

PREDICTIVE ONCOLOGY THROUGH FOUNDATION AI: INTEGRATING LONGITUDINAL CLINICAL DATA, MULTI-OMICS, AND DIGITAL TWINS

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Abstract: Predictive oncology is undergoing a transformative evolution through the integration of foundation artificial intelligence (AI) models, longitudinal clinical data, multi-omics technologies, and digital twin systems into comprehensive computational ecosystems capable of anticipating disease progression, therapeutic response, recurrence, and survival. Conventional oncology frequently relies on static clinical assessments and isolated molecular analyses, limiting accurate prediction of evolving tumor biology and individualized treatment outcomes. Recent advances in foundation AI models, multimodal transformer architectures, graph neural networks, self-supervised learning, reinforcement learning, and generative artificial intelligence have enabled seamless integration of radiological imaging, digital pathology, genomics, transcriptomics, proteomics, metabolomics, epigenomics, spatial biology, laboratory biomarkers, circulating tumor DNA, wearable physiological monitoring, electronic health records, biomedical literature, and longitudinal clinical outcomes into unified computational representations of cancer biology. These intelligent systems support precision diagnosis, biomarker discovery, prognostic prediction, therapeutic optimization, adaptive disease monitoring, digital twin simulation, intelligent clinical decision support, and personalized cancer care. Emerging technologies including multimodal large language models, agentic AI, federated learning, retrieval-augmented generation, explainable artificial intelligence, cancer knowledge graphs, cloud-native healthcare platforms, and digital health ecosystems further strengthen predictive oncology by enabling collaborative, privacy-preserving, transparent, and continuously adaptive biomedical intelligence. Despite remarkable technological advances, important scientific, technical, ethical, and regulatory challenges remain regarding multimodal data harmonization, computational scalability, interoperability, cybersecurity, clinical validation, regulatory acceptance, and equitable implementation. This review provides a comprehensive overview of predictive oncology through foundation AI, emphasizing integration of longitudinal clinical data, multi-omics, and digital twins for next-generation precision oncology.[1]

Keywords: Predictive oncology, Foundation models, Artificial intelligence, Digital twins, Longitudinal clinical data, Multi-omics, Precision oncology, Computational oncology, Personalized medicine, Clinical decision support.

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1. Introduction

Cancer is a biologically dynamic disease characterized by continuous genomic evolution, epigenetic remodeling, transcriptional dysregulation, proteomic adaptation, metabolic reprogramming, immune remodeling, stromal interactions, angiogenesis, therapeutic resistance, and evolving communication among malignant cells, immune populations, extracellular matrix, vascular structures, and host physiology. These interconnected biological processes evolve

throughout diagnosis, treatment, recurrence, metastasis, and survivorship, requiring computational systems capable of continuously integrating heterogeneous biomedical information across time.[2]

Modern oncology generates enormous quantities of biomedical information through radiological imaging, digital pathology, genomic sequencing, transcriptomics, proteomics, metabolomics, epigenomics, spatial biology, laboratory investigations, circulating tumor DNA, wearable

physiological monitoring, physician documentation, electronic health records, biomedical literature, and patient-reported outcomes. Although each modality contributes valuable biological insight, isolated interpretation frequently limits accurate prediction of disease evolution and individualized therapeutic decision-making.[3]

Foundation AI models provide a transformative computational framework capable of integrating longitudinal clinical data with molecular biology and digital twins, thereby enabling predictive precision oncology throughout the cancer care continuum.

2. Evolution of Predictive Oncology

Predictive oncology has evolved from conventional statistical prognostic models toward intelligent multimodal computational ecosystems capable of continuously learning from longitudinal biomedical information. Early predictive models primarily relied upon clinical staging, histopathological grading, demographic characteristics, and limited laboratory biomarkers. Although clinically valuable, these models frequently lacked molecular precision and adaptive learning capabilities.[4]

Deep learning substantially expanded computational capabilities by enabling automated feature learning from radiological imaging, digital pathology, genomics, and electronic health records. Transformer architectures subsequently revolutionized biomedical artificial intelligence through contextual learning across heterogeneous biomedical modalities.

Foundation AI models now acquire transferable biomedical knowledge through multimodal self-supervised learning, enabling generalized computational reasoning supporting biomarker discovery, prognostic prediction, therapeutic optimization, adaptive disease monitoring, and continuously personalized precision oncology.[5]

3. Principles of Foundation Models for Predictive Oncology

Foundation AI models differ fundamentally from conventional predictive algorithms because they acquire generalized biomedical representations from massive multimodal datasets before specialization for individual oncology

applications. Rather than learning isolated prediction tasks, these models develop transferable computational knowledge applicable across diagnosis, prognosis, biomarker discovery, therapeutic optimization, disease monitoring, translational research, and clinical decision support.[6]

Self-supervised learning enables discovery of latent biological relationships without requiring extensive manual annotation, while multimodal transformer architectures align radiological imaging, digital pathology, genomics, transcriptomics, proteomics, metabolomics, epigenomics, laboratory biomarkers, wearable physiological monitoring, physician documentation, patient-reported outcomes, biomedical literature, and longitudinal clinical trajectories within unified computational embedding spaces.

Graph neural networks further characterize interactions among genes, proteins, signaling pathways, metabolites, immune populations, imaging phenotypes, tissue architecture, therapeutic targets, physiological variables, environmental exposures, temporal disease evolution, and clinical outcomes, thereby enabling systems-level predictive reasoning throughout precision oncology.[7]

4. Computational Architecture

Modern predictive oncology platforms consist of interconnected computational layers responsible for biomedical data acquisition, preprocessing, multimodal representation learning, temporal reasoning, graph inference, predictive analytics, digital twin simulation, knowledge integration, and intelligent clinical decision support.[8]

The acquisition layer continuously integrates radiological imaging, digital pathology, genomic sequencing, transcriptomics, proteomics, metabolomics, epigenomics, spatial biology, laboratory investigations, circulating tumor DNA, wearable physiological monitoring, medication history, physician documentation, patient-reported outcomes, biomedical literature, pharmacological databases, and electronic health records. Advanced preprocessing pipelines normalize imaging studies, harmonize molecular datasets, encode biomedical narratives using natural language processing, synchronize temporal patient

information, and continuously incorporate emerging scientific evidence.

Foundation AI models subsequently generate generalized multimodal embeddings representing molecular biology, tissue architecture, imaging phenotypes, physiological function, environmental exposures, temporal disease evolution, and longitudinal clinical trajectories while enabling downstream predictive reasoning across diverse oncology applications.[9]

5. Longitudinal Clinical Intelligence

Longitudinal clinical information represents one of the most valuable resources for predictive oncology because it captures dynamic disease evolution throughout diagnosis, treatment, recurrence, metastasis, and survivorship. Foundation AI models continuously integrate serial radiological imaging, laboratory biomarkers, physician documentation, medication history, treatment response, toxicity profiles, hospitalization records, wearable physiological monitoring, and patient-reported outcomes into adaptive computational representations of evolving patient biology.[10]

Transformer architectures effectively model temporal dependencies among sequential clinical events, while graph neural networks characterize evolving interactions among molecular pathways, physiological adaptation, therapeutic interventions, and disease progression. Self-supervised learning further enables identification of previously unrecognized temporal biomarkers without requiring manually annotated datasets.

These computational advances substantially improve prediction of recurrence, therapeutic response, toxicity development, progression-free survival, and overall survival.[11]

6. Multi-Omics Integration

Comprehensive characterization of cancer biology requires seamless integration of genomics, transcriptomics, proteomics, metabolomics, epigenomics, immunomics, microbiomics, single-cell sequencing, spatial transcriptomics, and spatial proteomics. Foundation AI models harmonize these complementary molecular modalities using multimodal transformers and graph neural networks capable of generating

generalized biological representations of evolving tumor ecosystems.[12]

Artificial intelligence identifies latent biological relationships among genes, proteins, metabolites, signaling pathways, immune responses, epigenetic regulation, imaging phenotypes, histopathological architecture, and therapeutic targets while continuously integrating emerging biomedical evidence into adaptive computational representations.

These integrated molecular representations substantially improve biomarker discovery, molecular classification, therapeutic selection, precision immunotherapy, adaptive therapeutics, and translational cancer research.[13]

7. Predictive Biomarker Discovery

Identification of predictive biomarkers capable of anticipating therapeutic response, disease progression, recurrence, metastasis, and survival represents one of the most important applications of foundation AI models. Artificial intelligence integrates radiological imaging, digital pathology, molecular biology, laboratory biomarkers, circulating tumor DNA, wearable physiological monitoring, and longitudinal clinical outcomes into generalized computational representations capable of identifying latent biological signatures associated with future clinical events.[14]

Graph neural networks characterize interactions among genes, proteins, signaling pathways, immune responses, physiological adaptation, imaging phenotypes, and clinical trajectories while multimodal transformers continuously refine predictive biomarker performance through adaptive learning.

These computational advances substantially accelerate precision biomarker discovery while improving individualized therapeutic planning and clinical outcome prediction.[15]

8. Digital Health and Continuous Monitoring

Digital health technologies including wearable biosensors, mobile health applications, remote physiological monitoring, smart medical devices, patient-reported outcomes, and Internet of Medical Things (IoMT) platforms continuously generate longitudinal physiological information throughout the cancer care continuum. These technologies extend predictive oncology beyond

hospital settings by enabling continuous assessment of treatment response, toxicity, medication adherence, physical activity, cardiovascular physiology, metabolic health, sleep quality, stress, and quality of life.[16]

Foundation AI models integrate wearable physiological measurements with laboratory biomarkers, molecular biology, radiological imaging, digital pathology, and electronic health records using multimodal transformer architectures. Continuous physiological monitoring substantially improves early toxicity detection, adaptive disease monitoring, survivorship management, supportive care optimization, and real-world evidence generation. Digital health therefore represents an essential component of predictive oncology ecosystems.[17]

9. Integrated Predictive Clinical Intelligence

One of the greatest strengths of foundation AI models is their ability to unify longitudinal clinical data, radiological imaging, digital pathology, multi-omics, laboratory biomarkers, biomedical literature, pharmacological knowledge, electronic health records, digital biomarkers, patient-reported outcomes, and temporal clinical trajectories into comprehensive patient-specific computational representations. Rather than analyzing individual biomedical modalities independently, these models generate adaptive representations of evolving cancer biology capable of supporting diagnosis, biomarker discovery, prognostic prediction, therapeutic optimization, disease monitoring, recurrence prediction, survival estimation, multidisciplinary communication, and precision clinical decision-making. These generalized computational representations establish the foundation for predictive oncology, digital twins, intelligent clinical decision support, adaptive therapeutics, and continuously personalized precision medicine throughout the cancer care continuum.[18][19][20]

10. Digital Twins and Predictive Virtual Patient Modeling

Digital twin technology represents one of the most transformative applications of predictive oncology by creating continuously evolving virtual

representations of individual cancer patients synchronized with their biological counterparts. Foundation AI models integrate serial radiological imaging, digital pathology, genomics, transcriptomics, proteomics, metabolomics, epigenomics, spatial biology, laboratory biomarkers, circulating tumor DNA, wearable physiological monitoring, medication history, patient-reported outcomes, and longitudinal clinical information into adaptive computational patient models capable of simulating disease progression, therapeutic response, treatment-related toxicity, recurrence, metastatic dissemination, and survival.[21]

Unlike conventional predictive models based on static baseline measurements, digital twins continuously update their computational representations as new multimodal biomedical information becomes available. Integration of longitudinal clinical trajectories with molecular biology, imaging phenotypes, physiological monitoring, and predictive simulation enables virtual patients to evaluate alternative therapeutic strategies, optimize treatment sequencing, anticipate mechanisms of therapeutic resistance, personalize supportive care, and estimate long-term clinical outcomes according to evolving patient biology.

By integrating temporal clinical intelligence with adaptive predictive simulation, digital twins bridge computational oncology and personalized precision medicine throughout the cancer care continuum.

11. Intelligent Clinical Decision Support

Foundation AI models provide the computational infrastructure for next-generation clinical decision-support systems capable of integrating heterogeneous biomedical information into comprehensive patient-centered recommendations. Rather than independently interpreting radiological imaging, digital pathology, molecular diagnostics, laboratory investigations, physician documentation, patient-reported outcomes, biomedical literature, pharmacological knowledge, and evidence-based clinical guidelines, these systems synthesize diverse biomedical information into unified computational representations supporting multidisciplinary oncology practice.[22]

Interactive clinical dashboards generate individualized diagnostic summaries, molecular biomarker analyses, temporal risk assessments, radiomic and pathomic interpretations, digital twin simulations, therapeutic recommendations, toxicity estimates, recurrence probabilities, disease progression forecasts, survival predictions, and longitudinal treatment response assessments while facilitating collaboration among oncologists, radiologists, pathologists, surgeons, radiation oncologists, molecular biologists, pharmacists, nurses, genetic counselors, biomedical engineers, computational scientists, and translational researchers.

These intelligent systems improve workflow efficiency, strengthen multidisciplinary communication, reduce fragmentation of biomedical information, and promote evidence-based personalized cancer management throughout the cancer care continuum.

12. Continuous Learning and Adaptive Predictive Intelligence

A defining characteristic of predictive oncology through foundation AI is the ability to continuously evolve as new biomedical information becomes available. Artificial intelligence incorporates serial imaging examinations, computational pathology, circulating tumor DNA, laboratory biomarkers, wearable physiological monitoring, medication adherence, patient-reported outcomes, biomedical literature, pharmacological evidence, clinical guidelines, and real-world treatment outcomes into adaptive computational frameworks capable of continuously refining predictive accuracy throughout the patient's clinical journey.[23]

Continual learning algorithms enable incremental refinement of computational knowledge without catastrophic forgetting, while reinforcement learning optimizes prognostic prediction, therapeutic prioritization, disease monitoring, toxicity prediction, and survivorship planning through iterative evaluation of longitudinal patient outcomes. Foundation AI models further integrate clinician feedback and multidisciplinary tumor board recommendations into continuous model refinement.

This adaptive computational paradigm transforms predictive oncology into a continuously learning

scientific ecosystem capable of rapidly translating biomedical discoveries into individualized clinical practice.

13. Federated Predictive Oncology Networks

Development of highly generalizable predictive foundation AI models requires access to diverse longitudinal biomedical datasets representing multiple healthcare systems, imaging platforms, pathology laboratories, molecular technologies, wearable ecosystems, treatment protocols, and patient populations. Federated learning enables collaborative development of predictive oncology systems while preserving patient privacy and institutional governance through decentralized computational training.[24]

Participating healthcare institutions independently train local predictive models using radiological imaging, digital pathology, genomics, transcriptomics, proteomics, metabolomics, laboratory investigations, wearable monitoring, liquid biopsy, electronic health records, biomedical literature, and longitudinal clinical records while securely exchanging encrypted model parameters rather than identifiable patient information. This collaborative learning strategy substantially improves algorithm robustness, fairness, external validity, transparency, and generalizability across diverse healthcare environments.

Federated predictive oncology ecosystems therefore establish international computational oncology networks capable of accelerating scientific discovery, improving equitable access to precision medicine, reducing institutional bias, and supporting global cancer research while maintaining responsible biomedical data stewardship.

14. Explainability, Validation, and Ethical Governance

Successful implementation of predictive oncology requires transparent, interpretable, reproducible, and rigorously validated computational systems capable of supporting clinician confidence, patient trust, and regulatory approval. Explainable artificial intelligence (XAI) enables clinicians to understand predictive reasoning through temporal attention visualization, saliency maps, SHAP (Shapley Additive Explanations), integrated

gradients, feature attribution analysis, uncertainty estimation, confidence calibration, multimodal attention mapping, and counterfactual explanations identifying the imaging, molecular, pathological, physiological, pharmacological, and clinical variables responsible for predictive outputs.[25]

Clinical deployment additionally requires standardized multimodal datasets, interoperable computational infrastructure, prospective multicenter validation, external benchmarking, cybersecurity safeguards, continuous monitoring for algorithmic bias, transparent reporting standards, and compliance with evolving international regulatory frameworks governing AI-enabled healthcare technologies.

Responsible implementation further depends upon patient privacy, informed consent, transparency, accountability, fairness, equitable access, responsible data governance, continuous post-deployment surveillance, clinician education, and multidisciplinary oversight to ensure trustworthy integration of predictive foundation AI into routine oncology practice.

15. Future Perspectives

Future predictive oncology ecosystems will increasingly integrate multimodal foundation models, multimodal large language models, agentic artificial intelligence, graph neural networks, reinforcement learning, federated learning, digital twins, spatial multi-omics, single-cell sequencing, liquid biopsy, quantum computing, Internet of Medical Things (IoMT), cloud-native healthcare infrastructure, biomedical knowledge graphs, retrieval-augmented generation, explainable reasoning systems, and autonomous clinical intelligence into unified precision oncology platforms.[26]

These next-generation computational ecosystems will continuously integrate molecular biology, radiological imaging, digital pathology, laboratory medicine, wearable physiological monitoring, environmental exposures, electronic health records, biomedical literature, pharmacological databases, global clinical guidelines, and real-world clinical outcomes while autonomously coordinating biomarker discovery, adaptive therapeutics, personalized treatment planning, survivorship management, predictive risk

assessment, multidisciplinary communication, and continuous evidence synthesis.

Such intelligent predictive ecosystems are expected to transform oncology from reactive disease management toward predictive, adaptive, continuously learning, and precision-guided cancer medicine.

16. Discussion

Predictive oncology through foundation AI represents one of the most significant paradigm shifts in computational cancer medicine by integrating longitudinal clinical data, radiology, pathology, multi-omics, laboratory biomarkers, biomedical literature, pharmacological knowledge, digital biomarkers, digital twins, and foundation AI models into unified computational ecosystems capable of supporting comprehensive personalized cancer care. Unlike conventional prognostic models based upon static clinical variables, predictive intelligence continuously synthesizes heterogeneous temporal molecular, imaging, pathological, physiological, pharmacological, and clinical information into adaptive patient-specific representations capable of anticipating future biological and clinical events.[27]

Applications spanning computational pathology, radiogenomics, biomarker discovery, digital twins, precision immunotherapy, adaptive therapeutics, remote patient monitoring, federated collaboration, digital health, survivorship management, intelligent clinical decision support, and translational research demonstrate the extraordinary potential of predictive foundation models to redefine future oncology. Nevertheless, successful implementation requires continued advances in multimodal data harmonization, explainable artificial intelligence, interoperability, computational infrastructure, cybersecurity, regulatory science, ethical governance, clinician education, and sustained multidisciplinary collaboration.

As biomedical knowledge and healthcare data continue to expand exponentially, predictive oncology is expected to become one of the foundational computational infrastructures supporting precision oncology worldwide.

17. Conclusion

Predictive oncology through foundation AI is transforming personalized cancer care by integrating longitudinal clinical data, radiological imaging, digital pathology, multi-omics, laboratory biomarkers, biomedical literature, electronic health records, digital biomarkers, digital twins, and foundation AI models into unified computational ecosystems capable of supporting biomarker discovery, prognostic prediction, therapeutic optimization, adaptive disease monitoring, and precision clinical decision-making throughout the cancer care continuum.[28]

Advances in multimodal transformer architectures, graph neural networks, self-supervised learning, federated learning, reinforcement learning, multimodal large language models, explainable artificial intelligence, digital twins, agentic AI, retrieval-augmented generation, and generative artificial intelligence are expected to further strengthen predictive oncology ecosystems, enabling increasingly accurate molecular characterization, predictive clinical reasoning, adaptive therapeutics, continuous disease surveillance, and personalized precision medicine.[29]

Although important scientific, technical, ethical, regulatory, and implementation challenges remain, sustained collaboration among oncologists, radiologists, pathologists, molecular biologists, biomedical engineers, computer scientists, healthcare organizations, policymakers, industry partners, patients, and regulatory agencies will accelerate the responsible implementation of predictive foundation AI. These innovations have the potential to improve patient outcomes, enhance healthcare efficiency, reduce disparities in cancer care, accelerate translational research, facilitate predictive therapeutics, and establish a new era of intelligent, adaptive, and continuously learning precision oncology worldwide.[30]

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