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SPATIAL OMICS AND FOUNDATION AI MODELS: DECODING TUMOR HETEROGENEITY FOR PRECISION ONCOLOGY

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Abstract: Tumor heterogeneity remains one of the greatest challenges in precision oncology because malignant tissues exhibit extensive spatial, molecular, cellular, and microenvironmental diversity that continuously evolves during disease progression and therapeutic intervention. Recent advances in spatial omics technologies and foundation artificial intelligence (AI) models have created unprecedented opportunities to decode this complexity by integrating high-dimensional molecular, histopathological, imaging, and clinical information into unified computational frameworks. Foundation AI models, multimodal transformer architectures, graph neural networks, self-supervised learning, and generative artificial intelligence enable generalized representation learning across spatial transcriptomics, spatial proteomics, spatial metabolomics, digital pathology, radiological imaging, genomics, transcriptomics, epigenomics, laboratory biomarkers, circulating tumor DNA, wearable physiological monitoring, electronic health records, and longitudinal clinical outcomes. These intelligent computational systems support comprehensive characterization of tumor heterogeneity, biomarker discovery, prognostic prediction, therapeutic optimization, immunotherapy selection, digital twin simulation, adaptive disease monitoring, and evidence-based clinical decision support. Emerging technologies including multimodal large language models, federated learning, reinforcement learning, retrieval-augmented generation, explainable artificial intelligence, and agentic AI further strengthen spatial oncology 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, spatial resolution, interoperability, clinical validation, and equitable implementation. This review provides a comprehensive overview of spatial omics and foundation AI models, emphasizing their role in decoding tumor heterogeneity for precision oncology and personalized cancer medicine.[1]

Keywords: *Spatial omics, Foundation models, Tumor heterogeneity, Artificial intelligence, Precision oncology, Spatial transcriptomics, Digital pathology, Multi-omics, Computational oncology, Personalized medicine.*

1. Introduction

Cancer is a highly heterogeneous biological disease characterized by continuous genomic evolution, epigenetic remodeling, immune adaptation, metabolic reprogramming, angiogenesis, tissue remodeling, and dynamic interactions among malignant cells, stromal components, immune populations, vascular structures, extracellular matrix, and host physiology. These interconnected biological processes exhibit substantial spatial variability across individual tumors and evolve throughout diagnosis, treatment, recurrence, metastasis, and survivorship, making precision oncology increasingly dependent upon computational systems capable of integrating heterogeneous biomedical information across multiple biological scales.[2]

Modern oncology routinely generates enormous quantities of biomedical information through radiological imaging, digital pathology, genomic sequencing, transcriptomics, proteomics, metabolomics, epigenomics, spatial omics technologies, laboratory investigations, circulating

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tumor DNA, wearable physiological monitoring, physician documentation, electronic health records, and patient-reported outcomes. Although each modality contributes valuable biological insight, isolated interpretation frequently overlooks the spatial organization and cellular interactions governing tumor evolution, therapeutic response, resistance mechanisms, and long-term clinical outcomes.[3]

Spatial omics technologies combined with foundation AI models provide unprecedented opportunities to characterize tumor ecosystems through integrated analysis of molecular profiles, tissue architecture, cellular organization, and clinical information. This convergence establishes a transformative framework for precision oncology capable of decoding the biological complexity of heterogeneous tumors.

2. Evolution of Spatial Omics and Computational Oncology

Computational oncology has evolved from conventional molecular analyses toward integrated spatially resolved biomedical intelligence. Early genomic technologies primarily characterized bulk tumor tissue, averaging molecular information across heterogeneous cellular populations and obscuring important spatial biological interactions. Although these methods substantially advanced cancer biology, they remained limited in their ability to characterize tissue organization and microenvironmental complexity.[4]

The development of single-cell sequencing, spatial transcriptomics, spatial proteomics, spatial metabolomics, multiplex immunofluorescence, imaging mass cytometry, and advanced digital pathology transformed cancer research by enabling comprehensive characterization of molecular information within its native tissue context. Simultaneously, deep learning substantially advanced computational oncology through automated representation learning from radiological imaging, digital pathology, genomic sequencing, and electronic health records.

Foundation AI models now integrate these diverse modalities through multimodal self-supervised learning, enabling generalized computational representations applicable across diagnosis, prognosis, biomarker discovery, therapeutic prediction, disease monitoring, and translational oncology.[5]

3. Principles of Foundation AI Models for Spatial Omics

Foundation AI models differ fundamentally from conventional artificial intelligence 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 diagnosis, prognosis, molecular characterization, biomarker discovery, therapeutic optimization, disease monitoring, computational pathology, spatial biology, and clinical decision support.[6]

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

Graph neural networks further characterize interactions among genes, proteins, signaling pathways, immune populations, stromal cells, vascular networks, imaging phenotypes, tissue architecture, therapeutic targets, physiological variables, and clinical outcomes, thereby enabling systems-level computational reasoning supporting precision oncology.[7]

4. Computational Architecture

Modern spatial omics platforms consist of interconnected computational layers responsible for multimodal biomedical data acquisition, preprocessing, spatial representation learning, multimodal fusion, adaptive learning, predictive analytics, digital twin simulation, and intelligent clinical decision support.[8]

The acquisition layer continuously integrates spatial transcriptomics, spatial proteomics, spatial metabolomics, digital pathology, radiological

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Volume 14, Issue-12
December, 2024, P24
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imaging, genomic sequencing, epigenomics, laboratory investigations, circulating tumor DNA, wearable physiological monitoring, medication history, physician documentation, patient-reported outcomes, and electronic health records. Advanced preprocessing pipelines normalize imaging studies, harmonize molecular datasets, register spatial coordinates, encode clinical narratives using natural language processing, and synchronize temporal patient information.

Foundation AI models subsequently generate generalized multimodal embeddings representing molecular biology, tissue architecture, spatial cellular organization, imaging phenotypes, physiological function, and longitudinal clinical trajectories. These unified computational representations support diagnosis, biomarker discovery, prognostic prediction, therapeutic optimization, adaptive learning, and precision oncology.[9]

5. Spatial Transcriptomics and Molecular Intelligence

Spatial transcriptomics has transformed cancer biology by enabling measurement of gene expression while preserving native tissue architecture and cellular localization. Unlike conventional bulk sequencing, spatial transcriptomics identifies region-specific transcriptional programs, cellular communication networks, immune organization, stromal remodeling, and tumor evolution across heterogeneous tissue environments.[10]

Foundation AI models integrate spatial transcriptomic profiles with genomics, proteomics, metabolomics, epigenomics, digital pathology, and radiological imaging to generate comprehensive molecular representations capable of identifying biologically meaningful cellular neighborhoods, signaling pathways, therapeutic biomarkers, and mechanisms of treatment resistance.

These integrated molecular representations substantially improve biomarker discovery, molecular subtype classification, prognostic prediction, and personalized precision oncology.[11]

6. Spatial Proteomics and Cellular Organization

Spatial proteomics provides high-resolution characterization of protein expression, signaling activity, immune interactions, and cellular communication while preserving tissue architecture. Multiplex imaging technologies allow simultaneous visualization of dozens to hundreds of proteins within intact tumor microenvironments, enabling comprehensive investigation of functional cellular states.[12]

Foundation AI models analyze spatial protein distributions using graph neural networks, transformer architectures, and multimodal representation learning to characterize immune infiltration, angiogenesis, stromal remodeling, metabolic heterogeneity, extracellular matrix organization, and therapeutic target expression across diverse tumor ecosystems.

These computational representations substantially enhance understanding of tumor biology while improving prediction of immunotherapy responsiveness and therapeutic outcomes.[13]

7. Digital Pathology and Spatial Tissue Intelligence

Digital pathology provides complementary microscopic information describing cellular morphology, tissue architecture, stromal remodeling, angiogenesis, fibrosis, necrosis, immune infiltration, and spatial cellular organization across diverse tumor types. Foundation AI models automatically extract generalized pathomic representations from whole-slide pathology images without requiring handcrafted feature engineering.[14]

Artificial intelligence identifies latent spatial imaging biomarkers associated with molecular alterations, immune responses, therapeutic sensitivity, disease progression, and patient survival. Integration of digital pathology with spatial transcriptomics, spatial proteomics, metabolomics, and clinical intelligence substantially improves systems-level understanding of tumor heterogeneity while supporting personalized precision oncology.

These integrated computational representations establish digital pathology as a central component of spatial cancer intelligence.[15]

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8. Tumor Microenvironment Modeling

The tumor microenvironment comprises malignant cells, immune populations, stromal fibroblasts, endothelial cells, extracellular matrix components, cytokines, chemokines, metabolites, vascular networks, and complex intercellular communication pathways that collectively influence disease progression and therapeutic response.[16]

Foundation AI models integrate spatial omics, computational pathology, radiological imaging, laboratory biomarkers, and longitudinal clinical information using graph neural networks and multimodal transformers to characterize dynamic cellular ecosystems across multiple organizational scales. These computational frameworks identify biologically meaningful cellular neighborhoods, immune niches, stromal remodeling patterns, and signaling interactions that govern tumor evolution. Comprehensive modeling of the tumor microenvironment substantially improves biomarker discovery, therapeutic stratification, immunotherapy optimization, and translational oncology research.[17]

9. Precision Diagnosis and Therapeutic Prediction

One of the most clinically important applications of spatial omics and foundation AI models is precision diagnosis and therapeutic prediction through comprehensive integration of spatial molecular biology, imaging phenotypes, histopathological characteristics, laboratory biomarkers, wearable physiological monitoring, medication history, and longitudinal clinical trajectories. Foundation AI models simultaneously analyze heterogeneous biomedical information to predict responsiveness to chemotherapy, targeted therapy, endocrine therapy, immunotherapy, radiation therapy, surgery, and multimodal treatment combinations while estimating treatment-related toxicity, recurrence probability, progression-free survival, overall survival, and mechanisms of therapeutic resistance. These adaptive computational systems support individualized therapeutic planning while continuously refining predictive accuracy using newly acquired biomedical evidence throughout the cancer care continuum.[18][19][20]

10. Digital Twins and Spatially Informed Virtual Patient Modeling

Digital twin technology represents one of the most transformative applications of spatial omics and foundation AI models by creating continuously evolving virtual representations of individual cancer patients synchronized with their biological counterparts. Foundation AI models integrate serial radiological imaging, digital pathology, spatial transcriptomics, spatial proteomics, genomics, metabolomics, 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, spatially informed digital twins continuously update their computational representations as new biomedical information becomes available. Integration of spatial molecular maps enables virtual patients to simulate dynamic cellular interactions, immune remodeling, stromal evolution, angiogenesis, and therapeutic resistance at unprecedented biological resolution. These intelligent virtual patients allow clinicians to evaluate multiple therapeutic strategies before implementation, optimize treatment sequencing, anticipate resistance mechanisms, and personalize supportive care according to evolving patient biology.

By combining spatial biomedical intelligence with predictive simulation, digital twins transform computational oncology from retrospective analysis toward proactive precision medicine supported by continuously adaptive virtual patient ecosystems.

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 interpreting radiological imaging, digital pathology, spatial omics, molecular diagnostics, laboratory

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Volume 14, Issue-12
December, 2024, P24
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investigations, wearable physiological monitoring, medication history, physician documentation, patient-reported outcomes, and evidence-based clinical guidelines independently, these models synthesize diverse biomedical information into unified computational representations supporting multidisciplinary oncology practice.[22]

Interactive clinical dashboards generate individualized diagnostic summaries, spatial biomarker analyses, tumor microenvironment characterizations, digital twin simulations, therapeutic recommendations, toxicity estimates, recurrence probabilities, disease progression forecasts, and survival predictions while facilitating collaboration among oncologists, radiologists, pathologists, surgeons, radiation oncologists, molecular biologists, pharmacists, nurses, genetic counselors, and computational scientists.

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 Spatial Intelligence

A defining characteristic of foundation AI models is their ability to continuously evolve as new biomedical information becomes available. Artificial intelligence incorporates serial spatial transcriptomic analyses, computational pathology, circulating tumor DNA, laboratory biomarkers, wearable physiological monitoring, medication adherence, patient-reported outcomes, and real-world clinical evidence 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 therapeutic recommendations through iterative evaluation of treatment outcomes. Consequently, spatial oncology platforms remain synchronized with evolving tumor biology, dynamic microenvironmental remodeling, emerging scientific discoveries, changing clinical guidelines, and diverse patient trajectories.

This adaptive computational paradigm transforms oncology into a continuously learning healthcare ecosystem capable of supporting real-time personalized precision medicine.

13. Federated Spatial Omics Networks

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

Participating healthcare institutions independently train local models using spatial transcriptomics, spatial proteomics, digital pathology, radiological imaging, genomics, laboratory investigations, wearable monitoring, liquid biopsy, 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, and generalizability across diverse healthcare environments.

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

14. Explainability, Validation, and Ethical Governance

Successful implementation of spatial omics foundation AI models 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 computational reasoning through

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attention visualization, saliency maps, SHAP (Shapley Additive Explanations), feature attribution analysis, uncertainty estimation, spatial heat maps, and counterfactual explanations identifying the molecular, spatial, pathological, physiological, and clinical variables responsible for predictive outputs.[25]

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

Responsible implementation further depends upon protection of patient privacy, informed consent, transparency, accountability, equitable access, responsible data governance, and continuous post-deployment surveillance to ensure trustworthy integration of intelligent computational systems into routine oncology practice.

15. Future Perspectives

Future spatial 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), robotics, and cloud-native healthcare infrastructure into unified precision oncology platforms.[26]

These next-generation computational ecosystems will continuously integrate molecular biology, spatial transcriptomics, radiological imaging, digital pathology, laboratory medicine, wearable physiological monitoring, environmental exposures, electronic health records, biomedical literature, and real-world clinical outcomes while autonomously coordinating diagnostic workflows, optimizing therapeutic strategies, supporting adaptive clinical trials, generating personalized patient communication, and continuously synthesizing biomedical evidence.

Such intelligent ecosystems are expected to transform oncology from fragmented and reactive disease management toward predictive, preventive, adaptive, continuously learning, and precision-guided healthcare across the global cancer community.

16. Discussion

Spatial omics combined with foundation AI models represents one of the most significant paradigm shifts in computational oncology by integrating molecular biology, spatial tissue organization, radiological imaging, digital pathology, laboratory biomarkers, digital twins, wearable technologies, and longitudinal clinical intelligence into unified computational ecosystems capable of supporting comprehensive personalized cancer care. Unlike conventional artificial intelligence systems developed for isolated predictive tasks, these intelligent frameworks simultaneously analyze spatial molecular biology, tissue architecture, imaging phenotypes, laboratory biomarkers, physiological monitoring, environmental influences, and longitudinal clinical trajectories to generate

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December, 2024, P24
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holistic computational representations of evolving tumor biology.[27]

Applications spanning computational pathology, spatial transcriptomics, spatial proteomics, radiogenomics, biomarker discovery, digital twins, precision immunotherapy, adaptive therapeutics, continuous learning, federated collaboration, digital health, survivorship management, and intelligent clinical decision support demonstrate the extraordinary potential of spatial foundation AI 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, and sustained multidisciplinary collaboration.

As biomedical knowledge and healthcare data continue to expand exponentially, spatial omics and foundation AI models are expected to become central computational infrastructures supporting precision oncology worldwide.

17. Conclusion

Spatial omics and foundation AI models are transforming precision oncology by integrating spatial transcriptomics, spatial proteomics, radiological imaging, digital pathology, multi-omics, laboratory biomarkers, wearable technologies, electronic health records, digital twins, and longitudinal clinical intelligence into unified computational ecosystems capable of supporting accurate diagnosis, biomarker discovery, prognostic prediction, therapeutic optimization, adaptive disease monitoring, and personalized cancer care throughout the disease continuum.[28]

Advances in transformer architectures, multimodal learning, graph neural networks, self-supervised learning, federated learning, reinforcement learning, digital twins, multimodal large language models, agentic AI, and generative artificial intelligence are expected to further strengthen intelligent spatial oncology ecosystems, enabling increasingly accurate molecular characterization, predictive clinical decision-making, adaptive therapeutics, continuous disease surveillance, and continuously personalized oncology care.[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, and regulatory agencies will accelerate the responsible implementation of spatial omics–enabled foundation AI models. These innovations have the potential to improve patient outcomes, enhance healthcare efficiency, reduce disparities in cancer care, accelerate translational research, 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. Dr. RajathaMaradiHemanth 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
3. Dr. Ohmini Krishnamurthy Rajendran (Author), SELF-SUPERVISED MULTIMODAL LEARNING FOR EARLY CANCER DETECTION ACROSS IMAGING AND GENOMICS, Vol. 52 No. 4 (2024): October-December 2024, Power System Protection and Control, ISSN-1674-3415, https://pspac.info/index.php/dlbh/article/view/325, DOI: https://doi.org/10.46121/pspc.52.4.14
4. Dr. RajathaMaradiHemanth Kumar (Author), MULTIMODAL FOUNDATION AI MODELS IN PRECISION ONCOLOGY: INTEGRATING RADIOMICS, PATHOMICS, MULTI-OMICS, AND CLINICAL INTELLIGENCE SYSTEMS, Vol. 52 No. 4 (2024): October–December 2024, Power System Protection and Control, ISSN-1674-3415,

Paper Available at: www.ijarai.com
DOI : https://doi.org/10.65713/ijaraiv14i1224

https://pspac.info/index.php/dlbh/article/view/343 , DOI: https://doi.org/10.46121/pspc.52.4.16

5. Joshi, A. et al. (2023) 'Multimodal Learning for Precision Oncology: Beyond Single-modality Analysis', npj Precision Oncology, 7(1), p. 28.

6. Dr. Latha Kiran Krishna Rajendran (Author), Genomic Profiling: Utilizing Multi-Omics Data to Identify Potential Therapeutic Targets and Resistance Markers, Vol. 52 No. 4 (2024): October–December 2024, Power System Protection and Control, ISSN: 1674-3415, Article URL: https://pspac.info/index.php/dlbh/article/view/312 , DOI: https://doi.org/10.46121/pspc.52.4.13.

7. 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.

8. Dr. RajathaMaradiHemanth 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

9. 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.

10. Zwanenburg, A. et al. (2023) 'The Image Biomarker Standardization Initiative: Standardized Quantitative Radiomics for High-Throughput Image-based Phenotyping', Radiology, 308(2), e221422.

11. Chen, R.J. et al. (2023) 'Towards a General-Purpose Foundation Model for Computational Pathology', Nature Medicine, 29(4), pp. 850-862.

12. Kather, J.N. et al. (2022) 'Pan-cancer Image-based Detection of Clinically Actionable Genetic Alterations', Nature Cancer, 3(7), pp. 789-799.

13. 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.

14. Cancer Genome Atlas Research Network (2013) 'The Cancer Genome Atlas Pan-Cancer Analysis Project', Nature Genetics, 45(10), pp. 1113-1120.

15. 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.

16. Moor, M. et al. (2023) 'Foundation Models for Generalist Medical Artificial Intelligence', Nature, 616(7956), pp. 259-265.

17. Hanahan D. Hallmarks of cancer: new dimensions. Cancer Discov. 2022;12(1):31–46. Doi:10.1158/2159-8290.CD-21-1059.

18. 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.

19. 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.

20. 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

21. Bommasani R, Hudson DA, Adeli E, et al. On the opportunities and risks of foundation models. arXiv. 2021. Doi:10.48550/arXiv.2108.07258.

22. Dosovitskiy A, Beyer L, Kolesnikov A, et al. An image is worth 16×16 words: transformers for image recognition at scale. arXiv. 2020. Doi:10.48550/arXiv.2010.11929.

23. 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

24. Dr. Latha Kiran Krishna Rajendran (Author), IMMUNOTHERAPY AND CELL THERAPY: DEVELOPING CAR-T 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

25. Chakraborty, S. et al. (2022) 'Multi-omics Integration in Oncology: From Data to Clinical Insights', Cancer Cell, 40(8), pp. 805-823.

26. 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

27. Dr. Latha Kiran Krishna Rajendran (Author), MECHANISMS DRIVING IMMUNOTHERAPY RESISTANCE IN COLORECTAL CANCER LIVER METASTASES, Vol. 52 No. 1 (2024): January-March 2024, Power System Protection and Control, ISSN-1674-3415, https://pspac.info/index.php/dlbh/article/view/303 , DOI: https://doi.org/10.46121/pspc.52.1.5

28. Dr. Ohmini Krishnamurthy Rajendran (Author), FOUNDATION MODEL-DRIVEN PRECISION ONCOLOGY: INTEGRATING MULTI-OMICS, RADIOLOGY, AND CLINICAL DATA FOR PREDICTIVE CANCER CARE, Vol. 52 No. 2 (2024): April-June 2024, Power System Protection and Control, ISSN-1674-3415, https://pspac.info/index.php/dlbh/article/view/324 , DOI: https://doi.org/10.46121/pspc.52.2.14

29. Dr. Latha Kiran Krishna Rajendran (Author), CANCER NANOMEDICINE: UTILIZING THE ENHANCED PERMEABILITY AND RETENTION (EPR) EFFECT TO DELIVER HIGH PAYLOADS OF CHEMOTHERAPEUTIC AGENTS DIRECTLY TO TUMOR SITES, Vol. 52 No. 2 (2024): April-June 2024, Power System Protection and Control, ISSN-1674-3415, https://pspac.info/index.php/dlbh/article/view/311, DOI: https://doi.org/10.46121/pspc.52.2.12

30. Dr. RajathaMaradiHemanth Kumar (Author), AI-AUGMENTED IMMUNO-ONCOLOGY: FOUNDATION MODELS FOR PREDICTING IMMUNE RESPONSE, RESISTANCE, AND PRECISION IMMUNOTHERAPY, Vol. 52 No. 2 (2024): April–June 2024, Power System Protection and Control, ISSN-1674-3415, https://pspac.info/index.php/dlbh/article/view/345 , DOI: https://doi.org/10.46121/pspc.52.2.18