https://doi.org/10.48047/AFJBS.6.14.2024.6227-6237

Leveraging AI Models to Predict Potential Drug-Drug Interactions for Enhanced Patient Safety

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Article History

Volume 6, **Issue** 14, 2024 **Received**: 10 July 2024 **Accepted**: 19 August 2024 *doi: 10.48047/AFJBS.6.14.2024.6227-6237*

Abstract

Over a decade, pharmacy samples have been significant in treating diseases. Moreover, unknown drug-drug based interaction (DDIs) that cause unwanted hostile drug events (ADEs) in various regimens treatment remain a constant problem. Since artificial intelligence (AI) is universal existing today, various model based on AI have been incorporated to identify the significant drug interaction to assist clinicians in decision making across pharmacotherapies. Moreover, even though the models which is through DDIs have significantly used to help physicians in assisting to make decisions, but there is a concern concerning the AI models reliability due to their nature. Safety of the patients is promoted by Explainable AI (XAI) and depicts by showcasing the decision-making strategy of the AI models. *Keywords- Artificial Intelligence, Drug, Pharmacotherapies, Adverse Drug Reactions*

Introduction

The rapid growth of artificial intelligence (AI) has opened up new opportunities in healthcare, notably in the area of drug safety. Drug-drug interactions (DDIs) occur when two or more medications interact in a way that modifies their effects, potentially resulting in negative patient outcomes [1]. Predicting these interactions is critical for increasing patient safety, reducing undesirable side effects, and optimizing therapeutic results. Traditional techniques of detecting DDIs, which rely primarily on clinical trials and post-marketing surveillance, are timeconsuming and may miss some probable interactions, particularly rare or long-term ones [2]. AI models, particularly those that use machine learning and deep learning techniques, present a viable solution to this problem [3]. These algorithms can anticipate probable DDIs by analyzing massive amounts of biomedical data, such as drug chemical characteristics, patient information, and past interaction data. By identifying dangerous combinations early on, AI can help healthcare providers make better prescribing decisions, lowering the possibility of adverse medication responses.

The process of creating safe and effective medications is difficult, time-consuming, and expensive. According to a 2016 paper released by the Tufts Centre for the Study of medicine Development, producing a new medicine takes over 10 years and costs more than \$2.6 billion. [4]. Drug development is a multi-phase process that includes testing pre-clinical trials and regulatory sanction. Early diagnosis and mitigation of adverse drug-related reactions and medication-induced toxicity remain a major concern in the healthcare business[5]. Despite thorough research and regulatory monitoring, adverse drug reactions and toxicity continue to be major causes of mortality and morbidity globally, resulting in hospitalisation and significant healthcare expenses [6]. Traditional techniques of discovering hazards, such as after-market monitoring and negative event reporting, are reactive and may not detect detrimental effects until they affect many patients [7].

A comprehensive evaluation of observational research indicated that ADRs are responsible for a considerable percentage of hospitalisations globally, highlighting the ongoing healthcare dilemma. Additionally, drug-induced toxicity, a severe type of ADR, can cause organ damage and other serious health implications [8]. Drug-induced toxicity and ADRs have several effects. In clinical settings, they can injure patients and even lead to death. These conditions lead to high healthcare expenses, including longer hospital stays, more treatments, and lost productivity [9]. Finding effective solutions for the early diagnosis and reduction of ADRs and drug-induced harm is an important topic of study within the healthcare and pharmaceutical sectors. Improving early identification of ADRs and mortality might significantly minimize patient damage, improve patient safety, lower healthcare costs, and increase the effectiveness of the drug manufacturing procedure [10]. Traditional preclinical toxicity assessment requires lengthy in vitro and in vivo investigations, which are time-consuming, costly, and frequently fail to anticipate human-specific harmful consequences. Quantifiable Structure-Action Relationship (QSAR) representations have developed as key components of this strategy. QSAR methods service mathematical methods to predict a drug's biological action according to its chemical makeup, giving a cost-effective, quick, and somewhat accurate technique to assess drug toxicity [11].

Literature Review

A patient protection incident is characterised as various procedure, omission, or deed that causes hazardous healthcare circumstances and/or unexpected injury to the enduring [12]. Broadcasting patient protection occurrences is an effective way to improve patient protection [13]. Technique of broadcasting events was originally adopted in perilous sectors like aviation, fossil fuels, rail business, and so on to increase safety and boost organisational learning from failures. The technique was expanded to healthcare network with parameters including unidentified broadcasting, relevant feedback, and convenience of broadcasting [14]. Healthcare reporting systems capture and analyse adverse occurrences and near misses, providing safety professionals with actionable knowledge to reduce risks. Electronic patient safety reporting (ereporting) solutions have improved incident collection and analysis efficiency compared to paper-based methods [15]. However, the potential advantages of such systems for medicine have yet to be completely realized. Currently, we identify low-quality reports as a bottleneck that hinders the usability of data for improving quality and patient safety research. Data quality, including correctness, completeness, and timeliness, is a major challenge in EHR systems [16]. Research indicates that poor data quality and integration might lead to functional and usability issues. A well-designed system produces data of excellent quality. Similarly, an efficient ereporting system might act as a facilitator in improving data quality for the safety of patients [18]. Existing research shows that user interfaces and human factors can have an important impact on the quality and pace of event reporting. It was stated that an effective e-reporting system design should facilitate the social-cognitive procedure for potential reporters [19]. An efficient e-reporting system should lead reporters through the broadcasting process stepwise, saving time and effort. Research on e-reporting system design has been dispersed between research [20]. While there have been evaluations and relative analysis on broadcasting system strategy, they have focused on organizational culture rather than interface design. The study aimed to assess the present state of e-reporting, identify design features that enhance the quality of data, feature identification hierarchy based on development stage, and identify interest scientific gaps and challenges in developing e-reporting systems [21].

Data Set, Feature for Ai based Drug Analysis

As the number of pharmaceutical medications in the market has increased, drug-based data been updated and expanded to forecast DDIs [22]. Most DDI investigations used information from DDI Abstraction 2011, DDI Abstraction 2013, and the DrugBank catalogue. Public sources contain information on medication properties and DDI incidents, which may be used to develop AI techniques for DDI discovery. Quantitative information on DDIs is essential for developing the stated system [23]. Data records often use binary characters, with 1 indicating an interaction between medications and 0 indicating no known interaction.

Convolution AI based models for drug prediction

Advancements in computer science and network pharmacology have led to the use of multidimensional pharmacological characteristics in classical machine learning models as a potential way for predicting unknown drugs [24].

Drug prediction based on ensemble model

Ensemble approaches, which include many learning algorithms, outperform standalone models for DDI prediction. LibLINEAR, a combination of rectilinear the SVM, naive Bayesian, and Elective a perception system classifier, beat the imbalanced F-score-based train corpus model (71% vs 65%). A framework of various ML methodologies like Bayes theory (NB), the decision tree (DT), k-nearest neighbours (k-NN), LR, and SVM, significantly used to identify unidentified DDIs with an AUC of 0.67, outperforming separate procedures (NB:0.56, DT:0.465, k-NN:0.56, LR:0.565, and SVM:0.565) [25]. Various collaborative approaches, such as genetic algorithms and LR in algorithm collaborative rules, may predict DDIs with AUC values ranging to 1 and reliability above 90%, irrespective of whether authorized or unproven drug combinations are picked. Figure 1 illustrates the overall traditional workflow for prediction of drugs using AL and ML.

Fig.1. Overall workflow of traditional ML and DL for Drug Prediction

Artificial Neural Network (ANN)

This is a based-on data procedure that uncovers latent efficient relationships within a database. Artificial neural networks (ANN) use intricate interconnections to tackle either nonlinear or linear problems. Previous research has effectively used ANN models for DDI prediction tasks. Rohani et al. [26] employed a two-layer ANN model to operate on extracting features of various familiar media acquired from different distinct data foundations. Masumshah et al. [27] employed neural system that consists of feed-forward that is fully linked layer, with the activation purpose of ReLU serving as the sigmoid activation function for its result layer. In addition, used the ANN and transmission approach on DDI network nodes that resembled an adjacency matrix [28]. For the DDIs categorisation, they employed an XGBoost classifier that produced a binary value indicating whether the drug combinations interacted.

Convolutional Neural Network (CNN)

CNN, stimulated by the visual cortex of animals, is an excellent method for dealing with gridpatterned data. The primary purpose of this neural system is to convert the data into significant format without sacrificing forecast capability [29]. This feature types CNN a possible contender to DDI abstraction challenge, which demands valuable feature learning elements and enormous dataset scalability. These characteristics were then sent through an algorithm to get the normalised likelihood notch for every period. Quan et al. [30] use a word embedding to represent DDIs, which are then fed into a layer of network to extract features filters. The layer with maximum pooling collects crucial limited information and simplifies the perfect by lowering feature measurement [31]. Finally, in this framework, a coating known as softmax is employed to categorise DDI kinds.

CNN- Based Dependency

Feeding regional data into convolution in classic CNN is not practicable for long-distance associations amongst words in potential DDI instances. Enlarging the window may cause data sparsity issues. Convolutional method which is based on dependency known as Deep CNN was utilized to identify the dependencies amongst long separated words in a phrase and significantly gather DDIs from different instances.

Deep CNN

Deep CNN (DCNN) has been successfully used in computer vision to find complicated patterns in images and videos, making it a promising candidate for DDI extraction. Sun et al. [32] introduced a DCNN perfect that uses a tiny convolution building at the word level to extract embedding-based characteristics from raw biomedical text input. The softmax classifier will utilise these characteristics to retrieve DDIs from biomedical literatur

Fig.2. Progression of DDI estimation methods associated by different initial data and algorithms

Figure 2 depicts the Progression of Drug interaction methodology associated by various algorithms and data.

Opportunities and Challenges

Traditional machine learning (ML) was effective in extracting drug-drug interaction (DDI) from unstructured package inserts (also known as drug product labels) [33], but it still has limitations. Learning ML-based models from negative as well as positive data can be challenging in practical areas due to an absence of actual positive DDIs or a "gold standard" non-DDI. To avoid biassed sampling, it is important to detect positive data among unlabelled data with both positive and negative samples [34]. This may be accomplished using negative sampling of random values and verification group updates. It is unclear if there is a DDI amongst two medications for dataset which is negative in class, as unique drug combinations yet be recorded. There are several forms of DDI data, including security of drugs and physiological information, with varying sample sizes and database proportions and articles [35]. Traditional ML-based approaches require more effort to annotate and optimise parameters. However, we thought that future research should explore many options. Related to drugs textual information of data, including patent statistics, are crucial [36]. Second, it is unclear how to leverage drug area information or semi-organized medicines, like as paragraphs describing pharmacodynamics, method of binding protein and extraction of features, to develop predictive models [37]. DL's superior presentation and capacity to provide

task that classify hierarchical input which has sparked much study in the DDI prediction arena. Due to their lack of explainability, these deep learning algorithms are not widely accepted by medical professionals [38]. Few research has examined the explainability of DDI prediction models, leaving potential for improvement and innovation in ML-based models to assure predictive performance and interpretability. We believe that any technique can explain blackbox models.

Conclusion

Drug-drug interactions (DDIs) occur in pharmacy when one medicine alters the effects of another in an associated regimen. In therapy, cooperative activity and beneficial advantage are desired. Effective management of DDIs is essential for pharmacovigilance and medical practice, as they can lead ADEs and impact patient health. This study's major contribution is to provide a complete taxonomy of current approaches for predicting DDIs. Despite recent advances in DDI prediction, model interpretability remains a significant limitation. Further research is needed to fully explore the potential of XAI in DDI prediction. The exploration of AI models for forecasting probable drug-drug interactions (DDIs) demonstrates the enormous potential they have to improve patient safety. AI-driven techniques, particularly those based on machine learning and deep learning, provide a strong tool for analysing large amounts of complex biomedical data. These algorithms can uncover patterns and associations that older approaches may miss, allowing for the early detection of dangerous drug combinations. AI integration in clinical practice has the potential to transform how healthcare providers approach prescribing, resulting in more tailored and safe treatment programs. By identifying probable DDIs before they occur in real-world settings, AI models can help decrease adverse drug reactions, thereby improving patient outcomes and lowering healthcare costs.

Future Research

Future research should focus on developing high-accuracy white-box models, ensuring model fairness, and conducting strict sensitivity analyses for DDI prediction. This will increase trust and fairness in model performance, bringing it significantly closer to the clinical applications. XAI strives to know the algorithms in machine learning, not reduce their accuracy. Further research may reveal that XAI can reduce accuracy in DDI extraction tasks (NLP), particularly when text-based approaches are employed to refill databases and improve relationships in original sources.

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