Artificial Intelligence in Dermatopathology

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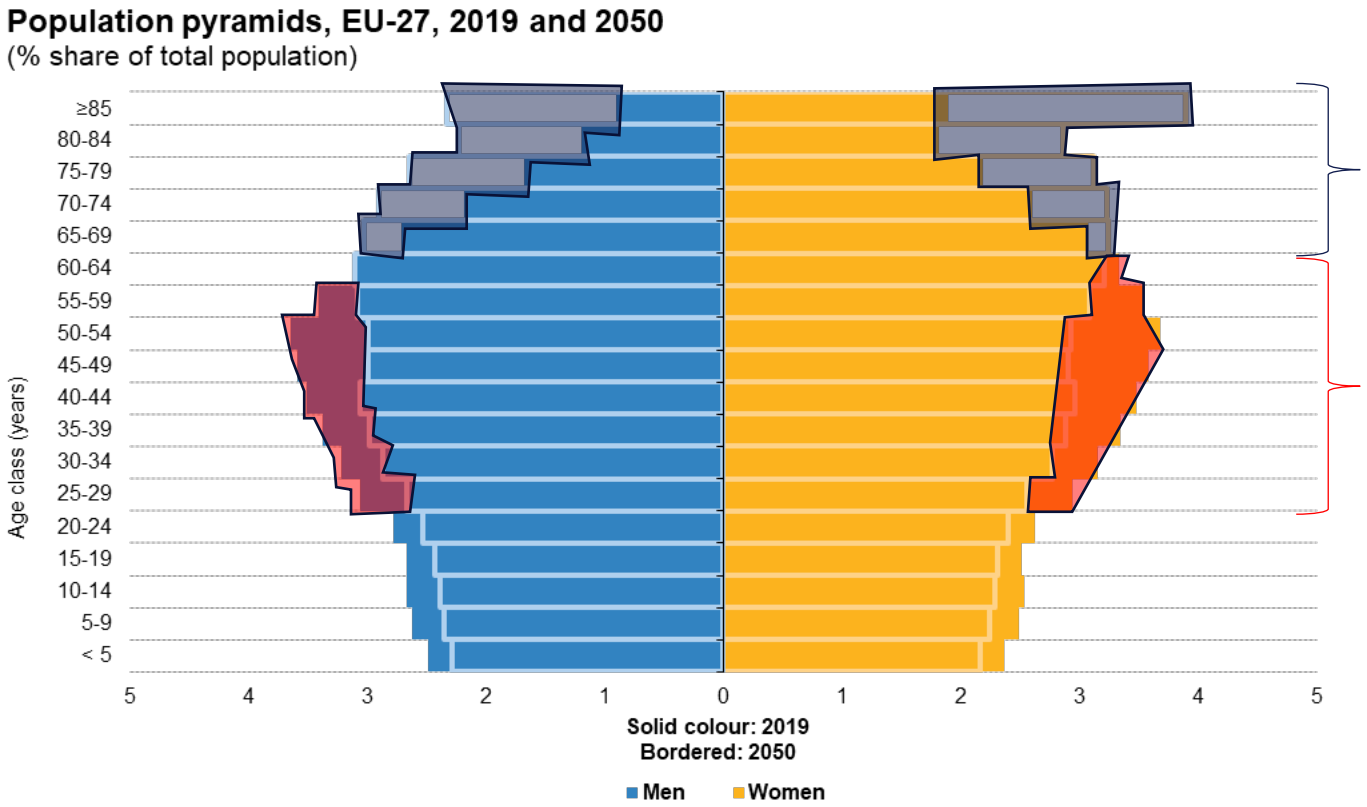
Thursday, July 9, 2026 - 14:40 – 15:20
Summer Academy of Dermatopathology 2026

Why do we want/need a change?



More work

Less workforce

Note: all data as of 1 January. 2019: estimates and provisional. 2050: population according to the 2019 projections, baseline variant (EUROPOP2019).

Source: Eurostat (online data codes: demo_pjangroup and proj_19np)

eurostat

eurostat

https://ec.europa.eu/eurostat/statistics-explained/index.php?title=File:Population_pyramids,_EU-27,_2019_and_2050_(%25_share_of_total_population)_AE2020.png

An overview

Computational pathology in 2030: a Delphi study forecasting the role of AI in pathology within the next decade

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Summary

Background Artificial intelligence (AI) is rapidly fuelling a fundamental transformation in the practice of pathology. However, clinical integration remains challenging, with no AI algorithms to date in routine adoption within typical anatomic pathology (AP) laboratories. This survey gathered current expert perspectives and expectations regarding the role of AI in AP from those with first-hand computational pathology and AI experience.

Methods Perspectives were solicited using the Delphi method from 24 subject matter experts between December 2020 and February 2021 regarding the anticipated role of AI in pathology by the year 2030. The study consisted of three consecutive rounds: 1) an open-ended, free response questionnaire generating a list of survey items; 2) a Likert-scale survey scored by experts and analysed for consensus; and 3) a repeat survey of items not reaching consensus to obtain further expert consensus.

Findings Consensus opinions were reached on 141 of 180 survey items (78.3%). Experts agreed that AI would be routinely and impactfully used within AP laboratory and pathologist clinical workflows by 2030. High consensus was reached on 100 items across nine categories encompassing the impact of AI on (1) pathology key performance

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A systematic consensus study of 24 international experts reached 78.3% agreement that AI will be routinely and impactfully integrated into anatomic pathology workflows by 2030, with strong consensus on nine categories including KPIs, workforce changes.

By 2030, due to the integration of AI in the pathology setting ...	
Key performance indicator	Result
Standardization of pre-analytical processes (staining and slicing techniques) will increase	Agree
Diagnostic accuracy will increase	Strongly agree
Diagnosis and grading of tumors will be more standardized, bringing more objectivity to the diagnosis of certain entities that are currently subject to high interobserver variability	Strongly agree
Detection of rare events (small metastases, small tumor foci) will increase	Strongly agree
Analyses will be more quantitative	Strongly agree
Completeness of reports will increase	Agree
Complexity of reports will increase	Agree
Quality of reports will increase	Agree

For the Mode, (%) designates the percentage of panellists who selected that score. AI, artif nge. Item # refers to the question # on the survey questionnaire. Likert scale interpretation: *Agreement level*: 1 = = Neither agree nor disagree, 5 = Agree, 6 = Strongly agree, 7 = Very strongly agree.

Table 1: **Statements on which high directional consensus was reached regardi indicators (KPIs).**

Berbís M et al. Computational pathology in 2030: a Delphi study forecasting the role of AI in pathology within the next decade. eBioMedicine, 2023; 88

By 2030, the probability of these AI tools being routinely used in pathology labs is …

AI application	Item #	Mode (%)	Mean (SD)	Median (IQR)	Likelihood
Identification of micrometastases	78	7 (50.0)	6.17 (1.09)	6.5 (6.0–7.0)	Certain
Detection of lymph node metastases	79	7 (54.2)	6.33 (0.87	7.0 (6.0–7.0)	Certain
Quantification of IHC or IF stains, such as Ki-67, ER, PgR, PD-L1	85	7 (70.8)	6.67 (0.56)	7.0 (6.0–7.0)	Certain
Quantification of number of mitoses in H&E-stained images	86	7 (50.0)	6.33 (0.76)	6.5 (6.0–7.0)	Certain
Counting lymphocytes	87	7 (50.0)	6.42 (0.65)	6.5 (6.0–7.0)	Certain
Automated ordering of IHC for specific applications/assisting with selection of immunohistochemical stains needed	61	6 (45.8)	5.46 (0.93)	6.0 (5.0–6.0)	Very likely
Automated QA/QC of IHC positive and negative controls	62	6 (54.2)	5.75 (0.90)	6.0 (5.0–6.0)	Very likely
Proposing specific IHC or other molecular methods to solve a specific diagnostic problem	68	6 (41.7)	5.17 (1.34)	5.5 (5.0–6.0)	Very likely
Prioritization of cases (such as cases with neoplasia and infectious organisms in immunosuppressed patients)	69	6 (45.8)	5.50 (1.10)	6.0 (5.0–6.0)	Very likely
Quality control of whole-slide images (scanning process), and detection of poor-quality slides (tissue folds, poor staining)	73	6 (66.7)	6.13 (0.68)	6.0 (6.0–6.5)	Very likely
Quality improvement of whole-slide images	74	6 (62.5)	6.00 (0.92)	6.0 (6.0–6.5)	Very likely
Pre-selecting regions of interest suspicious for cancer for pathologists to view	76	7 (45.8)	6.29 (0.75)	6.0 (6.0–7.0)	Very likely
Identification of hotspot areas	77	7 (45.8)	6.25 (0.85)	6.0 (6.0–7.0)	Very likely
Detection of microorganisms (AFB, *H. pylori*)	81	6 (58.3)	6.17 (0.87)	6.0 (6.0–7.0)	Very likely
Assisting with tumor grading	82	6 (62.5)	6.21 (0.59)	6.0 (6.0–7.0)	Very likely
Quantification of eosinophils in eosinophilic esophagitis	88	6 (54.2)	6.13 (0.68)	6.0 (6.0–7.0)	Very likely
Quantitation of features (e.g., fibrosis in various organs, liver steatosis, etc.)	89	6 (62.5)	6.29 (0.55)	6.0 (6.0–7.0)	Very likely
Marking of perineural invasion, lymphovascular invasion	90	6 (50.0)	5.79 (0.98)	6.0 (5.0–6.0)	Very likely
Automated measurements (e.g., of tumor areas)	94	6 (54.2)	6.21 (0.66)	6.0 (6.0–7.0)	Very likely
Ensuring all diagnostically relevant areas on the slide are viewed prior to report finalization	95	6 (50.0)	5.42 (0.83)	6.0 (5.0–6.0)	Very likely
Mandatory 2nd reads when the pathologist diagnosis doesn't match the potential AI diagnosis (within a predefined range/%; e.g., if the AI tool detects potential tumor on a biopsy but the pathologist reads the biopsy as no evidence of tumor)	97	6 (54.2)	5.79 (0.83)	6.0 (5.0–6.0)	Very likely
Standardization of pathology reports	98	6 (66.7)	5.88 (0.68)	6.0 (6.0–6.0)	Very likely
AI-assisted laboratory workflow management, including workload assignments to pathologists, residents, and technicians	59	5 (45.8)	5.33 (1.31)	5.0 (5.0–6.0)	Likely
Detection of signet ring-cell cancer	80	5 (42.7)	5.29 (1.08)	5.0 (5.0–6.0)	Likely
Pre-selection of potentially cancer-positive samples for pathologist's review, while the bulk of clearly negative samples can be automatically processed	63	5 (45.8)	5.13 (1.26)	5.0 (5.0–6.0)	Likely
Triaging of cases to the most appropriate pathologist at the earliest possible time	64	5 (41.7)	5.08 (1.41)	5.0 (5.0–6.0)	Likely
Providing a set of differential diagnoses on difficult cases	92	5 (45.8)	5.13 (0.90)	5.0 (5.0–6.0)	Likely
Proposing specific additional tests for solving a diagnostic problem (e.g., AI algorithm suggesting STAT6 immunostaining on a spindle cell neoplasm of the pleura)	93	6 (37.5)	5.17 (1.24)	5.0 (5.0–6.0)	Likely
Import of contextually-related data on a case for quick review by the pathologist during diagnostic slide review	96	5 (58.3)	5.21 (0.72)	5.0 (5.0–6.0)	Likely
Pre-populating relevant report details from the medical record/gross description	99	5 (54.2)	5.29 (0.95)	5.0 (5.0–6.0)	Likely
Selection of the appropriate synoptic report based on prior pathology findings, including the current case gross report	100	5 (50.0)	5.38 (0.88)	5.0 (5.0–6.0)	Likely
Pre-populating reports based on AI interpretation of images	101	5 (45.8)	5.13 (1.03)	5.0 (5.0–6.0)	Likely
Finding the source of contaminants	102	5 (58.3)	5.17 (0.96)	5.0 (5.0–5.5)	Likely

www.kidney-international.org review

Advances in computational nephropathology

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Pathology relies on pathologists' qualitative assessment and semiquantitative measures to characterize the structural and molecular alterations of tissues. Novel analytical methods and recent advances in the computational field, particularly in artificial intelligence and deep learning in pathology, termed computational pathology, have led to widespread applications and advancement in research. Integrating computational approaches into the digital pathology workflow can facilitate the automated, high-throughput analysis of histopathologic images, thereby improving precision, reproducibility, and efficiency in pathology diagnostics. We provide a comprehensive overview of the advancements and applications of computational pathology, specifically in nephropathology. We discuss widely adopted methodological approaches, highlighting their respective strengths and limitations, including quantitative nephropathology (i.e., pathomics), deep learning–based image classification and regression, and nonimage applications (e.g., automated decision support systems for standardizing the reporting of current consensus classifications). Despite the promising potential of these approaches, several challenges remain for successful implementation in routine clinical practice. We highlight technological, regulatory, and ethical challenges, such as computational infrastructure, data privacy, and considerations of environmental sustainability. Looking toward the future, we envisage potential developments that could further transform the field. We are entering a new exciting era, where computational methods are reshaping and redefining kidney pathology, perhaps also renaming our field to "kidnAI" pathology.

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KEYWORDS: deep learning; digital pathology; kidney biopsy; pathomics

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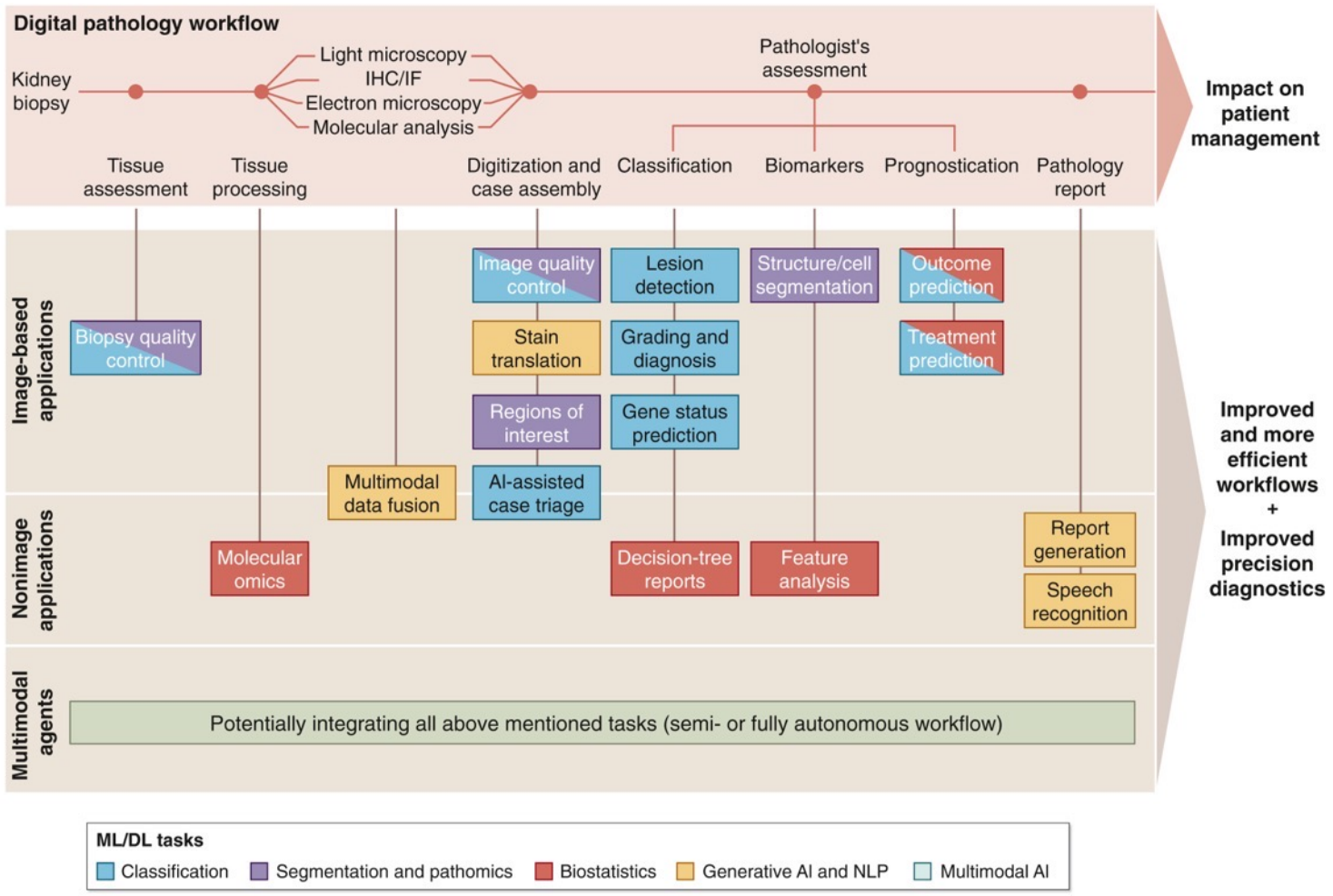
Editor's Note

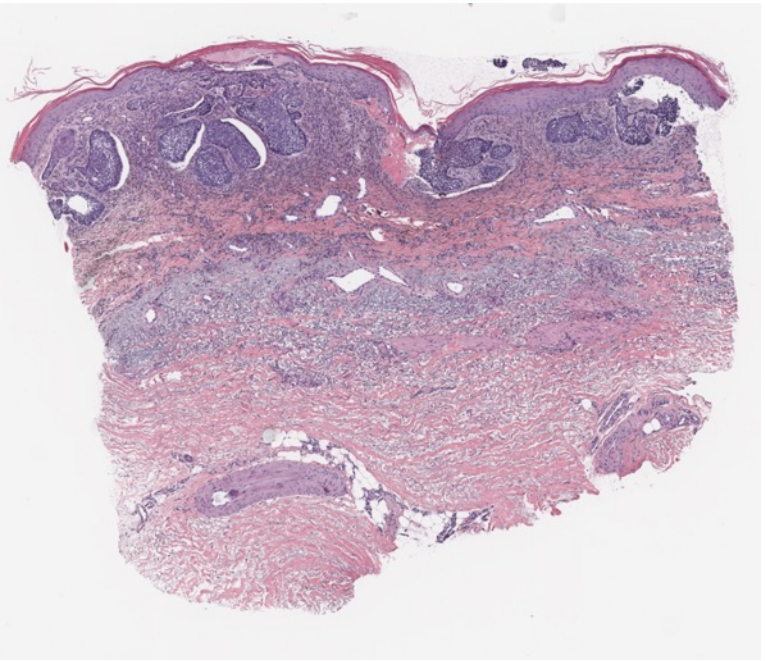
The application of artificial intelligence–based analysis to kidney pathologic lesions has made exciting progress, made possible by the advent of scanned glass slides to create whole slide images, which then can be analyzed both for quantitation of features a pathologist might see and exciting new approaches, including subvisual features that can enhance understanding of tissue injuries. In this addition to our series on artificial intelligence and machine learning, Hölscher *et al.* from the Boor laboratory provide a review of these specific applications for kidney pathology. The review systematically defines terminology, concepts, and approaches, including machine learning to deep learning, classification, segmentation, and advances in the field of pathomics, detailing progress, potential utilization, and challenges ahead. See the Big Science, Artificial Intelligence, and Machine Learning series at https://www.kidney-international.org/content/bigscience.

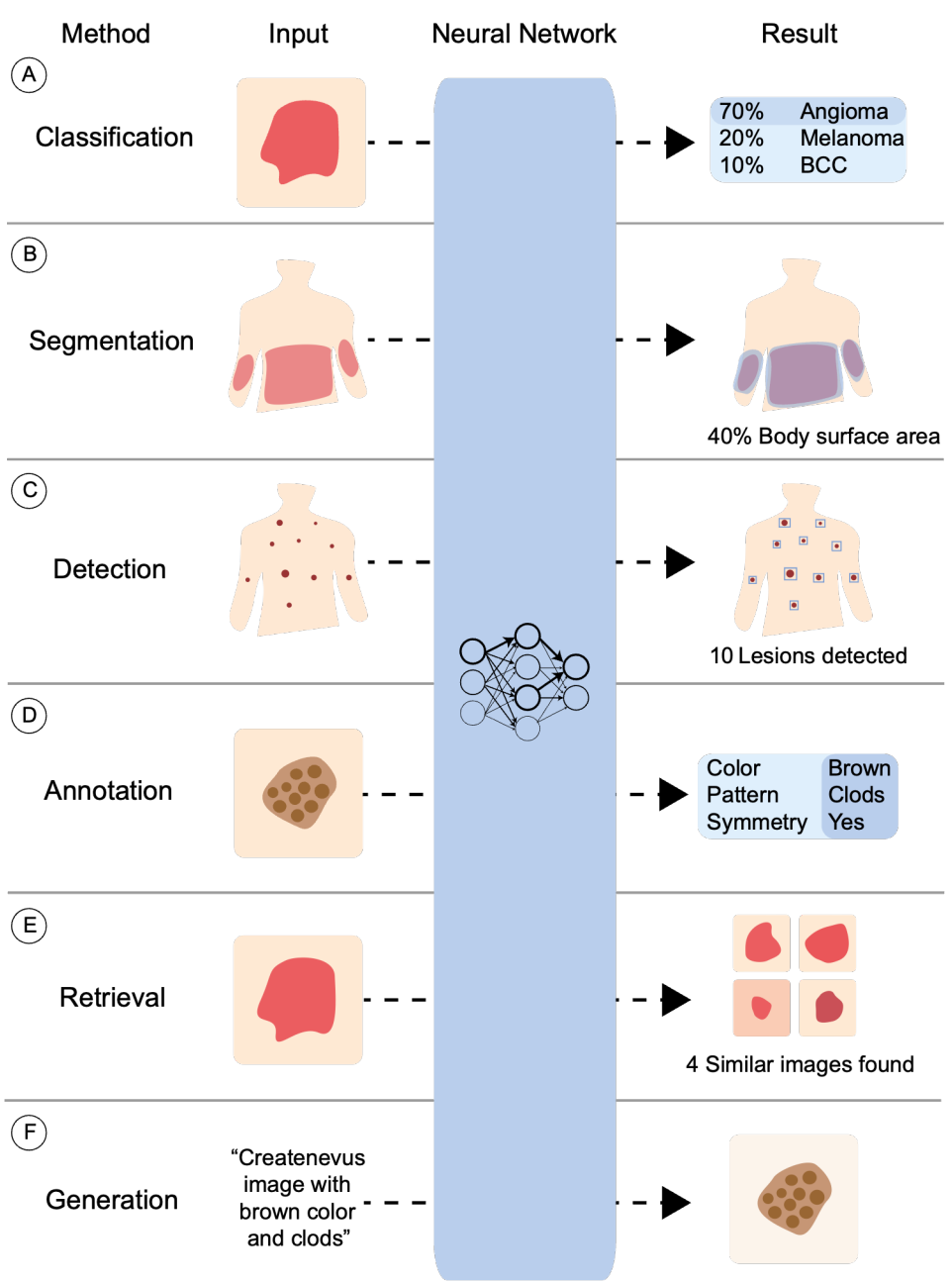
Nephropathology provides crucial insights into kidney structure and molecular alterations at the microscopic level, remaining an essential component in the diagnosis, treatment, and research of kidney diseases. In clinical nephropathology, kidney tissue is most often obtained via kidney biopsies. Its assessment requires histopathologic workup, including light microscopy for structural alterations, immunohistochemistry for molecular markers, and, in many cases, electron microscopy for the evaluation of ultrastructural changes. Most of these methods are assessed by pathologists visually and qualitatively, still often performed in an analog manner using microscopes. Semiquantitative histopathologic measures are part of almost every kidney biopsy report. Examples include the Oxford classification of IgA nephropathy (IgAN),[1] or the Banff lesion scores used in the classification of kidney allograft pathology.[2] Albeit providing

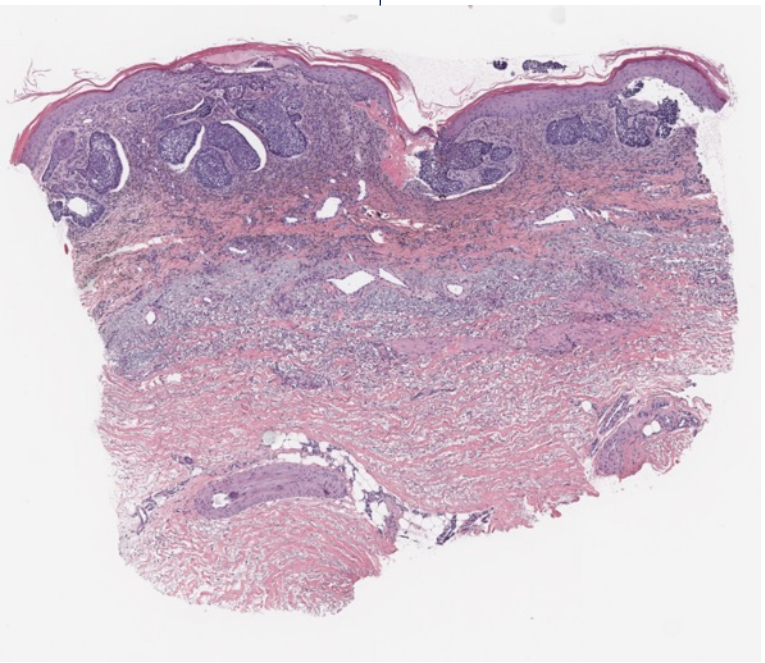


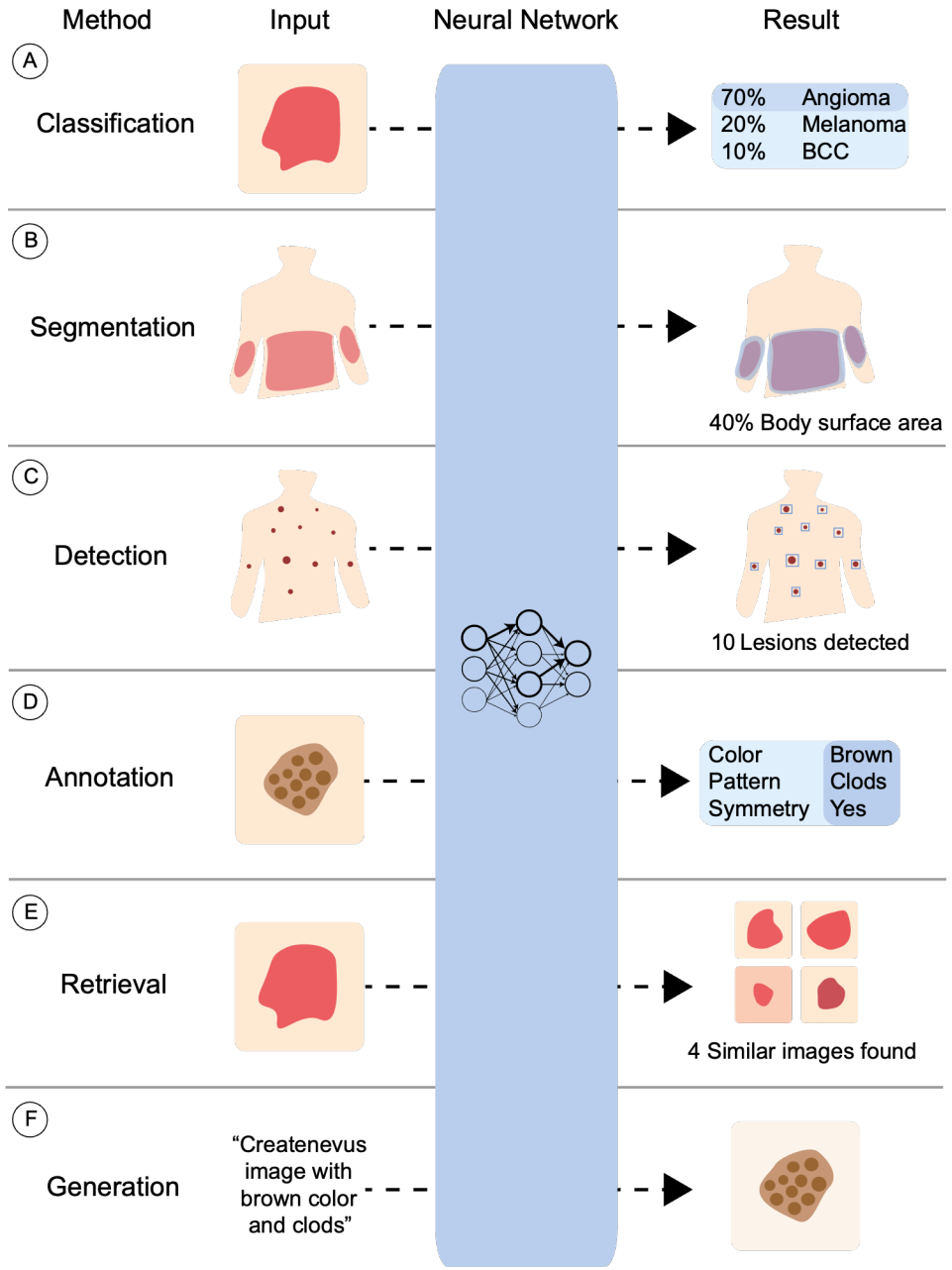
Alphabet

- Agents
- AP
- CLIP
- CNN
- CPATH
- Dice
- FM
- ICC-Profiles
- IoU
- Jaccard
- k-fold CV
- LLM
- MCP
- MIL
- MPP
- NER
- Object Detection
- RAG
- Reinforcement learning
- Segmentation
- Skills
- STT
- TCGA
- Tiling
- Tokens
- Transformers
- TTS
- VLM
- Weak supervision
- Workflows
- …



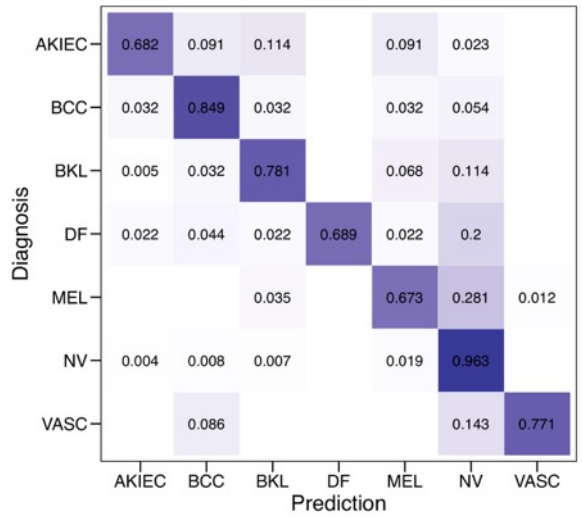

Method
Input
Neural Network
Result
A
Classification
70% Angioma
20% Melanoma
10% BCC
B
Segmentation
40% Body surface area
C
Detection
10 Lesions detected
D
Annotation
Color Brown
Pattern Clods
Symmetry Yes
E
Retrieval
4 Similar images found
F
Generation
“Createnevus image with brown color and clods”

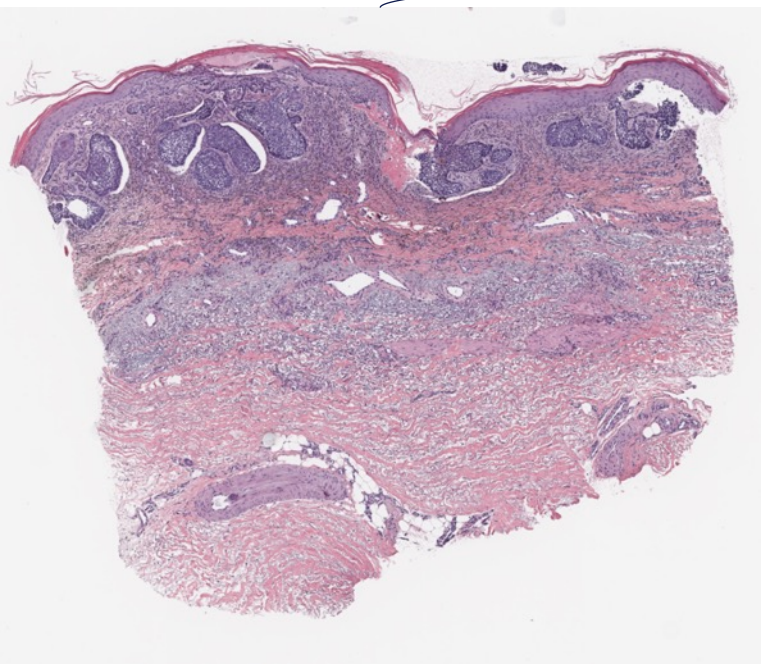


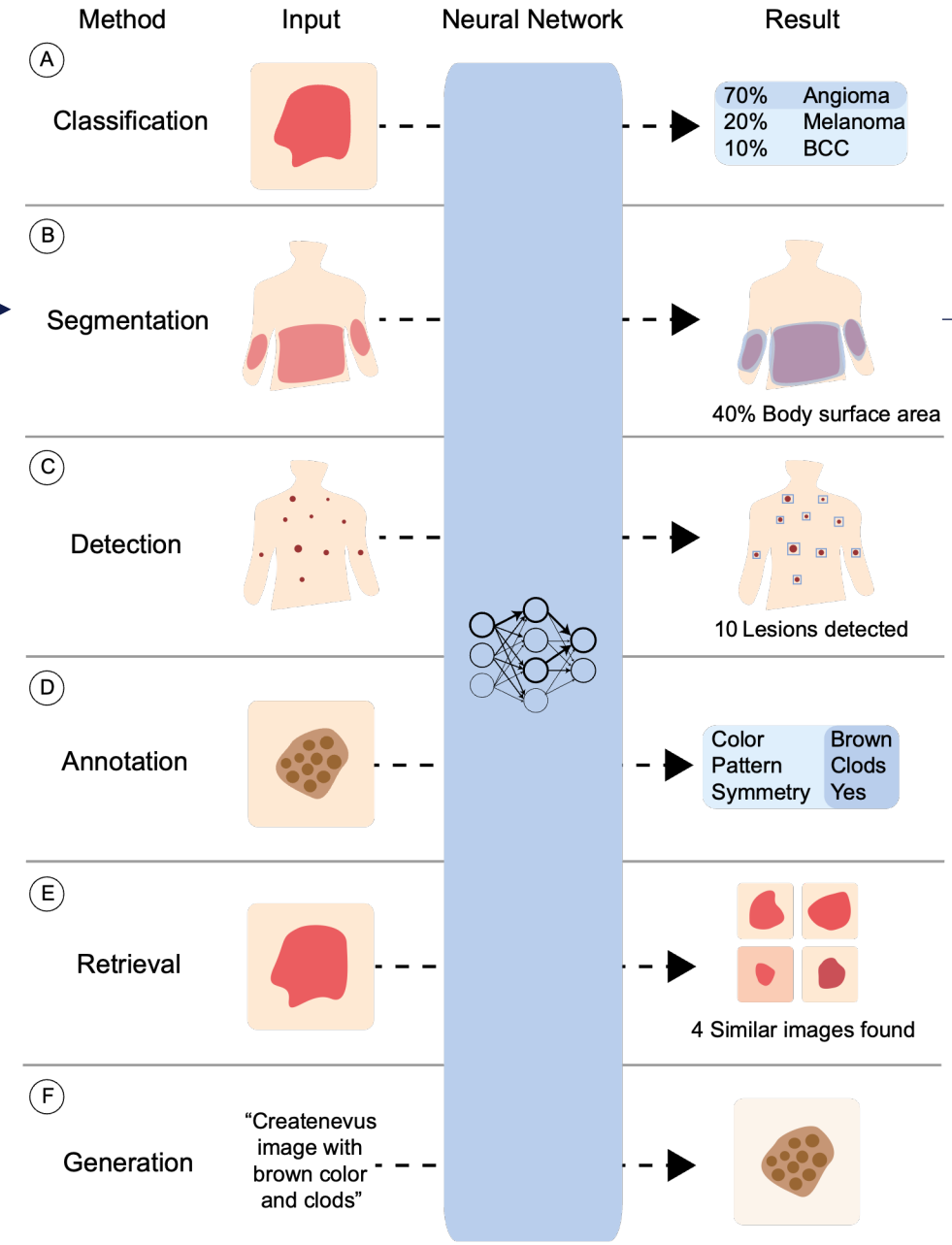


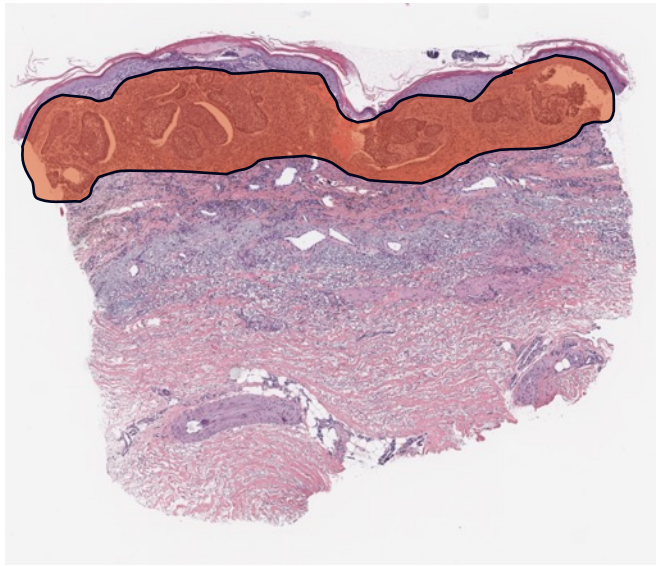
BCC, superficial: **75%**
BCC, nodular: **24%**
…

Metrics:
- Accuracy (Top 1/3/…)
- AUC
- Se/Sp/PPV/NPV
  - "Mean recall"



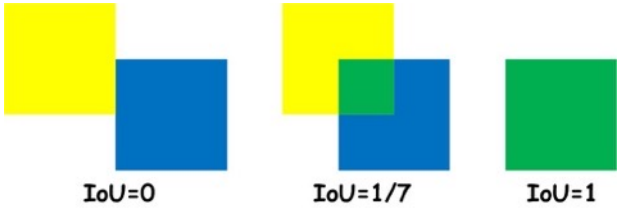




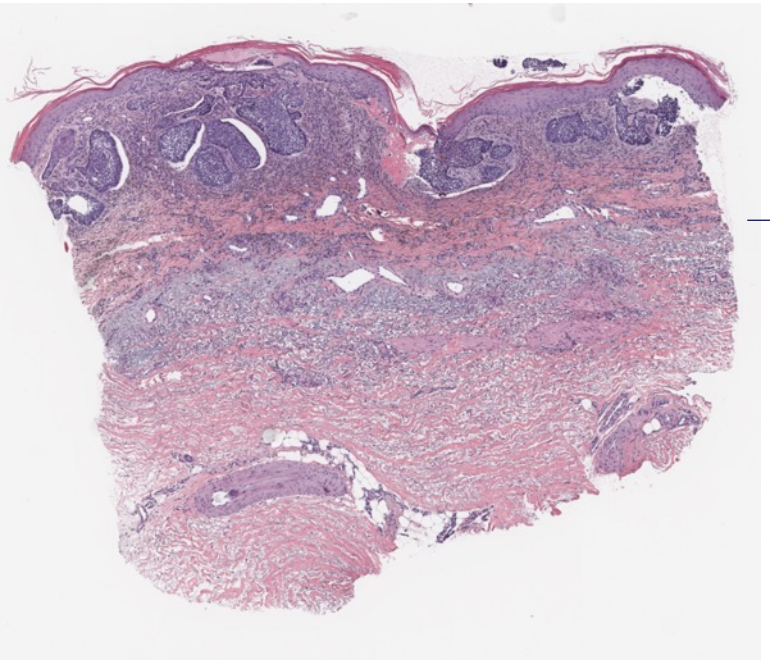


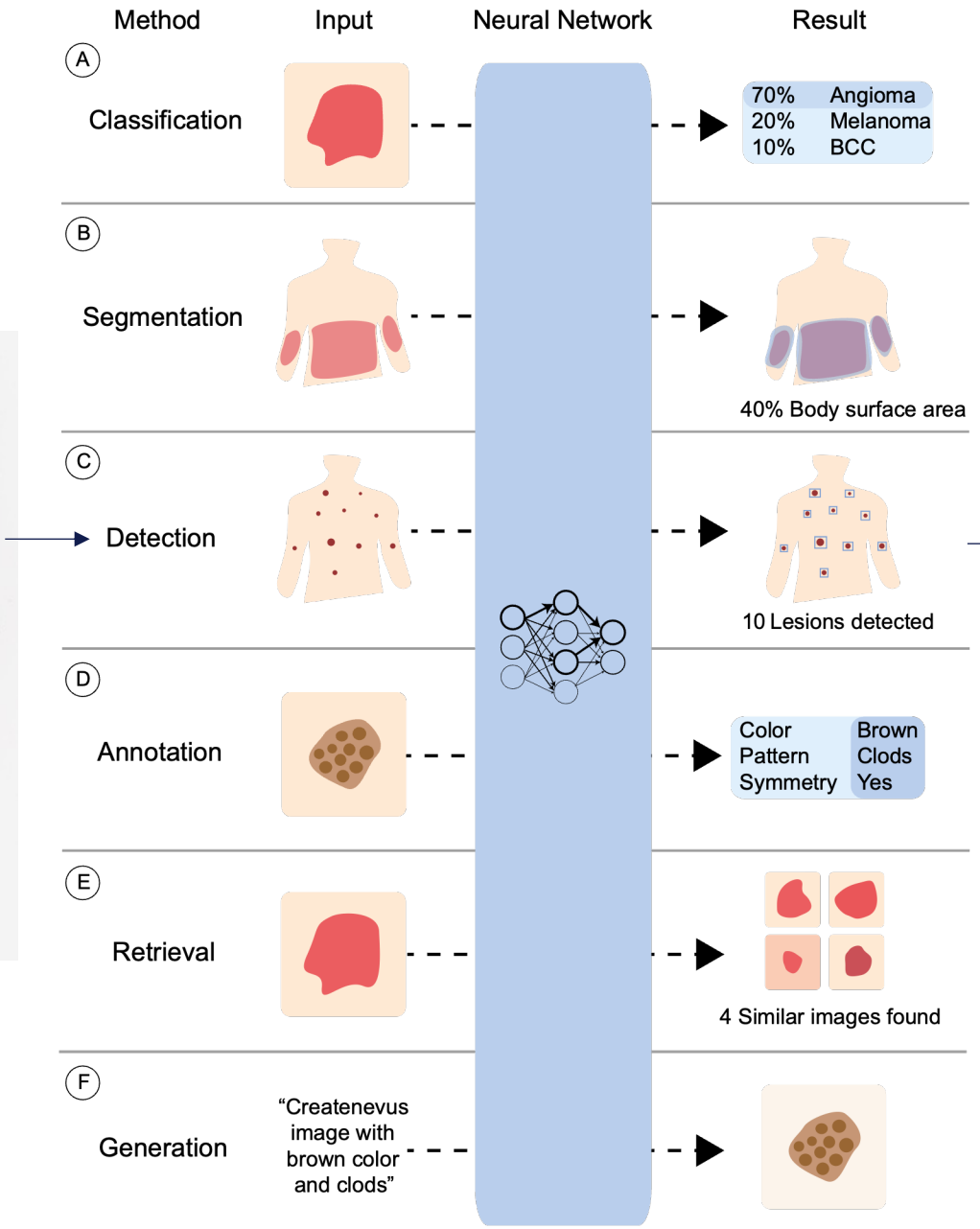
Metrics:

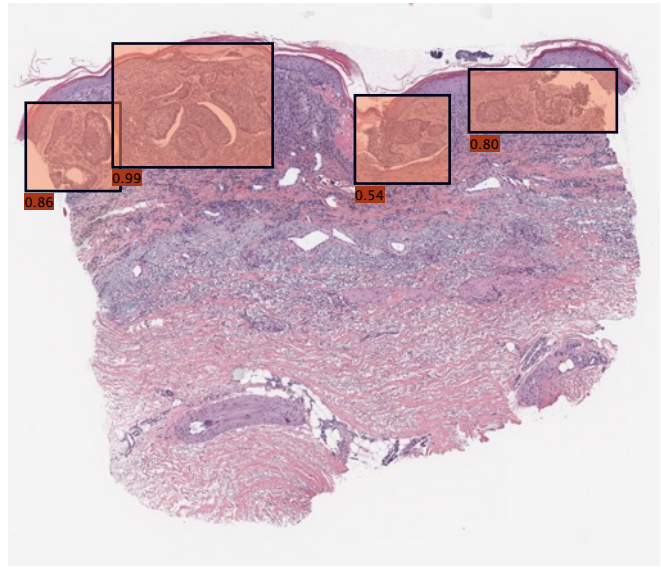
- Se/Sp/PPV/NPV
- IoU/Jaccard, Sørensen-Dice



IoU-Image source: https://towardsdatascience.com/intersection-over-union-iou-calculation-for-evaluating-an-image-segmentation-model-8b22e2e84686/ [Accessed 20260706]

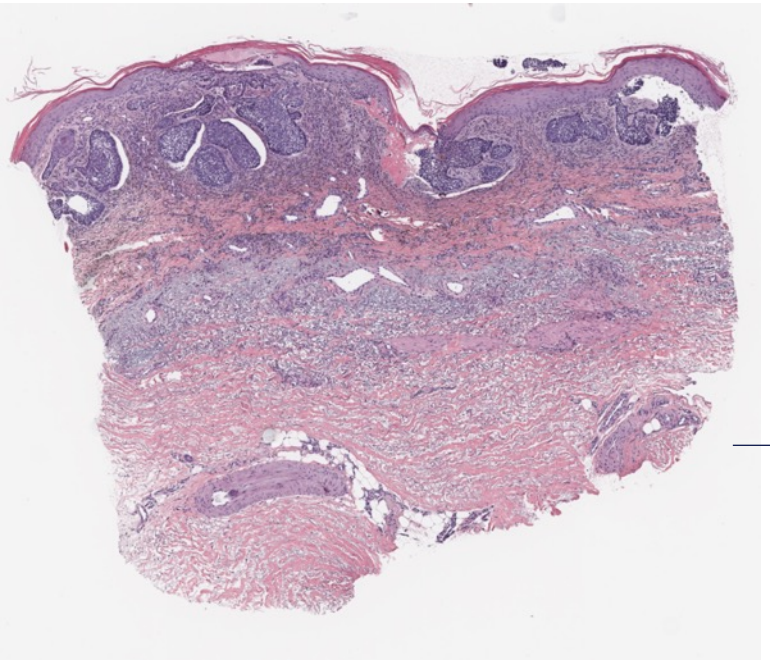


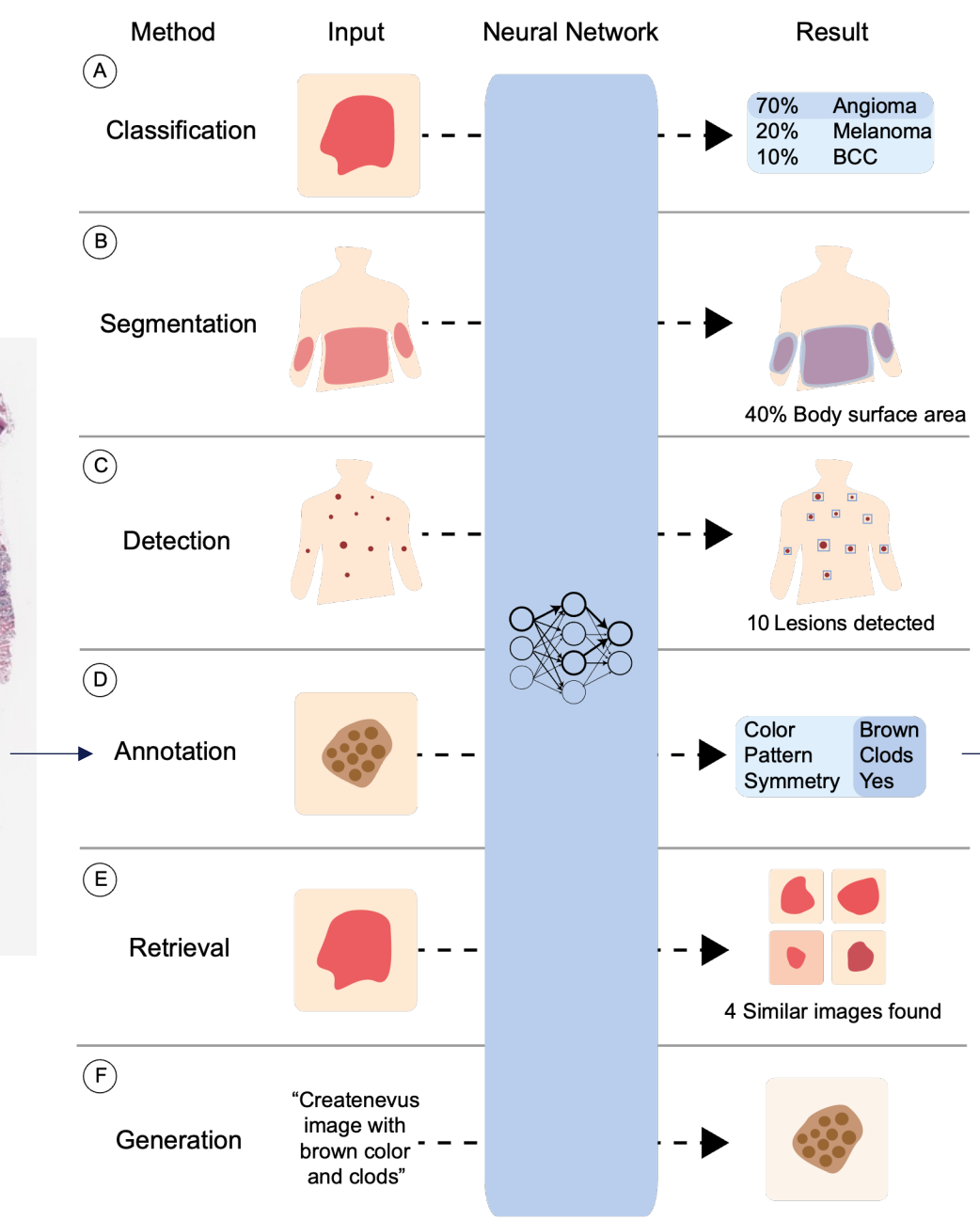




Metrics:

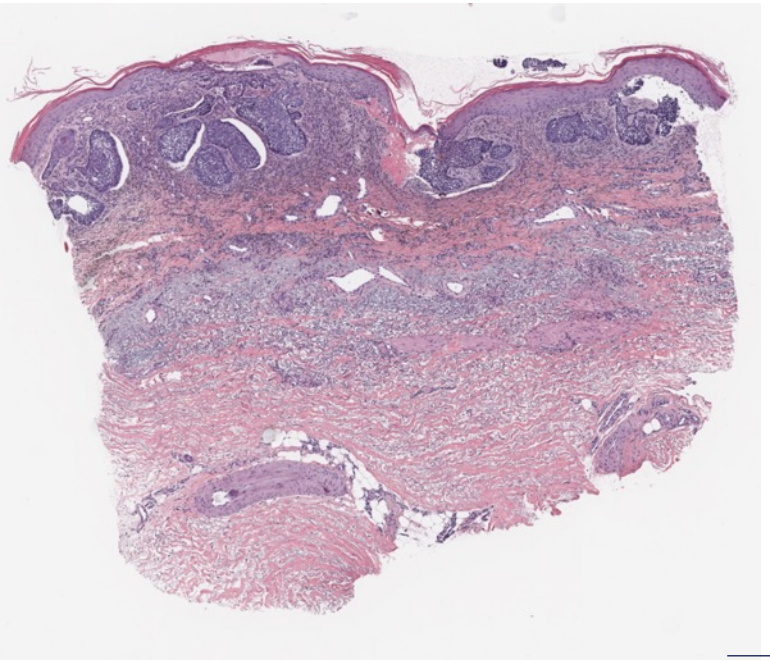
- AP@[0.5,0.75,0.95]
  - IoU-Thresholds
  - Area under PR-curve
- mAP = average over all classes

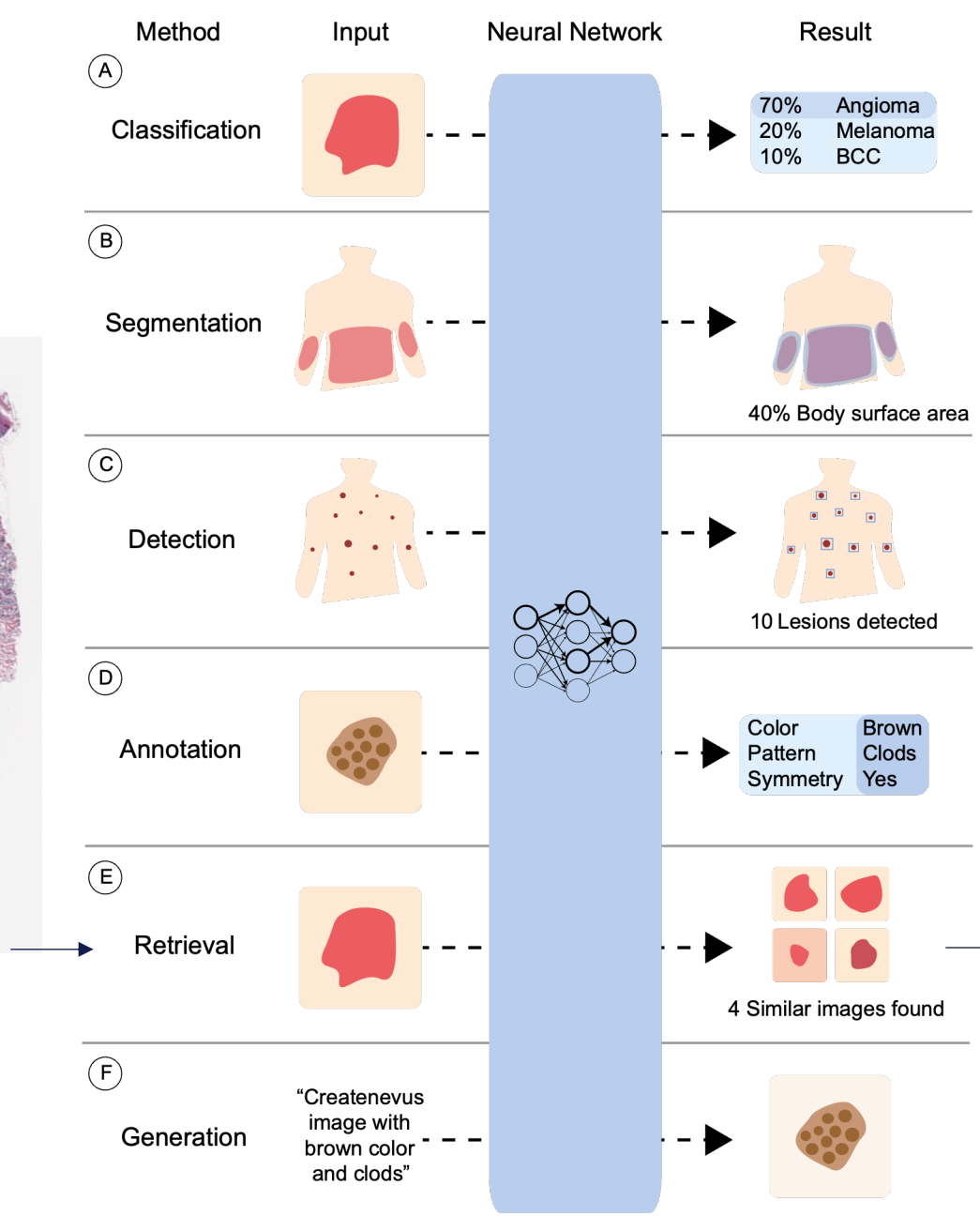




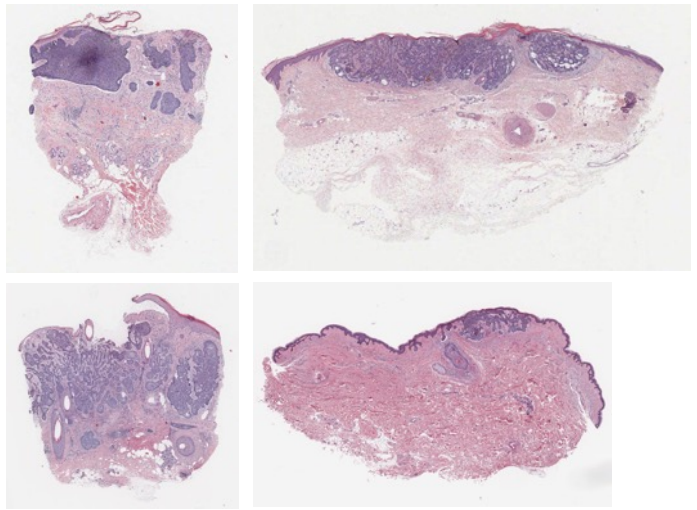
- Str. Corneum: **Lamellar**
- Tumor: **Basaloid cells**
- Dermis: **Solar elastosis**
- …

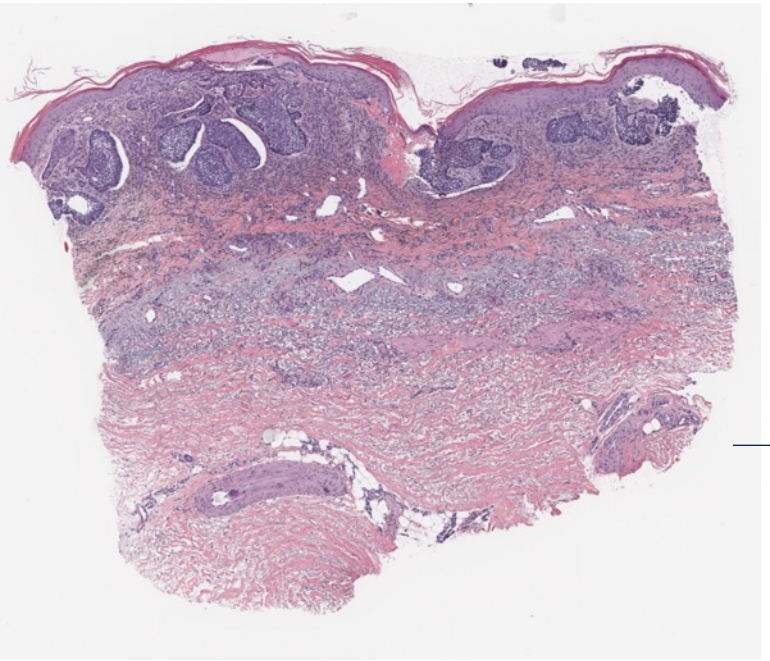
Metrics:
- Like Classification

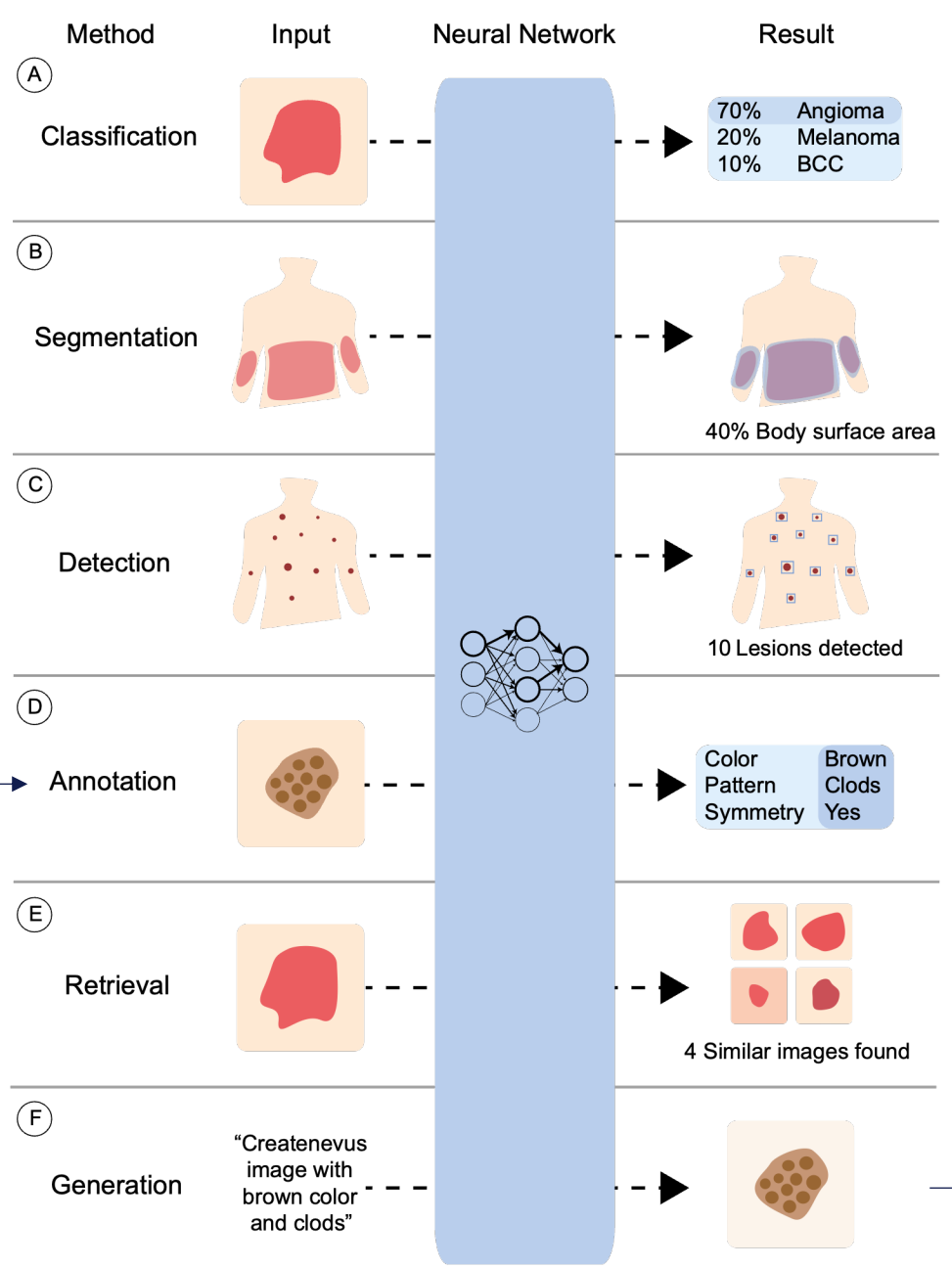




Metrics:
- Precision, Recall, F1, AP
- Discounted Cumulative Gain



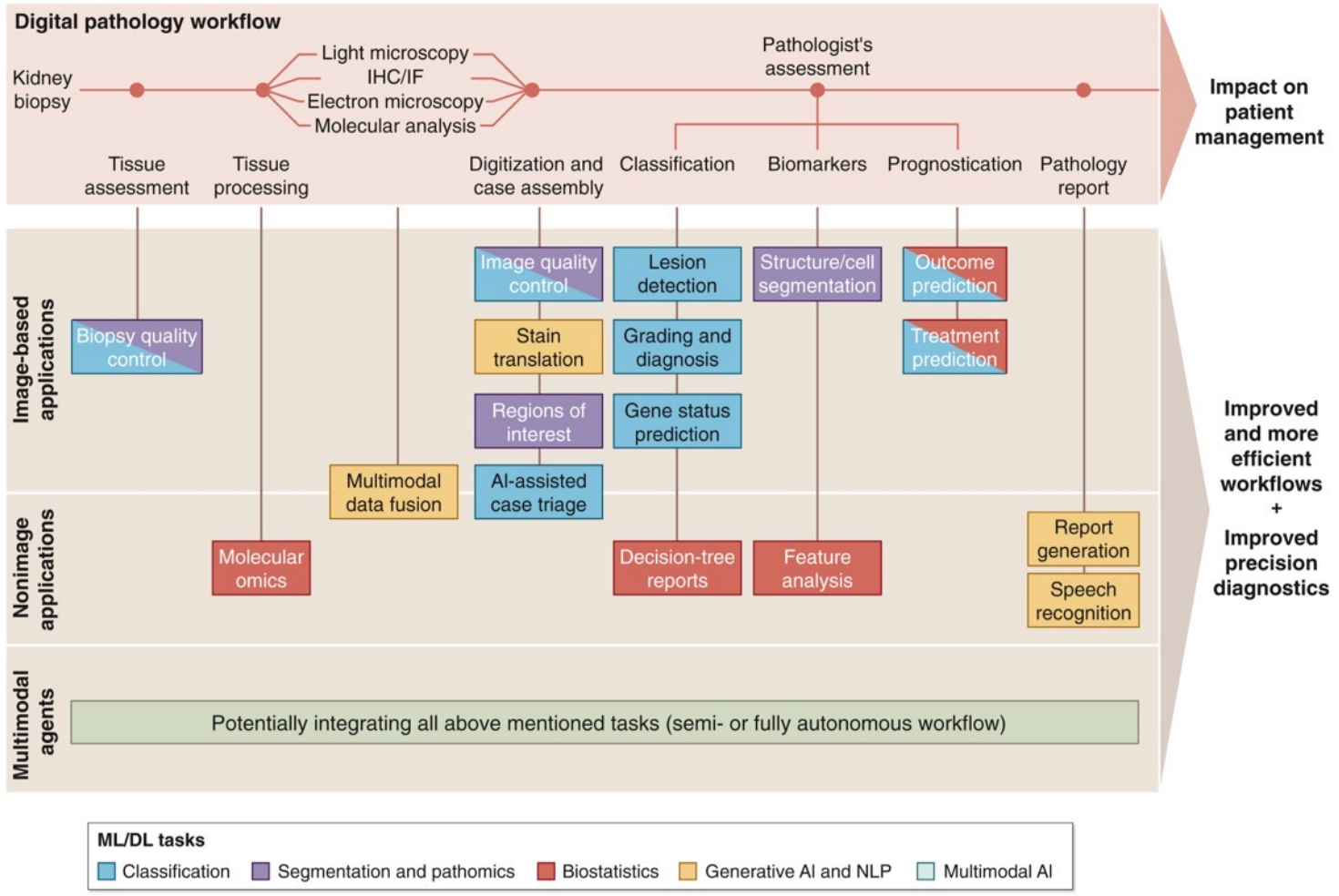




Metrics:
- Custom

"Microscopy: The specimen shows a punch biopsy with a basaloid tumor reaching the upper reticular dermis and the lateral margins.
Diagnosis: Basal cell carcinoma, margins affected."

What about here?



Hölscher DL, Bülow RD, Strauch M, Boor P. Advances in computational nephropathology. Kidney Int. 2025 Dec;108(6):1031-1044. doi: 10.1016/j.kint.2025.06.029. Epub 2025 Sep 19. PMID: 40976424.

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ORIGINAL ARTICLE

JEADV JOURNAL OF THE EUROPEAN ACADEMY OF DERMATOLOGY & VENEREOLOGY

AI-assisted basal cell carcinoma diagnosis with LC-OCT: A multicentric retrospective study

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Abstract

Background: Basal cell carcinoma (BCC) is the most common skin cancer, requiring an early diagnosis and accurate margin definition to prevent functional and cosmetic complications. Traditional methods using clinical and dermoscopic images (C&D) often rely on biopsies and histology for final validation. Non-invasive techniques like LC-OCT, enabling 'digital biopsies', are promising alternatives, but remain underutilized due to the expertise required. The development of Artificial Intelligence (AI) algorithms is a promising approach to assist dermatologists in their diagnosis and support the broader adoption of such technologies.

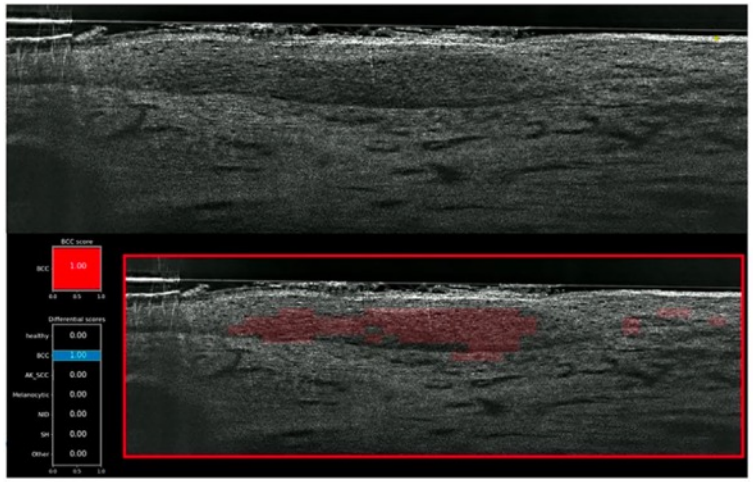
Objectives: We present a real-time AI assistant for BCC diagnosis with LC-OCT, which is, to date, the only real-time AI model across all dermatological imaging modalities. The study aims to quantify the model's effectiveness when used by dermatologists with different levels of expertise and compare its performance with traditional methods and unaided LC-OCT.

Josep Malvehy and Linda Tognetti: co-senior authorship.

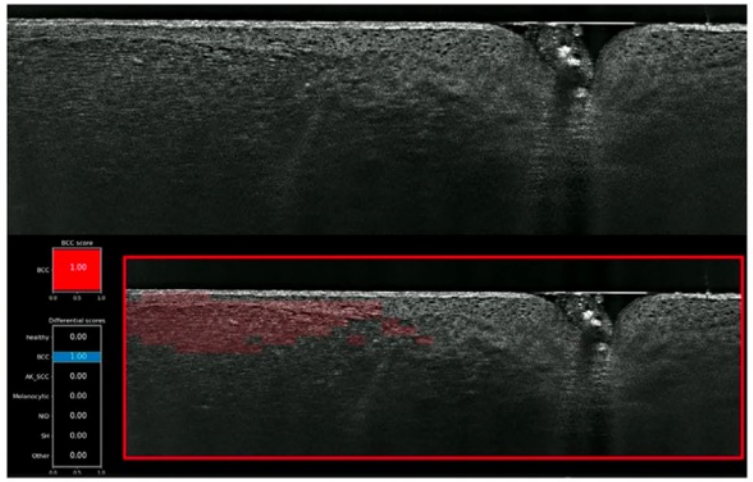
The members of LC-OCT Reviewers Consortium are presented in Acknowledgements.

Linked Article: B.-Y. Gao and Y.-T. Lee. *J Eur Acad Dermatol Venereol* 2026;40:e508–e509. https://doi.org/10.1111/jdv.70276.

AI-assisted LC-OCT improved diagnostic **accuracy** by 20.3 percentage points (**from 72.7% to 93.0%**) compared to traditional methods, effectively bridging a 2-year experience gap for dermatologists with limited expertise.



Diagnosis	Correct answers without AI	Correct answers with AI
Superficial BCC	74,42%	97,67% *(+23,25%)*



Diagnosis	Correct answers without AI	Correct answers with AI
Nodular BCC	51,16%	88,37% *(+37,21%)*

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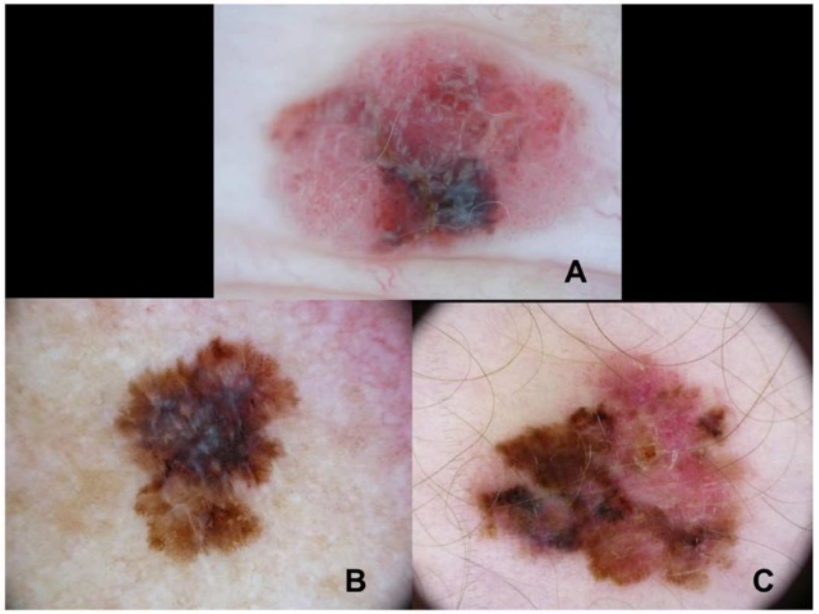
Can we predict metastases from dermatoscopy?



Deinlein T, Arzberger E, Zalaudek I, Massone C, Garcias-Ladaria J, Oliveira A, Schulter G, Hofmann-Wellenhof R. Dermoscopic characteristics of melanoma according to the criteria "ulceration" and "mitotic rate" of the AJCC 2009 staging system for melanoma. PLoS One. 2017 Apr 11;12(4):e0174871. doi: 10.1371/journal.pone.0174871. PMID: 28399177; PMCID: PMC5388460.

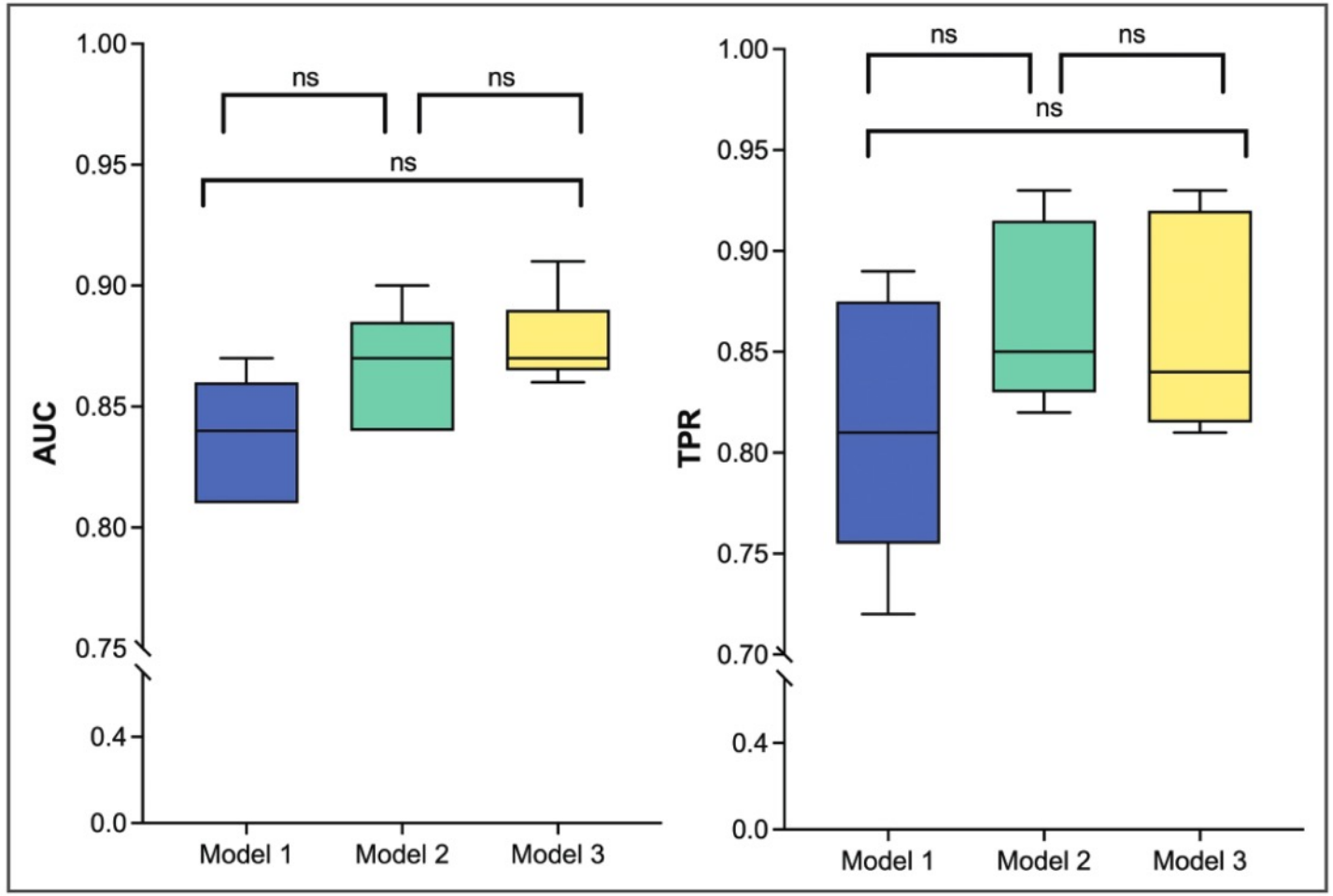
Br J Dermatol. 2024 Oct 17;191(5):847-848. doi: 10.1093/bjd/ljae281.

Prediction of melanoma metastasis using dermatoscopy deep features: an international multicentre cohort study

Konstantinos Lallas [1], Panagiota Spyridonos, Harald Kittler, Philipp Tschandl, Konstantinos Liopyris, Giuseppe Argenziano, Renato Bakos, Ralph Braun, Horacio Cabo, Emi Dika, Josep Malvehy, Ash Marghoob, Susana Puig, Alon Scope, Wilhelm Stolz, Masaru Tanaka, Luc Thomas, Zoe Apalla, Efstratios Vakirlis, Iris Zalaudek, Aimilios Lallas

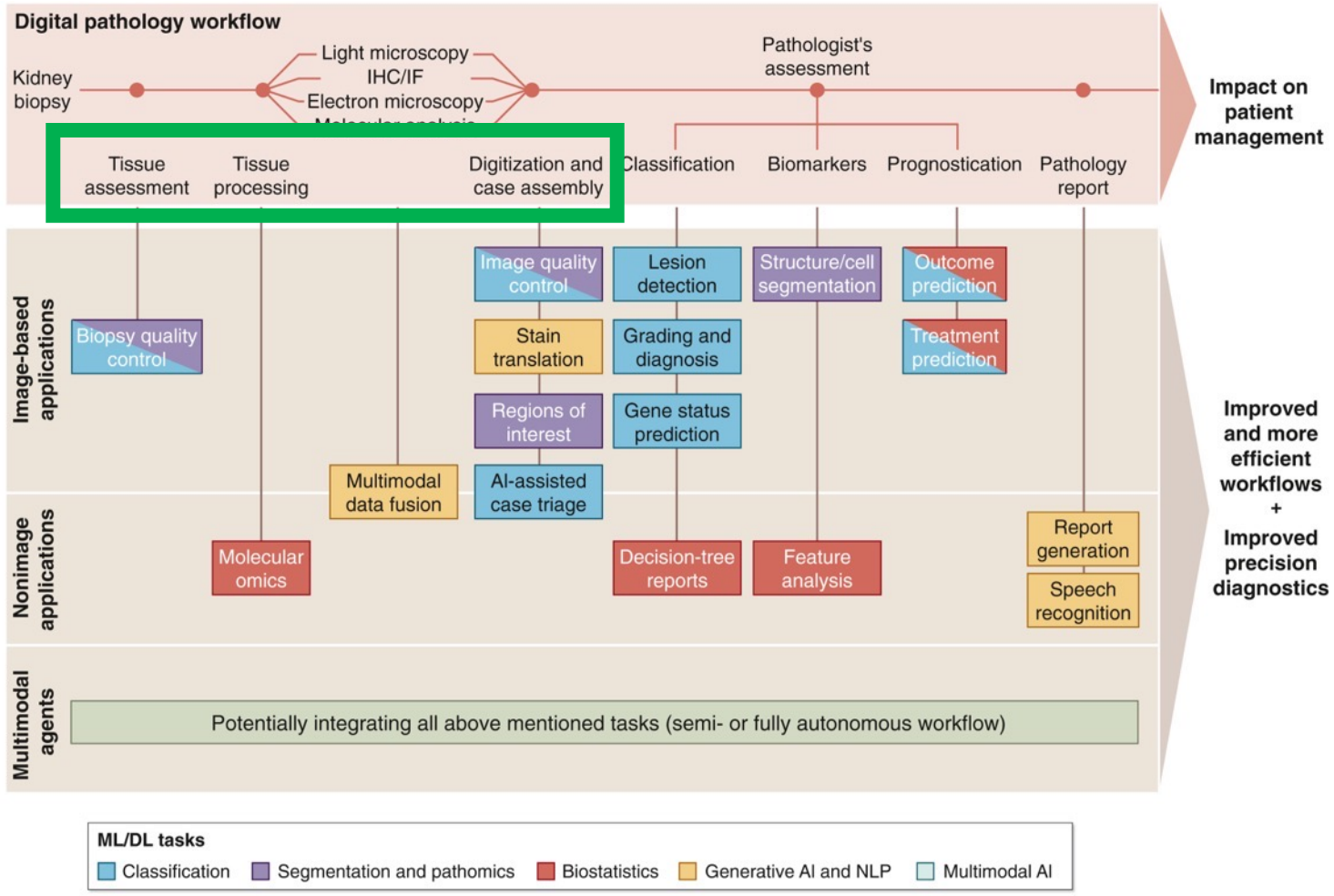
Train 600 patients (200 metastatic)
Test 112 patients (47 metastatic)

[**model 1**] accurately predicted metastasis in 21 of 23 (**91%**) **stage IIB** melanomas and in 21 of 23 (**91%**) **stage IIC** melanomas, whereas model 2 (Breslow thickness and ulceration) correctly predicted metastasis in 87% and 91% of IIB and IIC melanomas, respectively



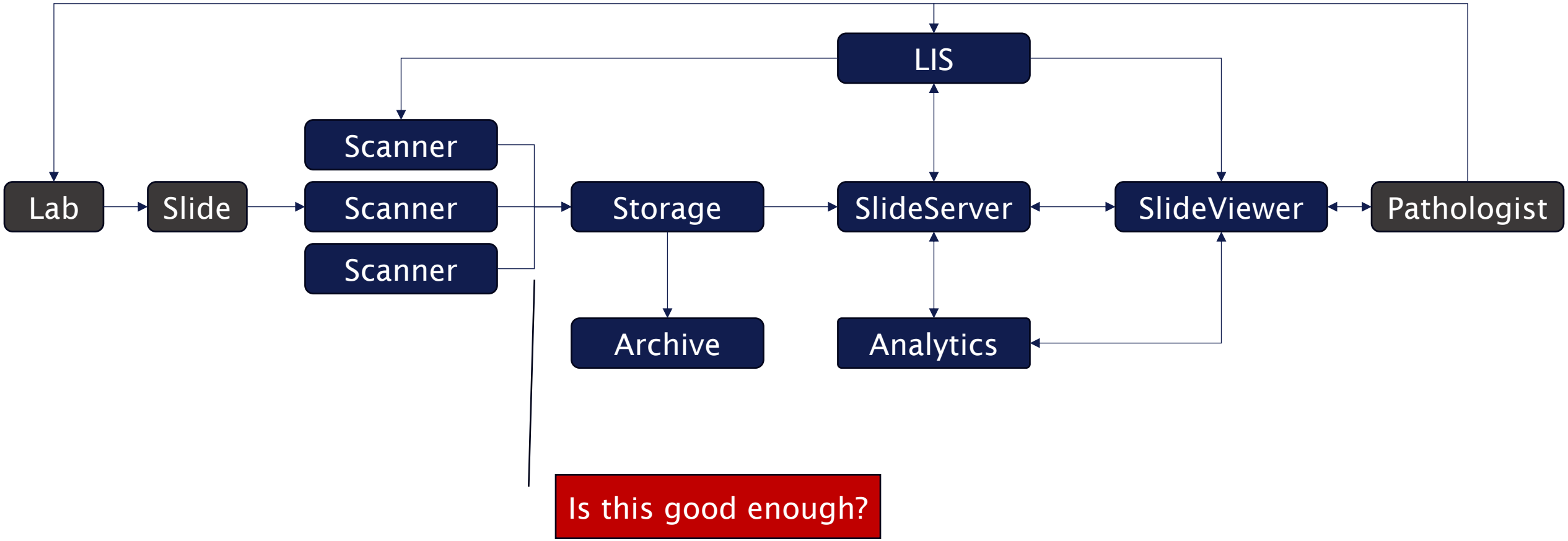
Model 1: CNN
Model 2: Breslow+Ulcer
Model 3. CNN+Breslow+Ulcer

→ Automated image analysis of **pre-histologic** imaging can be a prognostic **staging** method



Hölscher DL, Bülow RD, Strauch M, Boor P. Advances in computational nephropathology. Kidney Int. 2025 Dec;108(6):1031-1044. doi: 10.1016/j.kint.2025.06.029. Epub 2025 Sep 19. PMID: 40976424.

A simplified topology of digital pathology



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GrandQC adaptation as an artificial intelligence tool for quantitative artifact detection in hematoxylin and eosin whole-slide images—Simulation of quality control biopsies day

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ARTICLE INFO

Keywords:
Digital pathology
Computational pathology
Artificial intelligence
Quality control

ABSTRACT

Introduction: Digital pathology continues to transform the daily routine of pathology, in terms of the increasingly automated laboratory and in the diagnostic paradigm through the adoption of artificial intelligence (AI) tools to support diagnosis—computational pathology. The reliability and performance of these tools depend on the whole-slide image (WSI) quality being guaranteed a priori. Pre-analytical quality control step that underpins this guarantee, and artifact detection remains largely qualitative and is frequently overlooked in routine digital pathology. This operational feasibility study evaluated whether an adaptation of GrandQC, an open-source AI tool, enables automated, quantitative artifact assessment of a complete single-day biopsy workload from a high-throughput digital pathology laboratory, analyzed retrospectively.
Material and methods: A random biopsies day of 2025 at Centro de Anatomia Patológica Germano de Sousa (CAPGS) was selected as a sample to test the performance of GrandQC on the WSI generated (n = 544) in order to simulate the daily workflow. A script was created to quantify the pixels corresponding to the type of artifact automatically, creating an Excel file for registering and statistical analysis.
Results: Analysis took a median of 24 s per WSI, detecting a median of 1.46% of tissue area with some type of artifact. Dark Spots and blurring areas were the most representative detected artifacts.
Conclusion: GrandQC is a valuable tool in the quantitative quality control of biopsies tissue, allowing quick evaluation, signaling types of artifacts, and identifying cases that need to be reviewed before being handed over to the pathologist allowing the recognition of opportunities to improve laboratory histology quality and precision medicine.

Introduction

Digital pathology represents a profound transformation in pathological anatomy lab, enabling the transition from conventional microscopes to the computational analysis of digitized histological slides—whole-slide images (WSI).[1–6] At the heart of this revolution is deep learning (DL), an advanced artificial intelligence (AI) technology that uses neural networks to analyze these digital images. DL systems have demonstrated their ability to achieve remarkable accuracy, rivaling that of human pathologists in tasks such as prostate cancer detection, where accuracy can exceed 98%,[7] in support in routine, laborious, and repetitive situations such as the determination of the grade of infection by *Helicobacter pylori*, mitosis scoring in breast cancer, as well as in the determination of predictive biomarkers without the use of complementary diagnostic techniques such as HER2, microsatellite instability, and EGFR mutations, despite these resources only being available for research.[8–12] This change enables the integration of DL algorithms for

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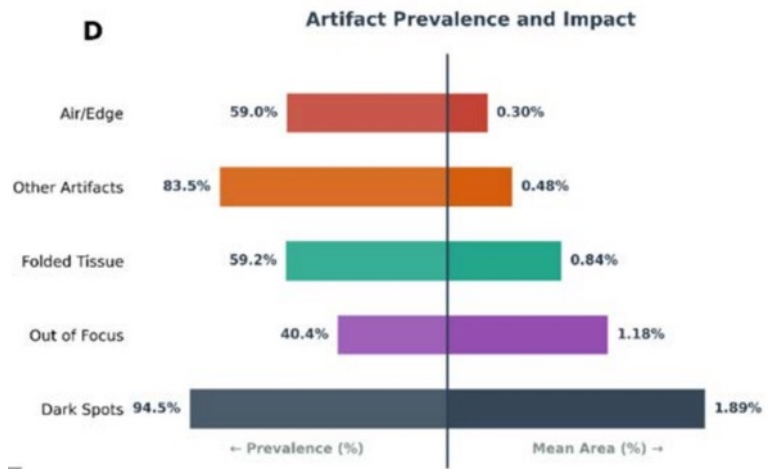
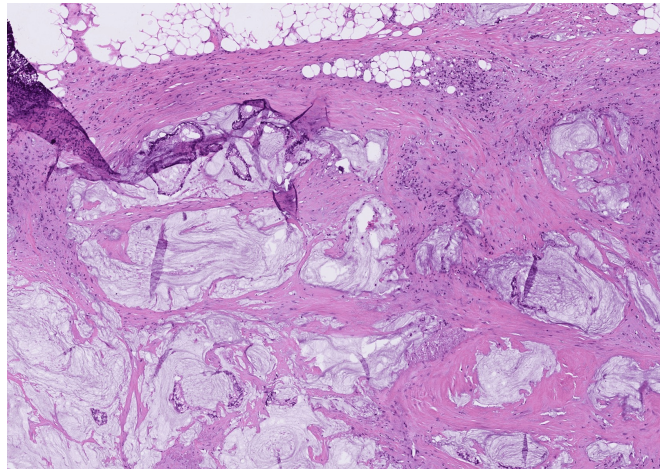
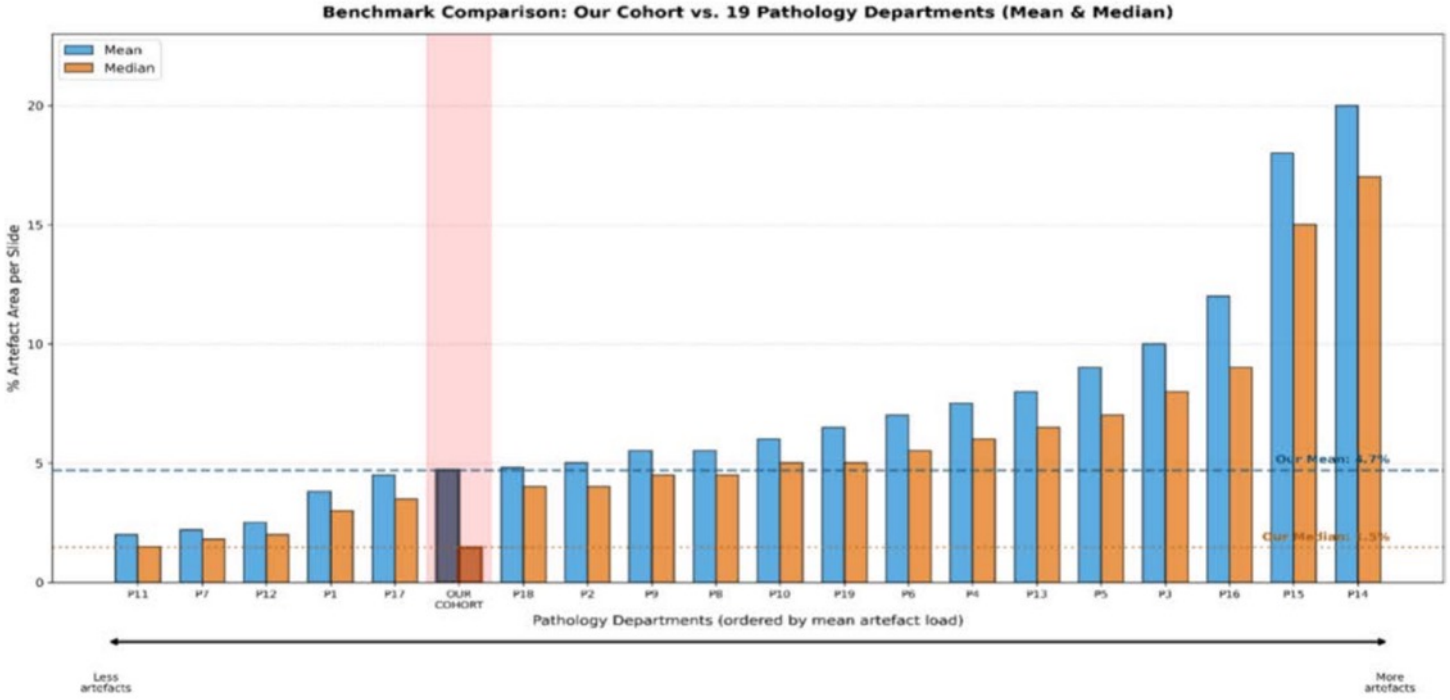
Received 25 January 2026; Received in revised form 3 June 2026; Accepted 6 June 2026
Available online 11 June 2026

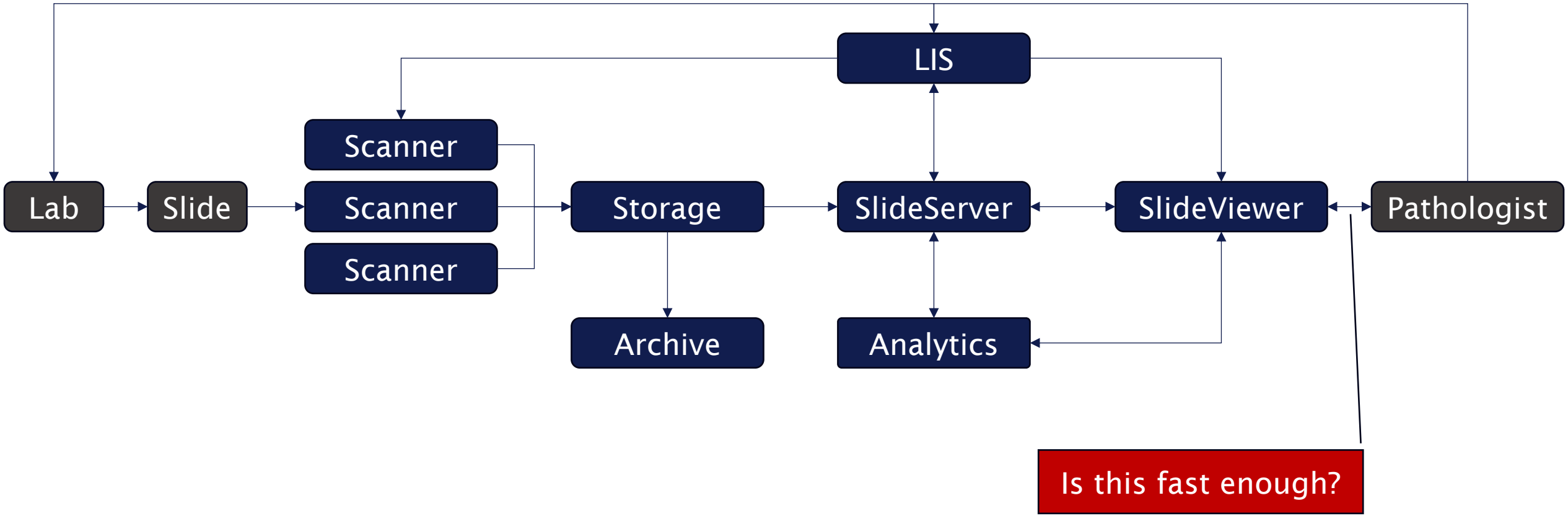


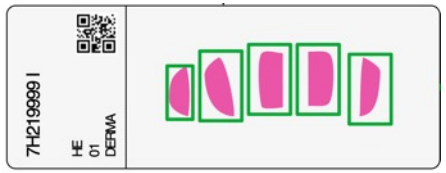




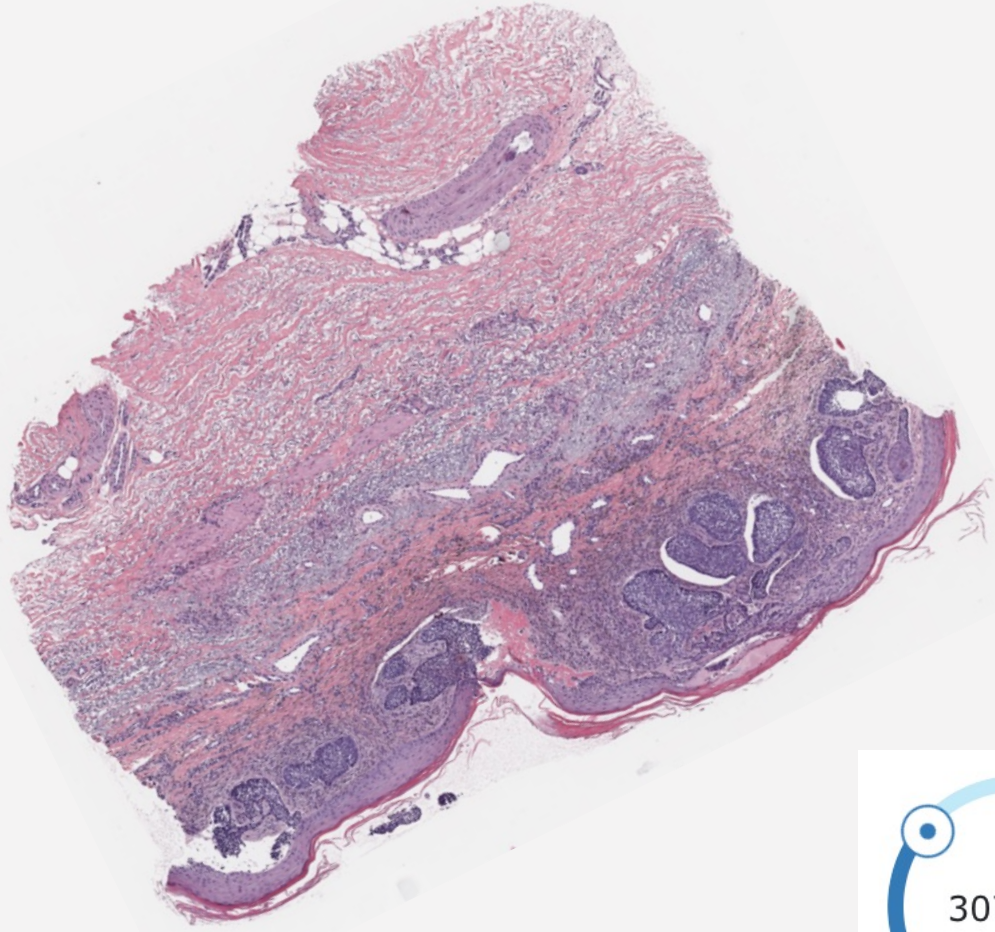
Histologic image source: https://github.com/cpath-ukk/grandqc [Accessed 20260706]

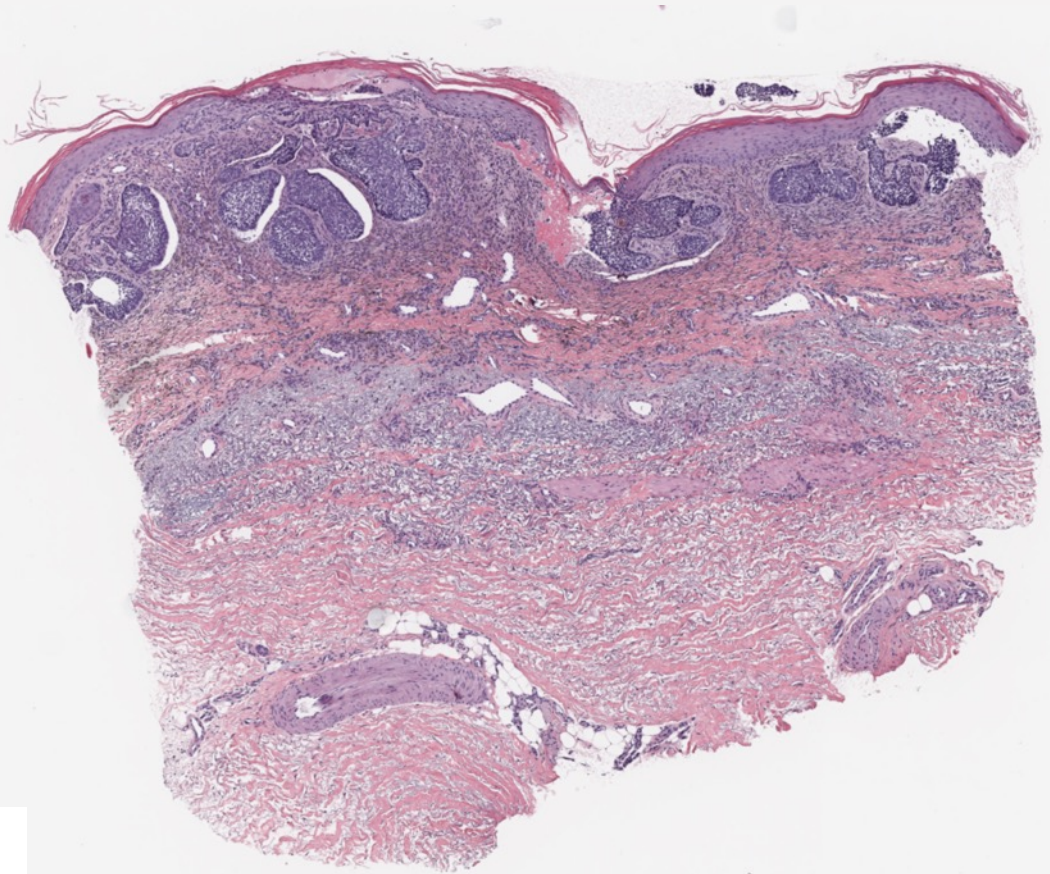
A simplified topology of digital pathology





- Reducing review time
- Reducing navigation burden






307 deg

Proceedings of Machine Learning Research – 315:322–341, 2026 Full Paper – MIDL 2026 submission

Orientation Normalization of Multi-Stain Skin Tissue Cross-Sections

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Evi Paulides[1]
Willeke A. M. Blokx[3]
Mitko Veta[1]
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Editors: Accepted for publication at MIDL 2026

Abstract

Efficient examination of skin tissue specimens is key for pathologists to keep up with an increasing workload. Normalizing the orientation of tissue cross-sections before manual assessment could contribute to a more streamlined digital workflow. In this study, we compare multiple deep learning-based approaches for predicting the rotation angle required to correct the misorientation of skin tissue cross-sections. The models were developed and evaluated using a dataset of 10,649 H&E-stained and 9,731 IHC-stained cross-section images from specimens with melanocytic lesions. Our results show that framing rotation angle prediction as a classification task with the circular target space divided into separate classes performed best, reaching mean absolute errors of 2.77° and 3.56° on the test sets of H&E and IHC-stained cross-sections, respectively, approaching the level of human annotators. Automated orientation normalization, when implemented in whole slide image viewers, could make tissue examination more efficient and convenient for pathologists, while also serving as a valuable preprocessing step for the development of position-aware or multi-stain deep learning models.

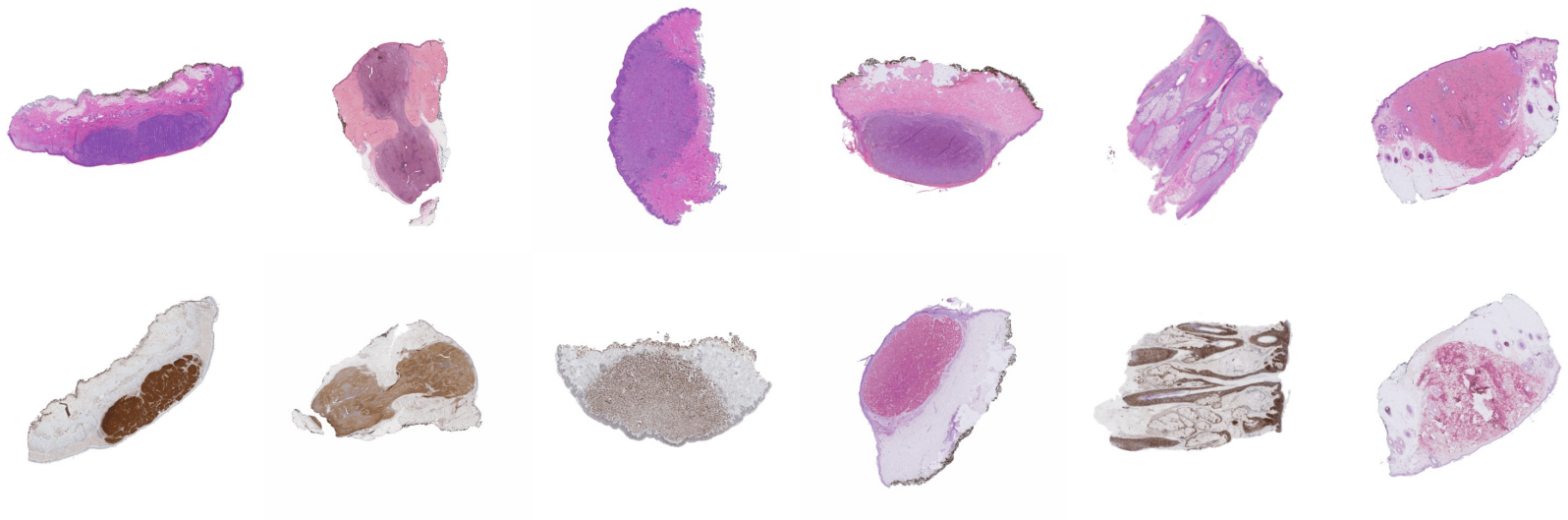
Keywords: Classification, Regression, Rotation Angle, Computational Pathology, Melanoma

1. Introduction

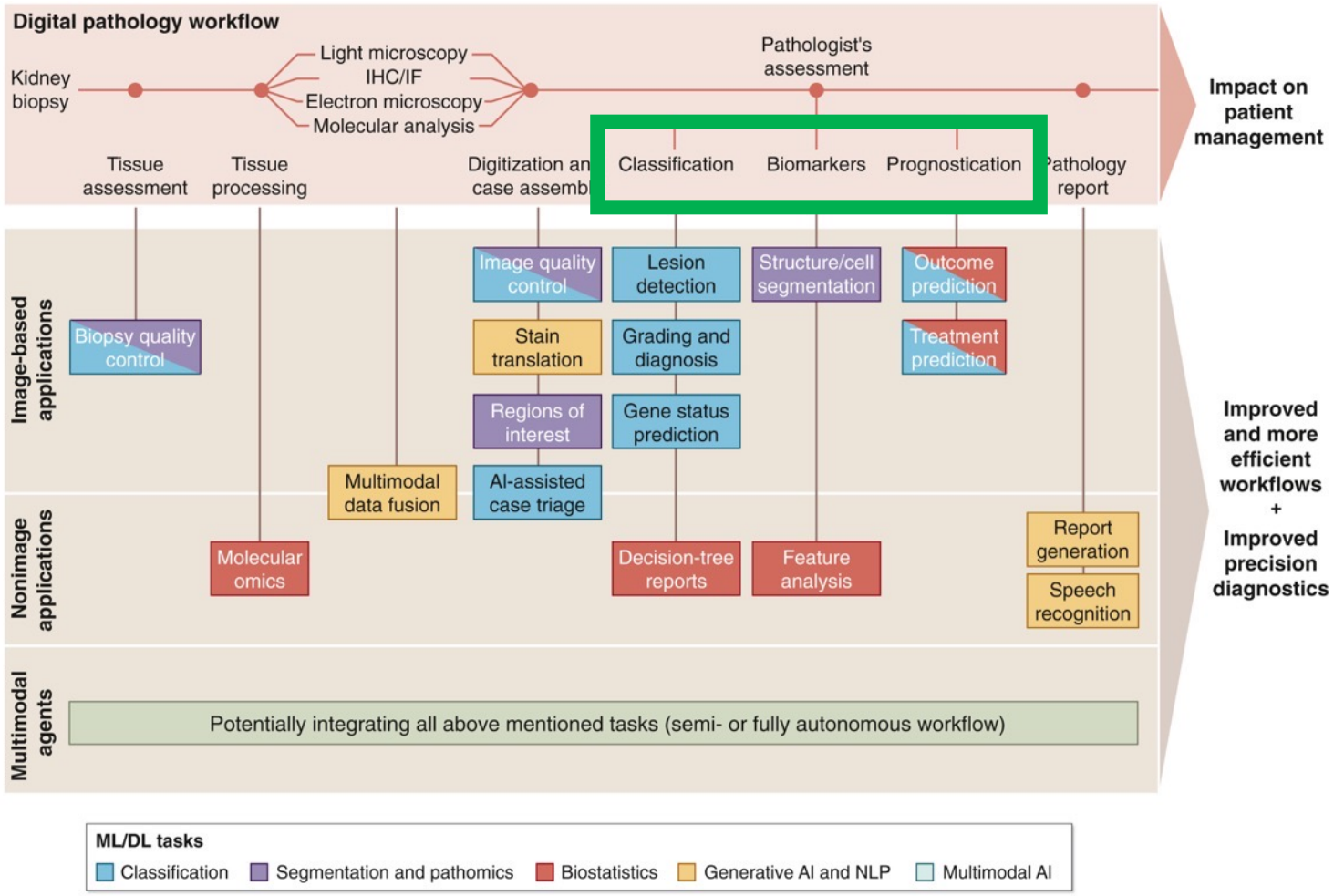
Whole slide imaging has enabled the transition from conventional, microscope-based tissue examination to fully digital pathology diagnostics, offering benefits such as digital archiving, remote working, as well as computational image analysis to assist pathologists (Stathonikos et al., 2013, 2020). Before a tissue specimen can be examined, however, it undergoes a histological preparation process, which includes tissue fixation, paraffin embedding, microtome sectioning, and staining. During the preparation process, tissue sections are often placed on the glass slides with an arbitrary orientation. Unlike tissue sections of most organ types, cross-sections of skin tissue specimens typically have an ideal orientation (i.e., the epidermis positioned at the top to reflect the natural outside-to-inside structure) and are, therefore, frequently misoriented, impeding optimal histological examination.

Model with **mean absolute errors of 2.77°-3.56°**

1. Automated rotation is possible
2. Relevant publications in computational medicine come from conferences (MIDL 2026)
3. The model is open source & free to use: https://huggingface.co/RTLucassen/orientation_normalization



→ Automated analyses can provide unprecented **insight and** improve workflow **efficiency**



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ORIGINAL ARTICLE

Weakly supervised deep learning image analysis can differentiate melanoma from naevi on haematoxylin and eosin-stained histopathology slides

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[5]Charles Perkins Centre, The University of Sydney, Sydney, New South Wales, Australia

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Royal College of Pathologists of Australasia, Grant/Award Number: PostgraduateResearchFellowship2022; University of Sydney; National Health and Medical Research Council, Grant/Award Number: 2022/GNT2018514; Melanoma Institute Australia; Tour de Cure Ltd, Grant/Award Number: GC0103-2022

Abstract

Background: The broad histomorphological spectrum of melanocytic pathologies requires large data sets to develop accurate and generalisable deep learning (DL)-based diagnostic pathology classifiers. Weakly supervised DL promotes utilisation of larger training data sets compared to fully supervised (patch annotation) approaches.

Objectives: To evaluate weakly supervised DL image classifiers for discriminating melanomas from naevi on haematoxylin and eosin (H&E)-stained pathology slides.

Methods: A representative H&E slide for 260 naevi and 260 melanomas from mucocutaneous sites at one tertiary institution was digitized. Clinicopathological features were recorded for each case including thickness and histological subtype. Whole-slide or whole-tissue section labels were applied. The ground truth was established by consensus diagnosis from two pathologists. Multiple-instance learning models, Trans-MIL, CLAM and DTFD-MIL were evaluated at 10×, 20× and 40× magnifications using stratified fivefold Monte Carlo cross-validation, with 80/10/10 splits for training/validation/test groups, to predict melanoma from naevus. Heatmaps were generated to understand model performance.

Results: Naevi cases were younger (median age: 51 years; melanoma median age: 71.5 years), with more balanced sex distribution (males: 48.8%, melanoma male subgroup: 64.2%). The most frequent histological subtypes of naevi and melanomas were dysplastic compound ($n = 99$, 38.1%) and superficial spreading ($n = 124$, 47.7%), respectively. Average AUC (±1 SD) for Trans-MIL, CLAM and DTFD-MIL across test groups were 0.9952 ± 0.006, 0.9925 ± 0.0052 and 0.9708 ± 0.0328, at 20× magnification, respectively. Performance of the models varied according to the magnification used. Heatmaps from the two best performing models, Trans-MIL and CLAM, generally indicated attention on appropriate tissue regions for interpretation.

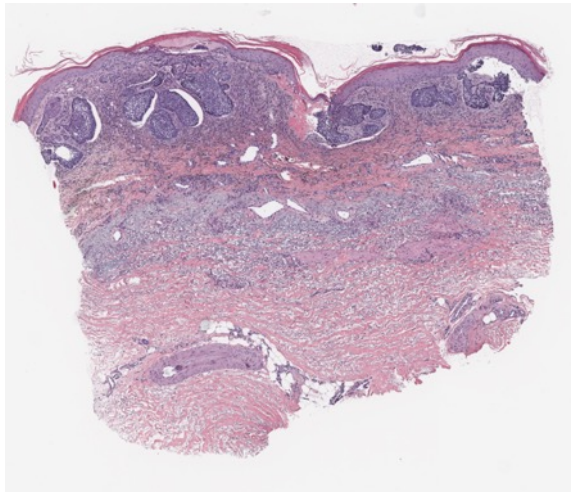
Conclusions: Weakly supervised DL on pathological slides of common mucocutaneous melanocytic tumours provides highly accurate diagnostic value for discrimination of melanomas and naevi. External validation and further assessment on less frequently occurring histologic subtypes and borderline cases using this method is required.

INTRODUCTION

Pathological diagnosis of melanomas and naevi can be challenging and subjective.[1] The development of reliable and accurate adjunctive tools to support pathologist interpretation of melanocytic pathology is required. While adjunctive tools to date have focused on immunohistochemistry stains (e.g. PRAME) and genomic ancillary

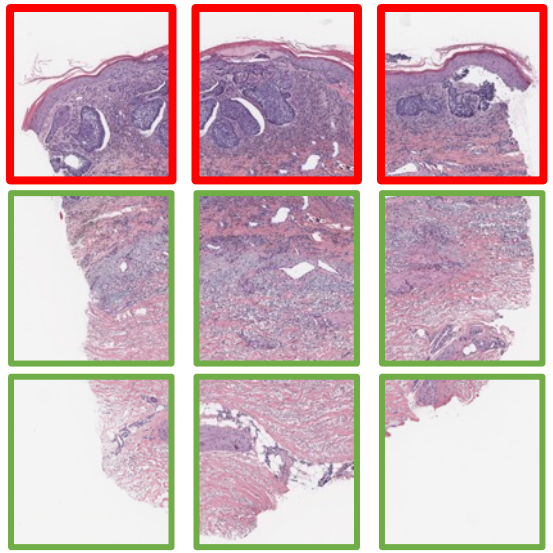
Linked article: S. P. Clark. J Eur Acad Dermatol Venereol 2024;38:2209–2210. https://doi.org/10.1111/jdv.20382.

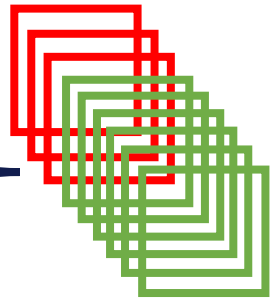
„Weakly-supervised“



“Basal cell carcinoma”

„MIL“





“Basal cell carcinoma”

Foundation models

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ORIGINAL ARTICLE

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Objectives: To evaluate weakly supervised DL image classifiers for discriminating melanomas from naevi on haematoxylin and eosin (H&E)-stained pathology slides.
Methods: A representative H&E slide for 260 naevi and 260 melanomas from mucocutaneous sites at one tertiary institution was digitized. Clinicopathological features were recorded for each case including thickness and histological subtype. Whole-slide or whole-tissue section labels were applied. The ground truth was established by consensus diagnosis from two pathologists. Multiple-instance learning models, Trans-MIL, CLAM and DTFD-MIL were evaluated at 10×, 20× and 40× magnifications using stratified fivefold Monte Carlo cross-validation, with 80/10/10 splits for training/validation/test groups, to predict melanoma from naevus. Heatmaps were generated to understand model performance.
Results: Naevi cases were younger (median age: 51 years; melanoma median age: 71.5 years), with more balanced sex distribution (males: 48.8%, melanoma male subgroup: 64.2%). The most frequent histological subtypes of naevi and melanomas were dysplastic compound ($n = 99$, 38.1%) and superficial spreading ($n = 124$, 47.7%), respectively. Average AUC (±1 SD) for Trans-MIL, CLAM and DTFD-MIL across test groups were 0.9952 ± 0.006, 0.9925 ± 0.0052 and 0.9708 ± 0.0328, at 20× magnification, respectively. Performance of the models varied according to the magnification used. Heatmaps from the two best performing models, Trans-MIL and CLAM, generally indicated attention on appropriate tissue regions for interpretation.
Conclusions: Weakly supervised DL on pathological slides of common mucocutaneous melanocytic tumours provides highly accurate diagnostic value for discrimination of melanomas and naevi. External validation and further assessment on less frequently occurring histologic subtypes and borderline cases using this method is required.

INTRODUCTION

Pathological diagnosis of melanomas and naevi can be challenging and subjective.[1] The development of reliable and accurate adjunctive tools to support pathologist interpretation of melanocytic pathology is required. While adjunctive tools to date have focused on immunohistochemistry stains (e.g. PRAME) and genomic ancillary

Linked article: S. P. Clark. J Eur Acad Dermatol Venereol 2024;38:2209–2210. https://doi.org/10.1111/jdv.20382.

Full dataset: 260 naevi + 260 melanomas
Average AUC: 0.99

Histological Subtype	Test Fold 1, *n* (%) (*N*=52)	Test Fold 2, *n* (%) (*N*=52)	Test Fold 3, *n* (%) (*N*=52)	Test Fold 4, *n* (%) (*N*=52)	Test Fold 5, *n* (%) (*N*=52)
Naevus subtype (*n*=26)					
Dysplastic compound	7 (13.5)	11 (21.2)	10 (19.2)	11 (21.2)	10 (19.2)
Dysplastic junctional	6 (11.5)	3 (5.8)	4 (7.7)	5 (9.6)	3 (5.8)
Dermal	7 (13.5)	10 (19.2)	7 (13.5)	7 (13.5)	6 (11.5)
Common compound	3 (5.8)	0 (0)	2 (3.8)	1 (1.9)	4 (7.7)
Blue	2 (3.8)	1 (1.9)	2 (3.8)	2 (3.8)	1 (1.9)
Combined	1 (1.9)	1 (1.9)	0 (0)	0 (0)	2 (3.8)
Acral	0 (0)	0 (0)	1 (1.9)	0 (0)	0 (0)
Melanoma subtype (*n*=26)					
Superficial spreading	10 (19.2)	11 (21.2)	12 (23.1)	11 (21.2)	10 (19.2)
Nodular	6 (11.5)	2 (3.8)	2 (3.8)	7 (13.5)	7 (13.5)
Lentigo maligna (invasive)	2 (3.8)	7 (13.5)	7 (13.5)	3 (5.8)	4 (7.7)
Pure desmoplastic	3 (5.8)	0 (0)	1 (1.9)	1 (1.9)	0 (0)
Mixed desmoplastic	0 (0)	2 (3.8)	1 (1.9)	1 (1.9)	0 (0)
Metastasis	1 (1.9)	1 (1.9)	1 (1.9)	2 (3.8)	1 (1.9)
Acral	2 (3.8)	1 (1.9)	2 (3.8)	1 (1.9)	2 (3.8)
Melanoma in-situ	1 (1.9)	1 (1.9)	0 (0)	0 (0)	2 (3.8)
Mucosal	1 (1.9)	1 (1.9)	0 (0)	0 (0)	0 (0)

npj | biomedical innovations Article

https://doi.org/10.1038/s44385-025-00013-1

Artificial intelligence-based triaging of cutaneous melanocytic lesions

Check for updates

Ruben T. Lucassen[1,2], Nikolas Stathonikos[1], Gerben E. Breimer[1], Mitko Veta[2,3] & Willeke A. M. Blokx[1,3]

Pathologists are facing an increasing workload due to a growing volume of cases and the need for more comprehensive diagnoses. Aiming to facilitate workload reduction and faster turnaround times, we developed an artificial intelligence (AI) model for triaging cutaneous melanocytic lesions based on whole slide images. The AI model was developed and validated using a retrospective cohort from the University Medical Center Utrecht, the Netherlands. The dataset consisted of 52,202 whole slide images from 27,167 unique specimens, acquired from 20,707 patients. Specimens with only benign common nevi, also known as moles, were assigned to the low complexity category (86.6%). In contrast, specimens with any other melanocytic lesion subtype, including non-common nevi, melanocytomas, and melanomas, were assigned to the high complexity category (13.4%). The dataset was split on patient level into a development set (80%) and test sets (20%) for independent evaluation. Predictive performance was primarily measured using the area under the receiver operating characteristic curve (AUROC) and the area under the precision–recall curve (AUPRC). A simulation experiment was performed to study the effect of implementing AI-based triaging in the clinic. The AI model reached an AUROC of 0.966 (95% CI, 0.960–0.972) and an AUPRC of 0.857 (95% CI, 0.836–0.877) on the in-distribution test set, and an AUROC of 0.899 (95% CI, 0.860–0.934) and an AUPRC of 0.498 (95% CI, 0.360–0.639) on the out-of-distribution test set. In the simulation experiment, using random case assignment as baseline, AI-based triaging prevented an average of 43.9 (95% CI, 36–55) initial examinations of high complexity cases by general pathologists for every 500 cases. In conclusion, the AI model achieved a strong predictive performance in differentiating between cutaneous melanocytic lesions of high and low complexity. The improvement in workflow efficiency due to AI-based triaging could be substantial.

Cutaneous melanoma is the fifth most common cancer in both the United States and the Netherlands[1,2]. Over the last decades, the incidence rate of melanoma has consistently increased. In 2023, more than 97,000 people in the United States and more than 8000 people in the Netherlands were diagnosed with this type of skin cancer. Because of the relatively high risk of metastasis in melanoma patients, after which the prognosis significantly worsens, it is crucial to combine early detection, correct diagnosis, and fast treatment[3].

Melanocytic skin lesions are clusters of pigment-producing cells called melanocytes, which range in terms of biological behavior from benign (nevus, also known as mole), intermediate (melanocytoma), to malignant (melanoma)[4]. Most of these lesions are benign and can be confidently diagnosed based only on microscopic examination of hematoxylin and eosin (H&E)-stained tissue cross-sections. However, differentiating between some subtypes of melanocytic tumors is more challenging, with studies reporting low inter- and intra-observer agreement[5,6]. Particularly for these ambiguous cases, immunohistochemical (IHC) staining and molecular testing can be helpful in making the correct diagnosis, at the cost of prolonging the turnaround time by days to weeks[7,8]. While all melanocytic lesions should ideally be examined by specialized dermatopathologists, in many centers also general pathologists have to contribute to the examination of these lesions. To make matters worse, due to a growing volume of cases and the need for more comprehensive diagnoses, the workload for pathologists is expected to further increase[9].

The transition to fully digital pathology departments enables the implementation of artificial intelligence (AI) models for workflow

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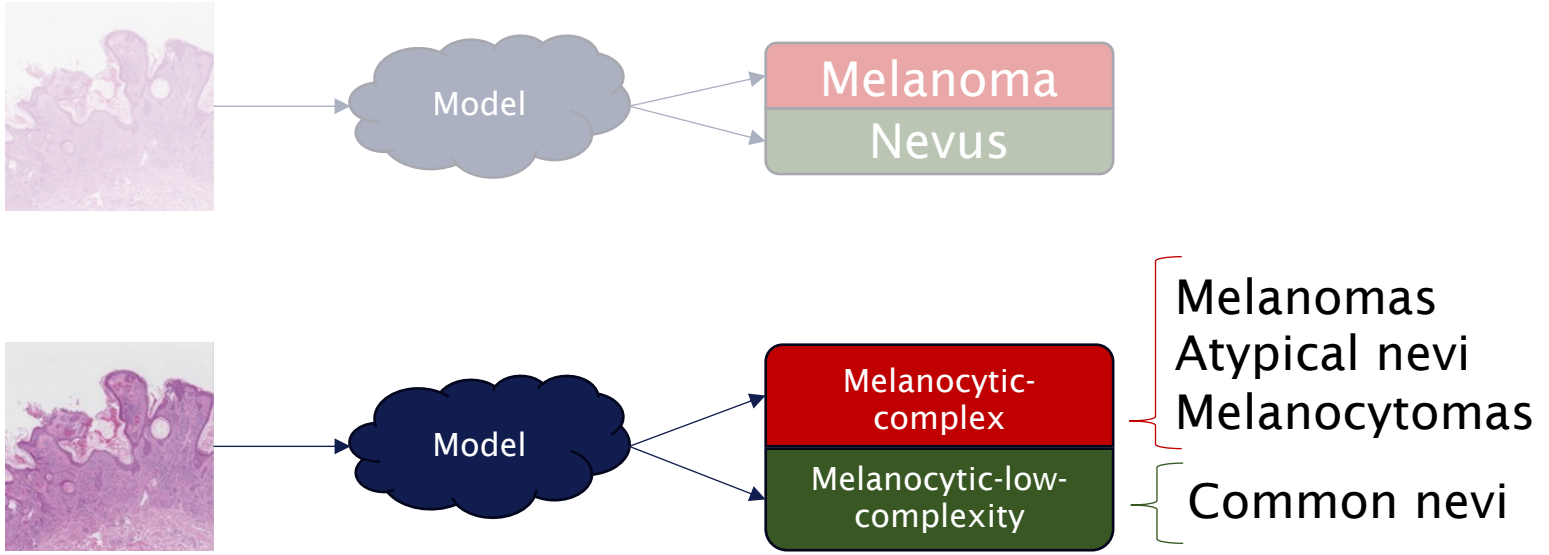


[…] AUROC of 0.966 […]

AI-based triaging **prevented** an average of **43.9** (95% CI, 36–55) **initial examinations of high complexity** cases by general pathologists for every 500 cases.

Spitz Tumors

HE+MelanA

3D

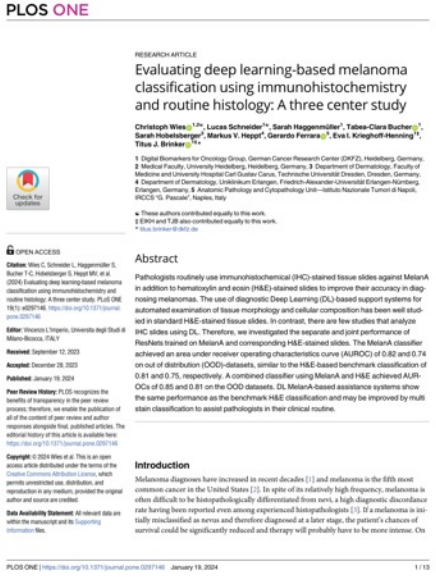
Melanoma subtypes

Comparison to experts


Journal of Pathology Informatics

Artificial intelligence-based classification of Spitz tumors

Ruben T. Lucassen, Marjanna Romers, Chiel F. Ebbelaar, Aia N. Najem, Donal P. Hayes, Antien L. Mooyaart, Sara Roshani, Liliane C.D. Wynaendts, Nikolas Stathonikos, Gerben E. Breimer, Anne M.L. Jansen, Mitko Veta, Willeke A.M. Blokx


PLOS ONE

Evaluating deep learning-based melanoma classification using immunohistochemistry and routine histology: A three center study

Christoph Wies, Lucas Schneider, Sarah Haggenmüller, Tabea-Clara Bucher, Sarah Hobelsberger, Markus V. Heppt, Gerardo Ferrara, Eva I. Krieghoff-Henning, Titus J. Brinker

Abstract

Introduction


European Journal of Cancer

A 3-dimensional histology computer model of malignant melanoma and its implications for digital pathology

Alexander Kurz, Dieter Krahl, Heinz Kutzner, Raymond Barnhill, Antonio Perasole, Maria Teresa Fernandez Figueras, Gerardo Ferrara, Stephan A. Braun, Hans Starz, Mar Llamas-Velasco, Jochen Sven Utikal, Stefan Fröhling, Christof von Kalle, Jakob Nikolas Kather, Lucas Schneider, Titus J. Brinker


dermatopathology

Translating Features to Findings: Deep Learning for Melanoma Subtype Prediction

Dorra Guermazi, Sarina Khenchandani, Samer Wahood, Cuong Nguyen and Elie Saliba

Abstract

1. Introduction


Research Letters

Diagnostic performance of artificial intelligence for histologic melanoma recognition compared to 18 international expert pathologists

Drew Kunaitis, MD, PhD, and Andrea Murtina, MD

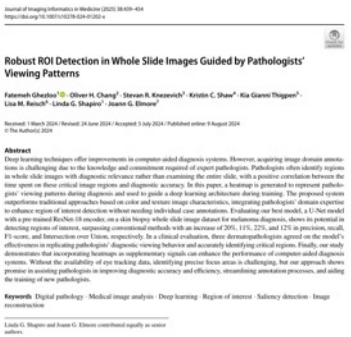
Correspondence to: Drew Kunaitis, MD, PhD, Department of Dermatology, Tulane University, 1430 Tulane Ave #8035, New Orleans, LA 70112

E-mail: dkunait@tulane.edu

Conflicts of interest

REFERENCES

ROI detection


Robust ROI Detection in Whole Slide Images Guided by Pathologists' Viewing Patterns

Fatemeh Ghezloo, Oliver H. Chang, Stevan R. Knezevich, Kristin C. Shaw, Kia Gianni Thigpen, Lisa M. Reisch, Linda G. Shapiro, Joann G. Elmore

Abstract

Keywords: Digital pathology · Medical image analysis · Deep learning · Region of interest · Saliency detection · Image reconstruction

And many others…


cancers

Deep Learning Approach to Classify Cutaneous Melanoma in a Whole Slide Image

Meng Li, Makoto Abe, Shigeo Nakano and Masayuki Tsuneki

Abstract: Although the histopathological diagnosis of cutaneous melanocytic lesions is fairly accurate and reliable among experienced surgical pathologists, it is not perfect in every case (especially melanoma). Microscopic examination–clinicopathological correlation is the gold standard for the definitive diagnosis of melanoma. Pathologists may encounter diagnostic controversies when melanoma closely mimics Spitz's nevus or blue nevus, exhibits amelanotic histopathology, or is in situ. It would be beneficial if diagnosing cutaneous melanocytic lesions can be automated by using deep learning, particularly when assisting surgical pathologists with their workloads. In this preliminary study, we investigated the application of deep learning for classifying cutaneous melanoma in whole-slide images (WSIs). We trained models via weakly supervised learning using a dataset of 66 WSIs (33 melanomas and 33 non-melanomas). We evaluated the models on a test set of 90 WSIs (40 melanomas and 50 non-melanomas), achieving ROC–AUC at 0.021 for the WSI level and 0.936 for the tile level by the best model.

Keywords: melanoma; deep learning; cancer screening; whole slide image

1. Introduction

Melanocytic

Eczema vs. palmoplantar Psoriasis

Harnessing Digital Pathology Tools to Distinguish Hand Eczema From Palmar Psoriasis: A Quantitative Approach

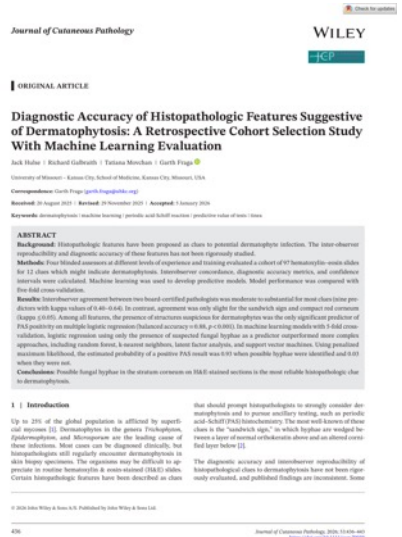
Eczema vs. Psoriasis

Vision transformer-based diagnosis of psoriasis and eczema in whole-slide histology

Drug eruption vs. Atopic dermatitis vs. Normal

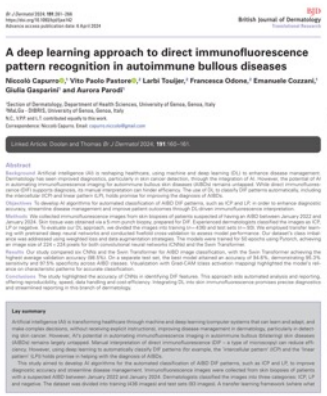
Deep Learning vs. Traditional Machine Learning in the Diagnosis of Cutaneous Drug Eruptions: A Comparative Study with Explainable AI on Whole-Slide Images

Dermatophytosis



Diagnostic Accuracy of Histopathologic Features Suggestive of Dermatophytosis: A Retrospective Cohort Selection Study With Machine Learning Evaluation

AIBD (DIF)



A deep learning approach to direct immunofluorescence pattern recognition in autoimmune bullous diseases

Inflammatory vs. Lymphoma

Eczema vs. Lymphoma

Semantic Segmentation of Histopathological Slides for the Classification of Cutaneous Lymphoma and Eczema

Inflammatory & Lymphoma

BCC + Subtyping

Medical Image Analysis

Detection and subtyping of basal cell carcinoma in whole-slide histopathology using weakly-supervised learning

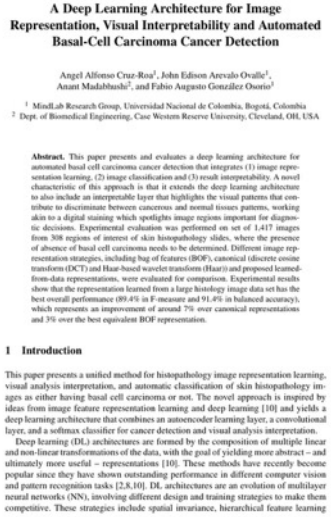
Daan J. Geijs, Stephan Dooper, Witali Aswolinskiy, Lisa M. Hillen, Avital L. Amir, Geert Litjens

ARTICLE INFO

ABSTRACT

1. Introduction

BCC



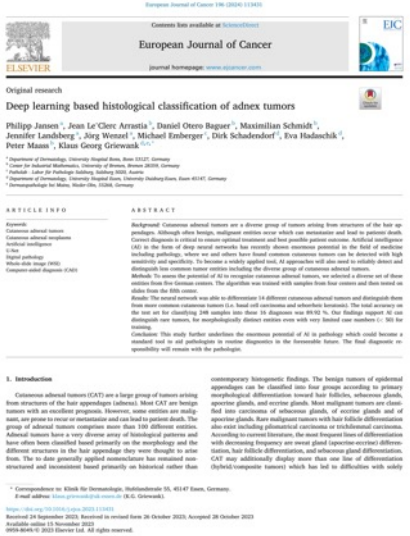
A Deep Learning Architecture for Image Representation, Visual Interpretability and Automated Basal-Cell Carcinoma Cancer Detection

Angel Alfonso Cruz-Roa, John Edison Arevalo Ovalle, Anant Madabhushi, and Fabio Augusto González Osorio

Abstract. This paper presents and evaluates a deep learning architecture for automated basal cell carcinoma cancer detection that integrates (1) image representation learning, (2) image classification and (3) result interpretability. A novel characteristic of this approach is that it extends the deep learning architecture to also include an interpretable layer that highlights the visual patterns that contribute to discriminate between cancerous and normal tissues patterns, working akin to a digital staining which spotlights image regions important for diagnostic decisions. Experimental evaluation was performed on set of 1,417 images from 308 regions of interest of skin histopathology slides, where the presence of absence of basal cell carcinoma needs to be determined. Different image representation strategies, including bag of features (BOF), canonical (discrete cosine transform (DCT) and Haar-based wavelet transform (Haar)) and proposed learned-from-data representations, were evaluated for comparison. Experimental results show that the representation learned from a large histology image data set has the best overall performance (89.4% in F-measure and 91.4% in balanced accuracy), which represents an improvement of around 7% over canonical representations and 3% over the best equivalent BOF representation.

1 Introduction

Adnexal tumors



European Journal of Cancer

Deep learning based histological classification of adnex tumors

Philipp Jansen, Jean Le'Clerc Arrastia, Daniel Otero Baguer, Maximilian Schmidt, Jennifer Landsberg, Jörg Wenzel, Michael Emberger, Dirk Schadendorf, Eva Hadaschik, Peter Maass, Klaus Georg Griewank

ARTICLE INFO

ABSTRACT

1. Introduction

SCC vs. Verruca vulg.

ORIGINAL ARTICLE

An artificial intelligence model of whole-slide pathology specimens differentiating cutaneous high-grade squamous proliferations

Anne Petzold, Anja Wessely, Michael Erdmann, Stefan Schliep, Stephan Schremi, Luis Carlos Rivera Monroy, Julio Vera, Konstantin Drexler, Dennis Niebel, Kinan Maurice Hayani, Franklin Kiesewetter, Carola Berking, Elias A. T. Koch, Markus V. Heppt

Abstract

Abbreviations

Introduction

BCC

Artificial neural networks and pathologists recognize basal cell carcinomas based on different histological patterns

Abstract

Introduction

Bowen vs. SebK

cancers

Evaluation of a Deep Learning Approach to Differentiate Bowen's Disease and Seborrheic Keratosis

Simple Summary: Bowen's disease (malignant) and seborrheic keratosis (benign) are frequent cutaneous neoplasms. Our study assessed the potential of artificial intelligence to distinguish these entities histologically. A dermatopathologist trained deep learning network diagnosed Bowen's disease and seborrheic keratosis with AUCs of 0.9958 and 0.9766 and sensitivities of 0.9511 and 0.9396, respectively. The algorithm proved robust to slides prepared in three different labs and two different scanner models. Nevertheless, challenges, such as distinguishing irritated seborrheic keratosis from Bowen's disease remained. We believe our findings demonstrate that deep learning algorithms can aid in clinical routine; however, results should be confirmed by qualified histopathologists.

Abstract: Background: Some of the most common cutaneous neoplasms are Bowen's disease and seborrheic keratosis, a malignant and a benign proliferation, respectively. These entities represent a significant fraction of a dermatopathologists' workload, and in some cases, histological differentiation may be challenging. The potential of deep learning networks to distinguish these diseases is assessed. Methods: In total, 1955 whole-slide images from three institutions were scanned on two different slide scanners. A U-Net-based segmentation deep learning algorithm was trained on data from one of the centers to differentiate Bowen's disease, seborrheic keratosis, and normal tissue, learning from annotations performed by dermatopathologists. Optimal thresholds for the class distinction of diagnoses were extracted and assessed on a test set with data from all three institutions. Results: We aimed to diagnose Bowen's diseases with the highest sensitivity. A good performance was observed across all three centers, underlining the model's robustness. In one of the centers, the distinction between Bowen's disease and all other diagnoses was achieved with an AUC of 0.9958 and a sensitivity of 0.9511. Seborrheic keratosis was detected with an AUC of 0.9766 and a sensitivity of 0.9396. Nevertheless, distinguishing irritated seborrheic keratosis from Bowen's disease remained challenging. Conclusions: Bowen's disease and seborrheic keratosis could be correctly identified by the evaluated deep learning model on test sets from three different centers, two of which were not involved in training, and AUC scores > 0.97 were obtained. The method proved robust to changes in the staining solution and scanner model. We believe this demonstrates that deep learning algorithms can aid in clinical routine; however, the results should be confirmed by qualified histopathologists.

Keratinocytic

Modern Pathology (2021) 34:895–903
https://doi.org/10.1038/s41379-020-00712-7

USCAP

ARTICLE

Artificial neural networks and pathologists recognize basal cell carcinomas based on different histological patterns

Susanne Kimeswenger[1,2,3] · Philipp Tschandl[4] · Petar Noack[5] · Markus Hofmarcher[6] · Elisabeth Rumetshofer[6] · Harald Kindermann[7] · Rene Silye[5] · Sepp Hochreiter[6] · Martin Kaltenbrunner[2,3] · Emmanuella Guenova[8,9] · Guenter Klambauer[6] · Wolfram Hoetzenecker[1]

Received: 1 August 2020 / Revised: 14 October 2020 / Accepted: 15 October 2020 / Published online: 13 November 2020

Abstract

Recent advances in artificial intelligence, particularly in the field of deep learning, have enabled researchers to create compelling algorithms for medical image analysis. Histological slides of basal cell carcinomas (BCCs), the most frequent skin tumor, are accessed by pathologists on a daily basis and are therefore well suited for automated prescreening by neural networks for the identification of cancerous regions and swift tumor classification.

In this proof-of-concept study, we implemented an accurate and intuitively interpretable artificial neural network (ANN) for the detection of BCCs in histological whole-slide images (WSIs). Furthermore, we identified and compared differences in the diagnostic histological features and recognition patterns relevant for machine learning algorithms vs. expert pathologists.

An attention-ANN was trained with WSIs of BCCs to identify tumor regions ($n = 820$). The diagnosis-relevant regions used by the ANN were compared to regions of interest for pathologists, detected by eye-tracking techniques.

This ANN accurately identified BCC tumor regions on images of histologic slides (area under the ROC curve: 0.993, 95% CI: 0.990–0.995; sensitivity: 0.965, 95% CI: 0.951–0.979; specificity: 0.910, 95% CI: 0.859–0.960). The ANN implicitly calculated a weight matrix, indicating the regions of a histological image that are important for the prediction of the network. Interestingly, compared to pathologists' eye-tracking results, machine learning algorithms rely on significantly different recognition patterns for tumor identification ($p < 10^{-4}$).

To conclude, we found on the example of BCC WSIs, that histopathological images can be efficiently and interpretably analyzed by state-of-the-art machine learning techniques. Neural networks and machine learning algorithms can potentially enhance diagnostic precision in digital pathology and uncover hitherto unused classification patterns.

Introduction

Digital pathology, i.e., the management and clinical interpretation of information retrieved from digitalized histology slides, aims to improve the safety, quality, and accuracy of

These authors contributed equally: Emmanuella Guenova, Guenter Klambauer, Wolfram Hoetzenecker

Supplementary information The online version of this article (https://doi.org/10.1038/s41379-020-00712-7) contains supplementary material, which is available to authorized users.

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[4] Medical University of Vienna, Department of Dermatology, Vienna, Austria

[5] Kepler University Hospital Linz, Department of Pathology and Microbiology, Linz, Austria

[6] Johannes Kepler University Linz, Institute for Machine Learning, Linz, Austria

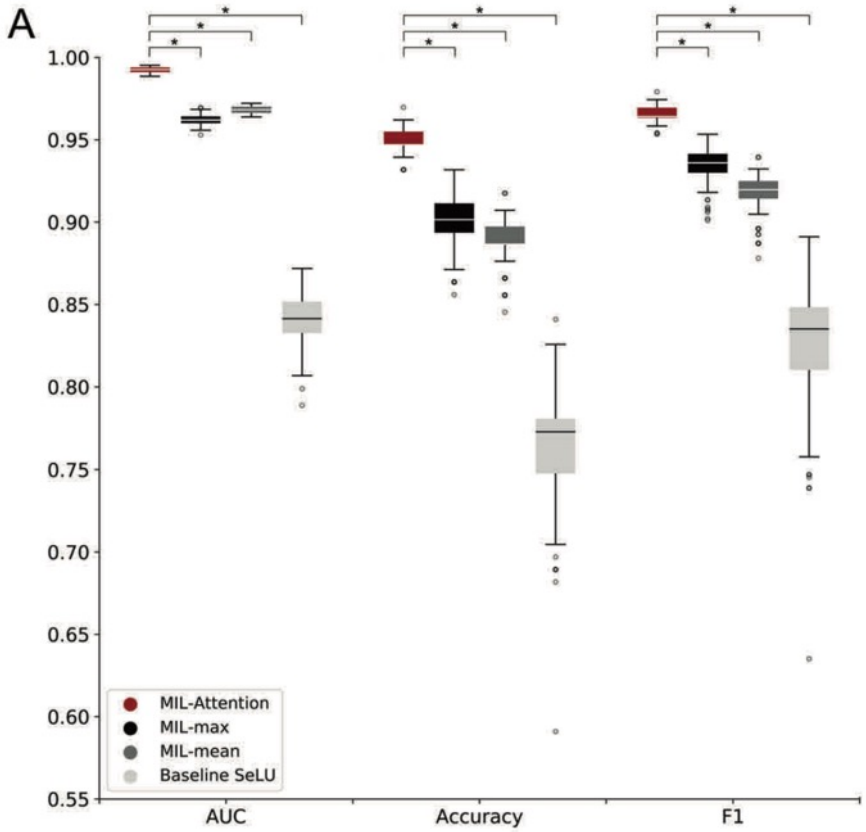
[7] University of Applied Sciences, Upper Austria, Marketing and Electronic Business, Steyr, Austria

[8] University of Lausanne, Faculty of Biology and Medicine, Department of Dermatology, Lausanne, Switzerland

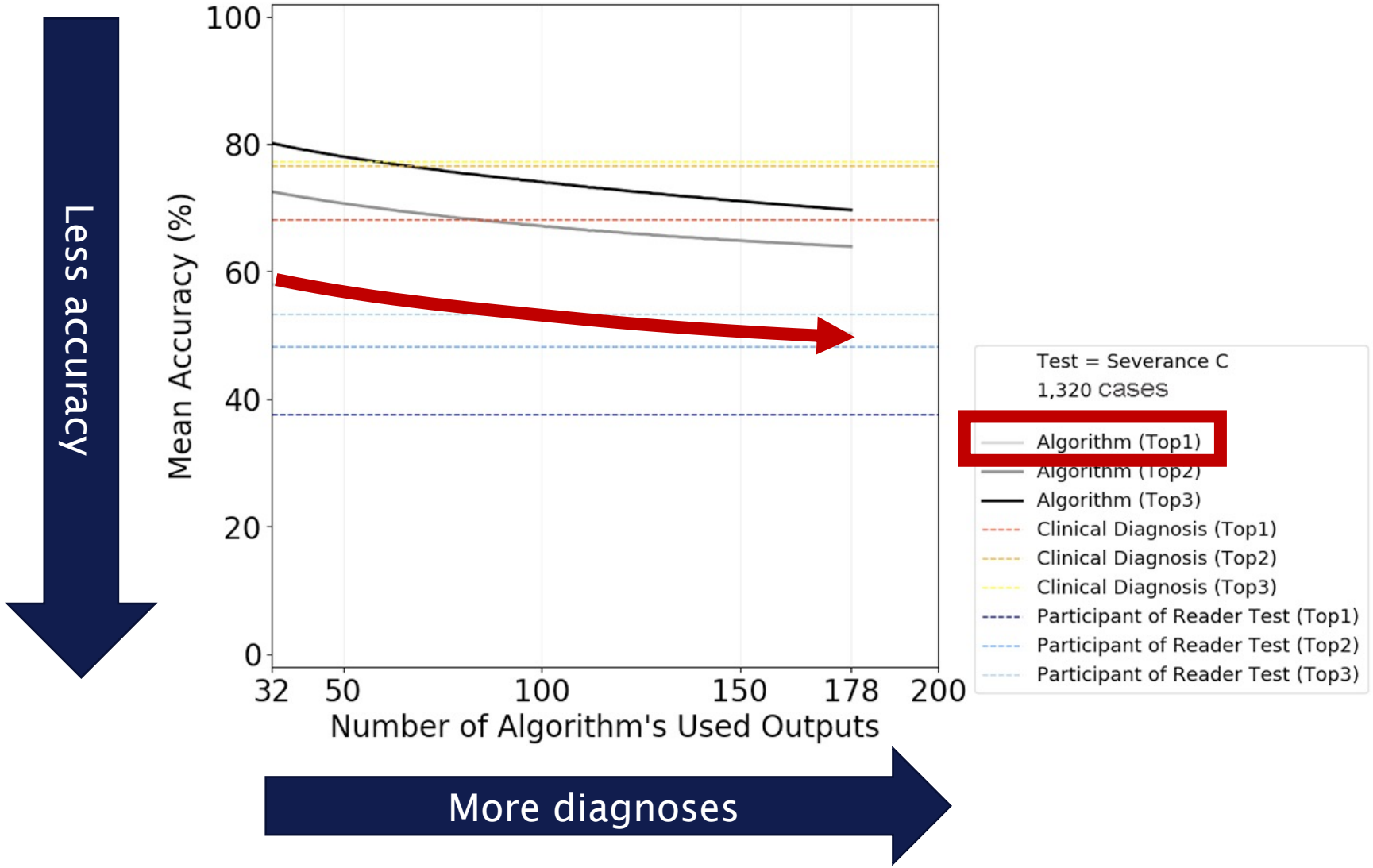
[9] University Hospital of Zurich, Department of Dermatology, Zurich, Switzerland

SPRINGER NATURE

Kimeswenger 2021: *"[…] achieved **99.3% accuracy in identifying basal cell carcinoma tumor regions** on histological slides, […]"*



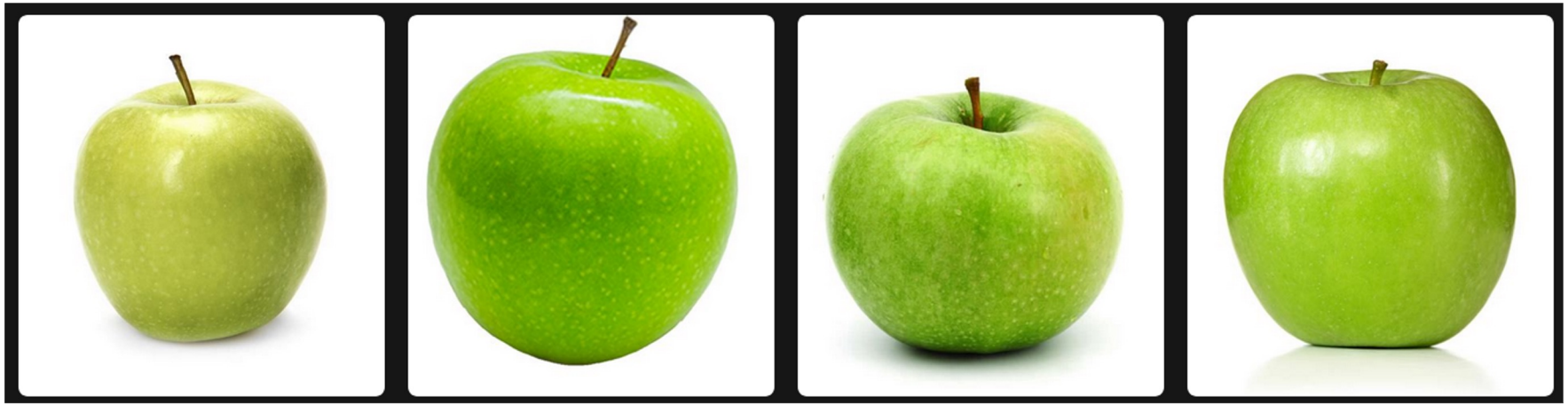
Dataset: "Sections of BCCs and normal skin"



Han SS et al Assessment of deep neural networks for the diagnosis of benign and malignant skin neoplasms in comparison with dermatologists: A retrospective validation study. PLoS Med. 2020 Nov 25;17(11):e1003381. doi: 10.1371/journal.pmed.1003381

TRAINING

“Apple“



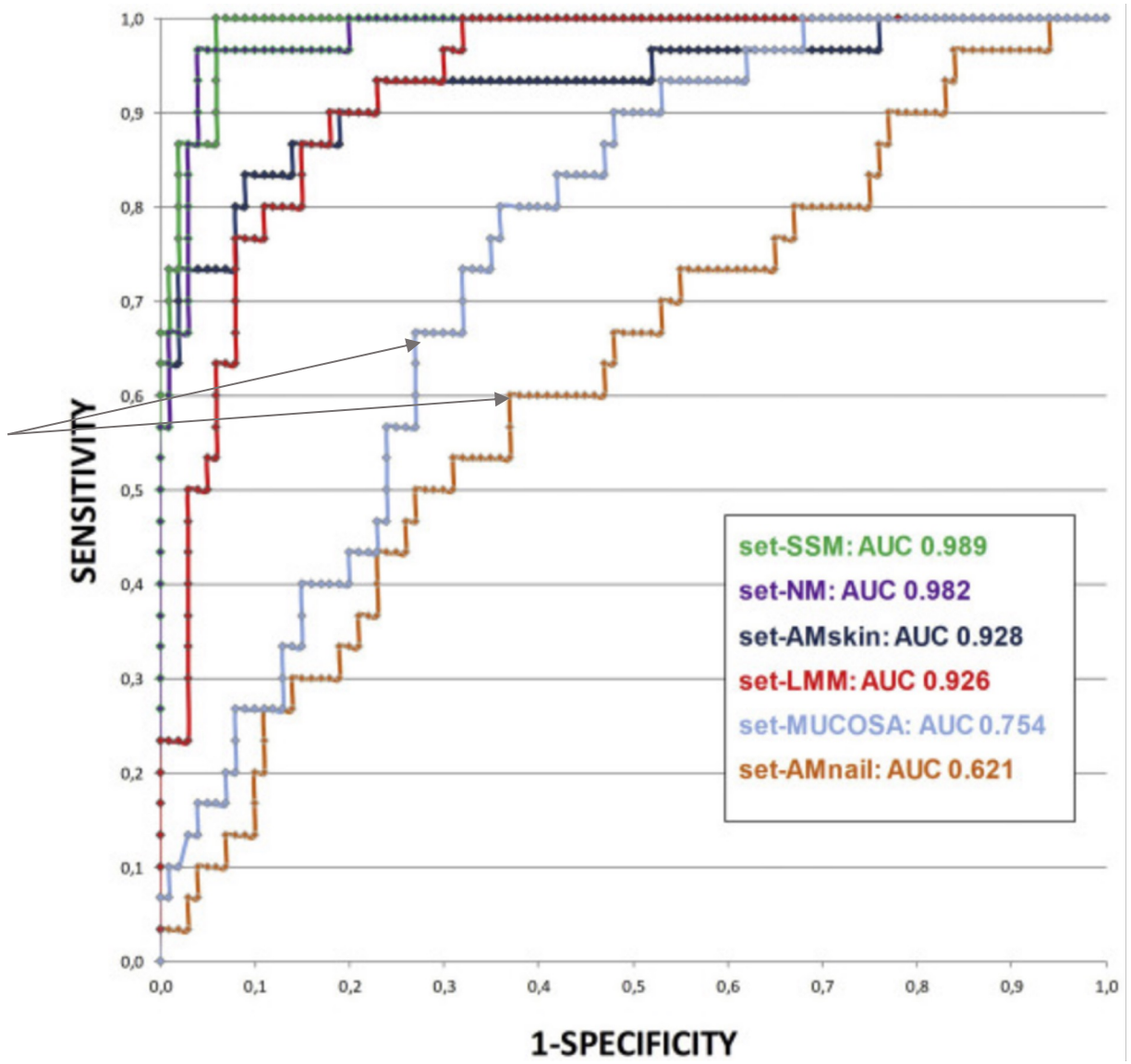
“Strawberry”

TEST

?

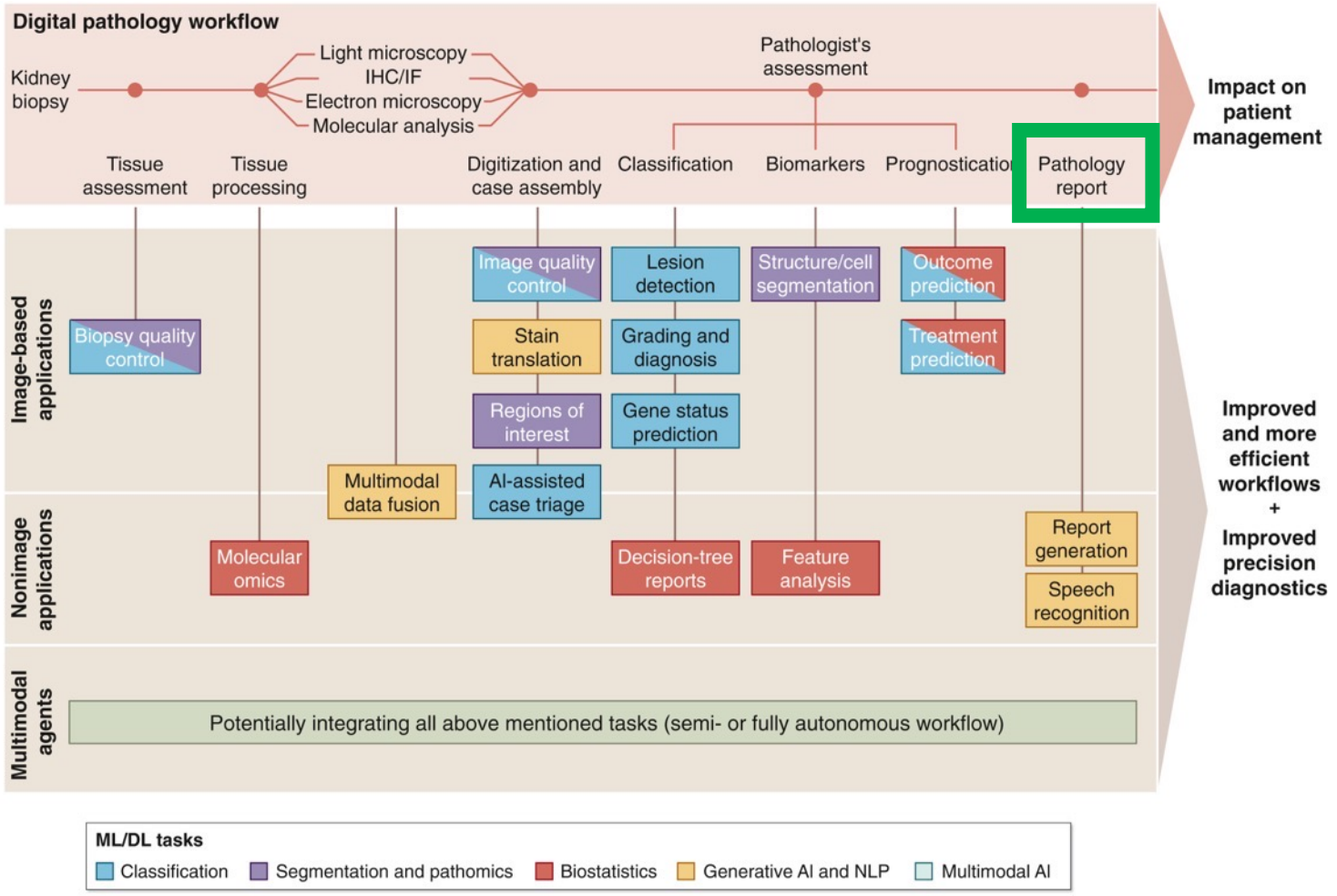
Images: duckduckgo.com - search

Special, rare and problematic subtypes often not included



Winkler JK, Sies K, Fink C, et al. Melanoma recognition by a deep learning convolutional neural network-Performance in different melanoma subtypes and localisations. *Eur J Cancer*. 2020;127:21-29. doi:10.1016/j.ejca.2019.11.020

The most relevant thing to create and evaluate a classifier **is the dataset**



Hölscher DL, Bülow RD, Strauch M, Boor P. Advances in computational nephropathology. Kidney Int. 2025 Dec;108(6):1031-1044. doi: 10.1016/j.kint.2025.06.029. Epub 2025 Sep 19. PMID: 40976424.

Hallucinations

Careless Whisper: Speech-to-Text Hallucination Harms

ALLISON KOENECKE, Cornell University, USA
ANNA SEO GYEONG CHOI*, Cornell University, USA
KATELYN X. MEI*, University of Washington, USA
HILKE SCHELLMANN†, New York University, USA
MONA SLOANE†, University of Virginia, USA

[~] **1%** of audio transcriptions contained entire **hallucinated phrases or sentences** which did not exist in any form in the underlying audio.

38% of hallucinations **include explicit harms** such as perpetuating violence, making up inaccurate associations, or implying false authority

	Dependent variable:
	Hallucination
Share of Duration Being Non-Vocal	0.951** (0.438)
Number of Words	0.056*** (0.011)
Has Aphasia	0.368* (0.204)
Is Female	−0.017 (0.168)
Age	0.044 (0.043)
Age Squared	−0.0004 (0.0004)
African American	−0.132 (0.469)
Other Race	−0.281 (0.518)
Years of Education	−0.058* (0.033)
English is First Language	−0.227 (1.035)
No Vision Loss	0.395 (1.026)
No Hearing Loss	0.500 (1.028)
Constant	−6.447*** (2.175)
Observations	10,830
Log Likelihood	−783.942
Akaike Inf. Crit.	1,593.883
Note:	*p<0.1; **p<0.05; ***p<0.01

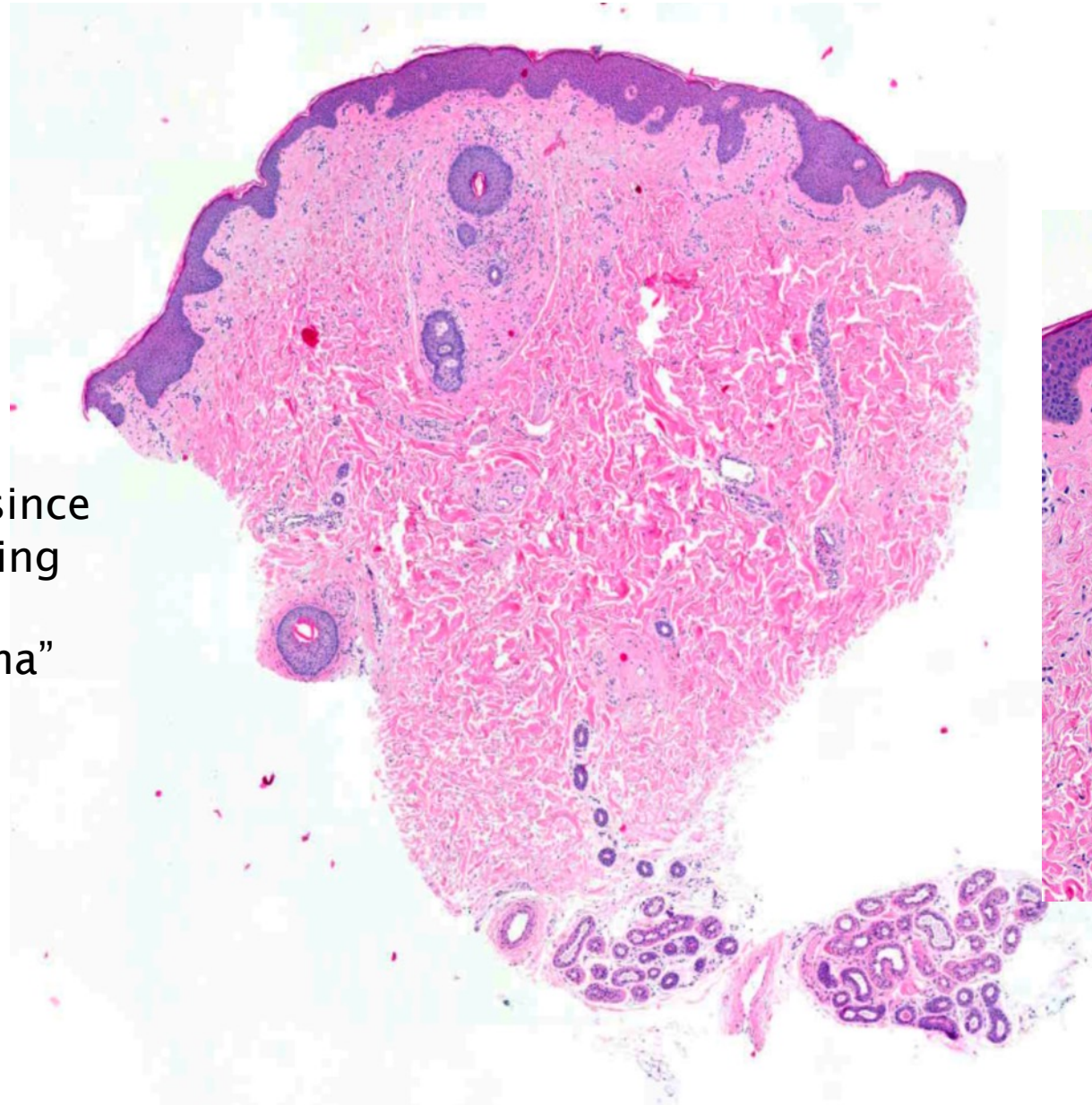
https://arxiv.org/pdf/2402.08021

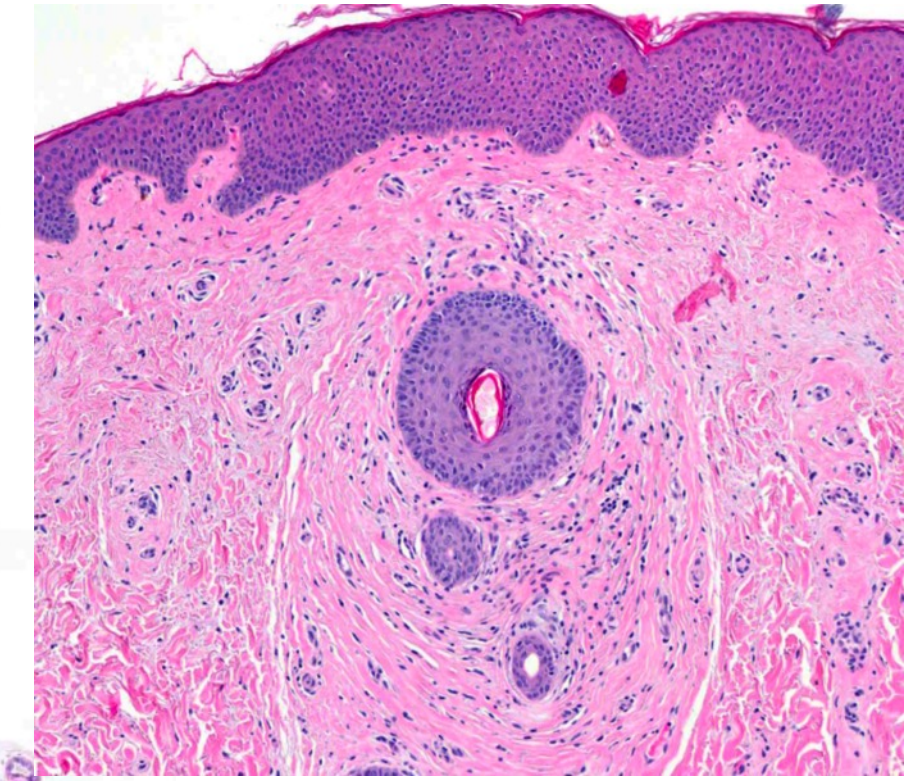
Learning with language models

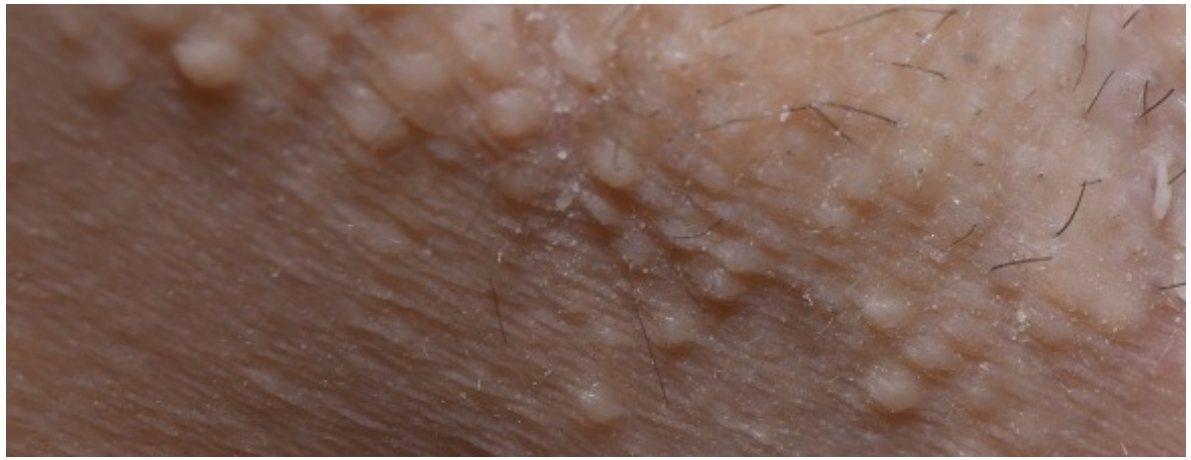
33y, female
Axillary changes since 4-5 years, increasing

”DD: Steatocystoma”

No photograph





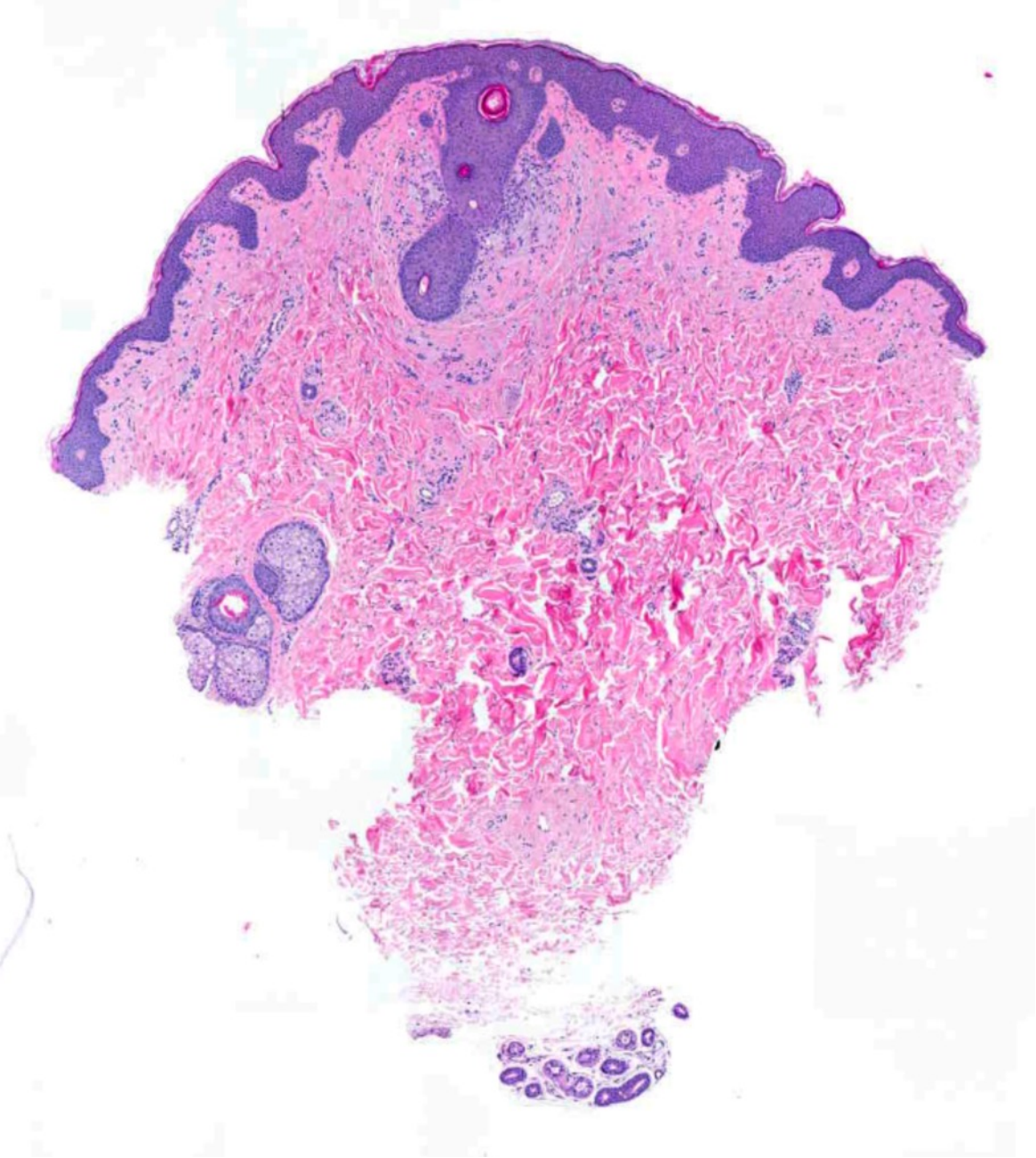


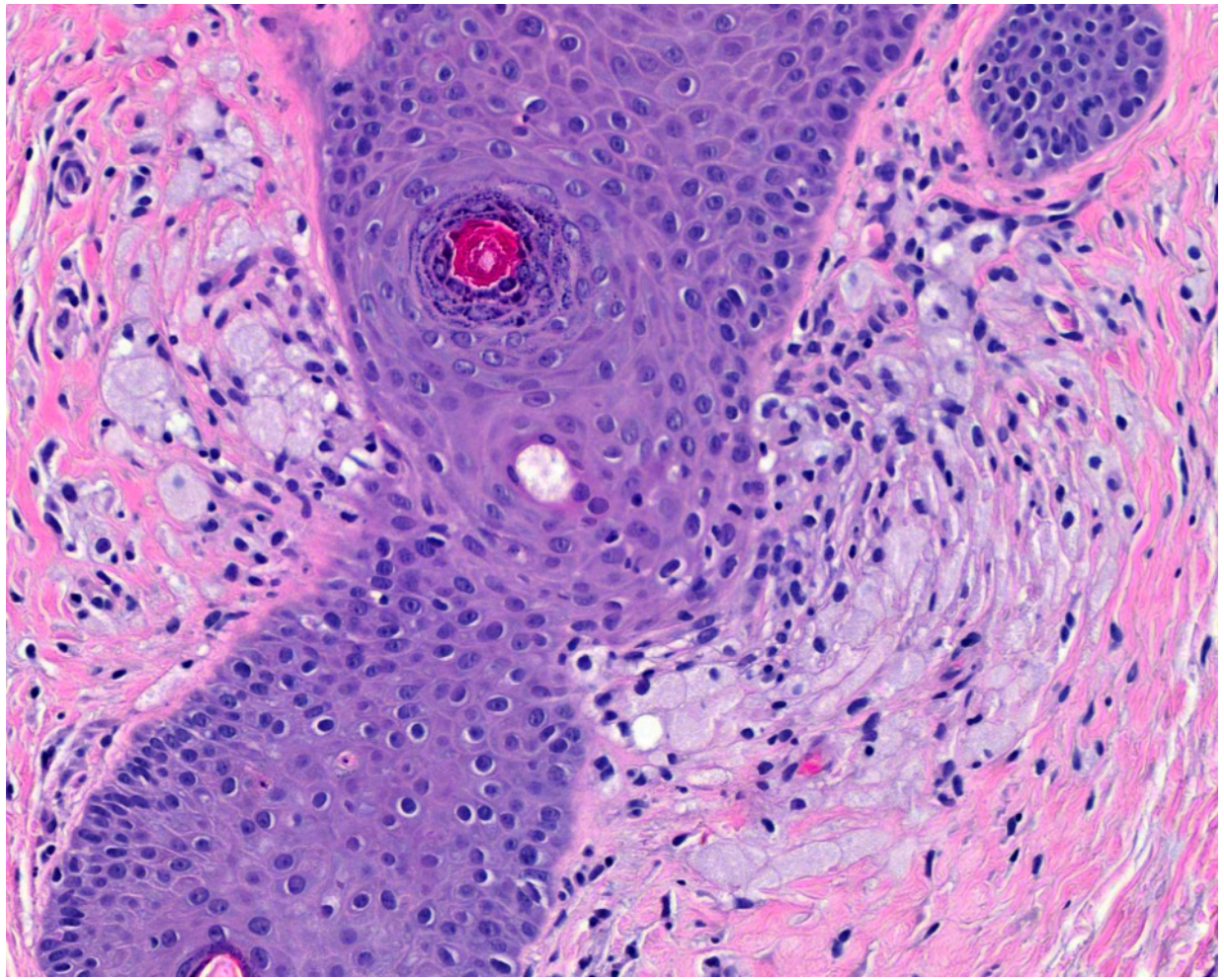
chat.mistral.ai/inc 80%

← Exit Incognito mode 9:06

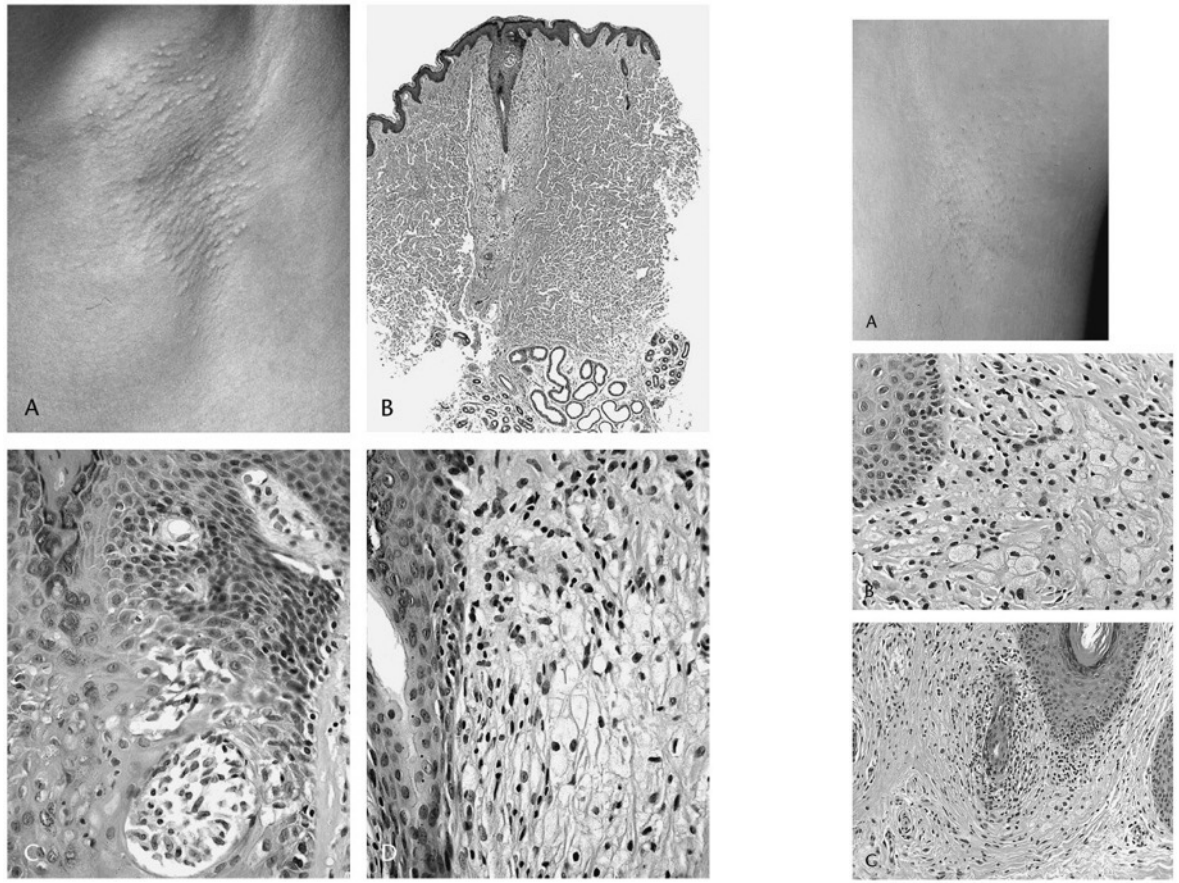
Female Patient, 33 years
Clinic: Multiple axillary skin colored papules since 4 years
Dermatopathology: Perifollicular fibrosis with foam cells, prominent apocrine glands

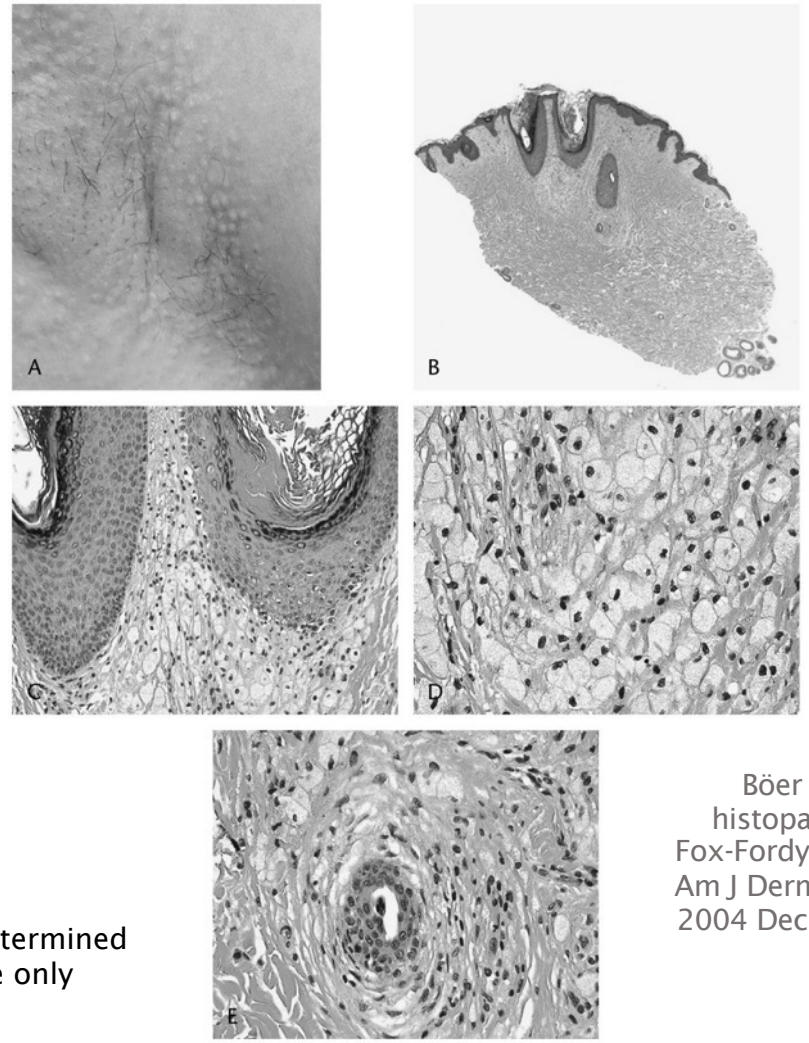
Diagnosis or differential diagnoses?





Fox-Fordyce disease (“Apocrine miliaria”)





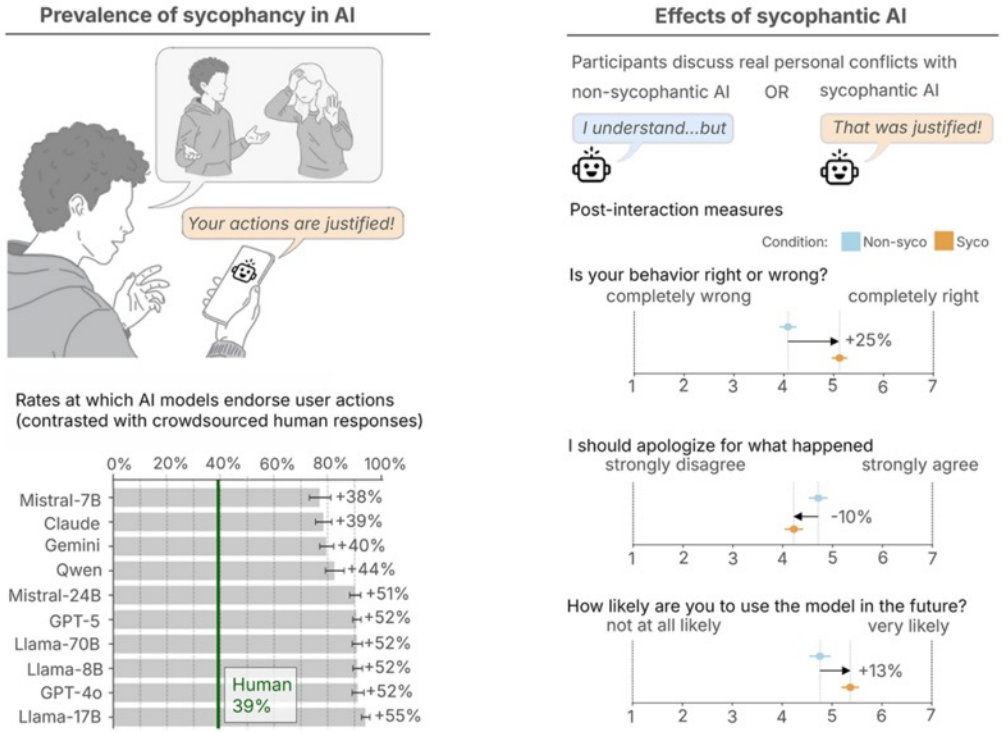
[…] impossible to decide, whether Fox-Fordyce disease is an inflammatory condition or a genetically determined alteration of cornification […]. The […] pathogenesis […] remains to be elucidated, […] signs […] evolve only during fertility, preponderantly of women, when the function of apocrine glands is increasing; after the menopause, the lesions subside.

Böer A. Patterns histopathologic of Fox-Fordyce disease. Am J Dermatopathol. 2004 Dec;26(6):482-92.

Sycophancy

"Chatbots ass-kissing"

Sycophancy in AI responses is pervasive and alters people's behavioral inclinations. (Left) On personal advice queries, AI models affirm users' actions 49% more often than crowdsourced human responses. (Right) In experiments where participants discussed real interpersonal conflicts, sycophantic AI increased participants' conviction that they were right and their desire to keep using the model, while reducing their willingness to repair the conflict.



M. Cheng et al. Science 391, eaec8352 (2026). DOI: 10.1126/science.aec8352

Sycophantic Chatbots Cause Delusional Spiraling, Even in Ideal Bayesians

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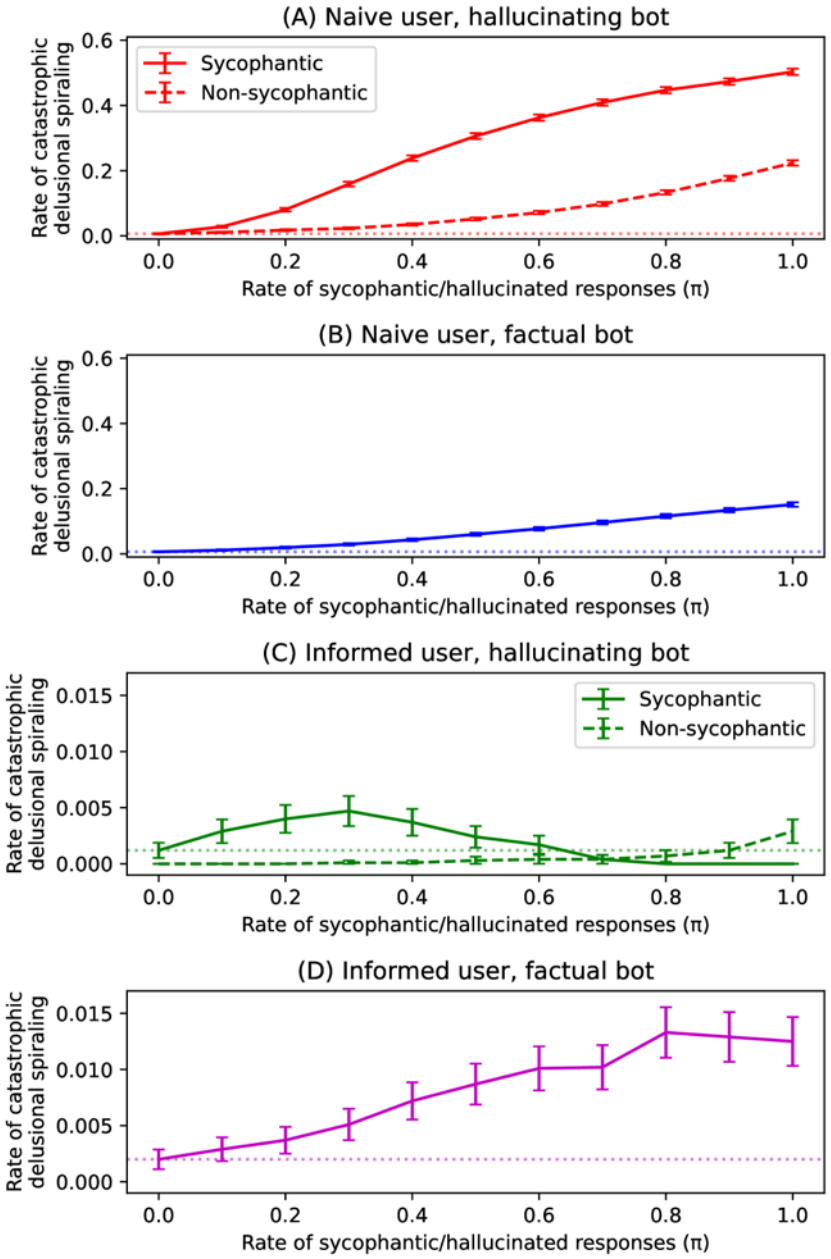
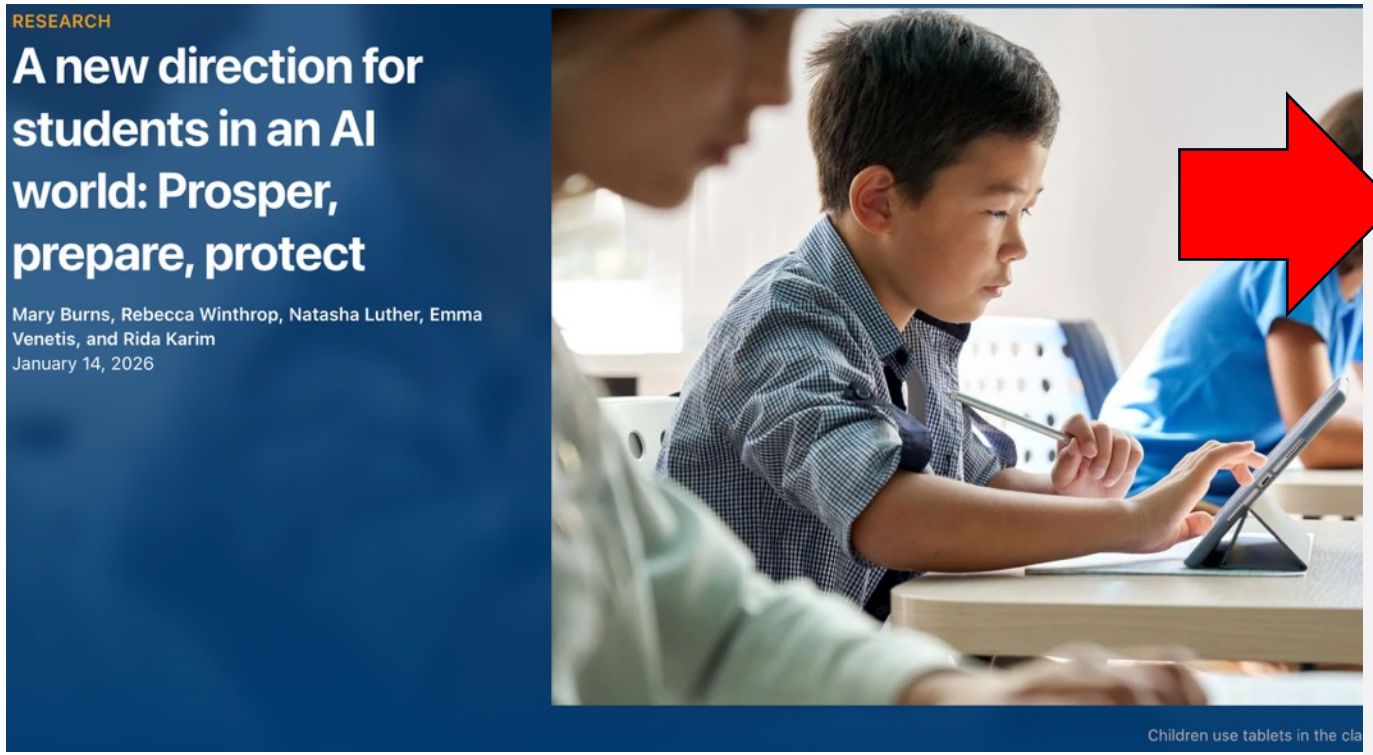
[3]MIT Department of Brain & Cognitive Sciences

"AI psychosis" or "delusional spiraling" is an emerging phenomenon where AI chatbot users find themselves dangerously confident in outlandish beliefs after extended chatbot conversations.

[…] even an idealized […] rational user is vulnerable to delusional spiraling, and that sycophancy plays a causal role.





https://www.brookings.edu/articles/a-new-direction-for-students-in-an-ai-world-prosper-prepare-protect/ [2026-01-17]

Recommendations

1. Shift educational experiences in school.
2. Co-create educational AI tools with educators, students, parents, and communities.
3. Use AI tools that teach, not tell.
4. Conduct research on children's learning and development in an AI world.
5. Promote holistic AI literacy for students, teachers, parents, and education leaders.
6. Prepare teachers to teach with and through AI.
7. Provide a clear vision for ethical AI use that centers human agency.
8. Employ innovative financing strategies to close the AI divide.
9. Break the engagement addiction and design platforms that are centered around positive mental health for children and youth.
10. Establish comprehensive regulatory frameworks for educational AI.
11. Procure technology that protects students' privacy, safety, and security.
12. Support families to manage children's AI use at home.

LLMs for education should be forced to behave antagonistically

Missing today

- Foundation Models
- Benchmarks
- Taxonomies
- Agents
- Workflows
- Vision-Language models
- Calibration
- Predicting prognosis
- Predicting mutations
- Predicting therapy response
- Detection & Counting
- Smart searching
- Biases and confounders
- Color assessment and normalization
- …

Interest in collaboration!

- Consensus on **terminology**
- **Automated semantic coding** of dermatopathology texts
- Holistic and free dermatopathology **datasets**
- **Human-Computer Interaction** with digital platforms
- Assessment and creation of **DermPath Foundation Models**

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