Integration of Artificial Intelligence and Omics Technologies for Precision Oncology

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ABSTRACT

This comprehensive review examines the integration of artificial intelligence (AI) and cancer treatment from an omics perspective. As cancer incidence and mortality rates continue to rise globally, understanding tumor heterogeneity and molecular subtypes has become essential for effective therapy. The review highlights the role of AI in analyzing omics data, including genomics, proteomics, transcriptomics, epigenomics, and metabolomics. AI-driven precision oncology significantly enhances diagnostics, treatment selection, and prognosis prediction by identifying complex patterns and correlations within large-scale datasets. By combining AI with various omics approaches, researchers are uncovering new insights into cancer biology, enabling more personalized therapeutic interventions. Additionally, the review explores the future potential of AI in oncology, focusing on the possibilities for improved patient outcomes and groundbreaking discoveries in cancer research.

Keywords: cancer, oncology, artificial intelligence, omics, precision medicine

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Introduction

Cancer is a disease characterized by the uncontrolled growth of abnormal cells that extend beyond their normal boundaries, potentially invading nearby tissues and spreading to distant organs. This progression, known as metastasis, disrupts and destroys organ function by obstructing the supply of nutrients and oxygen, leading to the accumulation of waste products. Cancer can affect almost any part of the body, presenting in various forms, and often spreads through the blood and lymphatic systems during advanced stages (Siegel et al., 2023). As a significant global health challenge, cancer is responsible for approximately 10 million deaths worldwide in 2020, with an estimated 1,958,310 new cases and 609,820 deaths projected in the United States alone in 2023 (Afolayan et al., 2024; Siegel et al., 2023). The incidence and mortality rates of cancer continue to rise globally, marking it as one of the leading causes of death (Sung et al., 2021). Additionally, a study predicts a consistent cancer death rate of approximately 0.24% in any country worldwide over the next century (Gaidai, Yan, & Xing, 2023).

Tumor heterogeneity, the variation in cell populations within tumors, is a universal feature of all cancer types. This heterogeneity includes differences between tumors of the same type among different patients (inter-tumor heterogeneity) and within individual tumors (intra-tumor heterogeneity) (Li et al., 2023). Recognized as a critical factor in cancer progression, tumor heterogeneity affects every stage, from initiation to metastasis and recurrence (Li et al., 2023). The sources of this heterogeneity include genetic, epigenetic, transcriptomic, proteomic, and metabolomic alterations (Li et al., 2023). Understanding these variations is essential for developing individualized therapies, particularly through cancer subtyping based on the molecular characteristics of primary tumors, which relies heavily on gene expression data (Shen et al., 2022). Although gene expression signature-based classification has shown promise, challenges such as platform differences, batch effects, and difficulties in classifying individual patient samples have limited its widespread implementation. The significance of cancer subtyping lies in its ability to guide the selection of specific therapies and the design of targeted treatments. While traditional cancer classification

methods rely on histopathological and clinical characteristics, gene expression profiling faces challenges from technical variations and experimental protocols, which can lead to non-biological batch effects (Gao et al., 2019). Within a single cancer type, multiple subtypes may exist, each influencing treatment decisions. For example, breast cancer is typically classified into subtypes such as LumA, LumB, HER2, Basal, and Normal, each guiding different treatment approaches (Luo et al., 2023). Similarly, prostate cancers exhibit diverse subtypes defined by specific gene fusions (e.g., ERG, ETV1/4, FLI1) or mutations (e.g., SPOP, FOXA1, IDH1), revealing highly varied genomic, epigenomic, and transcriptomic patterns (The Cancer Genome Atlas Research Network, 2015).

In recent years, artificial intelligence (AI) has emerged as a powerful tool for integrating and analyzing multi-omics data. The applications of AI in the medical field have expanded significantly, encompassing clinical practice, translational medicine, and biomedical research across various diseases, including cancer (Kourou et al., 2021). In oncology, AI is employed for a range of purposes, including risk assessment, automated segmentation, lesion detection, characterization, grading, staging, prognosis prediction, and therapy response evaluation (Cuocolo et al., 2020). AI's ability to accelerate the analysis of vast datasets, recognize patterns, and facilitate informed decision-making has made it instrumental in advancing medical research and practice (Xu et al., 2019). This review provides a comprehensive examination of the application of AI in cancer treatment, with a particular focus on its integration with multi-omics data. Additionally, it discusses the future potential of AI in advancing oncology, improving patient outcomes, and contributing to new discoveries in cancer research.

Omics and Artificial Intelligence

In the context of oncology treatment, Omics and Artificial Intelligence (AI) are emerging areas that play critical roles in advancing personalized medicine and improving cancer treatment outcomes.

Omics in Oncology

Omics refers to different areas of study that focus on various biological molecules in the body. These areas include: 1) Genomics: This is the study of genes

and DNA. In cancer treatment, genomics helps doctors understand which gene mutations cause cancer, so they can create specific treatments to target those mutations. (Micheel, Nass & Omenn, 2012) 2) Proteomics: This is the study of proteins. By studying proteins in cancer cells, scientists can learn how these cells work and find new ways to stop them. (Gillette, Jimenez & Carr, 2024). 3) Transcriptomics: This area focuses on RNA, which is made from DNA. Understanding RNA in cancer cells helps in discovering how these cells behave and in finding new treatment methods and 4) Metabolomics: This is the study of small molecules involved in metabolism. In cancer, studying these molecules can help identify new ways to diagnose and treat the disease. (Micheel et al., 2012).

Artificial Intelligence (AI) in Oncology

Artificial Intelligence (AI) is technology that uses computers to analyze large amounts of data. In cancer treatment, AI can: 1) Help Diagnose Cancer: AI can look at medical images like X-rays and help doctors detect cancer earlier and more accurately (National Cancer Institute, 2024). 2) Plan Treatments: AI can use patient data to predict how well a treatment will work, allowing doctors to choose the best treatment for each patient. (National Cancer Institute, 2024; National Institutes of Health, 2024). 3) Discover New Drugs: AI can help find new cancer drugs faster by predicting which ones might work based on the characteristics of the cancer and 4) Monitor Progress: AI can track how well a patient is responding to treatment and suggest changes if needed to improve outcomes. (National Cancer Institute, 2024; National Institutes of Health, 2024).

By combining omics with AI, cancer treatment is becoming more personalized. This means treatments are tailored specifically to each patient's cancer, which can make them more effective and reduce side effects.

Omics technologies in oncology

Molecules, such as genes, RNA, proteins, and metabolites, can be used to reveal the mechanisms underlying physiological processes and changes that occur during pathological conditions. Current technologies can obtain a huge number of molecular measurements from a biological sample. Many hundreds or thousands of molecules can be analyzed by high-throughput technologies termed as omics technologies. Examples of omics technologies include genomics, transcriptomics,

proteomics, and metabolomics, which correspond to global analyzes of genes, RNA, proteins, and metabolites, respectively. Those omics technologies can provide new insights into oncology.

Epigenetics refers to changes in gene expression that occur without altering the DNA sequence itself. These changes are influenced by various factors, including environmental exposures, lifestyle choices, and developmental processes. Epigenetic modifications can control which genes are turned on or off in different cell types, playing a critical role in regulating cellular functions and development. In the context of cancer, epigenetic alterations can lead to abnormal gene expression patterns that contribute to tumor initiation, growth, and metastasis. These changes may involve DNA methylation, histone modifications, and non-coding RNAs, among other mechanisms. AI technology is increasingly used to analyze large-scale genomic and epigenomic data sets, helping researchers uncover patterns and correlations that provide insights into the role of epigenetics in cancer. This integration of AI with epigenetics research holds great promise for improving our understanding of cancer biology and developing targeted therapies tailored to individual patients.

In cancer genomics, the widespread availability of genetic information facilitated by next-generation sequencing (NGS) technologies offers valuable insights into tumor genomic profiles. Additionally, germline mutations in cancer-predisposing genes like BRCA1/2 are identified to assess cancer susceptibility (Xu et al., 2019). Cell-free DNA (cfDNA) from dying tumor cells, exosomes, and circulating tumor cells (CTCs) serve as sources for tumor DNA, aiding in genomic profiling for risk prediction, disease diagnosis, and targeted therapy development (Xu et al., 2019). The study of whole genome sequences and DNA sequence variants, known as genome analysis, has significantly impacted medicine, enabling disease diagnosis, treatment response assessment, and prognosis prediction (Babu & Snyder, 2023). In colorectal cancer (CRC), genetic features such as KRAS mutation and microsatellite instability (MSI) status play pivotal roles in disease characterization (Gao et al., 2023). Although cancer is not primarily hereditary, the genome represents the entirety of genes within a cell, and genomics delves into the study of organisms' genetic make-up. Genome-wide

association studies (GWAS) have successfully pinpointed interacting genetic variants contributing to cancer risk (Shao et al., 2022).

Transcriptomics involves measuring the complete set of RNA transcripts and their abundance in cells or cell populations, serving as a read-out of cell state. The continual advancements in transcriptomics have brought about transformative changes in modern medicine, offering applications in disease diagnosis and prognosis. This technology enables the elucidation of how different genes interact within specific cell types over time (Babu & Snyder, 2023). In recent experiments, the Deep Convolutional Graph Network (DCGN) outperformed seven other cancer subtype classification methods when applied to breast and bladder cancer gene expression datasets. These findings highlight the superior performance of DCGN in classification tasks (Gao et al., 2019). Consequently, whole transcriptome-based cancer subtyping has emerged as an effective strategy for dissecting cancer heterogeneity. This approach integrates genetic, epigenetic, and micro-environmental features, providing insights into cancer biology and clinical presentation (Gao et al., 2019).

Proteomics involves quantifying the identity and abundance of all proteins within a sample. Mass spectrometry (MS)-based proteomics has demonstrated considerable potential by uncovering intricate and predictive biomarker signatures. These findings have not only enhanced clinical decision-making but have also facilitated the prediction of 118 patient trajectories through the application of machine learning techniques (Gillette et al., 2024).

Metabolomics involves studying small molecules in the body, typically those with a mass less than 1500 Da. Serving as the substrate for interactions between genetics, environment, microbiota, and exposome, metabolomics studies have driven advancements in biomedical research. These studies have applications in biomarker discovery, disease diagnosis, and prognosis (Babu & Snyder, 2023).

Integration of AI and Omics technologies

Cancer is a multifactorial disease and the development of cancer is complicated. Even though multi-omics technology can provide lots of information for better understanding the molecular and clinical features of cancers, the extensive volume of information is challenging for humans to analyze and gain deep insight. Through the AI capabilities, AI can process vast quantities of information obtained from omics technology to unveil in-depth insights into various types of cancer. Hence, AI can strengthen multi-omics technology to become a powerful tool for cancer research and medical oncology. In clinical practice, AI can be utilized for diverse purposes, such as risk prediction, investigation, diagnosis, and therapy response evaluation.

AI assists cancer research through its application in genomics, epigenomics, transcriptomics, proteomics, and metabolomics. In genomics, AI algorithms analyze vast genomic datasets to identify cancer genetic variations, aiding in the discovery of driver mutations and personalized treatment strategies. Epigenomic analysis with machine learning algorithm uncover patterns within large scale epigenomic datasets intricate DNA methylation patterns and histone modifications, shedding light on gene expression regulation in cancer cells and identifying potential therapeutic targets (Vinciguerra, 2023). AI assisted transcriptomic can analyze tumor heterogeneity (Figure 1), the tumor microenvironment, immune-related adverse event pathogenesis, drug resistance (Gui et al., 2023).

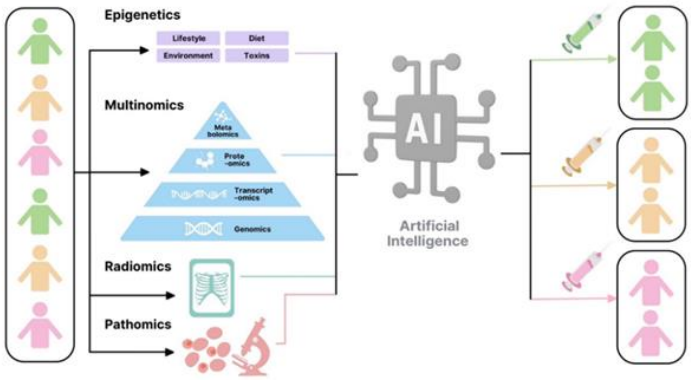

Figure 1 The synergistic integration of epigenetics, multi-omics, radiomics and pathomic data for AI-driven personalized patient management

AI-driven transcriptomics analysis uncovers dysregulated genes and pathways crucial for understanding cancer progression and classification. Moreover, AI facilitated proteomic analysis can predict complex protein biomarkers and interactions pivotal for elucidating cancer biology and developing targeted therapies. In addition, AI can identify risk factors, predict the likelihood of developing a disease (Gui et al., 2023). AI can be used to facilitate the integration of multi-omics information (Gao, Huang, & Xing, 2022). This integrated approach paves the way for the development of precision oncology, improving diagnosis and treatment outcomes for individual cancer patients.

Current Applications of Omics and AI

Genomic testing, particularly the Oncotype DX test, has greatly improved breast cancer treatment by analyzing the activity of 21 genes in a tumor. This test is crucial for patients with early-stage, estrogen receptor-positive (ER+), node-negative breast cancer. It helps predict the risk of cancer returning and the potential benefit of chemotherapy. By identifying which patients are likely to benefit from chemotherapy, the test also helps avoid unnecessary treatments for those at low risk (McVeigh & Kerin, 2017). The effectiveness of the Oncotype DX test is even better when combined with biomarkers like long non-coding RNA MALAT1, which provides additional information about cancer prognosis (Huang et al., 2021). The use of Oncotype DX in clinical practice is a major step forward in personalized medicine, allowing for more accurate treatment plans that match each patient's risk level, leading to better outcomes and fewer unnecessary treatments (McVeigh & Kerin, 2017; Huang et al., 2021).

In lung cancer, the combination of artificial intelligence (AI) and omics data has advanced screening and diagnosis. AI models using CT scans and radiomics have shown better accuracy in telling the difference between benign and malignant nodules compared to traditional methods, though issues like high false positive rates remain. Adding omics data, such as genomics and proteomics, makes these models more accurate by providing a deeper understanding of the disease, leading to more personalized treatments. Future research should work on improving these AI models

to reduce false positives and ensure they are effective for all patient groups (Cheng, Li, & Wu., 2024; Gharehbaghi et al., 2023).

In colorectal cancer (CRC), metabolomic profiling has highlighted important metabolic changes before and after surgery, particularly in pathways like arginine and proline metabolism. Zhuang et al. (2022) found that gamma-linolenic acid (GLA) levels, which were lower before surgery, returned to normal afterward, showing potential as a marker for CRC recurrence and prognosis. Proteomics has also helped in early cancer detection and personalized treatment by identifying specific protein biomarkers, allowing for customized therapies and monitoring treatment responses. Combining these omics approaches with AI enables a more efficient analysis of complex data, leading to more precise and individualized cancer care.

AI has also transformed the field of computational and digital pathology by integrating whole-slide imaging (WSI) with deep learning models like convolutional neural networks (CNNs). These AI-driven tools have greatly improved the accuracy and efficiency of diagnosing and classifying cancerous tissues, especially in prostate, colorectal, and breast cancer. AI has also made pathology more precise by reducing differences between observers and allowing for remote analysis, which was especially useful during the COVID-19 pandemic (Cui & Zhang, 2021; Bera et al., 2019; Baxi et al., 2022).

The combination of omics data with AI has also improved the ability to predict cancer outcomes and tailor treatments to each patient. For example, in colorectal cancer, AI models that include omics data have performed better than traditional methods in predicting patient outcomes, providing deeper insights into tumor biology and leading to more effective treatments (Cui & Zhang, 2021). Additionally, AI has advanced the discovery of biomarkers and patient stratification, particularly in immuno-oncology. AI-driven algorithms and multiplex immunohistochemistry (IHC) provide detailed information on immune cell distribution within tumors, improving predictions of responses to immune checkpoint inhibitors and supporting personalized treatment plans (Baxi et al., 2022).

However, the use of omics and AI in cancer care faces several challenges. One major issue is the variability in data quality and the need for standardization,

as differences in how samples are prepared and processed can affect the reliability of results (McVeigh & Kerin, 2017; Huang et al., 2021). The complexity of combining multi-omics data with AI models also makes the process difficult, requiring advanced computational tools and expertise (Cheng et al., 2024; Cui & Zhang, 2021). Additionally, many AI models, especially deep learning algorithms, are seen as "black boxes", making it hard for doctors to understand and trust their recommendations (Bera et al., 2019). High false positive rates in cancer screening and the risk of overfitting also present significant challenges, leading to unnecessary treatments and limiting the general use of AI models (Gharehbaghi et al., 2023). Ethical concerns about patient privacy and data security, as well as biases in AI algorithms, further complicate their use in clinical settings (Baxi et al., 2022). Additionally, the slow pace of clinical validation and regulatory approval, along with the high costs associated with these technologies, limits their availability, especially in areas with fewer resources (Zhuang et al., 2022). Addressing these challenges is essential to fully realize the potential of omics and AI in improving cancer care.

Conclusion

The integration of artificial intelligence (AI) into cancer care represents a major improvement over traditional methods that relied on manual analysis of omics data. Previously, cancer diagnosis and treatment were often slow and less accurate, with decisions based on general protocols rather than tailored to individual patients. AI has changed this by making data analysis faster and more precise, helping doctors to detect cancer earlier and choose the best treatment for each patient. By combining AI with omics technologies, it is now possible to create more personalized and effective treatment plans, which improves patient outcomes. As AI continues to develop, it will likely lead to even more advances in cancer research and care, offering new ways to understand and treat the disease at a deeper level. This progress holds the potential to greatly enhance the effectiveness of cancer treatments and improve the quality of care for patients worldwide.

Recommendation

To improve the use of omics and AI in cancer care, it is important to create clear guidelines for collecting and processing data to ensure that results are consistent and reliable. Making AI models easier to understand will help doctors trust and use them in their work. We also need to address ethical issues, such as protecting patient privacy and avoiding biases in AI. Testing these technologies thoroughly in clinical trials is necessary to prove they are safe and effective. Additionally, finding ways to lower costs and increase access, especially in areas with fewer resources, is essential. Continued research should focus on improving AI models and discovering new uses for omics to enhance personalized cancer treatment and patient outcomes.

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References

Afolayan, O.D., Firempong, C.K., Komlaga, G., Addo-Fordjour, P., Addy, B.S., & Emikpe, B.O. (2024). A review of preclinical evidence of *Cryptolepis nigrescens* (Wennberg) L. Joubert. and Bruyns., *Prosopsis africana* (Guill. and Perr.) Taub. and Pterygota macrocarpa K. Schum. traditionally used to manage tumours in Ghana. **Journal Ethnopharmacology**, 321, 117475.

Babu, M., & Snyder, M. (2023) Multi-Omics Profiling for Health. **Molecular & Cellular Proteomics**, 22(6), 100561.

Baxi, V., Edwards, R., Montalto, M., & Saha, S. (2022). Digital pathology and artificial intelligence in translational medicine and clinical practice. **Modern Pathology**, 35(1), 23-32. https://doi.org/10.1038/s41379-021-00919-2.

Bera, K., Schalper, K. A., Rimm, D. L., Velcheti, V., & Madabhushi, A. (2019). Artificial intelligence in digital pathology-new tools for diagnosis and precision oncology. **Nature Reviews Clinical Oncology**, 16(11), 703–715. https://doi.org/10.1038/s41571-019-0252-y.

Cheng, C., Li, Y., & Wu, F. (2024). Application value of early lung cancer screening based on artificial intelligence. **Journal of Radiation Research and Applied Sciences**, 17(2024), 100982. https://doi.org/10.1016/j.jrras.2024.100982.

Cui, M., & Zhang, D. Y. (2021). Artificial intelligence and computational pathology. **Laboratory Investigation**, 101(4), 412-422. https://doi.org/10.1038/s41374-020-00514-0.

Cuocolo, R., Caruso, M., Perillo, T., Ugga, L., & Petretta, M. (2020). Machine Learning in oncology: A clinical appraisal. **Cancer Letters**, 481, 55-62.

Gaidai, O., Yan, P., & Xing, Y. (2023). Future world cancer death rate prediction. **Scientific Reports**, 13(1), 303.

Gao, F., Huang, K., & Xing, Y. (2022). Artificial Intelligence in Omics. **Genomics Proteomics Bioinformatics**, 20(2022), 811-813.

Gao, F., Wang, W., Tan, M., Zhu, L., Zhang, Y., Fessler, E., Vermeulen, L., & Wang, X. (2019). DeepCC: a novel deep learning-based framework for cancer molecular subtype classification. **Oncogenesis**, 28(9), 44.

Gao, Q., Yang, L., Lu, M., Jin, R., Ye, H., & Ma, T. (2023). The artificial intelligence and machine learning in lung cancer immunotherapy. **Journal of Hematology & Oncology**, 16(1), 55.

Gharehbaghi, A., Partovi, E., & Babic, A. (2023). Parallel recurrent convolutional neural network for abnormal heart sound classification. **Studies in Health Technology and Informatics**, 302, 526–530.

Gillette, M.A., Jimenez, C.R., & Carr, S.A. (2024). Clinical Proteomics: A Promise Becoming Reality. Cell Stem Cell. **Molecular & Cellular Proteomics**, 23(2), 100688.

Gui, Y., He, X., Yu, J., & Jing, J. (2023). Artificial Intelligence-Assisted Transcriptomic Analysis to Advance Cancer Immunotherapy. **Journal of Clinical Medicine**, 12(4), 1279.

Huang, Z., Qin, Q., Xia, L., Lian, B., Tan, Q., Yu, Y., & Mo, Q. (2021). Significance of Oncotype DX 21-Gene Test and Expression of Long Non-Coding RNA MALAT1 in Early and Estrogen Receptor-Positive Breast Cancer Patients. **Cancer Management and Research**, 13, 587–593. https://doi.org/10.2147/CMAR.S276795.

Kourou, K., Exarchos, K.P., Papaloukas, C., Sakaloglou, P., Exarchos, T., & Fotiadis, D.I. (2021). Applied machine learning in cancer research: A systematic review for patient diagnosis, classification and prognosis. **Computational and Structural Biotechnology Journal**, 6, 5546-5555.

Li, J., Li, L., You, P., Wei, Y., & Xu, B. (2023). Towards artificial intelligence to multi-omics characterization of tumor heterogeneity in esophageal cancer. **Seminars in Cancer Biology**, 91, 35-49.

Luo, J., Feng, Y., Wu, X., Li, R., Shi, J., Chang, W., & Wang, J. (2023). ForestSubtype: a cancer subtype identifying approach based on high-dimensional genomic data and a parallel random forest. **BMC Bioinformatics**, 24(1), 289.

McVeigh, T. P., & Kerin, M. J. (2017). Clinical use of the Oncotype DX genomic test to guide treatment decisions for patients with invasive breast cancer. **Breast Cancer: Targets and Therapy**, 9, 393–400. https://doi.org/10.2147/BCTT.S109847.

Micheel, C.M., Nass, S.J. & Omenn, G.S. (2012). Evolution of Translational Omics: Lessons Learned and the Path Forward. **The National Academies Press (US).** Retrieved Aug 25, 2024, from: https://www.ncbi.nlm.nih.gov/books/NBK202165/.

National Cancer Institute. (2024). **Artificial intelligence in cancer research**. Retrieved Aug 25, 2024, from: https://www.cancer.gov/research/infrastructure/artificial-intelligence.

National Institutes of Health. (2024). **AI tool predicts response to cancer therapy**. Retrieved Aug 25, 2024, from: https://www.nih.gov/news-events/nih-research-matters/ai-tool-predicts-response-cancer-therapy.

Shao, D., Dai, Y., Li, N., Cao, X., Zhao, W., Cheng, L., Rong, Z., Huang, L., Wang, Y., & Zhao, J. (2022). Artificial intelligence in clinical research of cancers, **Briefings in Bioinformatics**, 23(1), bbab523.

Shen, J., Shi, J., Luo, J., Zhai, H., Liu, X., Wu, Z., Yan, C., & Luo, H. (2022). Deep learning approach for cancer subtype classification using high-dimensional gene expression data. **BMC Bioinformatics**, 23(1), 430.

Siegel, R.L., Miller, K.D., Wagle, N.S., & Jemal, A. (2023). Cancer statistics, 2023. **CA: A Cancer Journal for Clinicians**, 73(1), 17-48.

Sung, H., Ferlay, J., Siegel, R.L., Laversanne, M., Soerjomataram, I., Jemal, A., & Bray, F. (2021). Global Cancer Statistics 2020: GLOBOCAN Estimates of Incidence and Mortality Worldwide for 36 Cancers in 185 Countries. **CA: A Cancer Journal for Clinicians**, 71(3), 209-249.

The Cancer Genome Atlas Research Network. (2015). The Molecular Taxonomy of Primary Prostate Cancer. **Cell**, 163(4), 1011-1025.

Vinciguerra, M. (2023). The Potential for Artificial Intelligence Applied to Epigenetics. **Mayo Clinic Proceedings: Digital Health**, 1(4), 476-479.

Xu, J., Yang, P., Xue, S., Sharma, B., Sanchez-Martin, M., Wang, F., Beaty, K.A., Dehan, E. & Parikh, B. (2019). Translating cancer genomics into precision medicine with artificial intelligence: applications, challenges and future perspectives. **Human Genetics**, 138(2), 109-124.

Zhuang, F., Bai, X., Shi, Y., Chang, L., Ai, W., Du, J., Liu, W., Liu, H., Zhou, X., Wang, Z., & Hong, T. (2022). Metabolomic profiling identifies biomarkers and metabolic impacts of surgery for colorectal cancer. **Frontiers in Surgery**, 9, 913967. From: https://doi.org/10.3389/fsurg.2022.913967.