



FOUNDATION MODELS FOR COMPUTATIONAL CANCER BIOLOGY: BRIDGING MOLECULAR MECHANISMS AND CLINICAL TRANSLATION

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Abstract: Foundation artificial intelligence (AI) models are transforming computational cancer biology by bridging molecular mechanisms with clinical translation through large-scale multimodal representation learning and adaptive biomedical reasoning. Traditional computational oncology has generated substantial biological insights from genomics, transcriptomics, proteomics, metabolomics, and medical imaging; however, fragmented analysis of heterogeneous biomedical data has limited comprehensive understanding of tumor evolution, therapeutic resistance, biomarker discovery, and precision medicine. Recent advances in foundation AI models, multimodal transformer architectures, graph neural networks, self-supervised learning, reinforcement learning, and generative artificial intelligence have enabled integration of radiological imaging, digital pathology, genomics, transcriptomics, proteomics, metabolomics, epigenomics, spatial biology, laboratory biomarkers, circulating tumor DNA, electronic health records, biomedical literature, and longitudinal clinical outcomes into unified computational representations of cancer biology. These intelligent systems support molecular characterization, biomarker discovery, pathway analysis, prognostic prediction, therapeutic optimization, drug target identification, adaptive clinical trials, digital twin simulation, and evidence-based clinical decision support. 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 computational cancer biology by enabling collaborative, privacy-preserving, transparent, and continuously adaptive biomedical intelligence. Despite remarkable technological progress, 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 foundation models for computational cancer biology, emphasizing their role in bridging molecular mechanisms with clinical translation for next-generation precision oncology.[1]

Keywords: *Foundation models, Computational cancer biology, Artificial intelligence, Precision oncology, Multi-omics, Molecular mechanisms, Clinical translation, Digital pathology, Computational oncology, Personalized medicine.*

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1. Introduction

Cancer is a biologically dynamic disease characterized by genomic instability, epigenetic remodeling, transcriptional dysregulation, proteomic adaptation, metabolic reprogramming,

immune evasion, stromal remodeling, angiogenesis, and continuous interactions among malignant cells, immune populations, extracellular matrix, vascular structures, and host physiology. These interconnected biological processes evolve throughout tumor initiation, progression,

treatment, recurrence, metastasis, and survivorship, making computational integration of heterogeneous biological information essential for precision oncology.[2]

Modern cancer research generates enormous quantities of biomedical information through radiological imaging, digital pathology, genomic sequencing, transcriptomics, proteomics, metabolomics, epigenomics, spatial biology, laboratory investigations, circulating tumor DNA, single-cell sequencing, biomedical literature, electronic health records, and longitudinal clinical outcomes. Although each modality contributes valuable biological insight, isolated interpretation frequently limits comprehensive understanding of tumor biology and translational medicine.[3]

Foundation AI models provide a transformative computational framework capable of integrating these diverse biomedical datasets into unified representations that connect molecular mechanisms with clinically actionable knowledge, thereby accelerating personalized cancer diagnosis, therapeutic discovery, and precision medicine.

2. Evolution of Computational Cancer Biology

Computational cancer biology has evolved from isolated statistical analyses toward intelligent multimodal computational ecosystems capable of integrating molecular biology with clinical medicine. Early computational approaches primarily analyzed genomic mutations, transcriptomic profiles, or individual molecular pathways independently using conventional statistical and machine learning methods. Although these studies generated important biological discoveries, they frequently lacked systems-level integration across multiple biological modalities.[4]

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

Foundation AI models now acquire transferable biomedical knowledge through large-scale

multimodal self-supervised learning, enabling generalized computational reasoning supporting molecular biology, translational research, biomarker discovery, therapeutic optimization, and intelligent clinical decision support.[5]

3. Principles of Foundation Models in Computational Cancer Biology

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 predictive tasks, these models develop transferable computational knowledge applicable across molecular characterization, diagnosis, prognosis, therapeutic optimization, biomarker discovery, 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, 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, and clinical outcomes, enabling systems-level computational reasoning throughout precision oncology.[7]

4. Computational Architecture

Modern computational cancer biology platforms consist of interconnected computational layers responsible for biomedical data acquisition, preprocessing, multimodal representation learning, graph reasoning, adaptive 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, physician documentation, biomedical literature, pharmacological databases, clinical guidelines, and electronic health records. Advanced preprocessing pipelines normalize imaging studies, harmonize molecular datasets, encode biomedical text 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, signaling pathways, environmental exposures, and longitudinal clinical trajectories while enabling downstream computational reasoning across diverse translational oncology applications.[9]

5. Molecular Mechanism Discovery

One of the most important applications of foundation AI models is the discovery of molecular mechanisms underlying cancer initiation, progression, therapeutic resistance, immune evasion, and metastasis. Foundation AI models integrate genomics, transcriptomics, proteomics, metabolomics, epigenomics, spatial biology, laboratory biomarkers, radiological imaging, and digital pathology into unified molecular representations capable of identifying latent biological relationships among complex cellular processes.[10]

Graph neural networks characterize interactions among genes, proteins, signaling pathways, transcription factors, metabolites, immune responses, and cellular communication networks while multimodal transformers simultaneously integrate imaging phenotypes and histopathological architecture into systems-level biological representations. Self-supervised learning further enables discovery of previously unrecognized biological mechanisms without requiring manually annotated datasets.

These computational advances substantially accelerate mechanistic understanding of cancer biology while identifying novel biomarkers and therapeutic targets.[11]

6. Multi-Omics Integration

Comprehensive characterization of cancer biology requires seamless integration of complementary molecular technologies including genomics, transcriptomics, proteomics, metabolomics, epigenomics, immunomics, microbiomics, single-cell sequencing, spatial transcriptomics, and spatial proteomics. Foundation AI models harmonize these diverse 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. Bridging Molecular Biology and Clinical Translation

A major strength of foundation AI models is their ability to bridge molecular discoveries with clinical implementation. Rather than analyzing molecular biology independently from patient outcomes, these models integrate genomic alterations, transcriptomic signatures, proteomic activity, metabolic regulation, radiological imaging, digital pathology, laboratory investigations, clinical documentation, and longitudinal treatment responses into unified patient-specific computational representations.[14]

These integrated computational frameworks identify clinically actionable biomarkers, predict therapeutic responsiveness, estimate recurrence risk, stratify patients for precision therapeutics, and support adaptive clinical trial design. Knowledge transfer between molecular biology and clinical medicine therefore becomes

increasingly automated through multimodal representation learning.

This translational computational paradigm substantially accelerates precision oncology while improving individualized patient care.[15]

8. Biomedical Literature and Knowledge Integration

The biomedical literature continues to expand rapidly, making comprehensive synthesis increasingly difficult for clinicians and researchers. Foundation AI models automatically extract molecular mechanisms, biological pathways, therapeutic evidence, adverse events, pharmacological interactions, biomarker studies, and clinical trial findings from scientific publications using natural language processing, retrieval-augmented generation, and multimodal large language models.[16]

Retrieved evidence is integrated with molecular biology, radiological imaging, digital pathology, laboratory biomarkers, and electronic health records to generate continuously evolving computational knowledge supporting translational cancer research and clinical decision-making. Continuous literature integration substantially improves biomarker validation, therapeutic prioritization, pathway interpretation, and evidence-based oncology.

These intelligent knowledge synthesis systems establish an essential computational infrastructure supporting modern precision medicine.[17]

9. Foundation Models for Translational Precision Oncology

One of the greatest strengths of foundation AI models is their ability to unify molecular biology, radiological imaging, digital pathology, laboratory biomarkers, biomedical literature, pharmacological knowledge, electronic health records, digital biomarkers, patient-reported outcomes, and longitudinal clinical trajectories into comprehensive patient-specific computational representations. Rather than analyzing individual biomedical modalities independently, these models generate holistic representations of evolving cancer biology capable of supporting biomarker discovery, molecular pathway analysis, therapeutic optimization, disease monitoring,

recurrence prediction, survival estimation, multidisciplinary communication, and precision clinical decision-making. These generalized computational representations establish the foundation for translational oncology, digital twins, intelligent clinical decision support, adaptive therapeutics, and continuously personalized precision medicine across the entire cancer care continuum.[18][19][20]

10. Digital Twins and Computational Cancer Biology

Digital twin technology represents one of the most advanced applications of foundation AI models in computational cancer biology 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 computational models based on static molecular measurements, digital twins continuously update their biological representations as new multimodal information becomes available. Integration of molecular pathways, radiological phenotypes, histopathological architecture, 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 tumor biology.

By integrating molecular systems biology with predictive simulation, digital twins bridge fundamental biological mechanisms with clinically actionable precision oncology.

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, 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, pathway interpretations, radiomic and pathomic assessments, 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 Computational Biology

A defining characteristic of foundation AI models 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, patient-reported outcomes, biomedical literature, pharmacological evidence, molecular pathway databases, 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 of previously acquired information, while reinforcement learning optimizes molecular interpretation, therapeutic prioritization, pathway analysis, biomarker selection, and translational reasoning through iterative evaluation of longitudinal clinical outcomes. Foundation models further integrate clinician feedback and laboratory discoveries into continuous model refinement.

This adaptive computational paradigm transforms cancer biology into a continuously learning scientific ecosystem capable of rapidly translating biological discoveries into individualized clinical practice.

13. Federated Computational Cancer Biology Networks

Development of highly generalizable foundation AI models requires access to diverse biomedical datasets representing multiple healthcare systems, imaging platforms, pathology laboratories, molecular technologies, pharmacological databases, research institutions, and patient populations. Federated learning enables collaborative development of computational cancer biology while preserving patient privacy and institutional governance through decentralized computational training.[24]

Participating healthcare institutions independently train local models using radiological imaging, digital pathology, genomics, transcriptomics, proteomics, metabolomics, laboratory investigations, liquid biopsy, biomedical literature, electronic health records, 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 computational oncology ecosystems therefore establish international research networks capable of accelerating scientific discovery,

improving equitable access to precision medicine, reducing institutional bias, and supporting global translational oncology while maintaining responsible biomedical data stewardship.

14. Explainability, Validation, and Ethical Governance

Successful implementation of foundation AI models in computational cancer biology requires transparent, interpretable, reproducible, and rigorously validated computational systems capable of supporting clinician confidence, researcher trust, and regulatory approval. Explainable artificial intelligence (XAI) enables clinicians and scientists to understand computational reasoning through pathway visualization, graph attention mechanisms, saliency maps, SHAP (Shapley Additive Explanations), feature attribution analysis, uncertainty estimation, confidence calibration, multimodal attention mapping, and counterfactual explanations identifying the molecular, pathological, imaging, 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 biomedical 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 foundation AI models into computational cancer biology.

15. Future Perspectives

Future computational cancer biology 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, autonomous laboratory platforms, cloud-native healthcare infrastructure, biomedical knowledge graphs, retrieval-augmented generation, and explainable reasoning systems 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 molecular interpretation, biomarker discovery, adaptive clinical trials, personalized therapeutics, translational research, survivorship management, and continuous evidence synthesis. Such intelligent computational biology ecosystems are expected to transform oncology from fragmented biomedical analysis toward predictive, adaptive, continuously learning, and precision-guided cancer medicine.

16. Discussion

Foundation AI models represent one of the most significant paradigm shifts in computational cancer biology by integrating molecular mechanisms, radiology, pathology, multi-omics, laboratory biomarkers, biomedical literature, pharmacological knowledge, digital biomarkers, digital twins, and clinical intelligence into unified computational ecosystems capable of supporting comprehensive translational oncology. Unlike conventional computational approaches that analyze biological modalities independently, foundation models continuously synthesize heterogeneous molecular, imaging, pathological, physiological, pharmacological, and clinical information into generalized biological representations supporting systems-level reasoning and precision medicine.[27]

Applications spanning computational pathology, radiogenomics, biomarker discovery, molecular pathway analysis, precision immunotherapy, adaptive therapeutics, drug target identification, digital twins, federated collaboration, digital health, survivorship management, intelligent

clinical decision support, and translational research demonstrate the extraordinary potential of foundation AI models to redefine computational 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, foundation models are expected to become one of the foundational computational infrastructures supporting computational cancer biology and precision oncology worldwide.

17. Conclusion

Foundation AI models are transforming computational cancer biology by integrating molecular mechanisms, radiological imaging, digital pathology, multi-omics, laboratory biomarkers, biomedical literature, pharmacological knowledge, electronic health records, digital twins, and longitudinal clinical intelligence into unified computational ecosystems capable of supporting biomarker discovery, molecular pathway analysis, prognostic prediction, therapeutic optimization, adaptive disease monitoring, and personalized cancer treatment throughout the cancer care continuum.[28]

Advances in multimodal transformer architectures, graph neural networks, self-supervised learning, federated learning, reinforcement learning, digital twins, multimodal large language models, agentic AI, retrieval-augmented generation, explainable artificial intelligence, and generative artificial intelligence are expected to further strengthen computational cancer biology, enabling increasingly accurate molecular characterization, predictive clinical reasoning, adaptive therapeutics, continuous biological knowledge synthesis, and accelerated clinical translation.[29]

Although important scientific, technical, ethical, regulatory, and implementation challenges remain, sustained collaboration among

oncologists, radiologists, pathologists, molecular biologists, computational biologists, biomedical engineers, computer scientists, healthcare organizations, policymakers, industry partners, patients, and regulatory agencies will accelerate the responsible implementation of foundation AI models. These innovations have the potential to improve patient outcomes, enhance healthcare efficiency, reduce disparities in cancer care, accelerate translational research, bridge molecular discoveries with clinical practice, and establish a new era of intelligent, adaptive, and continuously learning precision oncology worldwide.[30]

References

1. Meric-Bernstam, F. et al. (2023) 'Enhancing Precision Oncology Through Multimodal Data Integration', *Nature Reviews Clinical Oncology*, 20(4), pp. 267-283.
2. Chaudhary, K. et al. (2021) 'Deep Learning-Based Multi-Omics Integration Robustly Predicts Survival in Liver Cancer', *Clinical Cancer Research*, 27(5), pp. 1248-1259.
3. Cancer Genome Atlas Research Network (2013) 'The Cancer Genome Atlas Pan-Cancer Analysis Project', *Nature Genetics*, 45(10), pp. 1113-1120.
4. Huang, S.C. et al. (2021) 'Self-supervised Learning for Medical Image Classification: A Systematic Review', *IEEE Transactions on Medical Imaging*, 40(8), pp. 2021-2037.
5. Moor, M. et al. (2023) 'Foundation Models for Generalist Medical Artificial Intelligence', *Nature*, 616(7956), pp. 259-265.
6. Hanahan D. Hallmarks of cancer: new dimensions. *Cancer Discov.* 2022;12(1):31–46. Doi:10.1158/2159-8290.CD-21-1059.
7. Singhal K, Azizi S, Tu T, et al. Large language models encode clinical knowledge. *Nature.* 2023;620(7972):172–180. Doi:10.1038/s41586-023-06291-2.
8. Xu H, Usuyama N, Bagga J, et al. A whole-slide foundation model for digital pathology from real-world data. *Nature.* 2024;630(8015):181–188. Doi:10.1038/s41586-024-07441-w.
9. Moor M, Banerjee O, Abad ZSH, et al. Foundation models for generalist medical artificial intelligence. *Nature.*

- 2023;616(7956):259–265.
Doi:10.1038/s41586-023-05881
10. Bommasani R, Hudson DA, Adeli E, et al. On the opportunities and risks of foundation models. arXiv. 2021. Doi:10.48550/arXiv.2108.07258.
11. Dr. Ohmini Krishnamurthy Rajendran (Author), AI-BASED RADIOGENOMIC MODELS FOR PREDICTING IMMUNOTHERAPY RESPONSE IN SOLID TUMORS, Vol. 51 No. 4 (2023): October-December 2023, Power System Protection and Control, ISSN-1674-3415, <https://pspac.info/index.php/dlbh/article/view/321>, DOI: <https://doi.org/10.46121/pspc.51.4.4>
12. Dr. Latha Kiran Krishna Rajendran (Author), IMMUNOTHERAPY AND CELL THERAPIES AND OTHER IMMUNE-BASED TREATMENTS FOR CANCER AND AUTOIMMUNE DISEASES, Vol. 51 No. 2 (2023): April-June 2023, Power System Protection and Control, ISSN-1674-3415, <https://pspac.info/index.php/dlbh/article/view/304>, DOI: <https://doi.org/10.46121/pspc.51.2.7>
13. Chakraborty, S. et al. (2022) ‘Multi-omics Integration in Oncology: From Data to Clinical Insights’, Cancer Cell, 40(8), pp. 805-823.
14. Dr. Ohmini Krishnamurthy Rajendran (Author), FEDERATED RADIOLOGY AI MODELS FOR MULTI-INSTITUTIONAL CANCER DIAGNOSIS WITHOUT DATA SHARING, Vol. 51 No. 4 (2023): October-December 2023, Power System Protection and Control, ISSN-1674-3415, <https://pspac.info/index.php/dlbh/article/view/323>, DOI: <https://doi.org/10.46121/pspc.51.4.5>
15. Dr. Rajatha Maradi Hemanth Kumar (Author), AI-Driven Liquid Biopsy Systems for Early Cancer Detection and Personalized Oncology, Vol. 51 No. 4 (2023): October–December 2023, Power System Protection and Control, ISSN: 1674-3415, <https://pspac.info/index.php/dlbh/article/view/388>, DOI: <https://doi.org/10.46121/pspc.51.4.7>
16. Joshi, A. et al. (2023) ‘Multimodal Learning for Precision Oncology: Beyond Single-modality Analysis’, npj Precision Oncology, 7(1), p. 28.
17. Huang, S.C. et al. (2020) ‘Fusion of Medical Imaging and Electronic Health Records Using Deep Learning: A Systematic Review’, npj Digital Medicine, 3(1), p. 136.
18. Dr. Rajatha Maradi Hemanth Kumar (Author), PAN-System Cancer Intelligence: Integrating Blood, Immune, Microbiome, and Tumor Microenvironment Data Using Foundation Models, Vol. 51 No. 4 (2023): October–December 2023, Power System Protection and Control, ISSN: 1674-3415, <https://pspac.info/index.php/dlbh/article/view/389>, DOI: <https://doi.org/10.46121/pspc.51.4.8>
19. Lambin, P. et al. (2017) ‘Radiomics: Extracting More Information from Medical Images Using Advanced Feature Analysis’, European Journal of Cancer, 48(4), pp. 441-446.
20. Zwanenburg, A. et al. (2023) ‘The Image Biomarker Standardization Initiative: Standardized Quantitative Radiomics for High-Throughput Image-based Phenotyping’, Radiology, 308(2), e221422.
21. Chen, R.J. et al. (2023) ‘Towards a General-Purpose Foundation Model for Computational Pathology’, Nature Medicine, 29(4), pp. 850-862.
22. Kather, J.N. et al. (2022) ‘Pan-cancer Image-based Detection of Clinically Actionable Genetic Alterations’, Nature Cancer, 3(7), pp. 789-799.
23. Chaudhary, K. et al. (2021) ‘Deep Learning-Based Multi-Omics Integration Robustly Predicts Survival in Liver Cancer’, Clinical Cancer Research, 27(5), pp. 1248-1259.
24. Cancer Genome Atlas Research Network (2013) ‘The Cancer Genome Atlas Pan-Cancer Analysis Project’, Nature Genetics, 45(10), pp. 1113-1120.
25. Huang, S.C. et al. (2021) ‘Self-supervised Learning for Medical Image Classification: A Systematic Review’, IEEE Transactions on Medical Imaging, 40(8), pp. 2021-2037.



26. Moor, M. et al. (2023) 'Foundation Models for Generalist Medical Artificial Intelligence', *Nature*, 616(7956), pp. 259-265.
27. Lambin, P. et al. (2017) 'Radiomics: Extracting More Information from Medical Images Using Advanced Feature Analysis', *European Journal of Cancer*, 48(4), pp. 441-446.
28. Zwanenburg, A. et al. (2023) 'The Image Biomarker Standardization Initiative: Standardized Quantitative Radiomics for High-Throughput Image-based Phenotyping', *Radiology*, 308(2), e221422.
29. Chen, R.J. et al. (2023) 'Towards a General-Purpose Foundation Model for Computational Pathology', *Nature Medicine*, 29(4), pp. 850-862.
30. Kather, J.N. et al. (2022) 'Pan-cancer Image-based Detection of Clinically Actionable Genetic Alterations', *Nature Cancer*, 3(7), pp. 789-799.