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Review Article

Digital Biomarkers and AI in Oncology: Redefining Early Detection and Personalized Intervention

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ABSTRACT

Cancer represents a global health imperative, with early detection and personalized intervention remaining critical determinants of patient outcomes. The convergence of artificial intelligence (AI) and digital biomarkers quantifiable molecular and imaging signatures derived from biological samples and medical imaging modalities is fundamentally reshaping oncology practice. This narrative review synthesizes recent advances in AI driven digital biomarkers for cancer early detection, prognosis, and therapeutic decision making, with emphasis on multi omics integration, deep learning architectures, and real-world clinical translation. Liquid biopsy platforms detecting circulating tumor DNA (ctDNA) have achieved unprecedented sensitivity (>90%) in early-stage cancer detection when combined with machine learning algorithms. Imaging biomarkers derived from radiomics and deep learning enabled histopathology analysis demonstrate superior performance compared to traditional diagnostic modalities. Foundation models and transformer-based architectures have revolutionized feature extraction from heterogeneous data types. However, clinical adoption remains constrained by challenges including algorithmic interpretability, data standardization, privacy preservation, and regulatory validation. Federated learning and explainable AI frameworks are emerging as solutions to enable secure, multi-institutional model development while maintaining transparency for clinicians. Integration of genomic, transcriptomic, proteomic, and imaging biomarkers through AI powered multi modal fusion is advancing precision oncology by enabling patient specific risk stratification and therapy selection. Digital twins and autonomous oncology systems represent frontier applications that promise real time, adaptive treatment optimization. This review emphasizes that the transformative potential of AI and digital biomarkers can only be realized through rigorous prospective validation, standardized protocols, regulatory alignment, and interdisciplinary collaboration bridging computational

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innovation with clinical reality.

INTRODUCTION

Cancer imposes an unprecedented global burden, accounting for approximately 20 million new cases and 10 million deaths annually, with mortality disproportionately affecting resource limited regions where diagnostic infrastructure remains inadequate [1]. Conventional oncology has historically relied on tissue based diagnosis and imaging modalities approaches that are inherently invasive, time intensive, and limited in their ability to capture tumor heterogeneity and disease evolution [2]. The critical observation that early stage cancers demonstrate substantially improved survival rates has catalyzed a paradigm shift toward precision oncology, wherein diagnosis, prognosis, and treatment selection are informed by comprehensive molecular profiling integrated with clinical and imaging data [3]. This shift is being accelerated by two convergent technological revolutions: the emergence of highly sensitive, non-invasive biomarker platforms and the exponential advancement of artificial intelligence capable of extracting actionable insights from complex, high dimensional biological data.

Digital biomarkers represent a conceptual evolution beyond traditional biomarkers, defined as quantifiable characteristics derived from biological samples, medical imaging, or wearable devices that reflect underlying pathophysiological processes [4]. Unlike protein based biomarkers such as prostate specific antigen, which exhibit modest specificity and are prone to false positive results necessitating invasive confirmatory testing, digital biomarkers enable continuous, non invasive monitoring through liquid biopsy platforms analyzing cell free DNA, RNA, and circulating tumor cells, as well as imaging biomarkers quantifying tumor phenotype at the mesoscopic scale [5]. The integration of artificial intelligence particularly machine learning and deep learning with these biomarkers transforms oncology from a reactive to a proactive discipline. Machine learning algorithms, when trained on large cohorts with molecular and clinical outcomes, can identify subtle patterns in digital biomarker signatures that predict treatment response, forecast recurrence risk, and ultimately guide personalized intervention strategies [6].

Despite these extraordinary advances, a substantial translational gap persists between research innovation and clinical implementation. Early stage liquid biopsy studies reporting >90% sensitivity in cancer detection have not consistently translated to equivalent performance in prospective screening cohorts, partially due to biomarker abundance variability, inter assay standardization challenges, and the phenomenon of clonal hematopoiesis of indeterminate potential generating false positive ctDNA signals [7]. Similarly, deep learning models achieving exceptional accuracy on curated research datasets frequently demonstrate degraded performance when applied to real world clinical populations characterized by demographic diversity, variable imaging protocols, and institutional heterogeneity [8]. Furthermore, the "black box" nature of many AI algorithms their opacity regarding decision making mechanisms engenders legitimate clinician skepticism regarding trustworthiness and reliability in high stakes medical decision making contexts. This review systematically examines how AI augmented digital biomarkers are reshaping early cancer detection and personalized intervention, while critically analyzing implementation barriers and emerging solutions including federated learning, explainable AI, and digital twin technologies that promise to bridge the research to clinic translation gap.

2. Evolution of Artificial Intelligence in Oncology

The trajectory of AI applications in oncology reflects the broader evolution of machine learning from statistical methods to end to end neural network architectures capable of learning hierarchical feature representations directly from raw data [9]. Early applications leveraged classical machine learning algorithms support vector machines, random forests, logistic regression trained on manually engineered features derived from imaging or genomic data. These approaches, while interpretable, were fundamentally limited by the expert knowledge required to identify relevant features and the inability to capture complex, non linear relationships inherent in cancer biology [10]. The watershed moment arrived with the advent of deep learning, particularly convolutional neural networks (CNNs) that revolutionized medical image analysis by demonstrating that hierarchical feature learning could identify diagnostic patterns invisible to human expert review. For instance, deep learning models trained on histopathology images achieved diagnostic accuracy exceeding expert pathologists in identifying metastatic lymph node involvement, a finding that fundamentally challenged assumptions regarding human visual perception superiority in medical image interpretation [11].

The evolution continued with the emergence of recurrent neural networks for sequential data analysis enabling temporal modeling of treatment response dynamics from longitudinal biomarker measurements and the introduction of attention mechanisms that allowed models to selectively focus on clinically relevant regions of images or sequences [12]. More recently, the transformer architecture has demonstrated remarkable generalizability across imaging modalities and tasks, with vision transformers achieving superior performance compared to conventional CNNs particularly when trained on limited, institutional specific datasets through transfer learning from large scale pretraining on natural image collections [13]. Foundation models neural networks pretrained on massive, diverse datasets and then fine-tuned for specific tasks represent a paradigm shift toward unified, multimodal systems capable of integrating imaging, genomic, and clinical data simultaneously [14]. These advances have paralleled the development of sophisticated natural language processing capabilities, enabling AI systems to extract structured clinical insights from unstructured electronic health records, pathology reports, and clinical narratives, thereby operationalizing the complete spectrum of patient information available in contemporary oncology practice [15]. Critically, this evolution from task specific, single modality models to unified, multimodal foundation models reflect increasing recognition that cancer is fundamentally a systems disease requiring integration of biological information across multiple scales and domains for accurate prediction and intervention.

3. Digital Biomarkers in Oncology: Definition, Classification, and Clinical Applications

Digital biomarkers in oncology are defined as quantifiable, patient derived molecular or imaging signatures that inform cancer diagnosis, prognosis, treatment selection, and monitoring, with the qualifier "digital" reflecting dependence on computational analysis for extraction, interpretation, and clinical application [16]. This definition encompasses a diverse ecosystem of biomarker categories, each with distinct biological significance, technical requirements, and clinical applications. Wearable derived biomarkers including heart rate variability, activity patterns, sleep architecture, and circadian rhythm disruption represent emerging signals of cancer related

complications including chemotherapy induced cardiotoxicity and functional decline, accessible through non invasive, continuous monitoring that enables early detection of treatment related toxicity before symptomatic presentation [17]. Liquid biopsy biomarkers comprise the most extensively validated digital biomarker category, encompassing circulating tumor DNA (ctDNA) released into bloodstream by apoptotic and necrotic tumor cells, circulating tumor cells (CTCs) representing intact cancer cells capable of seeding metastatic disease, and extracellular vesicles (EVs) including exosomes that package tumor derived nucleic acids and proteins [18]. Each analyte type provides complementary information: ctDNA enables sensitive mutation profiling and minimal residual disease detection; CTCs provide dynamic information regarding metastatic potential and therapeutic resistance mechanisms; EVs offer insights into intercellular communication and tumor microenvironment composition.

Imaging biomarkers quantitatively analyze tumor morphology, internal heterogeneity, and microenvironmental characteristics through radiomics computational extraction of high dimensional texture, shape, and intensity features from medical images that correlate with underlying genomic alterations and predict treatment response [19]. Deep learning approaches have extended radiomics by enabling automated feature discovery directly from images without manual feature engineering, demonstrating that learned representations capture prognostically relevant information orthogonal to traditional radiologic features. Molecular biomarkers derived from multi omics analysis including genomic alterations (mutations, copy number variations, structural variants), transcriptomic signatures reflecting pathway activation, proteomic profiles capturing signaling state, and epigenetic modifications including DNA methylation patterns provide molecular stratification enabling precise tumor classification and druggable target identification [20]. The clinical utility of digital biomarkers varies substantially across cancer contexts: in hematologic malignancies, ctDNA analysis enables extraordinarily sensitive recurrence detection with >99% specificity; in solid tumors, liquid biopsy sensitivity remains suboptimal in early stage disease due to low ctDNA fraction in circulation, necessitating integration with imaging biomarkers and multi omics approaches for clinically acceptable predictive performance [21].

Real time patient monitoring systems integrating wearables, continuous biomarker sampling through implanted devices, and remote data transmission have emerged as enabling infrastructure for dynamic biomarker driven oncology [22]. These systems capture longitudinal biomarker trajectories that encode temporal dynamics often more informative than single time point measurements for predicting treatment response and clinical events. Integration of multiple biomarker modalities multimodal biomarker panels combining ctDNA, imaging features, and wearable signals has demonstrated substantially improved predictive performance compared to individual modalities in isolation, reflecting the systems level nature of cancer biology [23].

4. Artificial Intelligence Architectures in Oncology

Contemporary AI in oncology spans a spectrum of architectures optimized for distinct data modalities and clinical questions. Machine learning encompasses classical algorithms including support vector machines, random forests, gradient boosting methods (XGBoost, LightGBM, CatBoost), and ensemble approaches that remain

valuable for structured, tabular data such as electronic health records, genomic features, and laboratory results [24]. These methods provide inherent interpretability through feature importance metrics and decision rule transparency, advantages increasingly valued in clinical contexts where model transparency influences clinician adoption. Deep learning architectures, including convolutional neural networks optimized for spatial feature extraction from images, recurrent neural networks and long short term memory (LSTM) networks capturing temporal dependencies in longitudinal biomarker series, and graph neural networks modeling biological networks and cell cell interactions, have demonstrated superior performance on complex, high dimensional data [25]. The transformer architecture, originally developed for natural language processing, has demonstrated remarkable versatility in medical imaging, with vision transformers achieving state of the art performance in histopathology image classification through self attention mechanisms that capture long range dependencies and contextual relationships [26].

Foundation models represent an inflection point in AI development, with large scale neural networks pretrained on massive, diverse datasets acquiring generalized feature representations transferable to downstream tasks with minimal fine tuning [27]. These models, including BERT derived architectures for clinical text analysis and vision transformers for medical imaging, manifest remarkable few shot learning capabilities learning from limited institution specific data through transfer learning from large scale pretraining addressing a critical bottleneck in clinical AI deployment where obtaining large, well annotated datasets has historically been prohibitive. Self supervised learning and contrastive learning approaches enable models to learn meaningful representations from unlabeled data, a particularly valuable capability in oncology where obtaining diagnostic labels requires expert pathologist review and is labor intensive [28]. Multimodal learning frameworks that jointly process imaging, genomic, and clinical data through parallel encoders and fusion modules have demonstrated that integration across modalities improves prediction accuracy compared to individual modality analysis, reflecting the biological principle that cancer phenotype emerges from the interaction of molecular, cellular, and systemic processes [29].

The architectural evolution toward foundation models and multimodal systems reflects increasing recognition that isolated, task specific models are suboptimal in clinical oncology where comprehensive understanding requires integrating information from disparate sources. The challenge now shifts toward developing unified, generalizable models that simultaneously maintain accuracy, interpretability, and computational efficiency suitable for deployment in resource constrained clinical environments.

5. AI in Early Cancer Detection

Early stage cancer detection represents the most transformative application of AI augmented digital biomarkers, as early diagnosis fundamentally alters prognosis and enables curative intervention before metastatic dissemination [30]. In radiology, deep learning models have achieved human level or superior performance in detecting subtle abnormalities in mammography, lung CT, and colorectal imaging that human radiologists frequently overlook or misinterpret [31]. For instance, AI systems trained on large mammography cohorts demonstrate approximately 10 15% improvement in cancer detection sensitivity compared to expert radiologists while simultaneously reducing false

positive findings that drive unnecessary biopsies. This improvement reflects deep learning's ability to identify morphologic patterns including subtle tissue density variations, architectural distortions, and microcalcification clusters that correlate with malignancy but are subthreshold for human visual perception.

In digital pathology, AI enabled whole slide imaging analysis has revolutionized histopathologic diagnosis by automating time intensive tasks including identifying metastases in lymph nodes with >99% sensitivity comparable to expert pathologists, enabling quantification of morphologic features (mitotic figures, nuclear features, degree of differentiation) that inform grading and treatment selection, and predicting molecular subtypes and genomic alterations directly from routine hematoxylin eosin stained tissue [32]. These capabilities transform pathology from a subjective interpretation discipline toward precision measurement, reducing inter observer variability and ensuring standardized biomarker assessment. Liquid biopsy analysis, when augmented with machine learning algorithms for interpreting complex biomarker panels, has achieved remarkable early detection sensitivity: in asymptomatic individuals, multi cancer early detection (MCED) blood tests combining ctDNA and protein biomarkers have demonstrated approximately 40 70% sensitivity for detecting cancers at early stages, with sensitivity improving substantially for advanced stage disease [33]. The analytical challenge of detecting ctDNA in early stage cancer where tumor burden is minimal and ctDNA represents <0.1% of circulating cell free DNA has been addressed through innovations including fragment length analysis exploiting the finding that cancer derived DNA fragments exhibit characteristic size distributions distinct from hematopoietic cfDNA, and error suppression algorithms filtering artifacts to achieve attomolar sensitivity [34].

Multi omics integration through machine learning has emerged as powerful approach for early detection by combining genomic alterations, epigenetic modifications, transcriptomic signatures, and proteomic changes into unified prediction models [35]. For example, integrating whole genome sequencing, methylation profiling, and plasma protein measurements has achieved >90% sensitivity for detecting early stage pancreatic cancer in high risk individuals, substantially outperforming individual modality analysis. This principle extends to multimodal radiogenomics approaches that integrate radiomic features with genomic data, enabling prediction of tumor genotype, treatment response, and prognosis without invasive biopsy [36].

6. Personalized Oncology and Therapeutic Decision Making

Precision medicine principles assert that optimal therapeutic outcomes are achieved when treatment selection is informed by patient specific tumor molecular characteristics, genetic predispositions, and predicted treatment sensitivity [37]. AI enables this vision by computationally predicting drug response based on tumor genomic and transcriptomic features: machine learning models trained on cell line drug sensitivity screens and tumor genomic data can predict chemotherapy response with 70 80% accuracy, substantially outperforming empirical selection [38]. Importantly, these models identify actionable targets for instance, predicting immunotherapy response through analysis of tumor mutational burden, microsatellite instability, neoantigen burden, and immune infiltration signatures that enable rational therapy selection and dose optimization. AI guided immunotherapy represents a particularly impactful application, as

computational prediction of checkpoint inhibitor response has achieved 75 85% accuracy by integrating genomic features (TMB, MSI, specific mutations), immune profiling (T cell density, PD L1 expression, immune activation signatures), and clinical parameters, enabling identification of responders likely to benefit from immunotherapy while sparing non responders from unnecessary toxicity [39].

Prognostic modeling through AI has revolutionized oncology practice by enabling personalized risk stratification that guides intensity of surveillance and aggressiveness of adjuvant therapy [40]. Deep learning models trained on multimodal data including imaging features, genomic alterations, clinical variables, and longitudinal biomarker trajectories achieve superior prognostic accuracy compared to traditional staging systems. For instance, in breast cancer, AI models integrating histopathologic features with genomic data and imaging characteristics predict long term recurrence risk more accurately than standard pathologic staging and Oncotype DX genomic assay scores alone. This enhanced prognostication enables treatment de escalation in low risk populations, sparing them from unnecessary chemotherapy toxicity while intensifying therapy for high risk patients likely to benefit from aggressive intervention. Adaptive treatment planning represents the frontier of AI driven therapeutic optimization, wherein longitudinal biomarker monitoring informs real time treatment modifications based on predicted drug resistance emergence [41]. For example, detecting early ctDNA emergence during chemotherapy prior to radiologic evidence of progression enables transition to alternative therapeutics before resistance mechanisms fully establish, potentially preventing acquired resistance driven treatment failure.

Patient stratification through clustering algorithms and unsupervised learning has identified novel cancer subtypes with distinct molecular signatures, prognostic implications, and therapeutic sensitivities [42]. These AI discovered subtypes frequently demonstrate superior prognostic stratification compared to traditional clinicopathologic classification, suggesting that machine learning identifies biologically meaningful tumor heterogeneity not captured by conventional diagnostic approaches. The promise of this stratification is increasingly realized through precision oncology trials that match patients to targeted therapies based on tumor genomic profiling; early data suggest that genomic matching improves response rates 1.5 2 fold compared to unmatched controls, with magnitude of benefit increasing when matching incorporates functional prediction of drug response rather than simply identifying mutations [43].

7. Explainable AI and Clinical Interpretability

The widespread adoption of AI in clinical oncology is fundamentally constrained by interpretability challenges: machine learning models, particularly deep neural networks, operate as "black boxes" wherein decision making mechanisms are opaque, limiting clinician understanding of which features drive predictions and undermining trust in AI generated recommendations [44]. This interpretability gap is particularly consequential in oncology, where treatment recommendations have profound implications for patient morbidity and mortality. Explainable AI (XAI) methodologies address this challenge through diverse approaches: post hoc explanation techniques including SHAP (SHapley Additive exPlanations) and LIME (Local Interpretable Model Agnostic Explanations) generate human comprehensible feature importance rankings indicating which patient

characteristics most strongly influenced model predictions; attention visualization methods including Grad CAM highlight regions of medical images most relevant to classification decisions, enabling verification that models focus on clinically appropriate anatomical structures [45]; and saliency mapping techniques visualize which image pixels contribute to predictions. These explanation methods have revealed both reassuring and concerning findings: in many contexts, AI models appear to focus on clinically relevant features (e.g., tumor boundaries in imaging classification, known driver mutations in genomic prediction); in other instances, models inappropriately rely on artifacts or confounders [46].

The integration of XAI into clinical workflows has been demonstrated to enhance clinician trust and adoption: when radiologists reviewing AI generated recommendations were provided with explanation visualizations highlighting clinically relevant imaging features, trust in AI predictions increased substantially compared to recommendations without explanations [47]. This finding underscores that explainability is not merely a scientific curiosity but rather an essential requirement for clinical implementation. Furthermore, XAI methods have identified concerning model biases: analysis of AI diagnostic systems has revealed that model predictions systematically vary by patient demographics (age, race, sex) in ways inconsistent with clinical appropriateness, suggesting that models are capturing demographic information that should not drive clinical decisions [48]. These findings have catalyzed development of fairness aware AI methods that explicitly constrain model reliance on demographic variables while maintaining predictive accuracy. The ethical imperative for transparent, unbiased AI in oncology where diagnostic errors and biased recommendations directly compromise patient outcomes is driving adoption of rigorous fairness assessment and XAI integration into AI development pipelines.

8. Federated Learning and Privacy Preserving Oncology AI

Clinical implementation of AI in oncology confronts a fundamental paradox: maximally powerful models require training on diverse, large scale datasets, yet patient privacy regulations including GDPR and HIPAA restrict centralized data aggregation [49]. Federated learning addresses this tension by enabling collaborative model training across multiple institutions without centralizing sensitive patient data. In the federated learning paradigm, each institution trains a local model on its own data, then shares only model parameters (weights and biases) with a central server that aggregates updates into a global model; raw patient data never leaves institutional servers, providing privacy preservation [50]. This approach has been successfully applied to oncology: federated training of deep learning models for brain tumor classification achieved comparable accuracy to centralized training (90 93%) while maintaining complete data locality, enabling multi institutional collaboration on diagnostic AI without privacy compromise [51]. Extensions including differential privacy mathematical techniques that inject calibrated noise into model updates to guarantee that individual patient data cannot be inferred from model parameters provide quantifiable privacy guarantees, albeit at modest accuracy cost [52].

The clinical translation advantages of federated learning in oncology are substantial: multi center model development addresses the critical problem that AI models trained in single institution contexts frequently demonstrate degraded performance when deployed at different institutions due to data distribution shifts,

equipment variation, population differences, and technical factors [53]. Federated learning naturally accommodates this heterogeneity through training on diverse, distributed data, often improving out of distribution generalization compared to single institution models. Furthermore, federated learning frameworks align with clinical workflows by eliminating requirements for data sharing agreements, enabling rapid collaborative model development among competing institutions [54]. The integration of explainable AI with federated learning ensuring that not only is training decentralized but also that resulting models provide interpretable predictions suitable for clinician review represents a critical next frontier [55]. Current challenges limiting federated learning adoption include communication overhead (model updates transmitted across networks require bandwidth), client heterogeneity (participating institutions have diverse computational resources and data characteristics), and the need for standardized protocols enabling interoperability across institutions using different electronic health record systems.

9. Future Perspectives: Digital Twins, Autonomous Systems, and Real World Evidence Integration

Digital twins represent a conceptual frontier in AI enabled precision oncology, wherein computational models simulate individual patient tumors at cellular and molecular resolution, enabling in silico prediction of treatment response and identification of optimal therapeutic strategies before clinical implementation [56]. These models integrate multi omics data, imaging information, treatment history, and longitudinal biomarker trajectories into mechanistic simulations that predict how tumors evolve under specific therapeutic perturbations. While currently in research phases, digital twins promise to transform oncology from trial and error empiricism toward first principles prediction: rather than attempting multiple sequential therapies observing response, digital twin simulations could identify optimal therapy sequences prospectively, potentially preventing acquired resistance driven treatment failure [57]. Autonomous oncology systems represent a speculative but plausible future wherein AI systems autonomously monitor patients through continuous biomarker analysis, integrate multi modal data, predict disease evolution, and recommend therapy modifications with minimal human intervention [58]. Such systems would require extraordinary advances in reliability, transparency, and regulatory acceptance, but conceptual frameworks are being developed that incorporate human in the loop oversight, ethical constraints, and explainability requirements [59].

Multimodal foundation models trained on massive, diverse oncology datasets (imaging, genomics, clinical records, scientific literature) promise to enable unified systems that simultaneously process heterogeneous data types and generate patient specific predictions [60]. These models would represent a departure from current paradigm of specialized models for specific tasks, instead providing generalizable representations from which diverse clinical questions can be answered through simple downstream processing. Real world evidence integration moving beyond traditional randomized controlled trials toward analysis of retrospective observational data, wearable derived information, and patient reported outcomes captured through digital platforms is being integrated with AI to understand therapeutic effectiveness, tolerability, and health outcomes in genuinely representative patient populations [61]. This approach has revealed important findings contradicting previous trial based conclusions,

suggesting that real world evidence integration through machine learning is essential for comprehensive understanding of treatment impacts.

10. Discussion

The review article demonstrates that artificial intelligence integrated with digital biomarkers is transforming modern oncology from conventional reactive treatment toward predictive, personalized, and minimally invasive cancer care. AI driven liquid biopsy platforms, radiomics, histopathology analysis, and multi omics integration have significantly improved early cancer detection, prognostic assessment, and therapeutic decision making. Deep learning and transformer based architectures enable extraction of clinically meaningful patterns from complex biological and imaging datasets that are often beyond human analytical capability. The article further highlights that multimodal biomarker fusion combining genomic, imaging, and wearable derived data provides superior predictive accuracy compared with single modality approaches.

Despite remarkable technological progress, several translational challenges remain unresolved. Clinical implementation is limited by issues including lack of standardized datasets, variability in biomarker sensitivity, interpretability concerns associated with black box AI systems, and regulatory uncertainties. The review also emphasizes the importance of explainable AI, federated learning, and privacy preserving computational frameworks in improving clinician trust and enabling collaborative model development across institutions. Emerging technologies such as digital twins and autonomous oncology systems are expected to further redefine precision oncology by enabling adaptive and real time treatment optimization. Overall, the article concludes that successful integration of AI and digital biomarkers into routine oncology practice will require rigorous clinical validation, interdisciplinary collaboration, ethical governance, and standardized regulatory frameworks.

CONCLUSION

The convergence of artificial intelligence and digital biomarkers is fundamentally redefining cancer diagnosis, prognosis, and treatment by enabling non-invasive, quantitative monitoring of disease state and prediction of clinical trajectories with unprecedented accuracy. The technical achievements are extraordinary: liquid biopsy combined with machine learning achieves >90% sensitivity for advanced cancers, deep learning enabled pathology exceeds expert diagnostic performance, and AI predicted therapy sensitivity correlates with clinical outcomes. Yet translating these achievements into widespread clinical benefit requires addressing interpretability gaps that undermine clinician trust, developing standardized protocols enabling cross institutional comparison, and deploying privacy preserving frameworks that enable collaborative development without compromising patient confidentiality. The trajectory toward precision oncology powered by AI is irreversible; the critical question is whether the oncology community can effectively bridge research innovation with clinical reality through rigorous validation, ethical guardrails, and interdisciplinary collaboration among computational scientists, clinicians, patients, and policymakers.

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