by CNN, potentially enabling molecular spatial inference from routine H&E slides without expensive transcriptomic assays. External validation and gene-level biological annotation of predicted clusters are planned as future work.

Keywords

Glioblastoma, Spatial transcriptomics, Deep learning, Digital pathology, ResNet18, GradCAM, Tumor heterogeneity.

References

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Prédiction de la mobilisation des cellules souches hématopoïétiques dans le cadre de l'autogreffe : modélisation par Machine Learning

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Abstract

La greffe de cellules souches hématopoïétiques constitue une option thérapeutique majeure pour de nombreuses pathologies hématologiques et non hématologiques. Le sang périphérique mobilisé est désormais la principale source de cellules souches, obtenues après stimulation par facteurs de croissance granulocytaires puis collecte par aphérèse. Toutefois, cette procédure reste longue, coûteuse et parfois contraignante, surtout lorsque plusieurs séances sont nécessaires, avec un impact sur le confort des patients et le rendement cellulaire.

Dans ce contexte, notre étude exploite les données démographiques, cliniques et biologiques de patients mobilisés par filgrastim pour autogreffe au centre de médecine régénérative du CHU Mohammed VI de Marrakech afin de développer un modèle basé sur l'apprentissage automatique(Machine Learning) capable de prédire l'état de mobilisation. L'objectif est d'anticiper les performances de collecte pour optimiser les stratégies de mobilisation et améliorer l'efficacité globale de l'autogreffe.

Ischemic Stroke Diagnosis: Machine Learning Approach Utilizing Whole Slide Thrombectomy Pathology Images.

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2: Pathology department, faculty of medicine, Alexandria university, Egypt

Background: Cerebral strokes are the second most common cause of death globally. Ischemic strokes are the predominant subtype, and it is classified according to its etiology into cardioembolic (CE) or large artery atherosclerosis (LAA). This classification is crucial for effective treatment and prevention of recurrence.

Objective: the diagnosis of ischemic stroke etiology by analysing the cellular components of thrombectomy specimens using classical machine learning approach.

Material and Methods: machine learning approach using XGBoost was applied on a dataset of whole-slide digital pathology images of thrombectomy specimens. High-resolution TIFF images of thrombectomy specimens (547 images associated with CE and 207 images associated with LAA etiology) were downloaded from the Mayo Clinic - STRIPAI Kaggle competition. They were stained with Martius Scarlet Blue (MSB).

Results: MSB stain was able to stain RBCs, WBCs and fibrin/platelets in yellow, purple and red/pink colours respectively. The proposed model was able to extract and analyse different colours of cellular components of thrombectomy specimen in images of both LAA and CE groups. LAA thrombi showed more RBCs and less WBCS, fibrins and platelets than CE. The proposed model achieved accuracy of 97% and a loss of 0.66588 in differentiating CE from LAA ischemic strokes.

Conclusion: the proposed machine learning approach was able to identify the etiology of ischemic strokes by analysing the cellular component of thrombectomy specimen. It came in fifth place on the leaderboard of Kaggle's competition private dataset.

Figure:

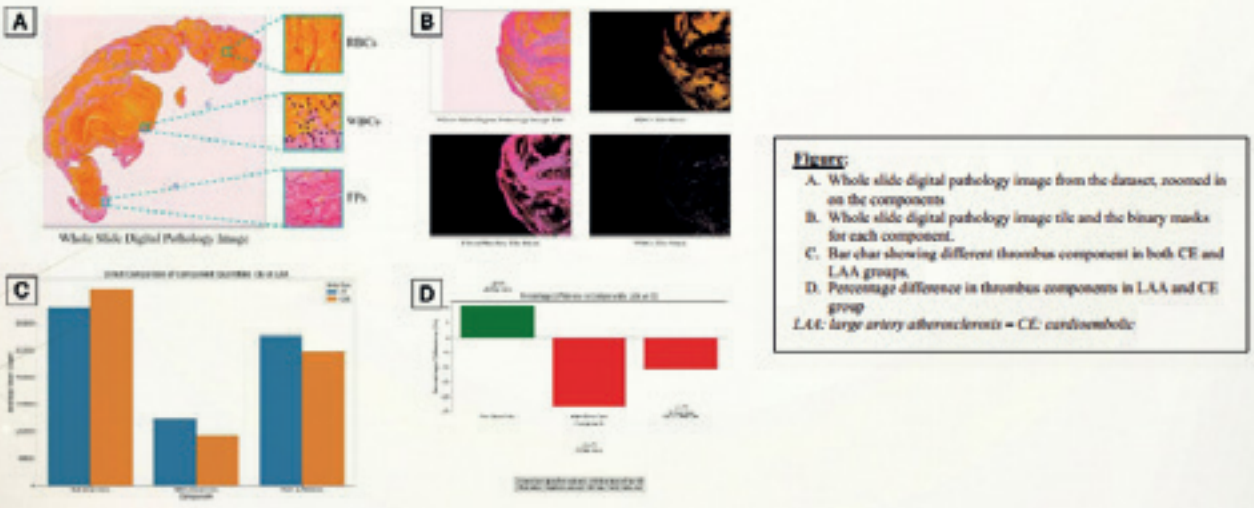

Figure:

A. Whole slide digital pathology image from the dataset, zoomed in on the components

B. Whole slide digital pathology image tile and the binary masks for each component.

C. Bar char showing different thrombus component in both CE and LAA groups.

D. Percentage difference in thrombus components in LAA and CE group

LAA: large artery atherosclerosis - CE: cardioembolic

Digital Pathology Assisted Semi-Automated Immunohistochemical Scoring of MMR and p53 in Endometrial Carcinoma: Interobserver Agreement and Clinicopathologic Correlation in a Resource-Limited Setting

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Background:

Molecular classification of endometrial carcinoma (EC), using immunohistochemistry (IHC) for mismatch repair (MMR) proteins and p53 offers a feasible surrogate for comprehensive genomic profiling in resource-limited settings. However, manual IHC scoring is subject to interobserver variability that may affect diagnostic accuracy. Digital Pathology assisted workflows using open-source QuPath software have shown reproducible IHC scoring in other tumor types but their performance for MMR/p53 interpretation in EC has not been validated in low- and middle-income country (LMIC) populations.

Methods:

We conducted a retrospective analysis of 132 consecutive patients with primary EC who underwent surgical resection from 2018 to 2021, examining MMR status using four antibody IHC panel (MLH1, PMS2, MSH2, MSH6) and p53 on tissue microarrays (TMA). Whole slide images were independently scored by two pathologists using conventional visual assessment and QuPath assisted semi-automated detection with pathologist validation (Figure 1). Interobserver agreement was assessed using Cohen's **k**.

Results:

MMR deficiency (MMR-d) was found in 28% (37/132) of cases mainly characterized by the combined loss of MLH1/PMS2 (81.1%). The p53 abnormal (p53abn) group was detected in 27.3% (36/132 cases). QuPath-assisted scoring significantly improved interobserver agreement for MMR (**k** = 0.89; 95% CI: 0.8-0.95; observed agreement 94.7%) compared with manual visual scoring (**k** =0.69; 95% CI: 0.55-0.8; observed agreement 88.6%). For p53, digital assisted k reached 0.96 (95% CI: 0.9-1; observed agreement 98.5%) versus manual k of 0.87 (95% CI: 0.8-0.96; observed agreement 94.7%). The p53abn subgroup showed the highest rate of advanced stage disease
(52.8%), lymph node metastasis (52.6%), and mortality (40.7%) compared to MMR-proficient/p53 wild type group (8.5%; 9.5%; and 5.8% respectively) ($p < 0.001$ for all).

Conclusion

The use of QuPath-assisted semi-automated IHC scoring enhances interobserver agreement for MMR and p53 assessment in EC and substantially exceeding manual visual scoring. This open source digital pathology workflow represents a scalable cost-effective approach for implementing IHC based molecular classification of EC in resource-constrained diagnostic settings, though multi-center validation with larger cohorts is warranted.

Keywords: Endometrial carcinoma; Digital pathology, Tissue microarray; interobserver agreement; resource-limited settings; immunohistochemistry.

MM-BCI 2026 enables population-adapted precision oncology in Morocco through MedGemma 1.5, MONAI 2.0, multimodal transformer fusion, and CURATE.AI v2 integration across TCGA-BRCA v2.0, CMMD, BreastEdge US, and UNI Pathology datasets.

Abdellah Liamani

CHU Mohammed IV Agadir

Abstract

Title: MM-BCI 2026: MedGemma 1.5, MONAI 2.0, Multimodal Transformer Fusion, and CURATE.AI v2 for Population-Adapted Breast Cancer Precision Oncology in Morocco

Background: Breast cancer constitutes Morocco's leading female cancer mortality cause (13.7/100k incidence), exacerbated by resource constraints, small local cohorts (<1k cases), and population-specific genetic factors (BRCA1 mutations 19.7%, CYP2C19*2 poor metabolizers 15%). Static protocols yield suboptimal pathological complete response (pCR) rates (35-65%) with Grade ≥3 toxicity approaching 40%. 2026 biomedical foundation models enable unprecedented LMIC transfer learning from global datasets to localized edge deployment.

Methods: MM-BCI 2026 integrates NVIDIA MONAI 2.0 Auto3DSeg for label-free US/photoacoustic segmentation (2mm vascular resolution) across TCGA-BRCA v2.0 (1,500+ AI-annotated cases), CMMD (3,728 mammograms+complaints), BreastEdge US (2k edge-optimized), and UNI Pathology 100M WSI. MedGemma 1.5 SigLIP provides clinical reasoning («IDC, Ki67 25%, recommend TCH») across radiology+clinical text. Hierarchical multimodal transformer fusion with crossmodal attention aligns five domains: radiology, pathology, genomics, longitudinal clinical data (CA15-3/ctDNA), pharmacogenomics. UNI Pathology foundation model enables zero-shot WSI subtyping (IDC vs ILC, F1 0.92). CURATE.AI v2 models individualized dose-response curves from 3-point biomarker trajectories. LoRA/PEFT fine-tuning adapts CHU Agadir/Casablanca EHR via FHIR, incorporating CYP2C19*2 pharmacogenetics and photoacoustic perfusion. BreastEdge AI pipeline ensures NVIDIA Jetson Orin edge deployment.

Expected Results: Multimodal transformer fusion achieves external AUC 0.96-0.98 subtype classification (+8% vs unimodal), pCR prediction AUC 0.92-0.93 (temporal modeling +10% vs static). NPV >97% early detection via MedGemma reasoning. CURATE.AI reduces Grade ≥3 toxicity 30% (doxorubicin 7558mg/m², neutropenia 40%12%). Data efficiency: 500 Moroccan patients + 10k MONAI BundleGen trajectories vs 10k traditional. SHAP analysis identifies ctDNA trajectory (42%

importance), vascular perfusion (28%) as primary pCR drivers. TCGA-IDC v2.0 validation confirms North African dense breast generalizability.

Conclusions: MM-BCI 2026 establishes North Africa's first edge-deployable precision oncology platform through MedGemma clinical reasoning, MONAI production deployment, transformer fusion, and CURATE.AI dynamic dosing. Population adaptation addresses Morocco's unique genetic landscape while reducing ineffective neoadjuvant exposure 25% and severe toxicity 30%. Continuous Agadir CHU learning creates self-improving clinical decision support, positioning Morocco as regional AI oncology leader.

CasePathTangier: Development of a Web-Based Educational Platform for Sharing Anonymized Pathology Cases Organized by Organ System

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Introduction

Case-based learning represents a fundamental pillar in pathology training. However, access to structured and ethically compliant educational platforms adapted to local contexts remains limited, particularly in resource-constrained environments. Therefore, there is a need for simple, secure, and pedagogically effective tools that facilitate the sharing of anonymized pathology cases for educational purposes.

Objective

To develop and evaluate a functional prototype of a web-based educational platform, CasePathTangier (accessible at https://casepathtangier-production.vercel.app/), dedicated to the structured sharing of anonymized pathology cases organized by organ system and supported by representative illustrative histological images.

Methods

An educational web platform (CasePathTangier) was developed and deployed online at https://casepathtangier-production.vercel.app/ using a lightweight architecture (Python/Django, SQLite, Bootstrap). Clinical cases were structured according to a WHO-style subspecialty classification of pathology. Only validated cases were made publicly accessible.

Each organ category was illustrated by a single representative, non-diagnostic H&E histological image, facilitating visual recognition and atlas-style learning. Strict ethical constraints were applied, including the removal of all identifiable patient information and the display of an explicit educational disclaimer. The platform was locally tested using several anonymized pathology cases.

Results

CasePathTangier provides an intuitive organ-based navigation system, allowing users to explore validated pathology cases accompanied by illustrative histological images. The interface emphasizes clarity, readability, and educational value while avoiding unnecessary technical complexity.

The platform, accessible online at https://casepathtangier-production.vercel.app/, demonstrates the feasibility of a low-cost, ethically compliant educational tool specifically designed for pathology training, with preliminary feedback indicating good usability and pedagogical value.

Conclusion

CasePathTangier demonstrates that a simple, organ-based web platform built on strict ethical principles can serve as an effective support for pathology education through the structured sharing of cases. This prototype may serve as a foundation for future academic, institutional, or multicenter educational initiatives in digital pathology education.

Keywords

Pathology; Medical Education; Case-Based Learning; Digital Pathology; Histopathology; Educational Platform

Transforming Diagnosis into Digital Pathology in Senegal: Microscopy, Scanning, and AI-A Preliminary Experience at the Laboratory of Pathological Anatomy and Cytology at Cheikh Anta Diop University in Dakar

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Introduction

Digital pathology improves the accuracy and speed of histopathological diagnosis and paves the way for the integration of artificial intelligence.
In resource-limited countries such as Senegal, its implementation remains constrained by a shortage of pathologists and the limitations of conventional optical microscopy.
The digitization of slides is a key step toward modernizing practices and building databases.

The objective is to describe the Senegalese experience in digital pathology and assess the feasibility of establishing a structured database for future artificial intelligence applications.

Materials and Methods

From August 2022 to December 2025, we used the Motic scanner in the Department of Anatomical and Cytopathology at the Faculty of Medicine and Pharmacy of Cheikh Anta Diop University in Dakar. As a university center, both experienced pathologists and pathologists in training were involved.
The study had two components: evaluating the concordance between digital reading and optical microscopy, and establishing a database for future algorithmic training. The data collection began with renal and cervical biopsies.
The renal biopsies consisted solely of normal cases without glomerular, tubulointerstitial, or vascular involvement. The cervical biopsies included inflammatory lesions, low- and high-grade dysplasias, and invasive carcinomas.
The digitized slides were independently reviewed under an optical microscope by senior pathologists to assess diagnostic concordance.

Results

A total of 5,134 cases were digitized, including 97% histology slides and 3% cytology slides. Among these, 824 cervical biopsies and 305 renal biopsies were analyzed.
The diagnostic concordance between the reading of digital slides and conventional optical microscopy was approximately 95%. The diagnostic turnaround time was reduced to 4–12 days, supporting the reliability of digital pathology.
A structured digital database was created from the renal and cervical biopsies according to predefined criteria.
This database represents a preliminary step toward future applications of artificial intelligence and the development of a dedicated platform.
Digital slide review also facilitated training, collaboration among pathologists, and diagnostic consensus.

Conclusion

This study demonstrates the feasibility of implementing digital pathology in our setting. The satisfactory concordance with conventional light microscopy confirms its reliability. The development of a structured database represents a key step toward the future integration of artificial intelligence in anatomic pathology.

Keywords

Scanning, Artificial Intelligence, Pathology.

Smart Diagnostic System Based Detection and Semantic Segmentation of Ganglion Cells in Gastrointestinal Histologic Sections

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Background: The presence of ganglion cells within the myenteric and submucosal plexuses is the histopathological hallmark of a functional Enteric Nervous System (ENS). Their absence, known as aganglionosis, is the definitive criterion for diagnosing Hirschsprung Disease (HSCR), a potentially fatal congenital disorder. Current diagnostic practice relies on the manual microscopic examination of hematoxylin and eosin (H&E) stained digestive biopsies to identify ganglion cells. This process is notoriously challenging due to the very low density of ganglion cells, their variable morphology, and significant inter-observer variability. The diagnostic dilemma is particularly acute in transition zones or in cases of hypoganglionosis. Consequently, there is a great need for an objective, accurate, and automated system to assist in the detection and quantification of ganglion cells to standardize diagnostics and reduce errors and time.

Materials and Methods: We developed a Multiclass Semantic Segmentation System based DeepLearning specifically designed to detect and characterize ganglion cells in gastrointestinal sections. The model was trained using our images dataset of cross section gastrointestinal specimen with ganglion cells spread in a large background of myenteric and submucosal tissues. We meticulously annotated the Region of Interest ROI in three Classes (Cytoplasm, Nucleus, Nucleolus) and Background. As we are dealing with very severe Imbalanced Dataset: 98% of pixels represent Background, and only 2% represent the ROI, we propose first to overcome this problem by generating a balanced Dataset and using data augmentation for enrichment. Different variants based U-Net architecture were experimented with different configuration parameters for adopting the best solution.

Results: Our proposed solution for Semantic Segmentation can in one hand detect the presence of plexus with F1-score ≈ 0.93, and on the second hand, extract the three regions of ganglion cells including Nucleoli, Nucleus and Cytoplasm with high precision even dealing with severe imbalanced Dataset with mDices=0.89. In fact, the proposed solution delivers groundbreaking performance in the automated analysis of myenteric plexus ganglion cells. It establishes new benchmarks for both plexus detection accuracy and multi-region cell segmentation precision, with results that far exceed the validation standards required for proof-of-concept evaluations in this domain.

Conclusion: We have successfully developed and validated a Smart System for automated detection and segmentation of ganglion cells in gastrointestinal histologic sections. This Smart Tool serves as a powerful decision-support system for histologists, enhancing the accuracy, efficiency, and standardization of HSCR diagnosis. By objectively quantifying ganglion cells and flagging suspicious areas of aganglionosis, it has the potential to reduce significantly diagnostic delays, efforts and errors.

PathoLearn: An AI-Assisted Interactive Platform for Learning General Pathology Using Quizzes, Flashcards and Clinical Cases

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Background

Teaching general pathology traditionally relies on lectures and static learning materials. However, medical students and pathology residents increasingly benefit from interactive and self-directed learning tools. Advances in artificial intelligence (AI) offer new opportunities to transform traditional educational resources into dynamic learning experiences. We developed PathoLearn (https://patholearn-app.vercel.app), an interactive educational platform designed to facilitate the learning and revision of general pathology through quizzes, flashcards and clinical cases supported by an AI assistant.

Methods

Educational content was extracted from structured pathology teaching materials and converted into a digital knowledge database including modules, chapters, multiple-choice questions, flashcards and clinical cases. The platform is organized into six main modules: elementary lesions, pathology techniques, inflammatory pathology, vascular pathology, tumor pathology and metabolic/storage disorders. The platform is built using a modern web architecture (Next.js and Supabase) utilizing Large Language Models (LLM) and RetrievalAugmented Generation (RAG) to ensure accurate and context-aware AI-assisted responses. An integrated AI assistant allows users to explore concepts, generate quizzes and simulate clinical cases interactively.

Results

The database currently hosts over 500 validated educational items, including more than 200 multiple-choice questions and over 50 structured clinical scenarios covering the six core pathology modules. The platform enables students and residents to review pathology concepts interactively and test their knowledge through dynamically generated quizzes. The AI assistant can generate additional educational material based on the structured database, including flashcards, targeted revision questions and clinical case simulations. Preliminary user testing among pathology residents demonstrated high engagement and positive feedback regarding usability and educational value.

Conclusion

PathoLearn illustrates how AI-assisted educational platforms can enhance modern pathology education. By integrating structured databases, automated quiz generation and AI-guided clinical case simulation, such systems may improve engagement, facilitate self-directed learning and support the teaching of general pathology.

Keywords

Pathology education; Artificial intelligence; Medical education; Interactive learning; Digital pathology training.

BeePath: A Web Platform for Collaborative and Assistive Computational Pathology in Low-Resource Settings

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Abstract

Background: Access to pathology expertise remains uneven in many African settings, with additional challenges related to training opportunities, case sharing, and the practical deployment of digital pathology tools. Although whole-slide imaging and artificial intelligence (AI) offer important opportunities to strengthen diagnostic workflows, available solutions are often fragmented and do not adequately combine slide review, annotation, collaboration, and education within a single accessible environment. Existing digital pathology platforms have established the feasibility of web-based WSI management, visualization, annotation, and collaborative analysis [1,2,3]. However, there remains a need for integrated platforms adapted to resource-variable settings, where browser accessibility, low-bandwidth operation, distributed expertise, and educational use are especially important. We aimed to develop BeePath, a web-based computational pathology workspace designed to support diagnostic review, pathology training, and AI-assisted analysis in such settings.

Methods: We developed a browser-based computational pathology platform designed to support diagnostic review, collaborative training, and AI-assisted analysis of whole slide images (WSIs) in low-resource settings. The system integrates a browser-based viewer enabling multi-resolution visualization and interactive annotation of WSIs, alongside collaborative tools allowing multiple users to review and label regions of interest. A backend pipeline performs patch-based processing of WSIs and incorporates state-of-the-art deep learning models for tissue detection, region classification, and assistive segmentation. AI-generated predictions are visualized as overlays to support expert interpretation and accelerate annotation workflows. The platform architecture emphasizes low-bandwidth optimization, scalable storage, and modular AI integration.

Results: The platform integrates core components of the digital pathology workflow within a single web environment, including WSI visualization, annotation, AI-assisted analysis, and collaborative case review. This design is intended to facilitate remote consultation, improve access to expert input, and support human-in-the-loop review of AI-generated outputs rather than isolated algorithmic use. Its educational functions also provide a practical framework for case-based teaching and supervision using digital slides. By reducing dependence on multiple disconnected tools and supporting access through the browser, the system is particularly relevant to settings where infrastructure, specialist availability, and training resources may be limited.

Conclusion: A unified web-based digital pathology workspace may help strengthen diagnostic support, expand access to pathology education, and enable responsible integration of AI into pathology practice in Africa. Such platforms may be especially valuable in resource-variable settings where collaboration, remote expertise, and scalable training are essential to improving pathology services.

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Quantitative and Digital Phenotyping of the Tumor Microenvironment in Non-Small Cell Lung Cancer: Multiplex Immunofluorescence and Digital Pathology Using QuPath

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Introduction: The tumor microenvironment (TME) plays a pivotal role in tumor progression and therapeutic response, particularly in the context of immunotherapy. In non-small cell lung cancer (NSCLC), conventional assessment of immune infiltrates by immunohistochemistry remains limited due to its semi-quantitative nature and interobserver variability. The advent of digital pathology and advanced image analysis tools now enables objective and reproducible quantification of cellular populations within their spatial context. Furthermore, multiplex immunofluorescence (mIF) technologies, when integrated with digital pathology, allow the simultaneous detection of multiple markers within a single tissue section, thereby enabling a comprehensive and spatially resolved characterization of the tumor cellular landscape. The aim of this study was to quantitatively characterize the TME in NSCLC samples using a multiparametric phenotyping approach based on multiplex immunofluorescence and digital image analysis with QuPath.

Methods: We conducted a retrospective study across two centers: the Department of Pathology at Ibn Rochd University Hospital (Casablanca) and the Thoracic Oncology Research Laboratory at the Léon Bérard Cancer Research Center (Lyon), including patients diagnosed with NSCLC.

Formalin-fixed paraffin-embedded (FFPE) samples were analyzed using multiplex immunofluorescence (mIF) with a panel of markers including CD3 (T lymphocytes), CD8 (cytotoxic T lymphocytes), FOXP3 (regulatory T lymphocytes), CD57 (natural killer cells), cleaved Caspase-3 (apoptosis), and CK1/3 (tumor epithelial cells). Slides were digitized using a multispectral fluorescence scanner and subsequently analyzed with QuPath, enabling automated cell detection, tumor–stroma segmentation, and phenotypic classification of cellular populations.

Results and Discussion:

Multiplex immunofluorescence (multi-IF) image analysis performed using QuPath enabled the identification of five phenotypic subpopulations: T lymphocytes (CD3: 5458 cells), cytotoxic T lymphocytes (CD8+: 3346 cells), regulatory T lymphocytes (FOXP3+: 1672 cells), mature NK cells (CD57+: 687 cells), and apoptotic cells of both tumor and immune origin (Caspase- 3+: 5312 cells).

Comparative analysis of tissue compartments revealed a higher density of CD8+ T lymphocytes and regulatory T cells within the tumor compartment compared to the stroma (CD8+: 1722 vs. 1624 cells, $p = 0.066$; Treg: 1647 vs. 25 cells, $p < 0.001$). This distribution suggests a tumor microenvironment characterized by a pronounced immunosuppressive component.

In addition, CD57+ cells, corresponding to differentiated cytotoxic effectors, exhibited a heterogeneous distribution within lymphocytic infiltrates. Analysis of apoptosis further demonstrated that Caspase-3+ cells were predominantly of immune origin compared to CK1/3+ tumor cells (2477 vs 124 cells; $p < 0.001$), indicating a predominance of immune cell apoptosis within the tumor microenvironment.

Conclusion:

This study demonstrates the feasibility and robustness of multiplex immunofluorescence combined with digital analysis using QuPath for an objective quantitative and spatial characterization of the TME in NSCLC. The findings highlight a high density of both cytotoxic (CD8+) and regulatory (FOXP3+) T lymphocytes within the tumor compartment, suggesting a potentially immunosuppressive profile, along with a predominance of apoptosis among immune cells. This multiparametric approach surpasses conventional methods in terms of reproducibility and precision, paving the way for the identification of predictive biomarkers of therapeutic response, particularly in the context of immunotherapy.

Keywords: Non-small cell lung cancer (NSCLC); Multiplex immunofluorescence (mIF); Digital pathology (QuPath); Image analysis; Cellular phenotyping; Digital quantification.

Spatial analysis of the tumor microenvironment in non-small cell lung cancer: intercellular distances and cluster organization as predictive biomarkers using multiplex immunofluorescence and digital pathology with QuPath

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Introduction:

Beyond simple quantification of cell populations, analysis of the spatial organization of the tumor microenvironment (TME) is emerging as a key factor in understanding mechanisms underlying responses to anticancer therapies. Evaluating intercellular distances, neighborhood interactions, and their organization into clusters provides a more precise understanding of immune dynamics within non-small cell lung carcinoma (NSCLC). In this study, we aimed to analyze spatial relationships between tumor and immune cells using multiplex immunofluorescence (mIF) images and digital pathology tools.

Methods:

We conducted a retrospective study at two centers: the Department of Pathology at Ibn Rochd University Hospital (Casablanca) and the Thoracic Oncology Research Laboratory at the Léon Bérard Cancer Research Center (Lyon), including patients with NSCLC. FFPE samples were analyzed using mIF with a panel of markers: CD3 (T lymphocytes), CD8 (cytotoxic T lymphocytes), FOXP3 (regulatory T lymphocytes), CD57 (NK cells), cleaved Caspase-3 (apoptosis), and CK1/3 (tumor epithelial cells). Slides were scanned using a multispectral fluorescence scanner and analyzed with QuPath. Intercellular distances were calculated in 2D between cellular centroids (nearest neighbor distances, µm) for pairs including CD8+-CK+, FOXP3+-Casp3+, and CD57+-Casp3+.
Cluster analysis was performed using density heatmaps and spatial clustering algorithms. Results were then correlated with response to chemotherapy.

Results & Discussion:

Intercellular distance analysis revealed reduced proximity between CD8+ T lymphocytes and CK+ tumor cells in responders compared to non-responders (45 vs. 120 µm, $p < 0.001$), suggesting potential direct interactions between these populations .
Furthermore, CD57+ cells were frequently located within 25 µm of apoptotic Caspase-3+ cells, indicating NK cell involvement in cytotoxic activity (Figure 2).
Cluster analysis revealed FOXP3+ regulatory T cell groupings associated with tumor recurrence ($p < 0.05$), reflecting the presence of immunosuppressive niches. In parallel,
mixed CD57+-Casp3+ hotspots were localized in apoptosis-rich areas, while spatial exclusion between CD8+ and FOXP3+ cells was observed in certain tumor regions, suggesting functional compartmentalization within the TME.

Conclusion: Spatial analysis of the TME using multiplex immunofluorescence and digital pathology uncovers complex cellular interactions not accessible through conventional approaches. Assessment of intercellular distances and cluster organization represents a promising strategy to identify relevant biomarkers, particularly in the context of NSCLC immunotherapies. This approach enables more refined patient stratification based on integrative spatial signatures.

Keywords: Spatial analysis; Tumor microenvironment; Multiplex immunofluorescence; QuPath; Intercellular distances; Cellular clusters.

An Intelligent System for Breast Cancer Cell Detection: First Experience at Burkina Faso

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Background: Early detection of breast cancer improves patient prognosis and remains a major public health challenge, particularly in low-resource settings. Digital pathology combined with artificial intelligence (AI) represents an innovative approach to support diagnostic activities. We report our first experience with an intelligent electronic system designed for the analysis of histopathological images and the detection of breast cancer cells at Bogodogo University Hospital, Burkina Faso.

Methods: Data were collected through the acquisition of digital images from routine histological slides of breast tissue. These images were analyzed using an intelligent electronic system based on image processing and AI algorithms. A descriptive and analytical assessment of the system's performance was conducted, focusing on cancer prediction, image validity, and concordance with the reference diagnosis established by pathologists.

Results: The system achieved a mean cancer prediction rate of 65%. Invalid image files represented 12% of the dataset, while 15% of cases were classified as benign. The overall concordance between the AI system and the pathologist's diagnosis was estimated at 79%.

Although the level of accuracy obtained is reasonable, it remains lower than that of expert pathologists, highlighting the need for further optimization.

Conclusion: This intelligent electronic system demonstrates potential value as a diagnostic support tool in digital pathology for breast cancer. An appropriate ethical framework is necessary to ensure data protection and clarify responsibility in the event of diagnostic errors.

Keywords: Artificial intelligence; digital pathology; breast cancer; Burkina Faso

Training-Free Inference-Time Enhancement for Zero-Shot Histopathology Classification

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Abstract:

Background: Vision-language models (VLMs) offer a promising training-free approach for digital pathology through zero-shot inference, reducing dependence on large annotated datasets and task-specific retraining. This is particularly relevant in histopathology, where expert annotation is costly and data variability across institutions can limit the scalability of supervised methods.

Aim: This work aims to investigate training-free inference-time enhancement strategies for zero-shot histopathology classification, combining completed results on colorectal pathology with ongoing work on brain tumor pathology from Egyptian clinical data.

Methods: Frozen VLMs were used in a zero-shot setting, with prediction improved at inference time through class-side refinement and image-side stabilization, without updating model parameters. For colorectal histopathology, experiments were conducted on the public NCT-CRC dataset. Training-free inference-time enhancement substantially improved zero-shot classification, increasing CLIP from 25.39% to 44.04%, PLIP from 63.17% to 87.88%, and MedSigLIP from 50.94% to 99.22% without fine-tuning. Ongoing work extends the same direction to a brain tumor pathology dataset derived from real Egyptian patients to assess robustness and clinical relevance on locally sourced data.

Conclusion: These findings show that inference-time enhancement can significantly improve zero-shot histopathology classification without fine-tuning. This approach offers a scalable and dataefficient direction for computational pathology across both public benchmarks and real-world African clinical datasets.

AI-Driven Prognostic Evaluation in Uveal Melanoma Through Automated Nucleolar Analysis

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Background & Objectives: The mean diameter of the ten largest nucleoli in uveal melanoma is a significant prognostic factor. However, measuring this parameter using conventional methods is often challenging, time-consuming, and prone to imprecision. This study proposes an automated artificial intelligence–based approach to accurately and efficiently assess this prognostic indicator.

Methods: A dataset of 1,280 histopathological images was selected for analysis. The images underwent preprocessing, including normalization and subsequent denormalization steps as part of the image processing pipeline. We then employed the discriminator component of a Generative Adversarial Network (GAN), used here as a classifier, to distinguish real data from those generated synthetically.

For image processing, images were converted from BGR to RGB format and subsequently transformed into grayscale. Thresholding was applied to define image boundaries and isolate relevant pixel intensity ranges. A mask was generated and applied, followed by a blurring step to reduce noise. Nucleolar contours were then detected, and closed contours were counted to determine the total number of cells. The diameters of the detected nucleoli were calculated, and the ten largest were selected to compute their mean diameter.

Results: The proposed automated method successfully identified and measured nucleolar diameters, enabling precise calculation of the mean diameter of the ten largest nucleoli.

Conclusion: Artificial intelligence–based automated methods represent an effective and time-saving tool in histopathology. They allow accurate, reproducible, and objective evaluation of prognostic factors in uveal melanoma.

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