WWW.IJRPR.COM

International Journal of Research Publication and Reviews

Journal homepage: www.ijrpr.com ISSN 2582-7421

Artificial Intelligence in Personalized Medicine: Advances in Pharmacogenomics for Diabetes, Hypertension, and Cancer Therapy

***T. Sakthimagendran* [(1)] *, *S. Mohankumar* [(2)]**

Department of Pharmaceutics, Pallavan Pharmacy College Kanchipurum-631502
Email: sakthimage2003@gmail.com

ABSTRACT

Personalized medicine seeks to enhance drug treatment by taking into account a patient's genetic makeup, clinical history, and lifestyle, thereby moving away from the "one-size-fits-all" model. At the heart of this approach is pharmacogenomics, which identifies interactions between genes and drugs that affect treatment effectiveness and potential side effects. Nevertheless, the implementation of pharmacogenomic knowledge in everyday practice faces obstacles due to the complexity and variation of the data in the patient's reactions for treatment. Artificial Intelligence (AI) has emerged as a groundbreaking tool, which prophesy the results of treatment with more accuracy, providing sophisticated computational methods to evaluate broad genomic and clinical data sets.This review checks how AI is changing pharmacogenomics in three major medical fields: diabetes, hypertension and cancer. In the management of diabetes, the AI-manual models combine individual blood sugar control, combining reactions to drugs such as metformin and SGLT 2 inhibitors combine genetic indicators with clinical and lifestyle information. In the case of hypertension, AI utilizes genetic variations, demographic information, and data from wearable devices to predict how patients will respond to ACE inhibitors, ARBs, and beta-blockers, thus allowing for the optimization of tailored therapies. Cancer treatment is the most developed area, where AI-powered platforms forecast a patient's reaction to chemotherapy and targeted therapies, aid in discovering biomarkers, and support decision-making in precision oncology. Despite these progresses, challenges still exist, including a lack of well -cured -cuisted dataset, algorithms in the algorithms, potential bias, regulatory challenges and moral issues related to privacy and privacy and consent. Future efforts should focus on the amalgamation of multi-ommics data, the development of clear AI and the use of federated learning techniques. By addressing these existing challenges, a-anhansed pharmacogenomics has the ability to replace clinical practices, which provide safe, more efficient and actually individual drug treatment.

INTRODUCTION:

Personalization of therapy has emerged as an important component of modern healthcare, taking away from the traditional "one-shaped-all" model based on the individual symptoms of each patient. By integrating genetic, clinical and environmental information, the purpose of individual drug is to increase treatment efficacy by reducing the risk of adverse drug effects. This strategy depends more on pharmacogenomics, which study how genetic variations affect the absorption, metabolism and reaction of the drug. However, the practical application of pharmacogenomic insight into regular clinical settings faces significant challenges due to the huge amounts of biomedical data, complexity and variability, despite great progress in genomic sequencing and biomarker identity. Recently, Artificial Intelligence (AI) has emerged as a powerful tool to resolve these challenges. Through the use of machine learning, deep learning and natural language processing, the AI system can analyze comprehensive multi-omics dataset, electronic health records, and real-time monitoring data that to highlight the hidden patterns directing the drug selection and dosage modifications. These abilities are especially encouraging for chronic and complex diseases, where the variation in treatment reactions creates a significant obstruction for effective healthcare. This review examines the potential integration of AI with pharmacogenomics in three major areas of therapy which are important for global health: diabetes, hypertension and cancer. Diabetes and high blood pressure, which rank in non-communicable diseases worldwide, perform remarkable variability in patient reactions for standard treatments, often leading to insufficient disease management. Conversely, cancer represents the most.

AI IN PERSONALISED MEDICINE:

Artificial Intelligence (AI) has become a transformative force in the healthcare sector, allowing for the analysis of intricate biomedical datasets that traditional statistical methods cannot adequately address. In the realm of personalized medicine, AI offers the computational resources and adaptive algorithms necessary to evaluate genomic, clinical, lifestyle, and environmental information, ultimately aiding in the provision of tailored therapeutic approaches.By revealing the pattern hidden within a broad dataset, AI not only improves pharmacogenomic research, but also increases clinical decision making because it happens.

MACHINE LEARNING (ML) :

It is the backbone of AI in terms of personal medicine. To promote various ML algorithms, such as random forests, support vector machines, and shields, is used to estimate on a large scale how individual patients will respond to the pinpoint biomarkers associated with drugs, risk groups and the results of treatment. For example, the ML model has been designed to predict glycemic control with diabetes with diabetes with diabetes to estimate the reactions of blood pressure for antihypertensive drugs with lifestyle information.

DEEP LEARNING (DL):

It is a particular area of ML, uses artificial nervous networks to understand complex and high-dimensional relationships that are characterized by biological systems. DL has proved valuable in particularly accurate oncology, where data of genomic, transcript and histopathological imaging is combined to forecast drug sensitivity or resistance. Its ability to process unnecessary data such as medical imaging and raw sequencing data provides a specific advantage in developing individual remedies strategies.

NATURAL LANGUAGE PROCESSING (NLP):

It makes the AI's access to AI by extracting important information from uncomfortable data such as Electronic Health Records (EHRS), educational papers and clinical notes. AIDS in the discovery of NLP drug-gene connection, adverse drug events and patient phenotypes, thus enhances pharmacogenomic database and promotes evidence-based personal treatment plans.

THE REINFORCEMENT LEARNING (RL):

It indicates a new range in personal medicine, where the algorithm receives through optimal treatment plans. In the context of chronic diseases like diabetes, the RL model has been used to create adaptive insulin dosing systems that adjust real-time fluctuations in glucose levels, diet and lifestyle factors. In addition, RL promises in oncology, where it can cure multi-drug therapy and dose program based on unique mobility of different tumors.

Together, these AI functioning are changing the field of individual medicine. By integrating ML, DL, NLP, and RL in pharmacogenomics, researchers and healthcare providers can predict the results of treatment, reduce adverse reactions and increase their ability to distribute highly customized drug remedies.

PHARMACOGENOMICS AND AI:

Pharmacogenomics, which checks how genetic differences affect drug reactions, is an important component of individual therapy. The genetic variations in the enzymes involved in drug metabolism, transporters and receptors can significantly affect the absorption, distribution, metabolism and elimination (ADME) of the drugs. However, traditional pharmacogenomic methods are constrained by selected genes and a narrow focus on limited dataset, which hinders the ability to capture the full spectrum of drug-gene interaction. Artificial Intelligence (AI) has emerged as a strong tool, which is capable of analyzing the huge amounts of genomic and clinical information to highlight the pre -exposed clinically important pattern.

Machine learning (ML) techniques like random forests, gradient boosting, and support vector machines can evaluate genome-wide association studies (GWAS) and sequencing data to identify new genetic variants linked to drug effectiveness and toxicity. Pharmacogenomics, which checks how genetic differences affect drug reactions, is an important component of individual therapy. The genetic variations in the enzymes involved in drug metabolism, transporters and receptors can significantly affect the absorption, distribution, metabolism and elimination (ADME) of the drugs. However, traditional pharmacogenomic methods are constrained by selected genes and a narrow focus on limited dataset, which hinders the ability to capture the full spectrum of drug-gene interaction. Artificial Intelligence (AI) has emerged as a strong tool, which is capable of analyzing the huge amounts of genomic and clinical information to highlight the pre -exposed clinically important pattern. Another significant use of AI in pharmacogenomics is found in biomarker discovery. By combining multi-omics data—including genomics, transcriptomics, proteomics, and metabolomics—AI systems can uncover predictive biomarkers for drug response or resistance. This broad integration provides valuable insight to physicians that cross individual gene assessments, providing a complete perspective on therapeutic results.
AI also improves the use of pharmacogenomic knowledge in clinicals by increasing clinical decision-support systems. For example, integrated AI tools in electronic health records may recommend drug options that match the patient's genetic profile. This increases safety and effectiveness of therapy.

APPLICATION IN ANTIDIABETIC THERAPY:

Diabetes mellitus is a common chronic condition marked by disrupted glucose metabolism, varying greatly among individuals with the results of treatment. Although there are many treatment options -as the difference in patients' reactions for metformin, sulfonylurus, DPP -4 inhibitors, GLP -1 receptor agonists, and insulin -in drugs often produce more likely in insufficient blood sugar control and complications. Research in pharmacogenomics has shown that drug transporters (such as metformin related to SLC22A1) and genetic diversity in enzymes and enzymes that metabolize drugs, affect how well the treatment works. However, applying this understanding to individual clinical practices requires advanced computational methods, in which

artificial intelligence (AI) plays an important role.Machine learning (ML) and deep learning (DL) techniques have been used to predict glycemic reactions for large -scale diabetes drugs. For example, the AI-based evaluation of the Genome-Wide Association Studies (GWAS) and Electronic Health Records (EHRS) has indicated genetic variations affecting metformin efficacy including polymorphism in ATM and SLC22A2. ML models that combine genetic, demographic, and clinical information can categorize patients into responders and non-responders, assisting in the personalized selection of medications. Similarly, DL strategies have been applied to analyze complex relations between multi-immix data and therapeutic results, which enhances the accuracy of predictions for best treatment plans.These "smart insulin dodging" systems reduce the possibility of hypoglycemia by promoting better long -term blood sugar control. Additionally, AI-driven digital health resources, including smartphone apps and wearable devices, continuously gather information on lifestyle and physiological parameters, empowering ML algorithms to refine treatment recommendations for each patient

APPLICATION IN ANTI HYPERTENSIVE THERAPY:

Hypertension is a condition in which consistently elevated blood pressure against the arteries, typically defined as a reading of 130/80 mm Hg . This ongoing high pressure compels the heart to work harder, significantly raising the risk of severe health issues like heart attacks, strokes, kidney disease, and heart failure. Despite the wide range of antihypertensive medications available—including ACE inhibitors, ARBs, calcium channel blockers, beta-blockers, and diuretics—variability in individual reactions to these treatments remains a significant clinical challenge. Various factors, such as genetic differences, demographic aspects, and lifestyle choices, contribute to the inconsistent management of blood pressure. Pharmacogenomics and artificial intelligence (AI) help us address these challenges in treatment.

Hypertension -related pharmacogenomics manifest genetic variations that affect reactions to drugs. For example, polymorphism in ACE genes can affect sensitivity to certain conditions, while the variations in the Add1 and Cyp3A5 are associated with different reactions for dietics and calcium channel blockers.. However, applying these findings in clinical practice necessitates advanced computational models to capture the intricate interplay between genetic, clinical, and environmental elements.The AI is well equipped to meet this requirement by analyzing multi-omics data and predicting treatment results to individual patients.

Machine learning (ML) methods have been utilized to predict blood pressure responses across various drug classes by integrating genetic data, clinical features, and longitudinal blood pressure records. The employment of deep learning (DL) has increased the future accuracy by highlighting complex, non-lectural relationships between genetic and phenotypeic variables, improving treatment strategies for the difficult patient population.Integration of AI with pharmacogenomics provides an important opportunity to increase high blood pressure management. By predicting drug responses, adapting to treatment and allowing real-time adjustment to therapy, AI-operated methods are the possibility of personal care for high blood pressure, making a reality in clinical practice.

APPLICATION IN ANTI CANCER THERAPY:

Cancer is one of the major global causes of death, characterized by significant changes in tumor biology and treatment reaction. Traditional remedies such as chemotherapy, targeted treatment, and immunotherapy often face issues related to incompatible efficacy and adverse side effects. As a result, individual oncology depends on pharmacogenomics to identify rapid genetic mutations, molecular profiles and biomarsers that guide treatment decisions. The integration of Artificial Intelligence (AI) in this domain has increased the ability to translate complex genomic information into practical clinical applications.

In the field of oncology, Pharmacogenomics has identified important drivers mutation and genetic changes including EGFR, KRAS and BRF, which affect the success of targeted remedies.Additionally, variations in genes connected to drug metabolism, such as TPMT and DPYD, influence how well patients tolerate chemotherapy. However, the huge amounts of genomic and clinical data generated in oncology require advanced computational devices for effective use. AI provides this ability through modeling an advanced future.

Machine learning (ML) and deep learning (DL) techniques have been widely applied to predict treatment results in oncology, classify patients and discover new biomarsers. For example, the ML models that integrate genomic, transcriptomic and histopathological information can predict the reactions to the inhibitor or platinum-based chemotherapy. DL technology expands this ability to medical imaging, enhancing the area of radiogenomics, where the features extracted from CT or MRI images are correlated with genomic data to estimate drug responses. These functioning significantly improve the accuracy of identifying patients who are most likely to benefit from specialized treatments. Natural Language Processing (NLP) increases cancer pharmacogen by examining drug-gene interaction and new treatment possibilities by examining huge biomedical literature, clinical testing data and electronic health records (EHR). This accelerates the application of findings into clinical decision-support systems that recommend personalized treatment approaches based on molecular and phenotypic traits. Reinforcement learning (RL)Joint drug represents a novel strategy in oncology for adaptation of treatment and treatment sequences. For example, RL algorithms can simulate tumor behavior in response to various medical combinations and propose adaptive treatment strategies that maximize effectiveness, reduce toxicity. Such systems are particularly beneficial for complex cancer that require combination treatment.In addition to clinical applications, AI intensifies drug discovery and re -introduction in oncology. The AI identifies potential drug goals, analyzing multi-omix data and predicts reactions to new compounds, thus reduces the time and cost associated with the development of cancer drugs.

CHALLENGES AND LIMITATIONS IN AI-DRIVEN PHARMACOGENOMICS

1. QUALITY AND DIVERSITY OF DATA:

The AI systems rely on wider, high-quality datasets. In pharmacogenomics, data often come from various sources such as genomic sequencing, electronic health records (EHRS), imaging studies and wearable techniques. Discrimination in data formats, missing data, and anomalies between populations reduce model accuracy and comprehensive glory. Additionally, insufficient representation of minority populations in genomic databases results in biased predictions, posing concerns regarding fairness in healthcare provision.

2.CLARITY OF AI MODEL:

Many AI systems, especially deep learning networks, serve as "black boxes", produce outputs without providing clear insights in logic behind their decisions .. In clinical pharmacogenomics, where treatment decisions may be important, lack of transparency, lacks transparency, reduces the acceptance of the physician trust and haemors.. The creation of explainable AI (XAI) frameworks is essential to ensure clinical reliability.

3. HEALTH CARE IMPROVES SETTINGS:

Even when effective AI models are present, embedding them into everyday health environment presents important difficulties. Clinical decision-support systems should obtain smooth integration with hospital EHR, follow data privacy rules, and provide user friendly interfaces for healthcare workers. Workflow combines the complexity of resistance implementation to lack of technical training between doctors and physicians.

4. FINANCIAL AND INFRASTRUCTURAL CHALLENGES:

The deployment of ai-interested pharmacogenomics demands sophisticated computational infrastructure, ongoing data management and interdisciplinary expertise. These requirements can be especially challenging for resource-complex environment, causing inequalities in access to personal treatment between high-income and low-medium-income countries.In summary, despite the important promises of A-provided pharmacogenomics, many obstacles need to be systematically addressed. Increase in data standardization, creating explanatory models, ensuring moral security, and promoting physician education are important measures.. Only completing these obstacles can lead to an infection in a reliable clinical resource in personal medicine with practical ability.

FUTURE DIRECTIONS AND OPPORTUNITIES IN AI-PHARMACOGENOMICS

The relationship between Artificial Intelligence (AI) and Pharmacogenomics is still developing, but the possibilities of increasing personal drug are important. New progress in computational techniques, data synthesis and clinical application has been designed to change medical decision making, resulting in improving efficacy and safety in drug management.

1. INTEGRATION OF MULTI-OMICS DATA:

Future AI technologies are expected to cohesively merge genomics with other omics disciplines, such as transcriptomics, proteomics, metabolomics, and epigenomics. By This integration of multi-ox, incorporating full biological complications of reactions to the disease and treatment, will increase the future accuracy and will help highlight the new drug goals. AI-operated systems that reconcile these versatile datasets will actually create a wide outline for personal medicine.

2. IMMEDIATE CLINICAL DECISION ASSISTANCE:

AI will be important in preparing real-time, adaptive clinical decision-support devices. By continuously evaluating electronic health records, data from wearable equipment, and genomic information, AI models can provide personal treatment suggestions at direct care points. This ongoing feedback mechanism will enable healthcare professionals to modify drug therapies in response to real-time data, enhancing patient outcomes while reducing unintended side effects.

3. TRUSTWORTHY AND EXPLAINABLE AI:

A key priority moving forward is the establishment of explainable AI (XAI) systems that offer clear insights into the prediction processes. These model physicians will increase the trust, reduce the path for regulatory approval, and support moral use. Emphasis on important genetic variations or biological routes affecting predictions, Xai will increase the clinical relevance of AI-Enhanced Pharaacogenomics.

4. DRUG DISCOVERY PROCESSES INCREASED:

AI is ready to change the landscape of the drug discovery by re-preparing existing drugs,

rebating existing drugs and simulating medical reactions before clinical trials.. This transformation will not only expedite the drug development process but also reduce costs, making tailored therapies more readily available.

5. BROADENING USES IN LOW-RESOURCE AREA:

As computational expenses are low, AI-supported pharmacogenomics can be sewn for application in low and medium-or-medals. COST-Effective, Cloud-based AI Solutions May Help to Bridge The Inequalities in Access to Personalized Medical Treatments.

Finally, the future of A-enhanced pharmacogenomics is the integration of multi-omix, real-time support to make clinical decisions, transparent models and global cooperation on data. These developments will facilitate the move from concept to standard practice in precision medicine, providing customized therapies that optimize benefits while minimizing risks for each patient.

CONCLUSION:

Artificial Intelligence (AI) has emerged as a transformational force in the field of individual medicine, especially through its integration with pharmacogenomics. By examining complex genetic, clinical and environmental data, AI facilitates anticipation of AIDS in creating individual drug responses and customized treatment strategies. It is particularly important for the management of complex diseases such as diabetes, hypertension and cancer, where traditional treatment methods often ignore individual differences.The use of AI is to predict drug reactions with machine learning algorithms to discovery of biomarkers, adapt treatment and even develop new drugs. Specifications such as deep learning, natural language processing, and reinforcement learning increase these functions by identifying non -linear connections, discovering comprehensive biomedical literature, and refining consistent treatment plans. In addition, the arrival of wearable technology and digital health platforms enables integration of real -time patient's information, which brings the dynamic and responsible treatment approach closer to real clinical practices.However, data diversity, algorithm transparency, moral issues, and adequate costs of infrastructure should not be ignored. These challenges emphasize the need for clear AI, standardized multi-omix dataset and cooperative structure to ensure fair and reliable clinical applications. Looking toward the future, the advancement of AI-powered pharmacogenomics will focus on integrating multi-omics data, providing real-time clinical decision support, fostering global collaboration via federated learning, and making technology accessible in low-resource environments. With such progress, personalized medicine is set to transition from a hopeful idea to a routine practice, delivering therapies that are not only effective but also safe and tailored to patients' distinct biological characteristics.

REFERNENCE:

1. Denny, J. C., Collins, F. S., & Roden, D. M. (2021). Pharmacogenomics in precision medicine: Progress, challenges, and opportunities. Nature Reviews Genetics, 22(12), 777–792. https://doi.org/10.1038/s41576-021-00380-4

2. Vamathevan, J., Clark, D., Czodrowski, P., Dunham, I., Ferran, E., Lee, G., … Bender, A. (2019). Applications of machine learning in drug discovery and development. Nature Reviews Drug Discovery, 18(6), 463–477. https://doi.org/10.1038/s41573-019-0024-5

3. Rajkomar, A., Dean, J., & Kohane, I. (2019). Machine learning in medicine. The New England Journal of Medicine, 380(14), 1347–1358. https://doi.org/10.1056/NEJMra1814259

4. Topol, E. J. (2019). High-performance medicine: The convergence of human and artificial intelligence. Nature Medicine, 25(1), 44–56. https://doi.org/10.1038/s41591-018-0300-7

5. Beam, A. L., & Kohane, I. S. (2018). Big data and machine learning in health care. JAMA, 319(13), 1317–1318. https://doi.org/10.1001/jama.2017.18391

6. Relling, M. V., & Evans, W. E. (2015). Pharmacogenomics in the clinic. Nature, 526(7573), 343–350. https://doi.org/10.1038/nature15817

7. Whirl-Carrillo, M., Huddart, R., Gong, L., Sangkuhl, K., Thorn, C. F., Whaley, R., … Klein, T. E. (2021). An evidence-based framework for evaluating pharmacogenomics knowledge for personalized medicine. Clinical Pharmacology & Therapeutics, 110(3), 563–572. https://doi.org/10.1002/cpt.2347

8. Caudle, K. E., Klein, T. E., Hoffman, J. M., Muller, D. J., Whirl-Carrillo, M., Gong, L., … Relling, M. V. (2017). Incorporation of pharmacogenomics into routine clinical practice: The Clinical Pharmacogenetics Implementation Consortium (CPIC) guideline development process. Clinical Pharmacology & Therapeutics, 102(2), 205–210. https://doi.org/10.1002/cpt.668

9. Amstutz, U., Henricks, L. M., Offer, S. M., Barbarino, J., Schellens, J. H. M., Swen, J. J., … Caudle, K. E. (2018). Clinical Pharmacogenetics Implementation Consortium (CPIC) guideline for dihydropyrimidine dehydrogenase genotype and fluoropyrimidine dosing: 2017 update. Clinical Pharmacology & Therapeutics, 103(2), 210–216. https://doi.org/10.1002/cpt.911

10. Relling, M. V., Schwab, M., Whirl-Carrillo, M., Suarez-Kurtz, G., Pui, C.-H., Stein, C. M., … Klein, T. E. (2019). Clinical Pharmacogenetics Implementation Consortium (CPIC) guideline for thiopurine methyltransferase (TPMT) and NUDT15 genotypes and thiopurine dosing: 2018 update. Clinical Pharmacology & Therapeutics, 105(5), 1095–1105. https://doi.org/10.1002/cpt.1304

11. Ramsey, L. B., Johnson, S. G., Caudle, K. E., Haidar, C. E., Voora, D., Wilke, R. A., … Klein, T. E. (2014). The Clinical Pharmacogenetics Implementation Consortium guideline for SLCO1B1 and simvastatin-induced myopathy. Clinical Pharmacology & Therapeutics, 96(4), 423–428. https://doi.org/10.1038/clpt.2014.125

12. Zhou, K., & Pearson, E. R. (2013). Metformin and genetic variation: From pharmacokinetics to pharmacodynamics. Diabetologia, 56(10), 2147–2154. https://doi.org/10.1007/s00125-013-2991-9

13. Zhou, K., Donnelly, L. A., Kimber, C. H., Donnan, P. T., Doney, A. S. F., & Pearson, E. R. (2011). Reduced-function ATM gene variant is associated with metformin response in type 2 diabetes. Nature Genetics, 43(2), 117–120. https://doi.org/10.1038/ng.735

14. Shu, Y., Sheardown, S. A., Brown, C., Owen, R. P., Zhang, S., Castro, R. A., … Giacomini, K. M. (2007). Effect of genetic variation in the organic cation transporter 1 (OCT1) on metformin action. Proceedings of the National Academy of Sciences, 104(7), 2628–2633. https://doi.org/10.1073/pnas.0610313104

15. Duarte, J. D., & Cooper-DeHoff, R. M. (2010). Mechanisms for blood pressure variability and pharmacogenomic implications. Pharmacogenomics, 11(5), 611–625. https://doi.org/10.2217/pgs.10.22

16. Turner, S. T., Bailey, K. R., Fridley, B. L., Chapman, A. B., Schwartz, G. L., Chai, H.-S., … Boerwinkle, E. (2012). Genomic association analysis of common variants influencing antihypertensive response to hydrochlorothiazide. Hypertension, 59(5), 974–981. https://doi.org/10.1161/HYPERTENSIONAHA.111.190892

17. Gong, J., Zhou, Q., & Chen, J. (2024). Pharmacogenomics-guided antihypertensive therapy: Current progress and AI applications. Frontiers in Cardiovascular Medicine, 11, 1432678. https://doi.org/10.3389/fcvm.2024.1432678

18. Kourou, K., Exarchos, T. P., Exarchos, K. P., Karamouzis, M. V., & Fotiadis, D. I. (2015). Machine learning applications in cancer prognosis and prediction. Computational and Structural Biotechnology Journal, 13, 8–17. https://doi.org/10.1016/j.csbj.2014.11.005

19. Iorio, F., Knijnenburg, T. A., Vis, D. J., Bignell, G. R., Menden, M. P., Schubert, M., … Garnett, M. J. (2016). A landscape of pharmacogenomic interactions in cancer. Cell, 166(3), 740–754. https://doi.org/10.1016/j.cell.2016.06.017

20. Garnett, M. J., Edelman, E. J., Heidorn, S. J., Greenman, C. D., Dastur, A., Lau, K. W., … Benes, C. H. (2012). Systematic identification of genomic markers of drug sensitivity in cancer cells. Nature, 483(7391), 570–575. https://doi.org/10.1038/nature11005

21. Barretina, J., Caponigro, G., Stransky, N., Venkatesan, K., Margolin, A. A., Kim, S., … Garraway, L. A. (2012). The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. Nature, 483(7391), 603–607. https://doi.org/10.1038/nature11003

22. Samstein, R. M., Lee, C.-H., Shoushtari, A. N., Hellmann, M. D., Shen, R., Janjigian, Y. Y., … Morris, L. G. T. (2019). Tumor mutational load predicts survival after immunotherapy across multiple cancer types. Nature Genetics, 51(2), 202–206. https://doi.org/10.1038/s41588-018-0312-8

23. Miotto, R., Wang, F., Wang, S., Jiang, X., & Dudley, J. T. (2018). Deep learning for healthcare: Review, opportunities and challenges. Briefings in Bioinformatics, 19(6), 1236–1246. https://doi.org/10.1093/bib/bbx044

24. Johnson, A. E. W., Pollard, T. J., Shen, L., Lehman, L.-w. H., Feng, M., Ghassemi, M., … Mark, R. G. (2016). MIMIC-III, a freely accessible critical care database. Scientific Data, 3, 160035. https://doi.org/10.1038/sdata.2016.35

25. Damanhouri, Z. A., Alkreathy, H. M., Alharbi, F. A., Abualhamail, H., & Ahmad, M. S. (2023). A review of the impact of pharmacogenetics and metabolomics on the efficacy of metformin in type 2 diabetes. International Journal of Medical Sciences, 20(1), 142–150. https://doi.org/10.7150/ijms.78902