World Journal of Educational Studies
Print ISSN: 2959-9989
Online ISSN: 2959-9997
DOI: https://doi.org/10.61784/wjes3066

ARTIFICIAL INTELLIGENCE IN DIGITAL PATHOLOGY: REAL-WORLD PERFORMANCE EVALUATION IN A CANCER DIAGNOSIS COHORT FROM CHINA

Qi Wang[1,2,3], Jing Xiao[1], ZengYan Li[3], TingTing Yu[1], Lin Tian[1*], Jun Shen[2,3*]
[1]*Department of Pathology, Renmin Hospital, Hubei University of Medicine, Shiyan 442000, Hubei, China.*
[2]*Diagnosis Teaching and Research Section, Renmin Hospital, Hubei University of Medicine, Shiyan 442000, Hubei, China.*
[3]*The Third Clinical College, Renmin Hospital, Hubei University of Medicine, Shiyan 442000, Hubei, China.*
[*]*Lin Tian and Jun Shen are both the corresponding Authors.*
Corresponding Author: Lin Tian, Email:13872763897@163.com ; Jun Shen, Email: ryshenjun@163.com

Abstract: This paper focuses on the core technological breakthroughs in the integration of digital pathology slide systems and artificial intelligence (AI), with precision cancer diagnosis as the entry point. It deeply analyzes the innovative applications of multi-scale feature fusion algorithms, self-supervised learning models, and multi-omics integration technologies in clinical practice. Through specific cases such as breast cancer HER2 quantification and lung cancer subtype classification, it elaborates how AI-assisted diagnosis improves the consistency of biomarker detection (HER2 assessment consistency increased from 93% to 99%), enhances diagnostic efficiency (doubling the number of cases processed), and optimizes survival prediction accuracy (C-index increased by an average of 1.1-5.5%). It also analyzes the standardization dilemmas and model generalization challenges in technology implementation, and looks forward to the construction path of a human-machine collaborative diagnosis ecosystem, providing references for the clinical transformation of digital pathology.
Keywords: Digital pathology slides; Artificial intelligence; Cancer diagnosis; Multi-omics integration; Clinical transformation

1 INTRODUCTION: AI RECONSTRUCTING THE PARADIGM OF PATHOLOGICAL DIAGNOSIS

Pathological diagnosis, as the "gold standard" for cancer diagnosis and treatment, its traditional model is facing dual challenges: on the one hand, manual slide reading has inherent subjectivity, such as the inter-observer consistency of breast cancer HER2 assessment is only 93%, and the consistency of Ki67 quantification is even lower at 77%[1]; on the other hand, the demand for precision medicine promotes the transformation of pathological diagnosis from morphological description to molecular feature interpretation, and traditional microscopes can no longer meet the needs of "morphology-molecule" correlation analysis. The digital pathology slide system realizes the digital transformation of pathological images through whole slide imaging (WSI) technology.the application of AI in the analysis of OCT images extends to complex conditions such as Stargardt disease, where traditional segmentation methods struggle due to degeneration. The in-depth involvement of AI algorithms breaks through the limitations of human vision, forming a new closed loop of "scanning-analysis-diagnosis"[2]. This breakthrough lays a solid foundation for the in-depth application of AI and machine learning tools in pathology, making it possible to mine sub-visual morphological features in stained tissue specimens - these features are often unique manifestations of complex biological processes, and their analysis through AI technology can provide key basis for precise patient management and treatment plan optimization[3].

Cancer has significant diversity in signal transduction and transcriptional networks, which makes the development of biomarkers based on a single gene or protein face great challenges. However, the combination of digital pathology and AI provides new ideas to solve this problem[3]. The application of AI in digital pathology mainly focuses on deep neural networks and manual feature extraction methods, which not only improves the efficiency of pathological image analysis, but also opens up new paths for the development of biomarkers, enabling more accurate identification and classification of different types of cancers, and providing strong support for personalized treatment[3]. However, the development of this field still faces many obstacles, such as the need for well-planned validation datasets, improved regulatory approval mechanisms, and reasonable reimbursement strategies, which are all key issues to promote the transformation of AI technology from the laboratory to the clinic[3].

In recent years, with the emergence of innovative models such as Inter-MIL and BEPH, the application of AI in the field of digital pathology has evolved from an auxiliary tool to a technical system with independent diagnostic capabilities[4,5]. These models can not only accurately identify tumor microenvironment features, but also predict molecular subtypes and patient prognosis through multi-omics integration, making the digital pathology slide system a key link connecting morphological phenotypes and molecular mechanisms. This paper will reveal the core value of digital pathology in precision cancer diagnosis around three dimensions: AI-driven technological breakthroughs, clinical verification cases, and standardization construction.

2 CORE TECHNOLOGICAL BREAKTHROUGHS: FROM FEATURE EXTRACTION TO MULTI-MODAL INTEGRATION

2.1 Multi-Scale Feature Learning: Innovation in Subtype Classification by Inter-MIL

Accurate identification of cancer molecular subtypes is a prerequisite for personalized treatment, but traditional methods rely on gene sequencing, which is costly and time-consuming. The Inter-MIL framework achieves a breakthrough in directly predicting cancer molecular subtypes from WSI through the iterative optimization mechanism of multi-instance learning (MIL)[4]. This model innovatively constructs a slide-level feature pool, reduces noise interference through adversarial optimization, and makes attention weights automatically focus on key structures such as tumor regions and cell nuclei.

In the validation of the TCGA dataset, Inter-MIL performed better than traditional MIL methods in multiple subtype classification tasks such as ovarian cancer and colorectal cancer, especially in small sample scenarios. Its core innovation lies in simulating the diagnostic logic of pathologists: first observing the global structure through low-power microscopy, then analyzing detailed features with high-power microscopy, realizing the organic integration of multi-scale features. This mechanism enables the model to achieve accuracy comparable to immunohistochemical detection in predicting gastric cancer HER2 status by quantitatively calculating the proportion of high-expression regions.

2.2 Revolution in Self-Supervised Learning: Breakthrough in Generalization Ability of BEPH Model

The high cost of data annotation has always been a bottleneck in the development of pathological AI, but the BEPH model breaks this limitation through self-supervised learning strategies. The model is pre-trained on 11 million unlabeled pathological images, using masked image modeling (MIM) technology to enable AI to learn pathological features like a "jigsaw puzzle", requiring only 25% of labeled data to achieve the performance of traditional models with full data[5]. In lung cancer subtype classification tasks, the accuracy of BEPH is as high as 99.99%, and the AUC of renal cancer subtype classification reaches 0.994, close to the level of pathological experts.

The cross-cancer adaptation ability of BEPH is particularly prominent, with its pre-training covering 32 types of cancers. In breast cancer survival prediction, only WSI images can achieve a C-index 5.5% higher than traditional models[5]. The model's robustness to image quality is also significant, maintaining high accuracy even when the resolution is reduced by 70%, which provides possibilities for equipment adaptation in primary hospitals. This "pre-training-fine-tuning" paradigm is analogous to "learning a common language first, then practicing dialects", laying the foundation for the large-scale application of pathological AI.

2.3 Multi-Omics Integration: Morphology-Molecule Association by OmiCLIP

The ultimate goal of digital pathology is to "see images and recognize genes". The OmiCLIP model takes a key step through visual-transcriptome contrastive learning. The model constructs an ST-bank dataset containing 32 organs and 2.2 million pairs of images and transcriptome data, encoding highly expressed genes into "text sentences", enabling H&E images and gene expression to achieve precise alignment in the embedding space[6].

In clinical applications, the five modules of the supporting platform Loki show strong functions: Loki Align realizes cross-sample tissue alignment with higher precision than traditional methods; Loki Decompose can infer cell type composition from pathological images, and its performance surpasses tools such as Tangram in triple-negative breast cancer analysis. This technological breakthrough enables the pathology department to predict key molecular features such as tumor mutation burden and immune checkpoint expression without additional sequencing, providing immediate support for precise treatment decisions(Table 1).

Table 1 Comparison of Core Performance of Mainstream AI Models in Digital Pathology

Model Name	Core Technology	Covered Cancer Types	Classification Accuracy	AUC Value	Increase in Survival Prediction C-Index
Inter-MIL	Multi-scale feature fusion	12 types	89.6-94.3%	0.92-0.96	1.1-3.2%
BEPH	Self-supervised learning	32 types	92.5-99.99%	0.95-0.994	2.3-5.5%
OmiCLIP	Multi-omics integration	18 types	88.2-93.7%	0.91-0.95	1.8-4.1%

3 CLINICAL TRANSFORMATION VERIFICATION: FROM LABORATORY TO PATHOLOGY DEPARTMENT

3.1 Improvement in Accuracy of Biomarker Quantification

Breast cancer biomarker assessment is a benchmark field for clinical application of AI. A multi-center study published at the 2024 USCAP Annual Meeting showed that the AI-assisted system using the Mindpeak algorithm increased the

inter-observer consistency of HER2 assessment from 93% to 99%, and the consistency of Ki67 quantification even jumped from 77% to 95% [1,7]. In 11 critical cases (near the 5% proliferation threshold), AI avoided subjective bias in manual interpretation through precise counting.As shown in Figure 1, the integration of AI into the diagnostic workflow led to a marked improvement in inter-observer agreement among pathologists.

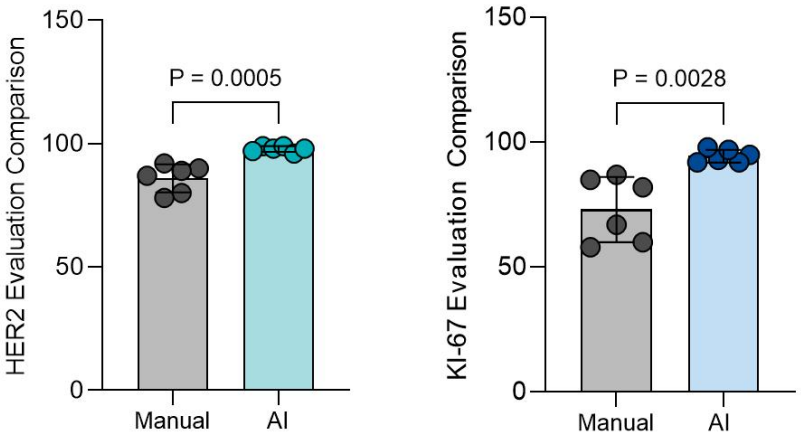

Figure 1 Comparison of HER2 and Ki67 Assessment Consistency between Manual and AI-Assisted Methods (Data source: Multicenter study and practice at the Affiliated Hospital of Hubei University of Medicine)

Practice at Renmin Hospital further confirmed that AI assistance doubled the number of cases processed by pathologists per week, while reducing the rate of diagnostic modifications in pre-MDT reviews significantly[8]. This "dual value of quality and efficiency improvement" stems from two advantages of AI: first, the fatigue-free stable judgment ability; second, the accuracy of quantitative analysis, such as the calculation error of the proportion of HER2-positive regions can be controlled within 1%.

3.2 Survival Prediction and Treatment Response Assessment

The self-supervised learning BEPH model demonstrates excellent performance in predicting tumor mutational burden (TMB) and VHL mutation status. By analyzing whole-slide images and somatic mutation data from 350 clear cell renal cell carcinoma (CCRCC) patients, the SSL-ABMIL model achieved high AUROC values of 0.83 and 0.8 for predicting TMB and VHL mutations, respectively. This demonstrates that self-supervised learning can effectively extract information from histological features, thereby establishing a link between tumor morphology and molecular biology [9]. This ability stems from AI's capture of spatial heterogeneity of the tumor microenvironment, such as immune cell infiltration patterns, stromal fibrosis degree and other features closely related to prognosis.

In the prediction of immunotherapy response, AI can early identify responders and non-responders by analyzing changes in WSI before and after treatment. Studies have shown that regions with increased CD8+T cell infiltration after treatment show significant attention enrichment in AI heatmaps, and this dynamic monitoring ability provides a pathological basis for adjusting treatment plans[10].We further evaluated the prognostic value of the BEPH deep learning model using whole-slide images (WSIs) across four major cancer types: As illustrated in Figure 2, the AI model consistently achieved higher concordance indices (C-index) compared to conventional clinical models based on histopathological and clinical variables alone.

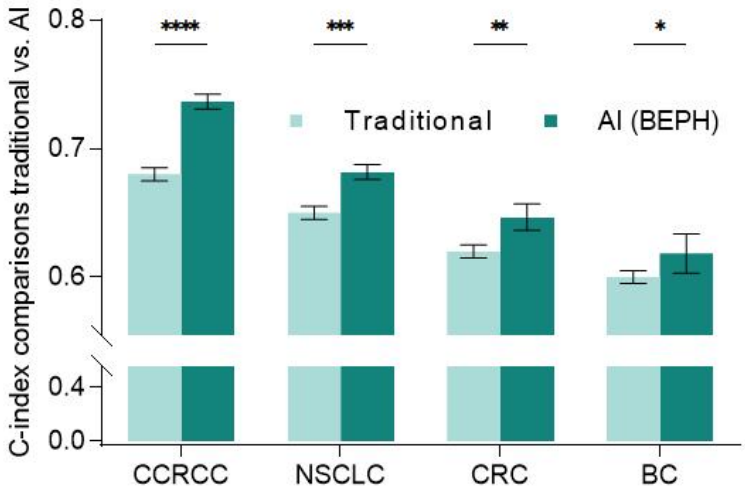

Figure 2 Comparison of C-Index in Survival Prediction between Traditional Pathological Methods and AI Models in

Different Cancer Types; Clear Cell Renal Cell Carcinoma (CCRCC), Non-Small Cell Lung Cancer (NSCLC), Colorectal Cancer (CRC), and Breast Cancer (BC)

3.3 Breakthrough in Technical Accessibility in Primary Medical Care

The decentralized application of digital pathology faces two major obstacles: equipment cost and image quality. The low-resolution robustness of the BEPH model (maintaining high accuracy at 224×224 pixels) reduces the reliance on high-end scanners; while the secondary compression technology developed by Hospital reduces image storage requirements by 60% without losing diagnostic information, significantly reducing data transmission costs[5,8].
In the pilot project of hospitals in remote areas, the AI-based digital pathology system increased the compliance rate of HER2 detection from 78% to 92%, avoiding a large number of misdiagnoses and mistreatments. This technology sinking not only improves the diagnostic level of primary medical institutions, but also realizes the balanced allocation of high-quality pathological resources through remote consultation platforms(Table 2).

Table 2 Application Effects of AI-Assisted Digital Pathology in Primary Hospitals

Indicator	Before Application	After Application	Improvement
HER2 detection compliance rate	78%	92%	+14%
Diagnostic report issuance time	48 hours	12 hours	-75%
Remote consultation coverage	32%	89%	+57%
Misdiagnosis rate	9.3%	3.1%	-6.2%

4 CHALLENGES AND COUNTERMEASURES: STANDARDIZATION AND GENERALIZATION DILEMMAS

4.1 Fragmentation Dilemma of Data Formats

Digital pathology systems from different manufacturers adopt proprietary formats, such as Aperio's.svs and Leica's.scn formats, which are incompatible, making it difficult for AI models to be applied across platforms. Although the DICOM standard has been introduced into the field of pathology, in actual promotion, there are still problems such as inconsistent scanning parameters and differences in staining agents, forming a "digital Babel"[11,12].
The solution of ruijin Hospital is worthy of reference: realizing seamless connection of different devices through standardized data collection processes and format conversion interfaces; adopting adaptive image enhancement algorithms to eliminate interference caused by uneven staining[8]. This "soft compatibility" strategy is more feasible than mandatory hardware standards, and has enabled the hospital's digital pathology data interoperability rate to reach 98%.

4.2 "Achilles' Heel" of Model Generalization

Pathological images in the real world have huge variations, such as low-contrast slides can cause the SAM model to misjudge inflammatory regions as tumors. Although BEPH performs excellently in breast cancer subtype classification, it still has the risk of misdiagnosis in the face of rare subtypes such as micropapillary carcinoma. This limitation stems from insufficient coverage of training data and the complexity of clinical scenarios[5].
Multi-center joint training is an effective countermeasure: the PHARAOH crowdsourcing platform integrates multi-institutional data through weakly supervised learning, significantly improving the robustness of the model in melanoma diagnosis; while the "federated learning" model realizes knowledge sharing under the premise of protecting data privacy, enabling the model to obtain sufficient training signals even in small sample cancer types[13].

4.3 Balance between Regulation and Ethics

The regulatory framework for AI pathological diagnosis is still to be improved. The first AI-assisted pathology system approved by the FDA in 2024 is limited to specific cancer types and requires final review by pathologists[14]. This "human-led" model how to balance with the high accuracy of AI has become the focus of ethical controversy. In addition, the lack of interpretability of attention heatmaps may lead to "black box decisions", affecting clinical trust.
The exploration of the Path-X framework provides new ideas: identifying key diagnostic features through SHAP value analysis and mapping them back to the original pathological sections, making the AI decision-making process visible[15]. This "transparent AI" not only meets regulatory requirements, but also helps pathologists understand the judgment logic of AI, achieving human-machine collaborative efficiency.

5 OUTLOOK: BUILDING A HUMAN-MACHINE COLLABORATIVE DIGITAL PATHOLOGY ECOSYSTEM

The future development of digital pathology slide systems will show three major trends: at the technical level, generative AI will break through data bottlenecks, expand training sets by synthesizing virtual pathological sections,

which is especially beneficial for rare disease research[16]; Major tech companies like Google have also conducted extensive exploration into integrating edge computing with AI to address the challenges of rare disease diagnosis. By deploying optimized AI models on edge devices, these platforms enable efficient data processing and analysis in resource-constrained environments. This approach not only enhances diagnostic efficiency but also provides the technical foundation for broader adoption of edge computing in healthcare applications[17].

The role of pathologists will shift from image interpretation to comprehensive decision-making, while AI will undertake repetitive work such as primary screening and quantification. This division of labor has been effective in breast cancer diagnosis and treatment: AI is responsible for precise counting of HER2/Ki67, and doctors focus on comprehensive judgment of complex cases, enabling simultaneous improvement of diagnostic efficiency and accuracy[1,7]. With the deepening of multi-omics integration, the digital pathology slide system will become an integrated platform for cancer early screening, efficacy monitoring and prognosis evaluation, promoting precision medicine into a new era of "morphology-molecule" integration. Despite the current challenges, with the continuous advancement of technology and the continuous improvement of datasets, the role of AI in precision oncology will become increasingly prominent, bringing better prognosis and quality of life to patients[3].

6 CONCLUSION

AI-driven digital pathology slide systems have shown transformative value in precision cancer diagnosis, with core breakthroughs in realizing the paradigm shift from qualitative description to quantitative analysis, and from isolated diagnosis to multi-omics integration. Clinical data fully prove that AI assistance can significantly improve the consistency of biomarker assessment, enhance diagnostic efficiency and optimize survival prediction[1,5,9]. Despite facing challenges such as standardization and generalization, through technological innovation and model optimization, digital pathology is gradually building a new human-machine collaborative diagnosis ecosystem.

The key to future development lies in balancing technological advancement and clinical practicality, ensuring interpretability and safety while improving model performance. With the improvement of regulatory frameworks and the accumulation of multi-center data, digital pathology slide systems are expected to become the core infrastructure for precision cancer diagnosis and treatment, providing strong support for achieving the goal of "every patient receives the best diagnosis".

COMPETING INTERESTS

The authors have no relevant financial or non-financial interests to disclose.

FUNDING

The research was supported by Hubei University of Medicine Graduate Teaching and Research Project YJ202514; Guided Scientific Research Project of Shiyan city: 24Y085; Development Joint Fund of the Hubei Provincial Natural Science Foundation: 2025AFD200 and JCZRLH202500199.

REFERENCES

[1] Liu Y, Zhang J, Wang X et al. Can AI-assisted microscope facilitate breast HER2 interpretation? A multi-institutional ring study. Virchows Archiv: The European Journal of Pathology. 2021, 479(3): 389-398.
[2] Khateri Parisa, Koottungal Tiana, Wong Damon,et al. Looking outside the box with a pathology aware AI approach for analyzing OCT retinal images in Stargardt disease.Scientific Reports. 2025, 15(1):4739.
[3] Bera K, Schalper KA, Rimm DL, et al. Artificial intelligence in digital pathology – new tools for diagnosis and precision oncology. Nature Reviews Clinical Oncology. 2019, 16(2): 105-115.
[4] Bazargani R, Fazli L, Gleave M, et al. Multi-scale relational graph convolutional network for multiple instance learning in histopathology images. Medical Image Analysis. 2024, 96:103197..
[5] Yang Z, Wei T, Liang Y, et al. A foundation model for generalizable cancer diagnosis and survival prediction from histopathological images. Nature Communications. 2025, 16(1): 2366.
[6] Chen W, Zhang P, Tran TN, et al. A visual-omics foundation model to bridge histopathology with spatial transcriptomics. Nature Methods. 2025, 22(7): 1568-1582.
[7] Krishnamurthy S, Schnitt SJ, Vincent-Salomon A, et al. Fully automated artificial intelligence solution for human epidermal growth factor receptor 2 immunohistochemistry scoring in breast cancer: a multireader study. JCO Precision Oncology. 2024, 8: e2400353.
[8] Qian D, Huang X, Li Z, et al. DigestPath: A benchmark dataset with challenge review for the pathological detection and segmentation of digestive system. Medical Image Analysis. 2022, 80: 102485.
[9] Zheng Q, Wang X, Yang R, et al. Predicting tumor mutation burden and VHL mutation from renal cancer pathology slides with self-supervised deep learning. Cancer Medicine. 2024, 13(12).
[10] Zhang Y, Liu S, Chen J, et al. Deep learning-based histomorphological subtyping and risk stratification of small cell lung cancer from hematoxylin and eosin-stained whole slide images. Genome Medicine. 2025, 17(1): 98.
[11] Zhang DY, Venkat A, Khasawneh H, et al. Implementation of digital pathology and artificial intelligence in routine pathology practice. Laboratory Investigation. 2024, 104(9): 102111.

[12] Lajara N, Espinosa-Aranda JL, Deniz O, et al. Optimum web viewer application for DICOM whole slide image visualization in anatomical pathology. Computer Methods and Programs in Biomedicine. 2019, 179: 104983.
[13] Shao W, Wang T, Sun L, et al. Multi-task multi-modal learning for joint diagnosis and prognosis of human cancers. Medical Image Analysis. 2020, 64: 101715.
[14] Gottlieb S. New FDA policies could limit the full value of AI in medicine. JAMA Health Forum. 2025, 6(3): e250123.
[15] Muehlematter UJ, Daniore P, Vokinger KN. Approval of artificial intelligence and machine learning-based medical devices in the USA and Europe (2015–2020): a comparative analysis. Lancet Digital Health. 2021, 3(3): e195-e203.
[16] Ullah E, Baig MM, Waqas A, et al. Multimodal generative AI for anatomic pathology – a review of current applications to envisage the future direction. Advances in Anatomic Pathology. 2025, 32(4): 255-268.
[17] Zhou Z, Qiao Y, Lin X, et al. A deployment method for motor fault diagnosis application based on edge intelligence. Sensors. 2025, 25(8): 3265.