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Digital Revolution in Medical Pathology: Integrating Ai, Genomics, and Molecular Imaging

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ABSTRACT

The current clinical pathologic diagnostic process using histological slide evaluation demonstrates inconsistent accuracy in medical diagnosis. Progress in digital pathology and other modern technologies now enables the utilization of AI for medical image diagnostics, along with genomic technology for profile assessment and molecular image functionality. This systematic review examines the impact of artificial intelligence technology combined with genomic analysis and molecular imaging systems on present-day pathological medicine advancement. The review includes research published between 2014 and 2025, obtained from the top five databases, to demonstrate how each technology improves diagnosis separately and collaborates for precise medicine advancement. The analysis evaluated ten studies that matched all the established criteria for inclusion. Medical diagnostics benefit from combined system platforms, which also strengthen patient classification systems and treatment selection. However, these platforms require improvements in data standards and workflow connections, as well as computational resources and moral framework requirements. The study defines the necessary criteria for government-connected data platforms and interpretive artificial intelligence models, and then creates regulatory mechanisms in collaboration with interdisciplinary partnerships to develop safe and equitable healthcare applications. A single organized system triggers an essential transformation that shifts pathology from traditional morphological practices toward complex multivariate modern data methods. The research delivers strategic recommendations to enhance future practice and policy development, which will enable these technologies to be widely used in clinical settings.

INTRODUCTION

The medical field of pathology maintains crucial importance for disease examination, which supports both diagnosis and treatment of patients (Ahuja & Zaheer, 2025). The pathological approach of tissue section examination under a microscope faces two drawbacks: it depends on subjective visual interpretation, and it produces variable results between different observers according to Madabhushi & Lee (2016). The diagnostic field of medicine underwent important changes in recent times because innovative technologies seek to enhance diagnostic accuracy, combined with quicker operations. Digital pathology brought about significant changes in healthcare through vigorous digitization of medical slides while creating opportunities for remote consultations and image analysis, and storing large amounts of valuable data (Ali & Saqib, 2023). Digital transformation has optimized operational processes and established conditions for advanced computational systems to enter modern pathological procedures (Shafi & Parwani, 2023). Computational algorithms linked with digital imaging created new methods to analyze information quantitatively which leads to more dependable measurement systems. The incorporation of Artificial Intelligence (AI) with genomics and molecular imaging into pathology practice leads scientific advancements in delivering precision medicine (Munari *et al.*, 2024). Artificial Intelligence delivers outstanding performance through deep learning algorithms that outstrips human competency during specific diagnostic examinations (Sussman *et al.*, 2022). Digital histopathological image analysis through AI models enables medical experts to detect different cancers (Abasher *et al.*, 2023), while measuring treatment effects and forecasting patient clinical results according to Salo *et al.* (2024). Massive data training enables such systems to detect faint patterns seen only by sophisticated machines which results in improved diagnostic accuracy. The molecular brightness of diseases has advanced significantly because of genomics (Ikwuka *et al.*, 2013). Modern sequencing methods provide full genetic alteration exploration capabilities which lead to biomarker discoveries for diagnostic testing and prognosis prediction and therapeutic aims (Munari *et al.*, 2024). The combination of genomic data analysis with tissue examination results enables detailed disease classification, especially in cancer cases, which leads healthcare providers to design individualised treatments (Asif *et al.*, 2023). Treatment effect, along with patient results improves with targeted therapy decisions based on specific genomic profile mutations. Through positron emission tomography (PET) and single-photon emission computed tomography (SPECT), which belong to molecular imaging technologies, researchers can observe functional biological processes within living patients.

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Medical experts use these diagnostic methods to monitor receptor expression levels along with metabolic activity by gaining additional secondary information from traditional anatomical imaging data (Fahmy, 2024). The combination of molecular imaging with AI algorithm enhancements facilitates better pathological detection alongside better pathological variation characterization through complex detection methods and exact identification (Rowe *et al.*, 2021). Better disease assessment capabilities within this combined system led to immediate, proper medical interventions.

Rationale for the Study

Pathological applications experience very limited AI advancements because genomic and molecular-imaging technologies fail to achieve sufficient collaborative development. Modern technologies demonstrate the capability to develop morphology-based pathology into an advanced data-based field that extends beyond traditional morphology-based practices. Better disease knowledge combined with superior patient outcomes becomes achievable when pathologists analyze disease observations together with genetic and molecular data according to Munari *et al.* (2024). The integration process reveals different challenges because it needs standardized data formats alongside system interoperability and training for specialized staff members. The implementation of these tools in healthcare facilities requires proper solutions to both data privacy concerns and algorithm transparency needs to sustain ethical clinical practice (Asif *et al.*, 2023). Healthcare providers and scientists alongside policy experts need to unite their efforts for developing standardized rules which defend patient safety and enable these tools to function in typical medical care.

Research Aim and Objectives

This study aims to explore the transformative impact of integrating AI, genomics, and molecular imaging into medical pathology. The specific objectives are:

1. To review the current applications and advancements of AI in pathological diagnostics.
2. To examine the role of genomic data in enhancing pathological assessments.
3. To evaluate the contributions of molecular imaging techniques in pathology.
4. To identify the challenges and limitations associated with the integration of these technologies.
5. To propose recommendations for effective implementation and future research directions.

MATERIALS AND METHODS

Study Design

The review implemented PRISMA guidelines throughout its systematic methodology (Page *et al.*, 2021). The research design brings together established studies about AI and genomic analysis with molecular imaging in pathology to achieve both less subjective decision-making and enhanced research reproducibility. The study used two independent reviewers who conducted dual screenings for data extraction concurrently until a third expert resolved any discrepancies. The review protocol established both eligibility requirements and data collection items and quality assessment instruments (CASP and Newcastle–Ottawa Scale) before starting the search process to avoid post-hoc decision-making. The PRISMA framework enhances research methodology, but is still unable to eliminate both publication bias and differences among research approaches. The system of registered protocols depends on certain assumptions about database availability, but does not identify research that exists outside database systems. The use of systematic registration during complete evidence synthesis helps researchers execute established guidelines correctly.

Inclusion Criteria

This study analyzed peer-reviewed original articles which met the following four conditions: (1) used AI algorithms with genomic analysis or molecular imaging applications in human pathology settings, (2) included clinical or histopathological specimen data such as biopsies and resection specimens, (3) provided diagnostic performance data together with workflow influences and patient-centered outcomes and (4) were published in English during January 2014 to March 2025. The analysis included clinical trials and cohort studies as well as case-control investigations and cross-sectional research and technology-validation studies for collecting evidence at multiple levels. The scope supports practical applications in medical practices through its multiple research method acceptance. The review only accepting English-language publications could potentially hide groundbreaking research from other languages which results in linguistic bias affecting the study results. The ten-year time boundary safeguards contemporary digital innovation studies without undermining earlier research conducted between 2014 and the present day. The research lacked geographic limitations letting participants from worldwide locations submit data yet this method brought increased variability among different healthcare facilities and their available resources.

Exclusion Criteria

The review excluded (1) non–peer-reviewed literature (editorials, commentaries, conference abstracts, theses), to focus on fully vetted research; (2) studies without direct pathology relevance (e.g., radiology-only AI applications or bioinformatics pipelines lacking histopathological correlation); (3) purely in vitro or animal-model investigations without human data; (4) articles lacking sufficient methodological detail or performance metrics; and (5) duplicates and extensions of the same primary dataset. The chosen data restriction criteria improve data review precision and quality but removes essential early-stage research that often presents at conferences. Language bias results from reports written in any language except English while publication bias becomes more prominent when gray literature is excluded. The team documented all excluded studies for potential use in future research updates that may include different types of evidence during the field's development.

Search Strategy

A systematic method was used for comprehensive literature search that combined Boolean operators along with Medical Subject Headings (MeSH) and free-text terms. The search terms were chosen specifically to represent digital pathology and artificial intelligence (AI) together with genomics and molecular imaging domains. The search included the following grouping of terms: "Digital pathology" OR "Whole slide imaging" along with "Artificial Intelligence" OR "AI in pathology" OR "Machine learning" OR "Deep learning" as well as "Histopathology" OR "Tissue analysis" and "Genomics" OR "Next-generation sequencing" OR "Genetic profiling" plus "Molecular imaging" OR "PET" OR "SPECT" together with "Precision medicine" AND "Pathology". The researchers used Boolean operators (AND, OR) to properly connect their selected concepts. For example: ("Digital pathology" AND "Artificial Intelligence") OR ("Genomics" AND "Histopathology") AND ("Molecular imaging" OR "Deep learning"). The literature search included PubMed/MEDLINE and Scopus and Web of Science and IEEE Xplore to complement Google Scholar. English-language peer-reviewed articles published since January 1, 2014 until March 31, 2025 made up the scope of this research. The authors performed their screening by PRISMA guidelines. The EndNote X9 program imported the search results for duplicate detection. Two separate researchers evaluated titles and abstracts of potential studies to determine their eligibility. Two researchers performed detailed reviews of articles that showed potential relevance. The research team excluded studies which failed to match the selection criteria while providing documented reasons. Any disagreement between reviewers was settled through mutual discussion or involvement of a third-party arbitrator. A systematic process followed by transparent methods enabled researchers to capture high-quality relevant studies that answered the study objectives.

Data Extraction and Management

A standardized extraction form was tested for clarity and consistency using ten randomly chosen medical studies before implementation on the remaining studies. The data collection process acquired information about study authors, publication dates, countries of origin as well as research design types and sample sizes, histology and cytology methods, AI system frameworks, genomic sequencing techniques, molecular imaging tracers, performance metrics, and documented clinical and workflow impact metrics. The extraction process took place independently between two reviewers who used Microsoft Excel software with automatic version tracking capabilities. The reviewers checked all measurements showing more than 10% deviation and met to reach consensus; disagreements escalated to a third expert validation.

Prisma

Transparent and rigorous selection followed the PRISMA 2020 guidelines during the study assessment process. The search process identified 1,374 records, which included database search results combined with manual reference tracking. The database search yielded 410 articles from PubMed and 340 from Scopus, together with 290 from Web of Science and 157 from IEEE Xplore and 177 from Google Scholar. Through the process of duplicate removal, 1,062 unique records persisted. Two independent reviewers reviewed titles and abstracts, which resulted in discarding 931 articles due to their irrelevance to the research topic and their non-human data or lack of digital pathology technology focus. A total of 131 full articles underwent a methodological assessment as well as a relevance review for their connection to AI, genomics, and molecular imaging applications in pathology. The analysis process excluded 121 articles because the research did not integrate the three technologies properly or lacked clinical applications or presented methodological issues. A total of ten high-quality studies fulfilled all requirements and became part of the systematic review evaluation. The authors conducted a critical assessment of the included studies, which followed thematic synthesis.

Methodology

This systematic review performed a synthesis of findings extracted from chosen research studies during data analysis. The research process included extensive database searches, which led to selecting relevant studies according to established eligibility standards about AI and genomic applications as well as molecular imaging in medical pathology. A structured data extraction process collected essential information, including research designs as well as technological methods, measured outcomes and application settings. The researchers separated studies according to their primary subjects, which examined AI diagnostic tool advancements and genomics applications in pathology and molecular imaging technique innovations. The research team analyzed each theme to detect typical patterns alongside current obstacles and new findings within this academic subject. A narrative synthesis method allowed researchers to organize and make sense of the study results while establishing relationships between different research works to present an extensive summary of medical pathology's up-to-date technologies. Researchers designed this study to demonstrate the expected improvements which these technologies would bring to diagnostic precision and patient recovery outcomes, and future pathology operations. A critical evaluation of the selected reports examined both study methodology and participant numbers alongside research design to guarantee that this review presents validated and dependable findings.

RESULTS AND DISUSSION

Technological Innovations and Diagnostic Performance

The combination of artificial intelligence with genomics and molecular imaging technologies enables precision diagnostics to transform pathology services by improving both diagnostic precision and individualized treatment of patients. Both significant potential advantages and critical assessment of strengths and weaknesses, together with combined implementation challenges, must be thoroughly evaluated. Such analysis demonstrates how complex these systems become when they are put into medical practice. Deep learning–based image analysis has proven effective in histopathology through Panayides *et al.* (2020) since their method reached area-under-curve (AUC) values upward of 0.90 for tumour recognition.

The obtained results demonstrate AI systems match pathologists' accuracy rates for sensitivity and specificity levels. The study demonstrates a major drawback because these models fail to maintain consistent performance when operating with diverse institutions or changes in staining protocols or slide quality (Cheng *et al.*, 2021). Large-scale generalization proves to be a major obstacle since controlled environment models struggle to perform correctly in actual clinical settings. Many AI algorithms maintain an untraceable decision-making process, which impedes clinicians from adopting them in practice settings (Prevedello *et al.*, 2019). The reliability of AI in pathology diagnostic settings comes into question because of such concerns, especially during critical medical determination moments. The diagnostic field has experienced significant transformation through genomic profiling because it identifies mutations and expression patterns to provide molecular insights. Tumour stratification in oncology, together with predictive treatment responses, increased to over 95% sensitivity after integrating next-generation sequencing (NGS) data with histopathological images according to Seyhan and Carini (2019). The reliability of genomic data faces various challenges according to Ahmad *et al.* (2021). The process of sequencing artifacts together with stringent tumour purity requirements can trigger incorrect test results that may confuse medical professionals during interpretation. Efficient bioinformatics pipelines provide solutions to analyse the large quantities of sequencing data which medical practitioners need for clinical applications. The bioinformatics pipelines containing AI systems develop recursive dependencies, which generate anxiety regarding analysis transparency and accumulated mistakes (Seyhan & Carini, 2019). Bioinformatics must implement strong, transparent procedures to enable genomic data usage in clinical decisions (Kermany *et al.*, 2018).

PET and SPECT techniques in molecular imaging enable real-time metabolic imaging of tissue structures beneath one centimetre, which traditional histological and genomic methods cannot visualise. The research by Tian *et al.* (2021) shows that these imaging modalities reach sensitivity rates above 90% for detecting small lesions to enhance early detection. PET and SPECT imaging methods face difficulties with specificity because tracer uptake happens in both malignant and benign tissues thereby causing false positive results. Traditional microscopic imaging provides higher spatial resolution than molecular imaging, which restricts the obtainable cellular details from this method. According to Panayides *et al.* (2020) and Simon *et al.* (2024), accurate interpretation and modality synergy between combined analytical techniques need precise standardisation of acquisition methods and image processing workflows.

These technological systems, united together, create potential major combined advantages. The convergence of image features and mutation profiles, and functional imaging within multimodal artificial intelligence systems leads to a 15% increase in prognostic accuracy according to Simon *et al.* (2024). The integration process comes with significant challenges that need to be addressed. The article by Gaffney and Mirza (2025) describes how the integration of these technologies becomes difficult due to data format inconsistencies between imaging and genomic platforms in addition to complex requirements for large dataset management infrastructure and divergent governance policies. The matter of algorithmic bias advances as a crucial problem in the field. The training of numerous AI models depends on minority-underrepresented datasets that result in performance differences during clinical use among diverse patient populations (Kim *et al.*, 2022).

Workflow Integration and Implementation Barriers Focus

The accuracy and efficiency of routine pathology diagnostics are set to improve significantly with the integration of workflow systems that bring together AI, genomics, and molecular imaging. These technologies encounter multiple complex problems while being integrated into current laboratory settings which require vital assessment before benefiting from their implementation. Shafi and Parwani (2023) state that automated whole-slide imaging (WSI) scanners introduced digital pathology but their implementation requires perfect LIS and reporting platform connectivity. Many current LIS systems operate using outdated protocols while missing essential APIs which would allow them to process large images of gigapixels and to connect genomic reports to histological analysis results. Pathology departments struggle with IT infrastructure built for transactional reporting which requires extensive hardware upgrades of high-throughput storage area networks and comprehensive network modification to handle image and sequence data according to Cheng *et al.* (2021). Panayides *et al.* (2020) emphasize that medical practices need proper data management structures based on standardized metadata schemas and data lakes to work efficiently. Healthcare data remains isolated throughout different systems because patients lack common data ontologies and tag classification structures (such as DICOM for images or HL7 FHIR for clinical information) which prevents multi-modality data search and integrated AI system development. Federated systems operate without centralized raw data storage because algorithms execute directly from source nodes to maintain privacy guidelines and achieve large-scale algorithms. The entire integrated workflow relies on data pipelines which pose the risk of becoming performance bottlenecks. The increase of "omics" datasets exceeds statistical capabilities which requires sophisticated computational frameworks based on Kubernetes clusters for handling large sequencing read volumes according to Seyhan and Carini (2019). The model performance becomes inconsistent when differences in scanner calibration and staining protocols and annotation granularity emerge in image acquisition and annotation pipelines according to Prevedello *et al.* (2019).

The use of centralized image-analysis competitions together with shared benchmarking datasets helps with both harmonization and ongoing validation process. The requirements for implementing this technology span technological resources and more. The paper explains how research clusters that incorporate GPUs or specialized AI accelerators for model training and inference also need to include object-storage solutions which handle petabyte-scale archives (Kim *et al.* 2022). The acquisition of capital to fund such infrastructure tends to face obstacles against core laboratory budgets which leads to resistance from senior management regarding investment returns according to Ahmad *et al.* (2021). The necessity for complete cost-benefit assessments emerges because reduced turnaround times together with lower error rates and possible future savings need to show how they balance initial investments. According to Gaffney and Mirza (2025) leadership frameworks need to adapt simultaneously to create specific guidelines regarding data protection together with security protocols and algorithm responsibility standards. The implementation of GDPR and HIPAA regulations necessitates role-based access controls along with audit trails along with data encryption when data rests or when it moves through networks. The absence of proper oversight exposes departmental operations to substantial regulatory penalties together with a deterioration of patient confidence. Human factors are equally critical. To achieve effective change management institutions must provide both tool proficiency training to pathologists and technical staff and education about system limitations. The adoption of AI outputs suffers from reduced pathologist acceptance because these systems fail to demonstrate their decision processes or explain their reasoning according to Cheng *et al.* (2021). The collaboration between IT, bioinformatics and clinical teams shows limited success because both departments work independently from each other according to Kim *et al.* (2022). Shafi and Parwani (2023) explain that "AI champions" who work in pathology laboratories connect these two different domains while addressing user concerns immediately and facilitate learning between colleagues, and drive continuous AI development. Successfully adopting AI solutions means providing ongoing support, like dedicated help desk staff, regular training sessions, and performance dashboards, to keep things running smoothly and ensure people continue to use the technology effectively.

Panayides *et al.* (2020) emphasize the necessity for integrative analytics platforms to have feedback systems that help laboratories enhance their algorithms and workflows using actual practice performance indicators. Laboratories can achieve reliable routine clinical care through proactive protocol adjustments by continuously monitoring indicators, which include error rates, model drift and user satisfaction (Oala, Flach & Ghalwash, 2022).

Ethical, Regulatory, and Data Governance Considerations

Combining AI with genomics and molecular imaging in pathology opens up incredible opportunities—but it also brings significant ethical challenges and regulatory hurdles that must be carefully addressed. The research by Gaffney and Mirza (2025) shows that patient privacy safeguards, together with accountability measures, need equal importance to technical performance when diagnostic algorithms enter clinical workflows deeply. The absence of strong governance systems will allow sensitive data to become compromised or lead to unauthorized uses of confidential information, which would compromise technological precision. According to Seyhan and Carini (2019), large-scale omics data consolidation poses significant threats through combining genomic sequences with high-resolution images for AI training models because this process centralizes vulnerable patient information. Ahmad *et al.* (2021) emphasise that advanced diagnostic democratisation should never violate patient consent or autonomy. Panayides *et al.* (2020) show how federated learning addresses this issue through model distribution since weight updates get encrypted before being shared, according to their research. These security systems need perfect encryption with strict key controls and accurate access protocols to prevent attackers from reassembling private information. The paper written by Kim *et al.* (2022) emphasizes that protecting infrastructure stands on par with importance. AI accelerators as well as GPUs need protected data centers to operate from, and these centres require ongoing monitoring procedures, alongside network segmentation, along automated audit log generation.

Cheng *et al.* (2021) emphasize that laboratories must comply with frameworks like ISO/IEC 27001 and HIPAA because nonexistence of formal policies for encryption and breach notification, and data retention leads to regulatory penalties, together with public trust deterioration. The majority of pathology departments encounter difficulties converting their legacy IT systems which operated for transactional reporting, into systems which handle multi-terabyte imaging and sequencing archives.

Transparency represents another essential foundation, according to the research by Prevedello *et al.* (2019). The secrecy of "black box" AI models prevents detection of scanning artifacts that both break user confidence and produce unpredictable mistakes, even when these models provide excellent accuracy. Shafi and Parwani (2023) explain that pathologists avoid implementing systems that lack explainable decision-making capabilities. The study from Kim *et al.* (2022) shows that explainable AI methods through attention maps and feature attributions help to show prediction formation, yet require accurate micro-level accuracy and clinical interpretation capabilities. The critical dashboard systems described by Panayides *et al.* (2020) help to find both model shifting patterns alongside novel biases which negatively impact minority populations.

The research conducted by Cheng *et al.* (2021) reveals that regulatory frameworks should advance their rules as new technological developments emerge. The FDA 510(k) clearance system and CE marking approach provide regulatory approval for software versions that remain unchanged but fail to cover the governance of AI systems that learn continuously. Shafi and Parwani (2023) highlight recent manufacturer approvals that include whole-slide imaging scanners plus a prostate-cancer AI algorithm, yet create unaddressed questions regarding update validation and how to verify retraining, along with adaptive learning procedures. Prevedello *et al.* (2019) suggest that mandates for uniform validation protocols should include multicenter prospective trials and standardised staining along with annotation benchmarking to provide regulators with equivalent datasets and metrics. The research by Gaffney and Mirza (2025) outlines how liability frameworks should specify the accountable parties when AI mishaps produce injuries. Pathology laboratories need to create oversight committees with pharmacovigilance board-like functions to verify AI-informed clinical assessments and modify consent arrangements for patients, together with adverse event tracking. The authors of Ahmad *et al.* (2021) support the development of "explainability audits" along with continuous post-market surveillance to detect rare critical failures. Footprint evaluation depends on clear organizational accountability along with rapid information feedback between organizations and technicians who maintain patient welfare through transparent reporting.

Implication

The research investigation identified multiple essential pathologic requirements that require combined technical and organizational answers. The highest level of data governance operation must take place. According to Seyhan and Carini (2019), the combination of "omics" and imaging data before training AI systems intensifies both privacy threats against patient data and potential abusive practices related to highly sensitive medical information. The federated learning method enables laboratories to maintain server-based private data protection and encrypted model updates exchange to access multiple institutional datasets according to Zhu *et al.* (2021) and Xu *et al.* (2020). The deployment requires authorised policies to establish end-to-end encryption together with strict key management protocols and role-based access control systems to fulfil the criteria set by ISO/IEC 27001 and HIPAA standards, according to Cheng *et al.* (2021) and Panayides *et al.* (2020). AI application infrastructure requires design specifications for its functionality. Modern healthcare facilities need GPU-powered computing clusters and AI accelerator systems that support encrypted storage with scale capabilities, according to the research by Kim *et al.* (2022). Modernization efforts must be deployed to legacy laboratory information systems, which need to use standardized APIs to receive digital slides and genomic reports according to Shafi & Parwani (2023) and Panayides *et al.* (2020). Organizations will need to show how the combination of faster test processing with fewer mistakes makes the upfront financing expense worthwhile (Ahmad *et al.*, 2021). All automated systems must implement transparency as an organizational foundation. The use of "Black box" predictive models damages trust while it simultaneously conceals any random connections that might exist within their results, according to Prevedello *et al.* (2019).

XAI tools with explanatory capabilities, such as HIPPO (Arvaniti *et al.*, 2024) as well as attention-based heatmaps (Chartrand *et al.*, 2022) provide evaluation functionalities for pathologists to analyze models' decision-making processes. Training programs must include specific units about understanding AI outputs and their boundary limitations (Rai, 2020; Holzinger *et al.*, 2022).

The approval process should evolve from receiving static approvals to active oversight. The current FDA 510(k) along with CE-mark approval processes, fail to meet the requirements of AI systems that learn in real time. Pathology departments need to implement procedures for software version control alongside retraining validation protocols and post-market safety checks, which resemble pharmacovigilance practices (Cheng *et al.*, 2021; Prevedello *et al.*, 2019).

Multiple healthcare organizations must establish ongoing learning systems together with cross-speciality supervision. Pathology departments should establish "AI governance committees" that unite medical specialists and bioinformatics professionals with legal experts and moral ethicists for checking new tools using standardised testing protocols and clinical effectiveness metrics (Gaffney & Mirza 2025). The necessary iterative refinement process requires performance dashboards which include indicators for model drift assessment and demographic sensitivity, and clinical impact evaluation (Panayides *et al.*, 2020). To advance precision diagnostics as an everyday practice which handles ethical standards, pathologists must implement organized investments that create secure infrastructure and federated architectures and adaptive governance, together with XAI capabilities and cultural changes.

Recommendation

The research findings produce multiple essential recommendations which direct the course of clinical practice, together with research activities and policy development. Every health institution needs to adopt AI and genomic instruments into digital pathology systems to boost diagnostic accuracy while providing individualized care. The integration of AI with genomic tools requires extensive training to build pathologists' abilities for responsible interpretation of AI-produced results together with genomic information. Policy officials and healthcare administrators need to create uniform guidelines that handle ethical problems, reveal algorithm operations, and guard patient information databases as the use of federated learning and data collaborations increases. The development of explainable AI requires an active enhancement of interdisciplinary relationships between computer scientists with molecular biologists, and clinicians to promote technological advances which remain clinically useful and patient-focused. Research funding for the evaluation of AI diagnostic systems in different patient populations remains necessary to stop health equity gaps from forming. Embracing people-centred, transparent, ethical methods represents the vital approach for achieving a complete medical revolution through AI genomics and molecular imaging.

CONCLUSION

This systematic review shows that integrating artificial intelligence (AI), genomics, and molecular imaging improves diagnostic precision and personalization in pathology. AI enhances image interpretation and predictive accuracy; genomics deepens molecular classification; and molecular imaging visualizes in vivo processes. Together, these modalities accelerate workflows, reduce error, and strengthen treatment planning and outcomes.

Major findings indicate strong performance: deep-learning histopathology models frequently achieved AUCs of 0.90 or higher, and multimodal systems that combine imaging with genomic features produced roughly a 15% gain in prognostic accuracy in comparative studies. Molecular imaging methods such as PET and SPECT demonstrated sensitivities exceeding 90% for detecting small lesions. In oncology stratification, integrating next-generation sequencing with histopathology achieved sensitivities above 95% in selected settings.

Clinical adoption remains constrained by data-format and interoperability gaps, privacy and bias risks, and limited explainability. Addressing these barriers requires robust data governance, investment in scalable compute and storage, and cross-disciplinary collaboration to develop transparent, validated models suitable for routine care.

Overall, the convergence of AI, genomics, and molecular imaging marks a shift toward precision diagnostics. With explainable AI and ethical oversight, these integrated approaches can deliver faster, reliable decisions, establishing a more patient-centered paradigm for pathology and improving outcomes across healthcare systems.

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