

Introduction to the JMI Special Section on Computational Pathology

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This [special section](#) of the *Journal of Medical Imaging* (JMI) highlights 11 studies that represent the current frontier of computational pathology. Together, they capture how artificial intelligence (AI), deep learning, and multimodal modeling are transforming histopathology into a data-driven discipline capable of bridging discovery science and clinical application. The studies featured in this section illustrate the field's growing maturity—from weakly supervised learning and explainable AI to longitudinal disease modeling and spatial omics prediction—demonstrating both technical innovation and translational readiness.

Weakly and semi-supervised learning are central themes across several contributions. Tan et al.¹ introduce HID-CON, a weakly supervised framework for intrahepatic cholangiocarcinoma subtype classification that employs contrastive hidden-class detection to differentiate subtle morphological phenotypes on whole slide images. Shao et al.² present a semi-supervised segmentation approach that combines diffusion modeling with collaborative learning to improve cell-nuclei delineation. Both papers exemplify how data-efficient learning strategies can enhance the precision of tissue characterization without relying on exhaustive manual labeling. Similarly, Mammadov et al.³ introduce a benchmark study demonstrating that self-supervision can strengthen instance-based multiple-instance learning methods, and that more efforts could be put into self-supervised learning methods for digital pathology. In addition, Aygunes et al.⁴ propose a patch relevance estimation framework with multilabel augmentation to better address label uncertainty in weakly supervised multiclass histopathology classification.

Several studies in this collection bridge methodological progress with clinical translation. Yu et al.⁵ present Glo-In-One-v2, a holistic deep learning framework capable of identifying glomerular cells, tissues, and lesions across human and mouse kidney histopathology. Ramos-Soto et al.⁶ contribute a reflective yet pragmatic discussion on the clinical implementation of artificial intelligence in medical imaging diagnosis, addressing issues of validation, generalizability, and workflow integration that remain barriers to routine clinical adoption. These papers collectively indicate a growing emphasis on designing AI models that are not only accurate but also clinically interpretable and deployable. Complementing these perspectives, the article by Shukla et al.⁷ presents a systematic review of federated learning in computational pathology, highlighting how decentralized training strategies can enable multi-institutional collaboration while preserving data privacy.

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Multiple-instance learning itself is a defining thread of this special section. Bilic et al.⁸ propose a Fourier-transform-based multiple-instance learning strategy for whole slide image classification, offering computational efficiency without sacrificing accuracy. Winzell et al.⁹ apply multiple-instance learning for longitudinal outcome prediction in prostate cancer patients on active surveillance. Both studies emphasize that the multiple-instance learning algorithms have strong and unique benefits for digital pathology AI.

The explainability of computational pathology is further demonstrated by Takagi et al.,¹⁰ who introduce a quantification-based explainable AI framework for hepatocellular carcinoma discrimination, integrating clustering and morphometric visualization to clarify deep learning decisions. In a complementary direction, Zhu et al.¹¹ introduce Img2ST-Net, a fully convolutional image-to-image framework that predicts high-resolution spatial transcriptomic maps directly from hematoxylin-and-eosin (H&E) images. This work exemplifies how computational pathology is expanding into spatial omics, linking morphology to molecular context and setting the stage for integrative tissue atlases.

Collectively, the papers in this special section highlight three converging trajectories that define modern computational pathology: efficiency, interpretability, and integration. Efficiency is realized through weakly and self-supervised paradigms that minimize annotation demands; interpretability emerges through explainable frameworks that convert model outputs into biologically meaningful features; and integration manifests in cross-modal systems connecting histology, outcomes, and molecular data. These studies reaffirm that computational pathology is no longer confined to algorithmic experimentation—it is rapidly evolving into a clinically relevant, biologically grounded science.

We thank all authors, reviewers, and associate editors for their exceptional contributions to this special section. Their collective work illustrates that the promise of computational pathology lies in its ability to merge computational intelligence with human expertise, enabling faster, more reproducible, and ultimately more insightful diagnoses. As the field advances, such integrative efforts will continue to redefine how pathology is practiced, taught, and translated to patient care.

References

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