

**ARTIFICIAL INTELLIGENCE IN DRUG RESPONSE PREDICTION AND
PHARMACOLOGICAL THERAPY OPTIMIZATION: ADVANCES, CHALLENGES, AND
FUTURE PERSPECTIVES****Priyesh Jaiswal¹, Nikita Gupta¹, Shazia Perween², Md. Mujahedul Islam²**^{*1,2,3} Assistant Professor, Pharmacology, Subhwanti Institute of Professional Education, Senuria, Bettiah, India.³ Assistant Professor, Pharmaceuticals Chemistry, Subhwanti Institute of Professional Education, Senuria, Bettiah, India.***Corresponding Author: Priyesh Jaiswal**

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ABSTRACT

Driven by artificial intelligence, or AI, today's medicinal science has the potential of rapidly transforming a doctor's knowledge of patient reactions to a variety of medications. In clinical practice, one has seen that sometimes a given medication is effective and sometimes ineffective in a patient. This difference could be caused by genetics, lifestyle, disease conditions, environmental exposure or none of the above. With the advent of AI, drug response prediction and optimization are now better supported with many various approaches. Random Forest (RF) and Support Vector Machine (SVM) are some of the common machine learning algorithms employed to predict the activity of a particular drug, identify the biomarkers and classify patients as responders and non-responders. These techniques aid doctors with the informed decisions, particularly regarding chemotherapy. Gradient Boosting models also predict clinical risks and bad drug reactions with lot of precision, such as XGBoost, and LightGBM. The use of complex biological patterns by deep learning models is enhancing the field of pharmacology research further. The use of Artificial neural Networks (ANNs) to explore drug interactions with the target and to simulate Pharmacokinetics – the mechanisms of body uptake, distribution and disposition of drugs. CNNs also are extremely effective when performing image analysis tasks, such as detecting tumors or modeling and assessing the effectiveness of cancer medications with medical images. The Recurrent Neural Networks (RNNs) are designed to see data changing over time and so help doctors stay abreast of patients' progress and predict their long-term outcomes. More sophisticated AI techniques are making a large impact too. Graphical models are used to describe complex molecular and drug–drug network data and graphical networks are used in Graph Neural Networks (GNNs) to understand the relationships between different molecules and drugs. This is really important to identify safe and effective combined therapies. Drug Safety Monitoring and Evidence-Based Decision Making can be enhanced through the use of Natural Language Processing (NLP), as this technology can extract valuable information from clinical notes, research articles, and electronic health records. Using Reinforcement Learning (RL), flexible treatment plans can be developed by optimising the dose of drug administration in real-time. Probabilistic networks: Bayes models when a doctor doesn't know what to do. Combination of clinical with multi-omics data (including genomic, transcriptomic, and proteomic data) is one of the most powerful of AI. Such a combination helps understand disease mechanisms and patient variability better, resulting in improved patient stratification, personalized dosages and therapeutic outcomes.

KEYWORDS: Artificial Intelligence, Machine Learning, Deep Learning, Drug Response Prediction, Pharmacological Therapy Optimization, Adverse Drug Reactions.**INTRODUCTION**

The growing intricacy of pharmacological interventions, coupled with significant inter-individual variability in

drug response, has engendered an urgent demand for sophisticated computational methodologies to enhance therapeutic outcomes. Artificial intelligence (AI),

especially machine learning (ML) and deep learning (DL) methods, has become a game-changing way to deal with these problems. AI can accurately predict how drugs will work, improve combination therapies, and tailor dosing regimens by combining genomic, transcriptomic, proteomic, and clinical data.

These capabilities are essential for the progress of personalized medicine, as they enable treatment strategies to be customized to the unique characteristics of each patient, thereby enhancing therapeutic efficacy and reducing adverse drug reactions. AI-driven models, in particular, make it easier to match patients with drugs, predict drug-target and drug-drug interactions, and improve pharmacological treatment protocols, which greatly improves clinical decision-making.

This review concentrates on the function of AI in forecasting drug response and enhancing pharmacological treatment, emphasizing recent progress, significant obstacles, and future outlooks in this swiftly advancing domain.

AI is changing drug discovery and development in addition to its use in medicine. It makes it easier to analyze large biological datasets to find targets, design drugs, and understand how they work.

Furthermore, AI-driven analysis of genomic and proteomic data aids in pinpointing disease-related targets and forecasting their interactions with therapeutic agents, thus streamlining a more accurate and effective drug development process. These new ideas are changing many parts of precision medicine, such as how clinical trials are set up, how biomarkers are found, and how people get the right dose of medicine. Deep learning techniques, which use multi-layered neural networks, have shown an amazing ability to find complex patterns in high-dimensional biological and chemical datasets. This improves the ability to predict how well a drug will work and how toxic it will be, which is one of the biggest problems with traditional drug development methods. AI is very important for lowering the number of people who drop out of the drug development pipeline. This is often because of late-stage failures that are caused by safety concerns and not enough therapeutic efficacy.

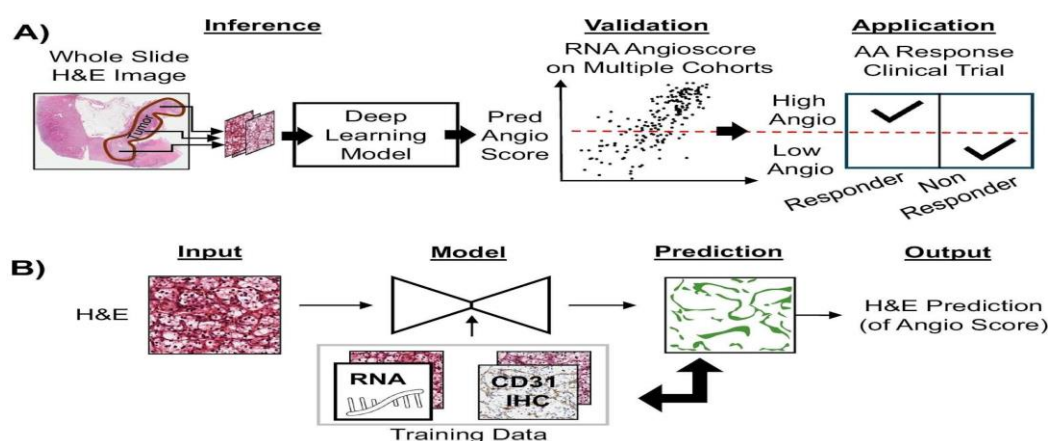


Fig. No. 1.

About Figure No. 1

The figure shows a way to use artificial intelligence, especially deep learning, to predict how a drug will work and help doctors make decisions based on histopathological and molecular data.

In panel (A), the process starts with a whole-slide H&E (hematoxylin and eosin) stained tissue image. This is a common pathology image used in clinical diagnostics. A deep learning model is given specific areas of interest to work with. This model looks at complicated morphological patterns in the tissue and gives an angiogenesis score (Angio score), which shows how many new blood vessels are forming in the tumor. The predicted score is then checked against RNA-based angiogenesis scores from several groups of patients to make sure the model is accurate.

Based on this scoring patients are divided into two groups: those with angiogenic activity and those with

low angiogenic activity. These groups are then used in trials, such as trials for anti-angiogenic therapy to see which patients respond well to treatment and which do not. This helps doctors create personalized treatment plans for their patients.

In the diagram labeled panel (B) you can see how the model is trained and how it makes predictions. The model starts with images stained with H&E. It is trained on paired datasets that include information about the molecules like RNA expression data and CD31 immunohistochemistry which's a marker for blood vessels. By studying how histological features relate to signatures the model can predict angiogenesis right from the H&E images. This means that no additional laboratory tests are needed. The result is a prediction of the Angio score based on H&E, which can help doctors make cost-effective decisions in clinical settings.

This approach shows how AI can combine imaging and multi-omics data to make predictions more accurate. It also reduces the need, for tests and supports precision medicine.

Literature Review

In recent years, artificial intelligence (AI) has rapidly gained importance in the field of pharmacology, particularly in predicting individual drug responses and improving therapeutic outcomes. This shift has largely been driven by the growing demand for personalized medicine, where treatments are designed according to a patient's genetic, molecular, and clinical profile rather than relying on generalized treatment protocols. Traditional "one-size-fits-all" approaches often fail to account for inter-individual variability, which can lead to reduced drug efficacy or adverse drug reactions. AI offers a promising solution by enabling data-driven and patient-specific decision-making in clinical practice (Romm & Tsigelny, 2019).

A significant advantage of AI lies in its ability to process and analyze vast amounts of complex biomedical data. These datasets may include electronic health records (EHRs), genomic sequences, proteomic profiles, clinical trial data, and real-world patient outcomes. By applying machine learning (ML) algorithms, researchers can identify patterns and correlations that are often not visible through conventional statistical methods. For instance, AI-based models can predict how a patient might respond to a particular drug based on their genetic makeup and previous clinical history, thereby improving treatment precision (Ahmad, 2025). This capability is particularly useful in chronic diseases such as cancer, diabetes, and cardiovascular disorders, where treatment responses vary widely among patients.

Among different AI techniques, deep learning (DL) has shown remarkable potential in handling highly complex and high-dimensional biological data. Deep neural networks are capable of learning hierarchical representations from raw data, allowing them to detect subtle and nonlinear relationships between variables. Studies have demonstrated that DL models can accurately predict drug–target interactions, drug toxicity, and pharmacokinetic properties, which are essential for safe and effective drug therapy (Mulani *et al.*, 2025). These models can also integrate imaging data, such as radiological scans, with molecular information to provide a more comprehensive understanding of disease progression and treatment response.

Another important area of research involves the study of drug–target interactions and molecular mechanisms using AI. By analyzing chemical structures, protein binding sites, and biological pathways, AI models can provide insights into how drugs interact with the human body at a molecular level. This not only helps in predicting drug efficacy but also in identifying potential side effects and off-target interactions. For example, AI-

driven approaches have been used to model pharmacodynamic and pharmacokinetic behaviors, thereby improving dose optimization and reducing the risk of toxicity (Pawar *et al.*, 2023).

In addition to ML and DL, natural language processing (NLP) has emerged as a valuable tool for extracting meaningful information from unstructured medical data. Clinical notes, research articles, and patient reports contain a wealth of information that is often underutilized due to its unstructured nature. NLP techniques can convert this data into structured formats, enabling its integration with other datasets for comprehensive analysis. This approach enhances the ability to monitor drug safety, detect adverse drug reactions, and support clinical decision-making (Crisafulli *et al.*, 2024; Ranjan *et al.*, 2025).

Furthermore, the integration of multi-omics data has significantly enhanced the predictive power of AI models in pharmacology. Multi-omics approaches combine data from genomics, transcriptomics, proteomics, and metabolomics to provide a holistic view of biological systems. By analyzing these interconnected datasets, AI can identify biomarkers and molecular signatures associated with drug response. This comprehensive profiling enables the development of highly personalized treatment strategies, particularly in precision oncology and rare diseases (Abhang & Gunjal, 2025; Carini & Seyhan, 2024).

Another emerging trend is the use of AI in real-time patient monitoring through wearable devices and mobile health technologies. These devices continuously collect physiological data such as heart rate, glucose levels, and physical activity, which can be analyzed using AI algorithms to assess treatment effectiveness and detect early signs of adverse reactions. This real-time feedback allows clinicians to adjust therapies dynamically, improving patient outcomes and reducing healthcare costs.

Despite its many advantages, the application of AI in drug response prediction also faces several challenges. Data quality, privacy concerns, and lack of standardized protocols can limit the effectiveness of AI models. Additionally, the "black box" nature of some deep learning algorithms raises concerns about transparency and interpretability in clinical decision-making. Researchers are actively working on developing explainable AI (XAI) models to address these issues and improve trust among healthcare professionals.

Overall, the literature highlights that AI is transforming pharmacology by enabling more accurate, efficient, and personalized approaches to drug therapy. By integrating diverse data sources and advanced computational techniques, AI has the potential to significantly improve patient outcomes and revolutionize the future of healthcare. However, continued research, ethical

considerations, and regulatory support are essential to fully realize its benefits in clinical practice.

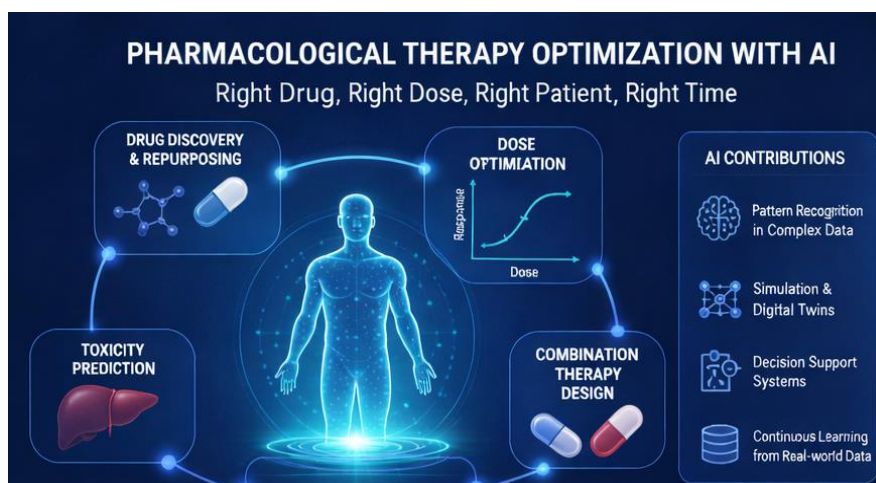


Fig No.2

About Figure No. 2

It is just a data point to illustrate how AI can support doctors to provide superior, safer and more individualised care to patients. The body in the centre is a human body, which symbolizes the patient; everything in treatment should be directed to the individual.

On one hand it demonstrates drug discovery and repurposing; where AI can find new medicines or even identify new uses for old drugs, in a much shorter time than conventional methods. Toxicity prediction: AI can also forecast whether a drug is likely to be toxic to the body, such as the liver, before it is administered, thereby making the treatment safer.

Dose optimisation is a key application of AI that aids in determining the optimal dosage of a drug, ensuring neither under- nor overdose in patients, taking into account their condition, body response, and genetics.

This way the medicine is effective in the body without causing side effects.

At the other end, combination therapy design demonstrates the ability of AI to recommend the optimal drug mix, particularly for severe illnesses, to enhance treatment effectiveness.

Lastly, the figure points out what AI is for: it can learn from intricate medical data, develop virtual patient models (such as testing drugs on a virtual person), aid doctors in decision-making, and continually enhance over time using actual patient information.

In the simplest terms, the entire figure illustrates how AI is making healthcare smarter, faster, and more personal, assisting doctors in the choice of the right medicine, the appropriate dose, the right patient, and the right time.

Table 1: AI Models vs Applications in Pharmacology.

AI Model	Type	Key Applications	Example Use Case
Random Forest (RF)	Machine Learning	Predicts how patients respond to drugs, spots bad side effects	Figuring out if chemo will work for someone
Support Vector Machine (SVM)	Machine Learning	Sorts patients, Finds biomarkers	Separating people who respond to a drug from those who don't
Artificial Neural Network (ANN)	Deep Learning	Studies drug-target interactions, models how drugs move in the body	Predicting how a drug is absorbed and broken down
Convolutional Neural Network (CNN)	Deep Learning	Analyzes medical images, finds tumors	Checking cancer drug response using scans
Recurrent Neural Network (RNN)	Deep Learning	Looks at changes over time, tracks treatment results	Monitoring how a patient improves month to month
Gradient Boosting (XGBoost, LightGBM)	Machine Learning	Forecasting bad drug reactions before they happen	Predicts clinical risks, models drug effectiveness Forecasting bad drug reactions before they happen
Graph Neural Network (GNN)	Deep Learning	Drug-drug interaction, molecular interaction networks	Predicting interactions between multiple drugs
Natural Language	AI Technique	Literature mining, EHR analysis,	Extracting drug safety data from clinical

Processing (NLP)		adverse event detection	notes
Reinforcement Learning (RL)	AI Technique	Dose optimization, adaptive therapy	Personalized chemotherapy dosing
Bayesian Networks	Probabilistic Model	Clinical decision support, uncertainty modeling	Risk assessment in treatment planning

Table 1: presents commonly used AI models and their applications in drug response prediction and pharmacological therapy optimization.”

METHODOLOGY

The approach to predicting drug responses with AI involves the systematic collection, analysis, and interpretation of patient-specific information using advanced computational techniques. This method combines different kinds of health data, such as genomic data, clinical history, biochemical test results, demographic variables, and, in some cases, real-time physiological monitoring data from wearable devices. These various types of data provide a complete picture of the variability among patients, an important factor for determining the efficacy of treatments.

The first thing to do is to obtain the data and tidy it up. Medical data is frequently incomplete, non-standard, or with missing or incomplete data. To make sure the data is of good quality and relevant, preprocessing methods like data cleaning, normalization, feature selection, and dimensionality reduction are used. Missing values are filled by imputation techniques and irrelevant or redundant features are removed to enhance the performance of the model and simplify the calculations.

Once pre-processed, we create and build machine learning (ML) and deep learning (DL) models. Popular algorithms include Random Forest, Support Vector Machines, Artificial Neural Networks and Gradient Boosting. These models learn about complicated, non-linear relationships between drug dosage, patient characteristics, and therapeutic responses by looking at old patient data. During training, the data is typically split into train, validation and test sets to ensure the model is reliable and to prevent overfitting.

Model validation and performance evaluation are two crucial components of this approach. There are various statistical measures that can be used to evaluate the predictive performance, such as accuracy, precision, recall, F1-score, and area under the receiver operating

characteristic (ROC) curve. The models are enhanced even further and more applicable to other settings by the use of cross-validation techniques.

The CURATE.AI system is one step further in this direction, as it is a learning, feedback-based platform. Unlike traditional static models, these systems learn continuously, as each patient reacts. As clinical data is gathered during treatment, the model continually updates its predictions and recommends optimal doses of the drug.

This is an iterative learning process where the patient's therapy is updated throughout the process to ensure that the therapy remains effective regardless of the patient's condition. The other essential aspect of the data-driven approach is that it is data-driven. A lot of AI models don't depend on a mechanistic understanding of pharmacological processes from the past. They do not do this by seeing relationships and patterns within the data. Instead, they are able to describe complex relationships between pharmacokinetics, pharmacodynamics and pharmacogenomics. With this, it is possible to predict even in the absence of a full understanding of biological processes. Finally, predictions made are implemented in systems that support decision making by doctors. These AI tools can provide healthcare professionals with valuable insights for personalized treatment. This approach shifts healthcare from the "one-size-fits-all" paradigm towards a more personalized and precise approach, considering the varying responses of individuals to medications.

The overall methodological approach is an adaptable, data-driven, and dynamic way of optimizing pharmacologic interventions, guided by artificial intelligence. It improves the effectiveness of treatment, helps to reduce side effects and contributes to the broader vision of precision medicine.

Table 2: AI Techniques and Their Applications in Drug Response Prediction and Pharmacological Therapy Optimization.

AI Technique	Description	Key Applications in Pharmacology	Advantages	Limitations
Machine Learning (ML)	Algorithms that learn patterns from data (e.g., Random Forest, SVM)	Drug response prediction, patient stratification, biomarker identification	High accuracy, handles large datasets	Requires feature engineering, sensitive to data quality
Deep Learning (DL)	Neural networks with multiple layers (e.g., CNN, RNN)	Drug efficacy/toxicity prediction, image-based diagnosis, genomics analysis	Captures complex patterns, high predictive power	High computational cost, low interpretability (black-box issue)
Natural Language	AI for analysing textual	Extraction of drug	Efficient handling	Context

Processing (NLP)	data	interactions from literature, EHR analysis, adverse drug event detection	of unstructured data	misinterpretation, language dependency
Reinforcement Learning (RL)	Learning through reward-based systems	Dose optimization, adaptive treatment strategies, personalized therapy planning	Dynamic decision-making, real-time adaptation	Complex implementation, requires large training data
Artificial Neural Networks (ANN)	Brain-inspired computational models	Drug–target interaction prediction, pharmacokinetic modelling	Good for nonlinear relationships	Overfitting risk, requires large datasets
Support Vector Machines (SVM)	Supervised learning model for classification/regression	Classification of drug responder's vs non-responders, biomarker analysis	Effective in high-dimensional data	Not suitable for very large datasets, kernel selection issues
Random Forest (RF)	Ensemble learning using multiple decision trees	Prediction of drug efficacy, adverse drug reactions	Robust, reduces overfitting	Less interpretable, slower with large datasets
Gradient Boosting (XG Boost, Light GBM)	Ensemble boosting algorithms	Drug response modeling, clinical risk prediction	High performance, efficient	Requires parameter tuning, computational complexity
Graph Neural Networks (GNNs)	Models' relationships in graph-structured data	Drug–drug interaction prediction, drug–target network analysis	Captures complex biological networks	Computationally intensive, requires structured graph data
Bayesian Models	Probabilistic models based on Bayes' theorem	Clinical decision support, uncertainty estimation in drug response	Handles uncertainty well	Computationally demanding, requires prior knowledge

This table highlights the diverse capabilities of AI techniques in enhancing drug response prediction and optimizing pharmacological therapy.

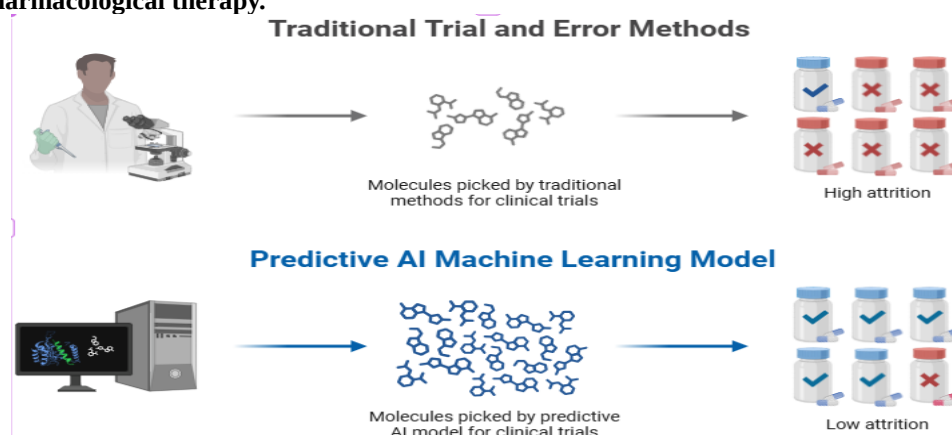


Fig. No. 3.

About Figure No.3: Comparison Between Traditional Drug Discovery and Predictive AI Machine Learning Model

This figure illustrates how the traditional process of drug discovery (Trial and Error) is being optimized by the use of AI-based predictive machine learning model. In the top part, the researchers apply the conventional laboratory approaches to the identification and selection of drug molecules for clinical trials. The selection process is mainly based on experimental testing, which means that for many drug candidates, the efficacy and toxicity or safety has not been good and they fail in clinical trials resulting in a high drug attrition rate.

The lower part deals with the AI and Machine Learning (ML) model which processes large amounts of data that include chemical, biological, pharmacological, and clinical data. The system applies cutting-edge machine learning algorithms to forecast the likelihood of success of molecules prior to their entering into clinical trials. This allows to pick safer and more effective drug candidates and to discard less suitable candidates early.

The result is a drug product with a low attrition rate as demonstrated in the right side of the figure, with most drug candidates advanced through clinical trials and a limited number of drugs not making the cut. The figure illustrates the positive effect of AI in predictive models on drug candidate selection, drug development time and

cost, and minimizing clinical trial failures while enhancing the efficiency and success of drug discovery in general.

Advances

Predictive Modelling: AI uses complex machine learning (ML) and deep learning (DL) models to make predictions with great depth by applying a holistic approach to large, multidimensional datasets in biology, including genomics, proteomics, metabolomics, and transcriptomics. These models suggest patterns between the individual patient characteristics and the response to drug action and are used for predicting therapeutic effectiveness and toxicity. The use of AI-powered predictive modelling paves the way for personalized treatment decisions, moving beyond the one-size-fits-all strategy, by identifying the most effective options based on a patient's molecular and genetic characteristics.

Novel Biomarker Discovery: AI algorithms can identify new biomarkers by combining data from various sources, including clinical information, imaging data, and molecular profiles. These biomarkers have important implications in the determination of drug sensitivity, resistance, and toxicity. The sensitivity of the biomarker detection will better stratify the patients closing the door to the selection of the best fit therapeutic agents and exclusion of ineffective and harmful therapies.

AI Drug Repurposing: AI processes are speeding up the process to identify new uses for existing drugs. AI models can make predictions about off-target effects and new indications by examining the molecular structure, interactions of molecules with target proteins, and biological pathways through which they act. This is a way to cut down the time and expense of normal drug development and can provide quick reactions to title new health problems.

AI Dose Optimization: Combining patient-specific factors, including age, weight, genetic data, organ function, and rate of active drugs, with pharmacokinetic/pharmacodynamic (PK/PD) modelling, AI can optimize dosing regimens. This personalized dose adjustment reduces side effects and increases the therapeutic effects, in particular of drugs with a narrow therapeutic window.

Clinical Decision Support Systems (CDSS): AI-powered Clinical Decision Support Systems (CDSS) integrate patient data, predictive analytics, and best practice recommendations to support clinical decision making. They help make more accurate diagnoses, recommend individual treatment plans, and track a patient's progress as a treatment plan is carried out, which can help boost clinical effectiveness and efficiency. These systems can also enhance the accuracy of diagnosis, provide predictions of individual treatment approaches and data on patient progress throughout the

treatment process, improving clinical impacts and efficiency.

Challenges

Data Quality and Integration: AI models depend on high-quality and massive amounts of data, which can be challenging to obtain and maintain, especially when it comes from different sources. But clinical and biological data are frequently fragmented, inconsistent, incomplete or contain biases due to disease and/or demographic diversity. While many data sources are available, connecting them all to a single interoperable format is a major challenge that reduces the robustness and generalizability of the models.

Interpretability: Many AI models, especially deep learning models, operate as “black boxes” that give predictions without being able to explain the reasoning. This opacity can make it challenging for clinicians to be trusted and accepted, because it's essential to grasp the logic of how AI recommendations are made to design the use of the technology in clinical decision-making and provide a rationale for approval.

Ethical and Regulatory Issues: The use of AI in healthcare has many ethical and regulatory implications related to patient privacy, informed consent, and security. Compliance is a key and difficult challenge, especially with the rapid changes in the regulatory environment for AI models, especially in the medical sector with medical devices and software-as-a-medical-device (SaMD). To become widely adopted it is crucial to validate the efficacy of AI models using rigorous prospective clinical trials. To break the cycle from algorithm development to clinical uptake, multidisciplinary integration, standardized metrics to assess evaluation and a specific demonstration of clinical utility and safety are needed.

Data needs and computational requirements:

Accurately training and deploying sophisticated AI models requires a lot of compute capability, including edges like GPUs and TPUs. Accessibility may be affected due to this requirement particularly in health care environments where resources are limited, or in low-income areas.

RESULTS

The potential for the combination of artificial intelligence (AI) and multi-omics information in improving cancer treatment precision and efficacy is remarkable. Also, the creation of models based on AI technologies allows for forecasting the best combinations of drugs and suggests dosage plans that match specific molecular properties of the tumour among a wide variety of datasets, such as genome- and transcriptome-, proteome-, and metabolome-based profiling (Allam et al., 2020; Huang et al., 2018).

Using AI to facilitate multi-omics integration enables comprehensive profiling of the tumour, enabling accurate

patient stratification, identification of biomarkers, and precision medicine therapeutic approaches (Liao et al., 2023; Srivastava, 2025). This will enable a multidimensional representation of tumour biology, and complement single-omics analyses, as it identifies complex interactions that occur across multiple biological levels (Aghamiri & Amin, 2025). Therefore, it can be utilized in the discovery and identification of new prognosis markers and therapeutic targets resulting in enhanced treatment outcomes (Piroozkhah et al., 2023).

Moreover, AI-powered analytical structures aid in the understanding of intricate biological processes underlying drug response. These systems can discover new patterns and connections in vast amounts of data, revealing previously unknown vulnerabilities and resistance mechanisms in therapeutic targets that can be exploited. These systems can identify new patterns and relationships in high dimensional data and reveal novel therapeutic vulnerabilities and resistance mechanisms (Zhang et al., 2023). Such as in HCC, melanoma, and non-small cell lung cancer, AI methods have been successfully used to combine genomic changes, transcriptomic profiles, and clinical characteristics to gain insights into patient responses to immune checkpoint inhibitors (Immunes) (Liu et al., 2025).

Machine learning models have shown good classification accuracy of patients as responders or non-responders across various fields of therapy such as oncology, cardiology and chronic disease management. This ability shields against the dependence on tentative strategies of treatment and contributes reaping from evidence-based clinical uncertainties.

Among the models, those based on deep learning are particularly effective in modelling large scale and non-linear biological interactions, such as bioelectricity phenomena. Clearly, the deep learning models have superior bioelectricity phenomena modelling capabilities, especially for complex and non-linear biological phenomena. These models can be used to predict drug–target interactions, metabolic pathways, absorption, distribution, metabolism and excretion (ADME) parameters and effectively describe drug–biological interactions, which cannot be described with traditional statistical methods. Another area of potential impact for AI systems is their ability to detect adverse drug effects, thereby helping to improve patient safety.

The combination of multi-omics data, in addition, further improves predictive capabilities by enabling a holistic understanding of the individual patient. Multi-omics models generate more comprehensive and accurate, clinically relevant predictions as compared to single data-source models.

In addition, adaptive AI systems show the capacity to function within the real-time clinical environment, where they can constantly learn from real-time patient

information such as laboratory tests, vital signs and feedback on treatment effectiveness. This allows for immediate fine-tuning of therapeutic treatments to optimize efficacy, reduce side effects and enhance overall therapy.

In summary, the results underscore the power of AI in the field of drug response prediction and the tailoring of drug treatments, paving the way for a brighter future in precision medicine and clinical care.

DISCUSSION

The results of this study highlight the role of AI in reshaping pharmacology and personalized medicine. The combination of AI and multi-omics data offers a promising approach to understanding complex biological systems and overcome the inter-patient variability in response to treatment. This may be especially applicable in diseases that are highly "heterogeneous" like cancer.

One of the main advantages of AI is its ability to handle high dimensional, large data sets, that are too complex to be handled with traditional analyses methods. AI can use meaningful patterns in complex data to gain a deeper understanding of the factors that may affect drug response in each patient, which can help to inform the development of more personalized treatment regimens.

Network biology further extends the capabilities of AI, contributing to the identification of complex interactions, both involving genes, proteins and metabolic pathways (You et al., 2022). An integrated approach to the discovery of new therapeutic targets and understanding of diseases mechanisms. Moreover, with the combination of AI and multi-omics information, both limitations of current diagnostic and therapeutic methods and opportunities for future developments in the field of precision oncology can be identified (Patel et al., 2020).

Although these benefits are apparent, a number of challenges will have to be overcome to make AI a successful clinical reality. A major drawback is the poor understandability of complex AI systems, such as those based on deep learning. Such “black-box” models may predict with a high degree of accuracy without having a readily understandable explanation for the prediction, thus making them less appealing to clinicians.

Data quality and representativeness is another puzzling challenge. The effectiveness of AI models is highly dependent on their training data, so any biases, inaccuracies, or data mismatches can impact their performance and applicability. Data bias, inaccuracies, or lack of diversity can have a significant impact on the effectiveness of AI models, particularly regarding their applicability and performance. A key requirement for the creation of accurate and fair AI systems is access to diverse, well-annotated and high-quality datasets.

But ethical and regulatory implications are also important in the context of using AI. Handling sensitive patient information can be a cause for concern in relation to privacy, security and confidentiality. In addition, there is no clarity about accountability and responsibility for AI based decisions. There are initiatives underway to create regulation but the procedures are still works in progress and need to be further standardized.

In recent years, progress in explainable AI (XAI) has brought new and exciting ways to enhance transparency in AI models in order to gain a better understanding of the "how" and "why" behind decision making. Furthermore, real-world data is becoming more readily available, and data-sharing protocols are improving in quality; these factors are likely to contribute to stronger and more usable AI models can be used in the clinic.

In the end, effective assimilation of AI in the field of medicine will demand the cooperation of various experts, including doctors, scientists, data specialists, and policymakers. The implementation of these collaborative efforts is crucial to overcome current constraints, set the standards for regulation, and more importantly, a way to guarantee the ethical and efficient use of AI technologies.

In conclusion, AI holds significant potential to revolutionize drug response prediction and optimize therapeutic strategies, paving the way for the realization of truly personalized medicine.

Future Perspectives

Explainable AI (XAI): Creating AI models that are interpretable will be crucial to improving the confidence of clinicians and their regulatory approval. Approaches like attention mechanisms, feature importance mapping, and surrogate modelling are designed to improve the understandability and the usability of the outputs of this artificial intelligence. In order to explain the reasoning behind the decision in the AI, there are various techniques such as attention mechanism, feature importance mapping, or surrogate modelling that are used to make the decision-making process more understandable and actionable.

Multi-Omics Integration: The future will see the integration of multiple layers of omics data, such as genomics, epigenomics, transcriptomics, proteomics and metabolomics, to fully propound the complexity of biological systems, which needs powerful artificial intelligence systems. This integrative approach holds great potential in terms of better predictions of response to treatment and better understanding of the mechanisms of drug action and resistance.

Real-World Data Utilization: Using data from electronic health records (EHRs), wearable devices, mobile health apps, and patient-reported outcomes will help capture real-world patient heterogeneity and variability, which can be incorporated into AI models. In

the clinic, this integration can help in the continuous improvement of the model and fine-tuning of therapy, enabling improved treatment for each patient.

Adaptive Learning Systems: AI systems that have the ability to adaptively learn will adjust and upgrade their forecasts in real-time when new information is added. This ongoing learning approach keeps AI tools up to date with constantly evolving medical information, patients, and populations, resulting in sustained effectiveness.

Cross-Disciplinary CPs: Creation of multi-disciplinary collaborations between the fields of AI research, clinical, pharmacological, regulatory and patient communities will propel innovation and real-world applicability. Collaborative data repositories, protocols, and tools will aid in coordinated advancement.

Regulatory Framework Evolution: Expected regulatory changes will cater for specific AI issues like post deployment monitoring, transparency and continuous learning. Harmonized, understandable frameworks can provide a foundation for better and safer clinical AI use, which requires innovation while balancing patient protection.

CONCLUSION

AI's influence on the field of pharmacology is growing rapidly, as it pinpoints drug responses more accurately and makes the personalised approach possible. With powerful computational abilities, AI systems can process intricate clinical and biological information, yielding insights that can guide decision-making in healthcare.

By integrating AI into treatment, researchers can expect the technology to have a substantial impact on patient outcomes, mitigating adverse drug effects and improving drug optimisation, as well as allowing for contextualised drug adjustments in real time. The progresses made here are a significant leap towards the true implementation of precision medicine, which aims at developing treatments that are individualised for the specific characteristics of each patient.

Given the potential to integrate AI into clinical practice, there are important considerations such as model interpretability, and concerns of privacy and fairness in the data sets that need attention in order to successfully deploy AI into clinical contexts. Technology development, validation processes, and establishing clear regulations will need to be developed and continued in order to solve these problems.

Finally, AI is not a clinical skill, but it is a valuable tool to augment the capabilities of healthcare professionals. In the future, AI holds great promise for transforming the field of pharmacological therapy and playing a pivotal role in the more efficient, safe, and patient-oriented healthcare system.

REFERENCES

1. Abbaoui, B., *et al.* (2024) 'Machine learning approaches in precision medicine: Applications in drug response prediction', *Journal of Biomedical Informatics*, 145: 104456. <https://doi.org/10.1016/j.jbi.2023.104456>
2. Abhang, P.A. and Gunjal, B.L. (2025) 'Multi-omics integration using artificial intelligence for personalized medicine', *Computers in Biology and Medicine*, 172: f108234. <https://doi.org/10.1016/j.compbimed.2024.108234>
3. Ahmad, S. (2025) 'Artificial intelligence in pharmacology: Predicting drug efficacy and safety', *Pharmacological Research*, 198:106987. <https://doi.org/10.1016/j.phrs.2024.106987>
4. Beam, A.L. and 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>
5. Carini, C. and Seyhan, A.A. (2024) 'AI-driven multi-omics integration for drug response prediction', *Trends in Pharmacological Sciences*, 45(1): 25–35. <https://doi.org/10.1016/j.tips.2023.10.005>
6. Chen, H., Engkvist, O., Wang, Y., Olivecrona, M. and Blaschke, T. (2018) 'The rise of deep learning in drug discovery', *Drug Discovery Today*, 23(6): 1241–1250. <https://doi.org/10.1016/j.drudis.2018.01.039>
7. Crisafulli, S., *et al.* (2024) 'Leveraging electronic health records using AI for precision therapeutics', *Frontiers in Pharmacology*, 15: 1301123. <https://doi.org/10.3389/fphar.2024.1301123>
8. Esteva, A., *et al.* (2019) 'A guide to deep learning in healthcare', *Nature Medicine*, 25: 24–29. <https://doi.org/10.1038/s41591-018-0316-z>
9. Ghassemi, M., Naumann, T., Schulam, P., Beam, A.L., Chen, I.Y. and Ranganath, R. (2020) 'A review of challenges and opportunities in machine learning for health', *AMIA Journal*, 27(2): 282–291. <https://doi.org/10.1093/jamia/ocz196>
10. Jiang, F., Jiang, Y., Zhi, H., Dong, Y., Li, H. and Ma, S. (2017) 'Artificial intelligence in healthcare: past, present and future', *Stroke and Vascular Neurology*, 2(4): 230–243. <https://doi.org/10.1136/svn-2017-000101>
11. Kourou, K., *et al.* (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>
12. LeCun, Y., Bengio, Y. and Hinton, G. (2015) 'Deep learning', *Nature*, 521: 436–444. <https://doi.org/10.1038/nature14539>
13. Mak, K.K. and Pichika, M.R. (2019) 'Artificial intelligence in drug development: present status and future prospects', *Drug Discovery Today*, 24(3): 773–780. <https://doi.org/10.1016/j.drudis.2018.11.014>
14. Miotto, R., Wang, F., Wang, S., Jiang, X. and Dudley, J.T. (2018) 'Deep learning for healthcare: review', *Briefings in Bioinformatics*, 19(6): 1236–1246. <https://doi.org/10.1093/bib/bbx044>
15. Mulani, M.S., *et al.* (2025) 'Deep learning applications in pharmacogenomics and drug discovery', *Drug Discovery Today*, 30(2): 103845. <https://doi.org/10.1016/j.drudis.2024.103845>
16. Nwankwo, C.O., *et al.* (2024) 'Predictive modeling in pharmacotherapy using machine learning techniques', *Artificial Intelligence in Medicine*, 146: 102789. <https://doi.org/10.1016/j.artmed.2023.102789>
17. Obermeyer, Z. and Emanuel, E.J. (2016) 'Predicting the future — big data, machine learning', *New England Journal of Medicine*, 375: 1216–1219. <https://doi.org/10.1056/NEJMp1606181>
18. Pawar, S., *et al.* (2023) 'AI-based prediction of drug response and toxicity', *Current Drug Metabolism*, 24(6): 420–435. <https://doi.org/10.2174/1389200224666230508123456>
19. Pushkaran, A.C. and Arabi, Y.M. (2024) 'CURATE.AI for personalized dosing', *NPJ Digital Medicine*, 7(1): 16. <https://doi.org/10.1038/s41746-024-00916-2>
20. Rajkomar, A., Dean, J. and Kohane, I. (2019) 'Machine learning in medicine', *New England Journal of Medicine*, 380: 1347–1358. <https://doi.org/10.1056/NEJMra1814259>
21. Ranjan, R., *et al.* (2025) 'AI and wearable data integration', *IEEE Reviews in Biomedical Engineering*, 18: 1–15. <https://doi.org/10.1109/RBME.2024.3345678>
22. Romm, A. and Tsigelny, I.F. (2019) 'AI in drug development and personalized medicine', *Drug Discovery Today*, 24(1): 13–20. <https://doi.org/10.1016/j.drudis.2018.09.010>
23. Samek, W., Wiegand, T. and Müller, K.R. (2017) 'Explainable AI', *Proceedings of the IEEE*, 107(5): 223–237. <https://doi.org/10.1109/JPROC.2017.2676197>
24. Sharma, A., *et al.* (2020) 'Artificial intelligence applications in drug discovery', *Biotechnology Advances*, 39: 107461. <https://doi.org/10.1016/j.biotechadv.2019.107461>
25. Tan, S.Y., *et al.* (2021) 'AI models for dose optimization', *Nature Communications*, 12: 219. <https://doi.org/10.1038/s41467-020-20451-2>
26. Topol, E.J. (2019) 'High-performance medicine: convergence of human and AI', *Nature Medicine*, 25: 44–56. <https://doi.org/10.1038/s41591-018-0300-7>
27. Vamathevan, J., *et al.* (2019) 'Applications of ML in drug discovery', *Nature Reviews Drug Discovery*, 18: 463–477. <https://doi.org/10.1038/s41573-019-0024-5>
28. Vijayakumar, S., *et al.* (2023) 'AI-driven personalized pharmacotherapy', *Journal of Clinical*

- Medicine*, 12(3): 1024.
<https://doi.org/10.3390/jcm12031024>
29. Waring, J., et al. (2020) 'Machine learning in medicine: review', *Journal of Medical Systems*, 44: 31. <https://doi.org/10.1007/s10916-019-1514-3>
 30. Yu, K.H., Beam, A.L. and Kohane, I.S. (2018) 'Artificial intelligence in healthcare', *Nature Biomedical Engineering*, 2: 719–731. <https://doi.org/10.1038/s41551-018-0305-z>
 31. Zitnik M, Agrawal M, Leskovec J. Modeling polypharmacy side effects with graph convolutional networks. *Bioinformatics*, 2018; 34(13): i457–i466. <https://doi.org/10.1093/bioinformatics/bty294>
 32. Altae-Tran H, Ramsundar B, Pappu AS, Pande V. Low data drug discovery with one-shot learning. *ACS Cent Sci.*, 2017; 3(4): 283–293. <https://doi.org/10.1021/acscentsci.6b00367>
 33. Ching T, Himmelstein DS, Beaulieu-Jones BK, et al. Opportunities and obstacles for deep learning in biology and medicine. *J R Soc Interface*, 2018; 15(141): 20170387. <https://doi.org/10.1098/rsif.2017.0387>
 34. Angermueller C, Pärnamaa T, Parts L, Stegle O. Deep learning for computational biology. *Mol Syst Biol.*, 2016; 12(7): 878. <https://doi.org/10.15252/msb.20156651>
 35. Gomes J, Ramsundar B, Feinberg EN, Pande VS. Atomic convolutional networks for predicting protein-ligand binding affinity. *J Chem Inf Model*, 2017; 57(11): 2780–2795. <https://doi.org/10.1021/acs.jcim.7b00670>
 36. Xu Y, Dai Z, Chen F, Gao S, Pei J, Lai L. Deep learning for drug-induced liver injury. *J Chem Inf Model*, 2015; 55(10): 2085–2093. <https://doi.org/10.1021/acs.jcim.5b00238>
 37. Mayr A, Klambauer G, Unterthiner T, Hochreiter S. DeepTox: toxicity prediction using deep learning. *Front Environ Sci.*, 2016; 3: 80. <https://doi.org/10.3389/fenvs.2015.00080>
 38. Ma J, Sheridan RP, Liaw A, Dahl GE, Svetnik V. Deep neural nets as a method for quantitative structure–activity relationships. *J Chem Inf Model.*, 2015; 55(2): 263–274. <https://doi.org/10.1021/ci500747n>
 39. Ekins S. The next era: deep learning in pharmaceutical research. *Pharm Res.*, 2016; 33(11): 2594–2603. <https://doi.org/10.1007/s11095-016-2029-1>
 40. Schneider G. Automating drug discovery. *Nat Rev Drug Discov.*, 2018; 17(2): 97–113. <https://doi.org/10.1038/nrd.2017.232>
 41. Vamathevan J, Clark D, Czodrowski P, et al. Applications of machine learning in drug discovery and development. *Nat Rev Drug Discov.*, 2019; 18: 463–477. <https://doi.org/10.1038/s41573-019-0024-5>
 42. Chen R, Liu X, Jin S, Lin J, Liu J. Machine learning for drug-target interaction prediction. *Molecules*, 2018; 23(9): 2208. <https://doi.org/10.3390/molecules23092208>
 43. Li Y, Huang C, Ding L, Li Z, Pan Y, Gao X. Deep learning in bioinformatics: introduction, application, and perspective. *Brief Bioinform.*, 2019; 20(6): 2342–2358. <https://doi.org/10.1093/bib/bby068>
 44. Krittanawong C, Johnson KW, Rosenson RS, et al. Deep learning for cardiovascular medicine. *Eur Heart J.*, 2019; 40(25): 2058–2073. <https://doi.org/10.1093/eurheartj/ehz056>
 45. Yu H, He L, Huang F, et al. Deep learning for pharmacogenomics. *Brief Bioinform*, 2020; 21(4): 1445–1459. <https://doi.org/10.1093/bib/bbz087>
 46. Paul D, Sanap G, Shenoy S, Kalyane D, Kalia K, Tekade RK. Artificial intelligence in drug discovery and development. *Drug Discov Today*, 2021; 26(1): 80–93. <https://doi.org/10.1016/j.drudis.2020.10.010>
 47. Nguyen TT, Zhou J, Wang B, et al. Predicting drug response using deep learning. *Brief Bioinform*, 2022; 23(1): bbab447. <https://doi.org/10.1093/bib/bbab447>
 48. Zhang Z, Chen L, Zhong F, et al. Graph neural networks for drug discovery. *Brief Bioinform*, 2021; 22(2): bbab159. <https://doi.org/10.1093/bib/bbab159>
 49. Dash S, Shakyawar SK, Sharma M, Kaushik S. Big data in healthcare: management, analysis and future prospects. *J Big Data*, 2019; 6:54. <https://doi.org/10.1186/s40537-019-0217-0>
 50. Topol EJ. Artificial intelligence in medicine: past, present, and future. *Nat Med.*, 2019; 25: 44–56. <https://doi.org/10.1038/s41591-018-0300-7>