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DEEP LEARNING-BASED CLASSIFICATION OF COLORECTAL ADENOMAS – A DATA-DRIVEN MODEL FOR RESOURCE EFFICIENCY

KLASIFIKACIJA KOLOREKTALNIH ADENOMA ZASNOVANA NA DUBOKOM UČENJU – MODEL ZASNOVAN NA PODACIMA ZA EFIKASNOST RESURSA

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Abstract
We evaluated the performance and practical impact of several deep learning models, including ResNet and transformer-based architectures, for classifying colorectal adenomas with and without high-grade dysplasia in histopathology images, to support an artificial intelligence-assisted triage workflow that reduces pathologist workload while maintaining diagnostic quality and workflow efficiency. Models were trained and validated on 1,669 histopathology image tiles from colorectal polyp samples (368 with high-grade dysplasia, 767 low-grade adenomas, and 534 non-neoplastic controls) that were expert-reviewed and analysed at 100× magnification. Performance was assessed using 5-fold cross-validation, and Grad-CAM++ heat maps were generated to visualise model attention and support explainable pathologist review. ResNet101 achieved 99.17% accuracy in the best fold and 97.40% on average. The explanatory heat maps consistently highlighted diagnostically relevant epithelial regions, supporting rapid pathologist verification. In a simulated workflow of 1,000 colorectal polyps, artificial intelligence-assisted triage reduced pathologist review volume by 41–61% while maintaining 98.91% detection accuracy for high-grade dysplasia and 99.47% accuracy for adenomas without high-grade dysplasia. These reductions correspond to meaningful full-time equivalent savings in high-volume gastrointestinal pathology practice, where repetitive biopsy assessment contributes substantially to the daily workload. These findings indicate that deep learning models can accurately classify colorectal adenomas and detect high-grade dysplasia, and that artificial intelligence-assisted triage and sign-out, supported by interpretable heat maps, may provide a practical pathway towards more sustainable and efficient digital pathology workflows.
Key words: Colorectal Neoplasms; Adenoma; Polyps; Deep Learning; Artificial Intelligence; Machine Learning; Computer-Assisted Diagnosis; Pathology

Sažetak
Procenili smo performanse i praktičan uticaj nekoliko modela dubokog učenja, uključujući *ResNet* i arhitekture zasnovane na transformerima, za klasifikaciju kolorektalnih adenoma sa displazijom i bez nje, visokog stepena na histopatološkim slikama, sa ciljem podrške radnom toku trijaže uz asistenciju veštačke inteligencije kako bi se smanjilo opterećenje patologa uz održavanje dijagnostičkog kvaliteta i efikasnosti radnog toka. Modeli su obučavani i validirani na 1.669 histopatoloških slika pločica iz uzoraka kolorektalnih polipa (368 sa displazijom visokog stepena, 767 adenoma niskog stepena i 534 ne-neoplastička kontrola) koje su pregledali stručnjaci i analizirali pri uvećanju od 100 puta. Performanse su procenjivane korišćenjem 5-podeljene unakrsne validacije, a Grad-CAM++ toplinske mape su generisane kako bi se vizualizovala pažnja modela i podržao objašnjivi pregled od strane patologa. *ResNet*101 je postigao tačnost od 99,17% u najboljoj grupi i u proseku 97,40%. Objašnjavajuće toplotne mape dosledno su isticale dijagnostički relevantne epitelne regije, podržavajući brzu verifikaciju od strane patologa. U simuliranom toku rada sa 1.000 kolorektalnih polipa, AI-podržana trijaža smanjila je obim pregleda od strane patologa za 41–61%, dok je održala tačnost detekcije od 98,91% za displaziju visokog stepena i 99,47% za ne-HGD adenoma – za benigni (nekancerozni) tumor žlezdanog tkiva. Ova smanjenja odgovaraju značajnim uštedama ekvivalenta punog radnog vremena u praksi gastrointestinalne patologije sa velikim obimom, gde ponovljene procene biopsija značajno doprinose svakodnevnom radnom opterećenju. Ovi nalazi ukazuju na to da modeli dubokog učenja mogu precizno klasifikovati kolorektalne adenome i detektovati displaziju visokog stepena, kao i da AI-podržana trijaža i zatvaranje pregleda, podržani interpretabilnim toplotnim mapama, mogu pružiti praktičan put ka održivijim i efikasnijim tokovima digitalne patologije.
Ključne reči: kolorektalni tumori; adenoma; polipi; duboko učenje; veštačka inteligencija; mašinsko učenje; kompjuterski asistirana dijagnoza; patologija

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Abbreviations

AI – artificial intelligence
CLIA – Clinical Laboratory Improvement Amendments
BMSs – biomedical scientists
GI – gastrointestinal
HGD – high-grade dysplasia
CNNs – convolutional neural networks
FTE – full-time-equivalent
ViT – Vision Transformer
DeiT – Data-efficient Image Transformer

Introduction

The field of histopathology is undergoing a shift as artificial intelligence (AI) is integrated into high-volume, low-complexity diagnostic tasks. The aim is to reduce specialist pathologist workload while improving workflow efficiency and resource allocation. Earlier workload-reduction strategies began with the American Society for Clinical Pathology's certification of cytotechnologists in the United States in 1957.

Later advances introduced digital and computer-assisted cytology screening systems, while maintaining compliance with Clinical Laboratory Improvement Amendments (CLIA '88) requirements that at least 10% of negative gynecologic cytology cases undergo rescreening and that all atypical cases be reviewed by a pathologist [1]. Automation therefore redistributed workload and allowed pathologists to focus on diagnostically complex cases.

In the United Kingdom, biomedical scientists (BMSs) have also adopted expanded roles in histopathology, particularly in gastrointestinal (GI) pathology, to help manage rising diagnostic volumes. This redistribution of routine tasks reduces consultant workload and supports an integrated team approach that improves efficiency while maintaining diagnostic quality [2]. These models demonstrate that structured task-sharing systems can support both service delivery and workforce sustainability.

In the United States, gastrointestinal endoscopy is performed at very high volumes, with an estimated 10–20 million endoscopies and colonoscopies annually [3-5]. Adenomatous polyps account for approximately 60–70% of colorectal lesions considered precursors to invasive carcinoma. Adenoma detection rates are estimated at 31–39% of endoscopies [6], while the risk of high-grade dysplasia (HGD) rises from 2.7–10% in small polyps to 51–85% in large polyps [7,8]. The large number of benign and low-grade adenomas requiring histologic assessment creates a substantial repetitive workload burden within GI pathology services.

Deep learning models, such as convolutional neural networks (CNNs) and transformer-based architectures, have demonstrated high precision in histologic image classification [9]. In pathology, these systems can replicate recognition of epithelial structures, nuclear atypia, and glandular patterns used by pathologists to grade dysplasia. When properly validated and implemented, AI systems may automate repetitive tasks, improve standardisation, and support more resource-efficient diagnostic service delivery [10].

Colorectal adenomas provide an ideal setting for this approach. Differentiating normal mucosa, low-grade adenomas, and HGD is morphologically straightforward but highly repetitive and time-consuming at scale [11]. Hospitals worldwide face increasing demands to deliver more care with fewer personnel and limited budgets. Within diagnostic services, pathology departments must balance rising specimen volumes with static or reduced staffing levels. Efficient management of workflow, turnaround time, and full-time-equivalent (FTE) allocation has therefore become a strategic priority. By assessing both diagnostic performance and operational impact, this study explores how AI-assisted digital pathology may function not only as a technical innovation but also as a practical tool for workflow redesign, workforce planning, and sustainable service delivery.

Material and Methods

Dataset

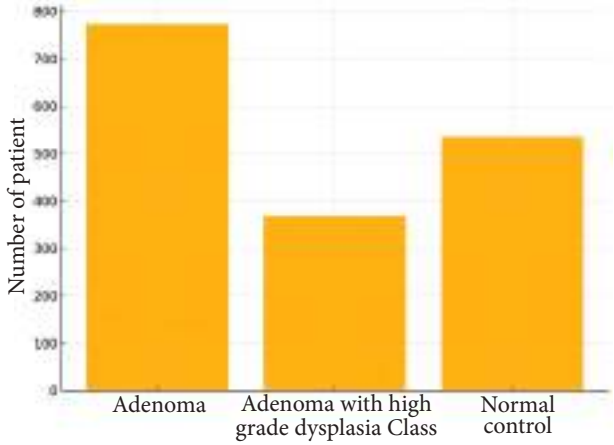
A total of 1,669 histopathological image patches of whole-slide colorectal tissue were analysed. Each patch had a resolution of 2,560 × 1,920 pixels and was captured as a JPG at 100× magnification using a Leica DMC 4500 camera mounted on a Leica DM 2000 LED microscope (Leica Microsystems, Wetzlar, Germany). Images were manually labelled into three diagnostic categories: adenoma (n=767, 46%), adenoma with high-grade dysplasia (n=368, 22%), and normal control tissue (n=534, 32%) **(Table 1; Graph 1).**

Test dataset

For evaluation, a fixed test dataset of 240 images (14.4% of the total) was held out from all cross-vali-

Table 1. Number of images per class in the dataset (N=1,669)

Class	Images	Share (%)
Adenoma	767	46
Adenoma with high-grade dysplasia	368	22
Normal control	534	32



Graph 1. Image count per class in the complete dataset

dation experiments. It contained 80 images per class, ensuring balanced distribution and comparability across models **(Graph 2).**

Model architectures

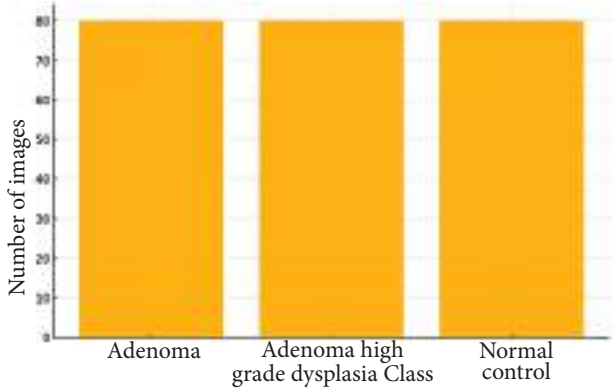
Two families of deep learning models were evaluated. Residual Networks (ResNet-18, ResNet-50, and ResNet-101) were tested as convolutional neural networks with skip connections, using resized inputs of 640 × 480 pixels. Transformer-based architectures included the Vision Transformer (ViT) and the Data-efficient Image Transformer (DeiT), both trained with input resized to 224 × 224 pixels.

Training protocol

All models were trained using 5-fold stratified cross-validation to preserve class balance. ResNet-101 was initialised with ImageNet-pretrained weights; the final fully connected layer was modified to match the three diagnostic categories, and all parameters were fine-tuned end-to-end. Training employed the AdamW optimiser (initial learning rate 1×10^{-4}, weight decay 1×10^{-4}) with a ReduceLROnPlateau scheduler. Each model was trained for 30 epochs per fold.

Hyperparameter optimization

Architecture-specific optimisation was performed with the Optuna framework, varying optimiser, learning rate, weight decay, and scheduler parameters.



Graph 2. Number of images per class in the fixed test dataset

Explainability

To support clinical interpretability, Gradient-weighted Class Activation Mapping++ (Grad-CAM++) was applied to generate class-specific heat maps that highlight the histological regions most relevant to each prediction.

Results

Baseline performance

Baseline performance is summarised in **Table 2.** ResNet architectures achieved the strongest results, with ResNet-101 and ResNet-18 both reaching 96.67% accuracy in the best fold. On average, ResNet-101 achieved 94.75% accuracy compared with 93.92% for ResNet-18, while transformer models performed worse (ViT, 85.10%; DeiT, 92.90%). Importantly, at this stage, ResNet-101 correctly identified the majority of HGD cases, though three HGD cases were misclassified as adenomas and three adenomas were misclassified as HGD. This demonstrates strong, though not perfect, separation of dysplastic from non-dysplastic lesions.

Confusion matrix analysis

The baseline confusion matrix for ResNet-101 **(Figure 1)** shows excellent classification for normal controls, with only 1 error among 80 cases. Adenomas without HGD were also detected with high accuracy, though a small proportion overlapped with

Table 2. Baseline accuracies on the fixed test set (5-fold cross-validation)

Model	Best fold accuracy (%)	Average accuracy (%)
ResNet-18	96.67	93.92
ResNet-50	95.83	94.42
ResNet-101	96.67	94.75
ViT	86.25	85.10
DeiT	95.00	92.90

Table 3. Accuracy after Optuna hyperparameter optimisation

Model	Best fold accuracy (%)	Average accuracy (%)
ResNet-101	99.17	97.40
ViT	97.08	96.30
DeiT	96.67	95.25

HGD. Conversely, HGD was detected in more than 95% of cases, confirming the model's capacity to flag advanced lesions while revealing the main challenge lies in distinguishing borderline adenomas.

Hyperparameter optimisation

Across the complete dataset using 5-fold cross-validation, HGD detection reached 98.91%, adenomas without HGD 99.47%, and normal controls nearly 100%. On the independent hold-out test set, the optimised ResNet-101 model correctly classified 78 of 80 HGD images (97.5%) **(Table 3, Figure 2).**

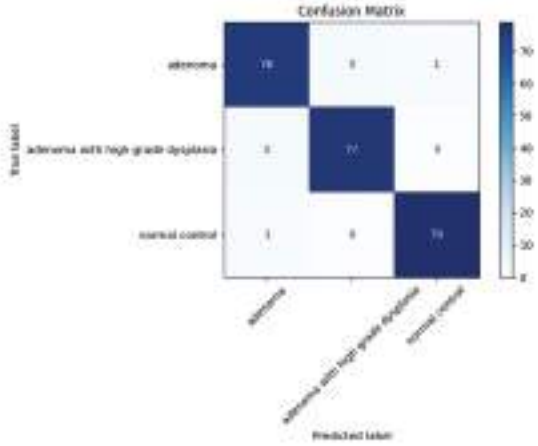


Figure 1. Confusion matrix of the baseline ResNet101 model on the test set

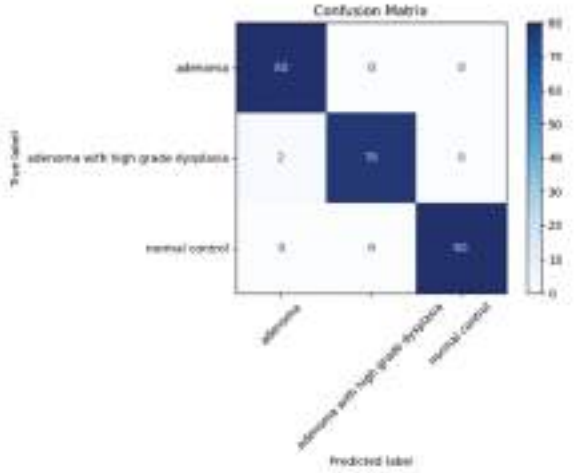


Figure 2. Confusion matrix of the optimised ResNet101 model after Optuna hyperparameter tuning

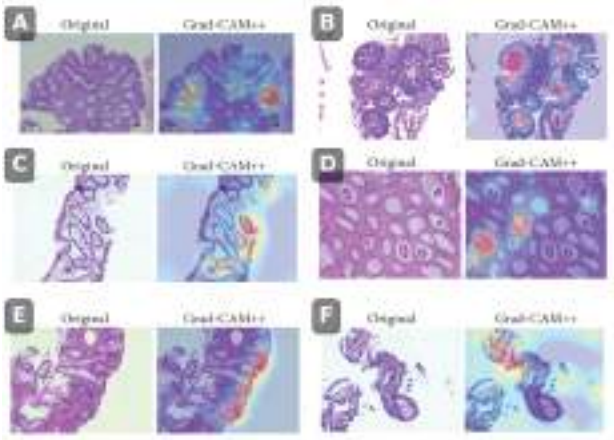


Figure 3. Grad-CAM++ visualisations of model attention for selected test images

Legend: (A) Adenoma without high-grade dysplasia: H&E (left) and heat map (right) showing regions evaluated as adenoma without high-grade dysplasia; (B) Adenoma with high-grade dysplasia: H&E (left) and heat map (right) showing regions evaluated as adenoma with high-grade dysplasia; (C) Normal colonic mucosa: H&E (left) and heat map (right) showing regions evaluated as normal colonic mucosa; (D) Normal colonic mucosa misclassified as adenoma without high-grade dysplasia: H&E (left) and heat map (right); (E) Adenoma without high-grade dysplasia misclassified as adenoma with high-grade dysplasia: H&E (left) and heat map (right): (F) Adenoma without high-grade dysplasia misclassified as normal colonic mucosa: H&E (left) and heat map (right), showing absence of a focused region of evaluation.

Explainable AI results

Grad-CAM++ heat maps **(Figure 3)** showed that ResNet-101 focused on epithelial regions with nuclear atypia and glandular irregularity, the same features pathologists use to diagnose HGD. The alignment of network attention with diagnostically relevant structures supports clinical confidence, indicating that high accuracy in HGD detection corresponds to recognition of the correct microscopic features rather than spurious artefacts.

Discussion

This study demonstrates that deep learning can be integrated into diagnostic histopathology not merely as a technical adjunct, but as a practical framework for workflow redesign and management-level change. By focusing on colorectal adenomas - a high-volume, relatively low-complexity diagnostic category - we demonstrate how validated AI performance can be translated into measurable operational outcomes, including reduced workload, improved effi-

ciency, and potential FTE savings in gastrointestinal pathology services [12]. Similar to how cytotechnologists and biomedical scientists have historically supported specialist pathologists by prescreening routine cases, AI may assume responsibility for common lesions while pathologists to focus on diagnostically complex or clinically significant specimens [13]. This tiered diagnostic model aligns with the broader trend toward task-shifting and workforce optimisation in laboratory medicine [14].

Evidence from multiple disciplines supports the feasibility of this approach. In prostate cancer screening, AI-assisted triage reduced the number of biopsy cores requiring pathologist review by nearly 80% while maintaining detection of clinically significant disease [15]. Likewise, a meta-analysis of radiology workflows demonstrated that AI integration reduced reading volume by 44–62% and reading time by approximately 27% while improving sensitivity without compromising specificity [16]. A large systematic review of more than 152,000 whole-slide images across 100 pathology studies further confirmed that AI systems can achieve expert-level diagnostic performance, with pooled sensitivity of 96.3% and specificity of 93.3% [9]. Together, these findings demonstrate that AI can safely serve as a prescreening and workload redistribution tool across diagnostic specialities. In other areas of medicine, AI systems have also been shown to screen, follow up, and manage patients while reducing consultant workload and supporting service efficiency, including within orthopaedic fracture liaison services [17].

Our study extends this concept to colorectal adenomas. The optimised ResNet-101 model achieved a best-fold accuracy of 99.17% and an average accuracy of 97.40%. Across the entire dataset, using 5-fold cross-validation, the model correctly identified 364 of 368 adenomas with HGD (98.91% detection rate) and 99.47% of adenomas without HGD. In the independent hold-out test set, the optimised model correctly classified 78 of 80 HGD cases (97.5%), while all adenomas without HGD and all normal control cases were correctly classified **(Figure 4).** Errors across the entire dataset were limited, with only three adenomas overcalled as HGD, one adenoma labelled as normal mucosa, and four HGD lesions missed. Importantly, the model achieved near-perfect recognition of normal mucosa and low-grade lesions, a feature with direct operational relevance, as accurate exclusion of low-risk tissue reduces unnecessary manual review and allows pathologists to redistribute time to clinically demanding cases. These findings are consistent with previous work in gastrointestinal pathology, including the study by Faghani et al., which demonstrated high sensitivity and specificity for deep learning detection of dysplasia in Barrett's oesophagus [18].

Beyond diagnostic accuracy, our findings demonstrate how validated AI output can function as an operational management tool. In modelled clinical workflows, AI could independently evaluate diminutive low-risk adenomas, while pathologists selectively review larger lesions, AI-flagged HGD cases, and a proportion of AI-negative cases for quality assurance. Applying published polyp size distributions, this approach would reduce pathologist review volume by approximately 41–61%, corresponding to a potential saving of approximately 0.5 FTEs in high-volume gastrointestinal pathology practice, where daily colonoscopy biopsy volumes are substantial [8]. Such gains do not represent the replacement of professional expertise, but rather redistribution of cognitive effort from repetitive visual confirmation to integrative diagnostic interpretation, multidisciplinary discussion, and consultative activities.

These projected efficiency gains are supported by emerging real-world implementation data. In a community pathology laboratory, practical AI deployment reduced turnaround times by approximately nine hours and decreased immunohistochemistry utilisation by one-third without compromising diagnostic quality [19]. If replicated at scale, such workflow improvements could help alleviate workforce shortages, reduce burnout, and improve service sustainability within increasingly pressured pathology systems.

Explainability remains essential for clinical adoption. AI systems cannot function as "black boxes" if they are to be trusted in routine diagnostic workflows. Historical parallels exist in haematology, where automated blood film analysers identify atypical cells for operator review while achieving performance comparable to experienced laboratory scientists. In histopathology, explainability tools such as Grad-CAM++ heat maps provide a similar interpretive bridge between algorithmic prediction and human review. Retamero et al. demonstrated that AI-assisted detection of breast cancer lymph node metastases improved sensitivity among less-experienced pathologists and reduced review time by directing attention to diagnostically relevant regions [20]. In our study, Grad-CAM++ heat maps consistently focused attention on epithelial regions demonstrating nuclear atypia and glandular irregularity – the same morphologic features used by pathologists to distinguish low-grade from high-grade dysplasia. In misclassified cases, however, heat maps occasionally failed to emphasise dysplastic regions,

instead highlighting benign structures, illustrating both the promise and current limitations of explainable AI systems.

From a systems perspective, these findings support a broader framework for data-driven resource management within pathology departments. Once validated prospectively, AI-generated diagnostic metrics could inform staffing models, identify workflow bottlenecks, guide workload balancing across sites, and support evidence-based allocation of personnel resources [10]. In this way, AI evolves from a purely diagnostic technology into a strategic management tool that supports hospital-level operational decision-making [21].

Several limitations should be acknowledged. The dataset was derived from a single institution, and variations in staining protocols, scanner hardware, and image acquisition may affect generalisability across centres [22]. In addition, the projected workload reductions and FTE savings remain theoretical and depend on digital infrastructure, regulatory governance, and the successful integration of AI triage into routine diagnostic pathways. Prospective multi-site validation studies incorporating cost-effectiveness analyses and real-world implementation metrics will therefore be essential before widespread adoption.

Conclusion

Ultimately, the question is not whether artificial intelligence can recognise high-grade dysplasia - our data and prior studies demonstrate that it can - but how it can be integrated safely into routine pathology workflows in a way that improves efficiency without compromising patient care. We envisage a stepwise implementation model beginning with artificial intelligence-assisted case previewing within digital worklists, progressing to real-time diagnostic assistance during sign-out, and eventually enabling supervised automatic sign-out of low-risk, high-volume lesions under structured quality assurance frameworks. This trajectory mirrors the historical evolution of task-sharing roles within pathology and offers a credible pathway toward sustainable diagnostic practice in the era of digital medicine.

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