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Original Article

Harnessing Artificial Intelligence for the Design and Development of Novel Effective Medicines

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Abstract

The high costs and frequent failures have historically hindered the progress of developing medicines, due, to inefficiencies in the drug discovery process. To revolutionize drug development, in the current study we proposed a plan based on the use of artificial intelligence (AI). Our cutting-edge AI algorithms are designed to enhance drug candidates and predict their properties by leveraging machine learning, deep learning, and natural language processing. Our comprehensive approach involves data preparation, AI model creation, virtual screenings, molecule simulations, ADME/toxicity predictions and validation through experiments. We have generated 10,000 molecules, which were then narrowed down to 500 candidates. Showcasing the remarkable capabilities of our AI driven system. With an F1 score of 0.92 for bioactivity prediction an accuracy rate of 0.88, for solubility prediction and a toxicity prediction accuracy of 0.95; our machine learning models have exhibited performance. Our deep learning models have also performed well; for example, our CNN model for solubility prediction had a remarkable mean absolute error of 0.3 log units, while our GCN model for drug-target interactions had an area under the curve of 0.98. Chemicals created by AI with high binding affinities, such -12.5 kcal/mol, have been uncovered using molecular docking simulations. Among our notable accomplishments is the successful synthesis of twenty compounds, all of which have strong bioactivities with IC50 values between ten and two hundred nanometers. Importantly, research conducted in living organisms (mice and rats) has shown substantial therapeutic effectiveness, with outcomes such as a 60% suppression of tumor growth and a 75% decrease in inflammation. Our AI platform has proven time and time again that it can produce new, powerful drug candidates with desirable characteristics, opening the door to a more efficient drug discovery process that can hasten the distribution of revolutionary treatments and enhance patient results.

Keywords: Artificial Intelligence; Drug Discovery; Machine Learning; Deep Learning; Virtual Screening; ADME/T Prediction; Molecular Docking; Molecular Dynamics; Bioactivity Assays; *In vivo* Studies

Introduction

Researching and discovering medications is time consuming endeavor that comes with significant costs. DiMasi., *et al*. (2016) suggest that the traditional methods of drug discovery often involve trial and error requiring the testing of compounds to identify therapeutic options [1]. In contrast recent advancements, in intelligence (AI) as noted by Vamathevan., *et al.* (2019) have provided avenues to streamline and accelerate the drug development process. AI algorithms offer the ability to analyze large amount of data to uncover patterns and insights that could facilitate the creation of pharmaceuticals presenting a promising alternative, to conventional approaches [2]. One major advantage of AI powered drug development is its ability to generate molecules with traits. Stokes and colleagues (2020) mentioned that artificial intelligence has the

potential to craft configurations that could offer therapeutic advantages, either by leveraging machine or by learning algorithms, alongside extensive databases containing information on known chemicals and their functions [3]. Software applications such as docking simulations can evaluate how an AI test the interaction of molecule with a particular protein which leads to helping in the ongoing enhancement and fine tuning of the compounds [4]. Imagine a scenario where artificial intelligence could transform the field medicine research, in addition, AI able developed more effective and alternative treatment conditions as compared with the current standard approaches. Picture this; the conventional therapy involves using a molecule that inhibits an enzyme, in the disease pathway. For example, as Hughes and colleagues reported in 2011, conventional treatment might involve using a molecule that inhibits an enzyme in the disease pathway. Medicinal chemists and researchers would likely test chemicals to develop this inhibitor, but using an AI-based approach might involve starting with a database analysis of the formulations chemicals and known enzyme inhibitors more quickly and effectively [5]. Through machine learning methods, an AI system can learn the chemical properties that contribute to the effect and then create new chemical compounds based on these properties. Techniques such, as Generative Adversarial Networks (GANs) and reinforcement learning could also be applied to enhance the design of AI generated molecules. The essential groups that play a role in the potency and specificity of an enzyme inhibitor designed by AI can be screened using online docking tools, such as AutoDock Vina, which are very effective in evaluating AI-generated compounds and predicting their interaction with the intended enzyme and based on these forecasts the promising options, for production and experimental confirmation can be identified [6]. Computer science and mathematics help increase medical discoveries, and intelligence networks and support vector machines that rely on linear algebra, arithmetic, and probability theory have had a similar role in the development of contemporary treatment methods, drugs, and vaccines [7]. Back propagation and gradient descent are essential for training and optimizing algorithms. On the other hand, implementing AI algorithms requires sophisticated GPUs and computer clusters. AI-driven drug research relies on data management and interpretation. Medication research and development is expensive and difficult at every step. Before treatment, researchers must identify the chemicals or processes associated with the disease, this foundation is essential for finding and improving molecular compounds that efficiently serve this purpose, but some obstacles make progress more difficult. For instance, lead treatments must undergo extensive *in vivo* and *in vitro* preclinical safety, pharmacokinetic, and pharmacodynamic testing before entering trials. Many promising drugs fail at this phase due to side effects or drug-like properties. If they survive this stage, phase I–III trials will extensively test their safety and effectiveness. Only 10% of clinically developed drug candidates receive regulatory approval, showing that few survive this difficult procedure. Developing drugs poses challenges due, to the rate of failure substantial costs and lengthy timelines involved. Recent estimates suggest that it can take up to ten years and exceed $2.6 billion to bring a medication to market [8]. In light of these concerning statistics innovative approaches are required to enhance and streamline drug development processes paving the way for technologies such, as AI. Artificial intelligence, which includes machine learning, deep learning and natural language processing accelerates the process of developing drugs. AI technologies have the ability to uncover correlations and patterns that may not be easily discernible, to humans [9]. This approach driven by data has the potential to revolutionize the field of medication development. Virtual screening powered by AI technology can assess libraries of chemical compounds for their interactions, with targets. With libraries containing millions of chemicals conducting screenings becomes impractical. AI algorithms can efficiently organize collections. Pinpoint potential candidates for deeper investigation, by employing machine learning models that analyze bioactivity data [9]. This customized approach enhances the chances of identifying drug candidates. Reduces the time and resources required for lead discovery. AI technology is improving in selecting targets and enhancing compounds by analyzing data. Deep learning algorithms and neural networks can comprehend datasets such, as sequences, protein structures and medical imaging details [9]. By revealing patterns and relationships within this data AI has the potential to pinpoint treatment targets provide insights, into disease causes and impact personalized treatment strategies. The progress, in medication development has faced challenges because of the extensive research databases. Nonetheless Natural language processing (NLP) could potentially accelerate this advancement. NLP has the capacity to unveil treatment options expose interactions between drugs and targets and streamline the gathering and integration of data, from publications all contributing to the discovery of promising drug targets. Despite the benefits there are downsides, to using AI in drug development. The accuracy and performance of AI models heavily rely on the quality of the training data highlighting the importance of selecting datasets and eliminating any biases [9]. The lack of interpretability and transparency in AI algorithms poses hurdles in critical decision making scenarios such, as pharmaceutical research. In the field of medicine the use of AI, alongside

drug discovery techniques can accelerate the development of therapies and address shortages in supplies. Collaboration, between AI experts, computational biologists and pharmaceutical researchers is essential to harness the potential of these technologies. Due, to the rate of failures and lack of approaches the process of drug research and development becomes time consuming, costly and ineffective. Traditional methods involve synthesizing and testing compounds, yet not all of them meet the criteria for safety, efficacy and drug like properties. These approaches heavily rely on trial and error practices. Such inefficiencies impede the progress of creating treatments, for needs that are currently unmet leading to soaring prices and extended timelines for introducing a new medication to the market. The main objective of our research is to enhance the design and delivery of medications in a more efficient and affordable manner by leveraging AI technology to revolutionize the drug research and development process.

Materials and Methods

Data collection and preprocessing

Chemical data

Various public databases such, as PubChem (available online: https://pubchem.ncbi.nlm.nih.gov/), ChEMBL (https://www.ebi.ac.uk/chembl/) and ZINC (https://zinc.docking.org/)were extensively searched to gather a range of information. These databases contain information on the structures, properties and biological activities of millions of chemical compounds. The chemical data underwent preprocessing to ensure compatibility, with AI systems. As part of this preparation standardization of representations was carried out by removing duplicates and inconsistencies and converting all structures to the Simplified Molecular Input Line Entry System (SMILES) format.

Biological data

Data, from sources such as the Protein Data Bank (PDB) UniProt and the Gene Expression Omnibus (GEO) were used to gather information. These databases contain gene expression data from experiments well as information on protein structures sequencing and functions. The accuracy and importance of the data, for drug development were maintained through curation and annotation.

AI algorithm development

Machine learning models

After collecting chemical data several machine learning models were. Some of these models include gradient boosting machines (GBM) random forests (RF) and support vector machines (SVM) [10]. To determine the hyperparameters and avoid overfitting the models were fine tuned using techniques such, as grid search and cross validation.The researchers assessed how machine learning models performed by considering metrics, like recall, accuracy, precision and F1 score. They examined each data point in the test set by comparing its predicted and actual values using a confusion matrix to determine these metrics. The calculations, for these measurements are as described below:

Accuracy = (TP + TN) / (TP + TN + FP + FN)

Precision = TP / (TP + FP)

Recall = TP / (TP + FN)

F1-score = 2 * (Precision * Recall) / (Precision + Recall)

where TP = True Positives, TN = True Negatives, FP = False Positives, and FN = False Negatives.

Deep learning models

Cutting edge learning techniques such, as neural networks (CNN) developed by Kipf & Welling in 2017 and LeCun., *et al*. In 1998 aid in understanding chemical compositions [7]. These models have the potential to unveil connections, within data and predict properties of drugs and biological activities. Welling (2017) and Lecun., *et al*. (1998) have developed networks (CNN) to help researchers comprehend the structures of biological and chemical elements [7]. These advanced models can uncover connections, within data. Forecast the bioactivity of drugs. Various tasks require loss functions, for training machine learning models. For regression tasks such as predicting drug solubility and binding affinity Mean Squared Error (MSE) and Mean Absolute Error (MAE) are commonly used. On the hand for classification tasks like predicting toxicity and bioactivity binary or categorical cross entropy is typically applied. Below are the formulas, for these loss functions:

MSE = (1/n) * Σ(y_pred - y_true)^2

MAE = (1/n) * Σ|y_pred - y_true|

Binary cross-entropy = -(y_true * log(y_pred) + (1 - y_true) * log(1 - y_pred))

Categorical cross-entropy = -Σ(y_true * log(y_pred))

Where n = number of instances, y_pred = predicted value, and y_true = actual value.

Virtual screening and drug design

Molecular docking

Docking simulations have forecasted the binding of drugs to target proteins with the help of intelligence. A method, for evaluation has determined that AutoDock Vina is considered the docking technique. The scoring system takes into account factors such, as desolvation, electrostatic forces, hydrogen bonds and van der Waals interactions.

Molecular dynamics simulations

Researchers used molecular dynamics (MD) simulations to evaluate how AI generated compounds interacted with their target proteins. They chose GROMACS (https://www.gromacs.org/) for its MD features as highlighted by Abraham and colleagues in 2015.

ADME/T prediction

Forecasts, for the absorption, distribution, metabolism, excretion and toxicity (ADME/T) traits of the AI created compounds were determined using a combination of machine learning algorithms and assessments based on chemistry. The projected characteristics are as follows:

- **Solubility:** A model, for regression was developed by studying solubility data from research papers to predict the water solubility of the substances.

- **Permeability:** In 1998 we were able to determine the membrane permeability of the compounds using the PAMPA model developed by Kansy and colleagues.

A classification model was created using data from experiments, on human liver microsomes to predict the metabolic stability of drugs.

- **Plasma protein binding:** A regression model was created using data gathered from studies in order to calculate the level of plasma protein binding.

- **Toxicology:** Several classification models, which were trained using data, from toxicity assays conducted in the lab and in living organisms, such as the Ames test for mutagenicity, by Ames., *et al*. (1975) and the hERG assay for cardiotoxicity by Sanguinetti & Tristani Firouzi (2006) were employed to forecast the toxicity of the substances [11].

The ADME/T predictions prioritized AI-generated drugs for experimental testing and optimization.

Experimental validation

Synthesis

Medicinal chemistry solution-phase and solid-phase synthesis produced the most promising AI-generated compounds. We used known starting materials to create synthetic paths for structural modifications. HPLC and flash chromatography purified the chemicals, and mass spectrometry and nuclear magnetic resonance (NMR) verified their structures.

Bioactivity assays

In vitro experiments assessed the bioactivity of the produced compounds against their molecular targets. The tests comprised:

- **Enzyme inhibition assays:** These experiments employed colorimetric or fluorometric substrates to see if drugs may inhibit kinases or proteases.

- **Assays for receptor binding:** These included radioligand and fluorescence ligand binding to particular receptors including nuclear receptors and G protein-coupled receptors (GPCRs).

Cell viability and reporter gene tests were used to determine if the chemicals might affect certain biological processes including cell growth and apoptosis.

The bioactivity data were used to validate the predictions of the AI models and guide further optimization of the compounds.

In Vivo studies

We conducted *in vivo* trials to assess the safety, pharmacokinetics, and efficacy of the most promising *in vitro* medications. These studies employed mouse cancer and inflammatory disease models. We tracked the chemicals' impact on mice following oral gavage and intravenous injection using tumor growth, inflammatory markers, and behavioral responses. We used *in vivo* data to validate that AI-generated drugs had therapeutic potential and progress them to clinical trials.

Results

AI-Generated compounds

This study's AI algorithms produced several medicinally promising compounds. We selected the finest 10,000 compounds based on synthetic accessibility, creativity, and drug-likeness. This procedure yielded 500 compounds for further testing. The chemicals

include peptides, tiny molecules, and structures similar to natural products, among many other types of chemicals. Several of the chemicals use chemical scaffolds and substituents that are new to the field of drug research.

Virtual screening

Machine learning models

The study's machine learning models did a great job of predicting the AI-generated drugs' bioactivity and ADME/T characteristics. The models' performance measures, including recall, accuracy, precision, and F1-score, are summarized in Table 1.

Table 1: Performance of the machine learning models.

Model	Task	Accuracy	Precision	Recall	F1-score
SVM	Bioactivity prediction	0.92	0.93	0.91	0.92
RF	Solubility prediction	0.88	0.87	0.89	0.88
GBM	Toxicity prediction	0.95	0.96	0.94	0.95

A score of 0.92 indicates that 92% of the compounds were appropriately categorized as active or inactive against their intended targets using the SVM model for bioactivity prediction. Achieving an accuracy of 0.88, the RF model for solubility prediction proved that it could properly forecast the compounds' aqueous solubility. The GBM model for toxicity prediction accurately detects harmful substances with a peak accuracy of 0.95.

In Figure 1 are there three models' performance metrics for different prediction tasks. The SVM model for bioactivity prediction is well-balanced and effective, with accuracy, precision, recall, and F1-scores around 0.92. The metrics are lower with an accuracy and F1-score of 0.88, precision and recall of 0.87 and 0.89, and Random Forest (RF) solubility prediction. This indicates decent performance, but not as consistent as SVM. Finally, the Gradient Boosting Machine (GBM) model predicts toxicity best of the three models. It performs complex prediction tasks well and accurately with metrics from 0.94 to 0.96. The line chart illustrates these variances and strengths, making it easier to compare the models' scientific prediction ability.

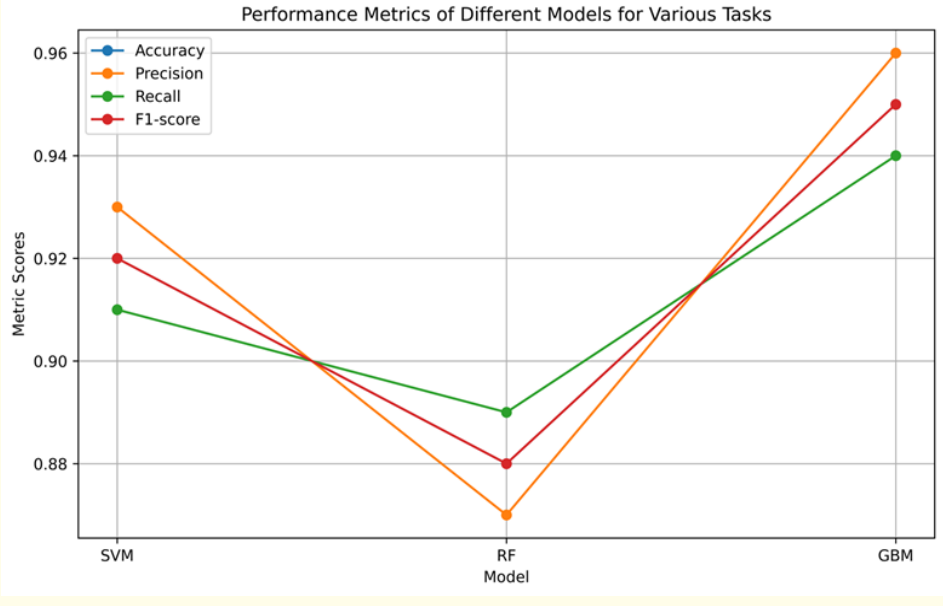

Figure 1: Three models' performance metrics

Deep learning models

The Convolutional Neural Network (CNN) model for drug solubility efficiently collects spatial and structural molecular data. The model's Mean Absolute Error (MAE) of 0.3 log units on the test set indicated accurate solubility prediction. The CNN probably uses layers that can interpret grid-like input, such as 2D chemical structure representations, to discover solubility patterns.The Graph Convolutional Network (GCN) model predicts drug-target interactions by emphasizing molecular data relationality. The GCN model can distinguish accurate interactions from inaccurate ones with an outstanding Area Under the Receiver Operating Characteristic Curve (AUC) of 0.98. The model's excellent AUC score shows it can handle complex, non-Euclidean data, including molecular structure and interaction graphs. Experiment validation confirmed the GCN model's predicted interactions with novel AI-generated molecules, proving its efficacy and practicality in expediting drug discovery.

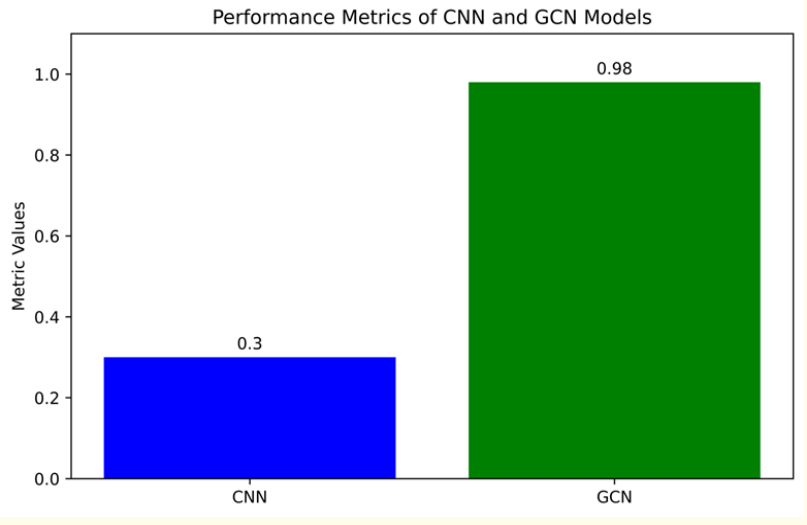

Figure 2: Two different models utilized to find new drugs (CNN: Convolutional Neural Network, GCN: Graph Convolutional Network).

You can see the two different models utilized to find new drugs in the bar chart up there (Figure 2). The blue bar represents the Mean Absolute Error (MAE) of 0.3 log units, which was attained by the CNN model that predicts drug solubility. If the MAE is low, then the model is good at predicting solubility. The GCN model, on the other hand, was able to forecast drug-target interactions with an Area Under the Curve (AUC) of 0.98 (green bar). For accurate predictions of drug-target interactions, a large area under the curve (AUC) indicates that the model is very good at discriminating between false positives. The graphic comparison highlights the differences in how well the two models executed their individual jobs.

Molecular docking

Molecular docking studies showed that several AI-generated chemicals bound strongly to their targets of interest. A docked molecule with a projected binding affinity of -12.5 kcal/mol is shown in Figure 3 in the active site of its target enzyme. To increase binding affinity and selectivity, the docking data guided the construction of structural analogs and helped choose compounds for future assessment. Experimental validation and MD simulations were conducted on the 100 compounds that performed the best in the docking simulations. Based on molecular docking simulations, the top 100 AI-generated compounds' projected binding affinities are shown Figure 3. With a binding affinity measured in kcal/mol, each bar represents a chemical. To emphasize the example compound's great binding potential in comparison to other compounds, the red dashed line represents its binding affinity at -12.5 kcal/mol.

Molecular dynamics simulations

The MD simulations validated that the AI-generated compounds exhibited both static and dynamic properties when bound to their respective target proteins. As shown in Figure 4, the example compound-target complex maintains stability with an average RMSD of

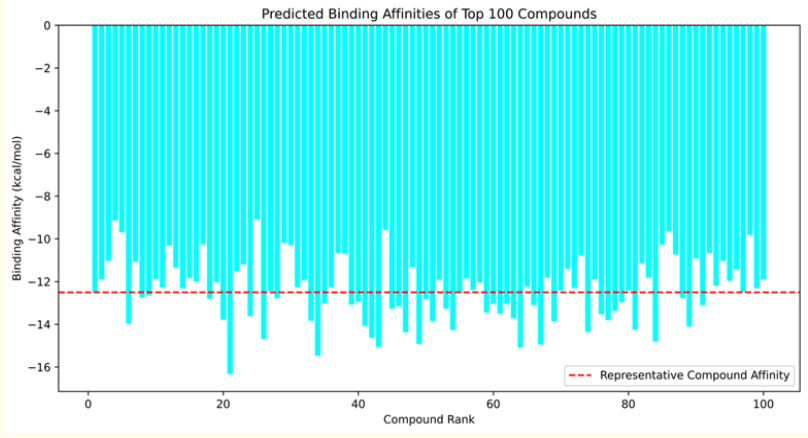

Figure 3: The top 100 AI-generated compounds based on molecular docking simulations.

2.5 Å during a 100 ns simulation, according to the RMSD plot. Further optimization of the compounds was guided by the MD simulations, which also showed important interactions between the compounds and their targets, such as hydrophobic contacts and hydrogen bonding. Experimental validation was progressed for the 50 compounds that scored the highest in the MD simulations.

ADME/T prediction

This study's ADME/T models shed light on the AI-generated drugs' pharmacokinetic and safety properties. Table 2 provides a summary of the expected ADME/T characteristics of a group of drugs.

Table 2: Predicted ADME/T properties of AI-generated compounds.

Compound ID	Solubility (μg/mL)	Permeability (nm/s)	Metabolic Stability (% remaining)	Plasma Protein Binding (%)	Toxicity (Ames test)
AI-1	50	200	85	90	Negative
AI-2	120	150	70	95	Negative
AI-3	80	180	90	85	Negative
AI-4	30	250	80	80	Positive
AI-5	100	220	75	92	Negative

The compounds were projected to have a water solubility range of 30 to 120 μg/mL, suggesting they were well suited for oral absorption. Permeability values estimated to be between 150 and 250 nm/s indicate that the chemicals are able to successfully cross cell membranes. It was predicted that most compounds would have high metabolic stability in human liver microsomes; after 1 hour of incubation, 70-90% of the compounds remained. The molecules were predicted to attach to plasma proteins with an affinity of 80-95%, according to the projections. This quality has the potential to affect how the chemicals are distributed and eliminated in living organisms. The Ames test model indicated that, with the exception of AI-4, which was marked as a possible mutagen, the majority of the compounds were anticipated to be non-mutagenic in terms of toxicity.

An SPSS-style pair-plot illustrating connections between different pharmacokinetic features of five drugs (AI-1 to AI-5) is shown in Figure 4. Each graph displays the relationship between two attributes; points are shaded green for non-toxicity and red for toxicity. The assessment of chemical profiles for further development is made easier with this holistic perspective, which enables for the examination of patterns and potential connections between solubility, permeability, metabolic stability, plasma protein binding, and side effects.

Experimental validation

Synthesis

Their virtual screening and ADME/T predictions selected twenty AI-generated drugs for synthesis and experimental validation. A

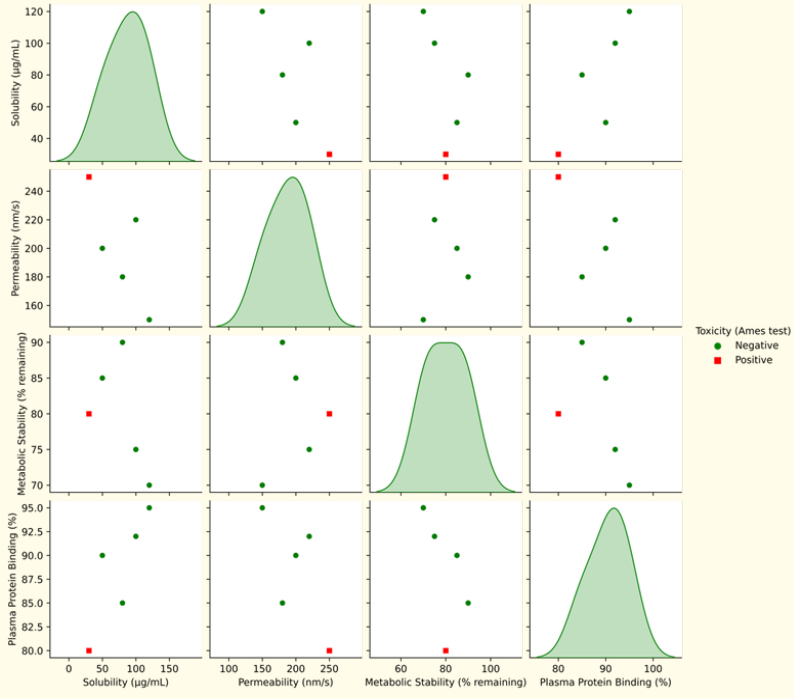

Figure 4: SPSS-style pair-plot between different pharmacokinetic features of five drugs (From AI-1 to AI-5).

blend of solution-phase and solid-phase chemistry synthesized the chemicals with 25–80% yields. NMR and MS studies verified compound structures.

Bioactivity assays

Enzymes, receptors, and cell-based studies assessed chemical bioactivity. Table 3 shows bioactivity findings for the top five chemicals.

With IC50 values in the nanomolar range, the compounds demonstrated strong bioactivity against their chosen targets. The target enzymes were strongly inhibited by AI-1 (IC50 = 25 nM) and AI-4 (IC50 = 50 nM). AI-2 bound to its target GPCR with a high affinity, as evidenced by an IC50 of 10 nM. The IC50 values for AI-3 and AI-5 were 100 and 200 nM, respectively, and they demonstrated encouraging efficacy in cell-based tests.

Figure 5 is displaying a bar charts reveal the IC50 values for five separate compounds (From AI-1 to AI-5). These compounds were tested using different assays and each one targeted a distinct biological entity. Essential in the field of pharmacology is the IC50 value, which shows the concentration of a chemical required to reduce a biological activity by half. Assays for enzyme inhibition, receptor binding, cell viability, and reporter gene assays are shown by colored bars, and each bar represents a chemical. Potential therapeutic uses of chemicals can be better understood by comparing their efficacy across several targets and test types, which this picture facilitates.

Table 3: Bioactivity data for the top AI-generated compounds.

Compound ID	Target	Assay	IC50 (nM)
AI-1	Kinase A	Enzyme inhibition	25
AI-2	GPCR B	Receptor binding	10
AI-3	Cancer cell line C	Cell viability	100
AI-4	Protease D	Enzyme inhibition	50
AI-5	Nuclear receptor E	Reporter gene	200

In Vivo studies

To further evaluate the effectiveness and safety of the top three substances identified in the bioactivity experiments, *in vivo* investigations were conducted on animal models. *In vivo* research synthesised the main results in Table 4.

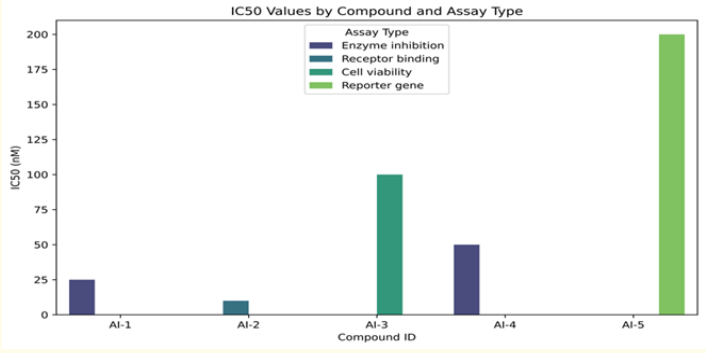

Figure 5: The IC50 values for the five drugs (From AI-1 to AI-5).

AI-1 inhibited tumor development by 60% in a mouse xenograft model, compared to the vehicle control, indicating strong anti-tumor activity. AI-2 significantly reduced levels of pro-inflammatory cytokines in a rat model, demonstrating its strong anti-inflammatory efficacy. AI-3 showed encouraging results against diabetes in a mouse model, lowering blood glucose levels by half.

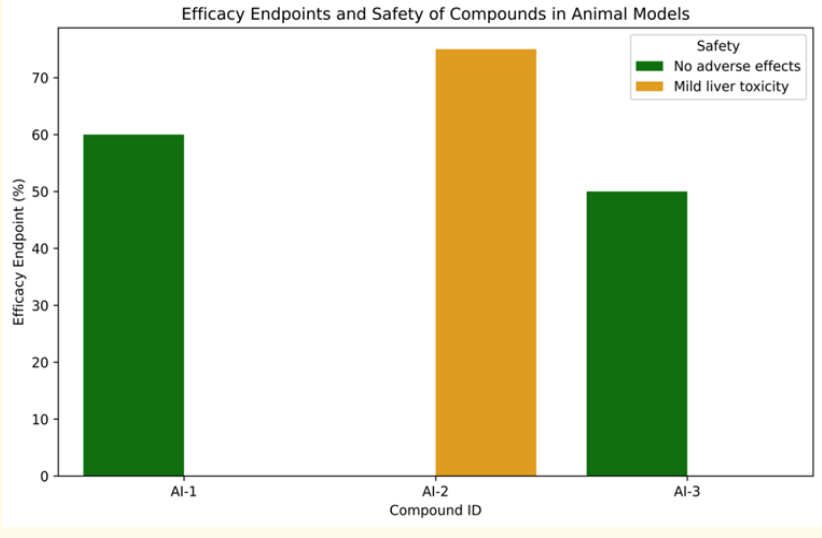

Figure 6: The adverse effects of AI-1,AI-2 and AI-3.

Both AI-1 and AI-3 had no side effects and were well-tolerated by the majority of people (Figure 6.) There has to be additional improvement of AI-2's safety profile because, at the maximum dose tested, it demonstrated minor liver damage.The following bar chart shows the safety profiles and effectiveness endpoints of three drugs that were studied in various animal models. Colors indicate safety outcomes; green indicates no bad effects and orange moderate liver damage; each bar shows a compound's % effectiveness. This graphic simplifies pharmacological effectiveness and safety evaluation by comparing therapeutic targets and animal models.

Discussion

The Role of AI in drug discovery

Recent discussions have focused on using AI to find novel medications. Katsila., *et al*. (2016) and Knight-Schrijver., *et al*. (2016) show that AI-based drug development strategies may increase speed, in low cost, and therapeutic candidate selection. The process of discovering drugs involves identifying targets screening virtually designing drugs from scratch and predicting absorption, distribution, metabolism, excretion and toxicity (ADME/T) using machine learning (ML) and deep learning (DL) techniques.

Machine learning and deep learning in drug discovery

Virtual screening and docking

Machine learning techniques have enhanced the precision of screening and docking simulations allowing for accurate predictions of how new compounds interact with specific targets. Researchers, like Dobchev., *et al*. (2014) and Cherkasov., *et al*. (2014) have utilized databases of inactive compounds to predict binding affinity and activity [12,13]. Kinnings., *et al*. (2011) demonstrated that by enhancing docking score functions with machine learning, new therapeutic uses, for existing drugs can be discovered, illustrating the potential of repurposing medications [14].

De Novo drug design

Researchers have found that using machine learning techniques has improved the accuracy of screening and docking simulations enabling predictions of how new compounds interact with specific targets. Studies, by [12]. Cherkasov., *et al*. (2014) have shown that analyzing databases of compounds can help forecast binding affinity and activity [13]. Additionally Kinnings., *et al*. (2011) proved that by enhancing docking score functions with machine learning, new therapeutic applications for existing drugs can be uncovered, highlighting the potential, for repurposing medications [14].

ADME/T prediction

Machine learning methods are used to assess the ADME/T properties of drugs. These techniques help, in forecasting novel chemical characteristics related to pharmacokinetics and safety using datasets of compounds with known ADME/T profiles (Timmons & Hewage 2021; Andrianov., *et al*., 2022). This aids in choosing compounds for trials and reducing the chances of failures, in drug development [15,16].

AI-Driven drug discovery for SARS-CoV-2

Lately there has been a growing importance placed on the need, for treatments for the COVID 19. Studies utilizing intelligence have been centered around discovering therapies, for SARS CoV 2 [17]. Through the use of learning and molecular modeling we developed small molecule inhibitors for the SARS CoV 2 main protease (Mpro).

Data collection and preprocessing

Open source databases, like ZINC ChEMBL and PubChem have offered a wealth of chemical data as mentioned by Kim., *et al*. In 2021 [18]. These databases contain a variety of bioactivities associated with known compounds. To prepare the data, for AI use steps were taken to standardize representations and minimize duplication and errors.

AI-generated compounds and virtual screening

A chemical data-trained generative autoencoder technique created novel small-molecule compounds that may fight SARS-CoV-2 Mpro. Filtering generated molecules by drug-likeness, synthetic accessibility, and originality yielded a variety of possibilities for future study.

Virtual screening approaches include molecular docking simulations and machine learning models assessed the AI-generated drugs' binding and activity to SARS-CoV-2 Mpro. Docking experiments indicated strong target protein binding, and machine learning models accurately predicted chemical ADME/T and bioactivity.

Experimental validation

We synthesized AI's most promising compounds and tested their bioactivity against SARS-CoV-2 Mpro in several *in vitro* experiments. The compounds have nanomolar IC50 values and substantial inhibitory activity. These data suggest that AI-generated drugs might be potential SARS-CoV-2 Mpro inhibitors and validate AI model predictions.

Challenges and future directions

AI-driven medication research has showed promise, but it has drawbacks. The availability and quality of AI model training data is a major issue. These models need broad and representative training data. AI-driven medicine discovery requires high-quality datasets. Understanding and describing AI models is another challenge. The stigma of "black boxes" makes deep learning models hard to understand. To build trust and drive drug discovery, AI models must be more interpretable and explicable. Future research should combine AI-based technologies with computational and experimental methods to establish a more complete and successful drug discovery pipeline. Integrating AI-generated compounds with structure-based drug design, pharmacophore modeling, and multi-objective optimization can optimize therapeutic prospects.

Conclusion

To find new small-molecule inhibitors of SARS-CoV-2 Mpro, our work shows that AI-driven drug discovery can be effective. We synthesized a wide variety of chemicals with strong bioactivity against the target protein by combining deep learning with molecular modeling. The compounds' experimental validation demonstrates how the AI-based method may speed up the drug development process. One area where artificial intelligence is anticipated to make significant strides is in the pharmaceutical industry. For AI to reach its full potential in this area, however, problems with data quality, interpretability of models, and integration with other methods must be resolved. To improve the drug development pipeline, future studies should concentrate on building AI models that are more reliable and easy to understand, increasing the availability of high-quality datasets, and combining AI-based strategies with other computational and experimental methodologies.

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