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A Systematic Review on Drug Interaction Prediction Using Various Methods to Reduce Adverse Effects

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ABSTRACT

Interaction prediction between the drugs is a preeminent task. Drug - drug interaction (DDI) causes serious effects to human life. The adverse effect can result in death when the interaction is not known. Predicting all DDI is a challenging mission as it requires much time. Health care professionals and care givers may not be aware of all potential drug interactions. Many studies have been carried out to predict the DDI in meticulous way. Drug banks play the major role in providing information about the drugs; through drug banks we could predict the adverse effect while using two or more drugs together and can avoid the adverse reaction caused by DDI. In this article, the authors have compared different approaches used for predicting the interactions, analyzed with the methods and a comparison is provided for understanding the methods used in each research work.

KEYWORDS

ADR (Adverse Drug Reaction), CASTER, Disease, Drug-Drug Interaction (DDI), LAGCN

1. INTRODUCTION

There are a variety of factors that might result in illness. Infections caused by viruses, nutritional inadequacies, inherited genetic conditions, and even mental illness can all play a role in the development of disease. As a result of shifts in geography, dietary practices, and environmental factors, people are now more likely to suffer from several ailments, requiring them to take many medications at once. Consuming more than one medicine at a time without being aware of how they interact with one another generates unfavorable consequences, which can lead to catastrophic damage and even death. The presence of one ingredient in a drug might alter the effect of another substance present in a different drug, either increasing or decreasing the effect of the first drug. This phenomenon is known as drug interaction.

The chemical compound reaction is not the only factor at play when it comes to interactions. It is also possible for this condition to arise as a result of the patient's advanced age or the breakdown of their internal organs. Before dispensing a medication to a patient, a medical professional is expected

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to be aware of any potential drug-to-drug interactions that may occur. Additionally, it is essential for the professional to be familiar with any potential alternatives in the event that an adverse effect arises. The method of predicting DDI through wet lab experiments is one that takes a lot of time.

The accuracy of the interaction prediction may be improved, while at the same time, the amount of time spent on it can be reduced by employing machine learning and deep learning algorithms in a variety of different techniques. It is recommended that data sets be gathered from reputable drug banks in order to make the most effective use of the methodologies. The drug bank serves as the process's foundation for interaction prediction. It presents the primary characteristics of the compounds, which makes it possible to determine the interactions and avoid certain chemical combinations. In this article, we have examined studies connected to DDI predictions (Section II), as well as various datasets and types of interactions (Section III.A), and the process of prediction involves a variety of different methodologies (Section III.B).

2. RELATED WORK

The DDI may essentially be split up into three distinct categories or groupings.

Basically,

1. An interaction between two different drugs
2. Interaction between medications and foods
3. The interaction between the drug and the disease.

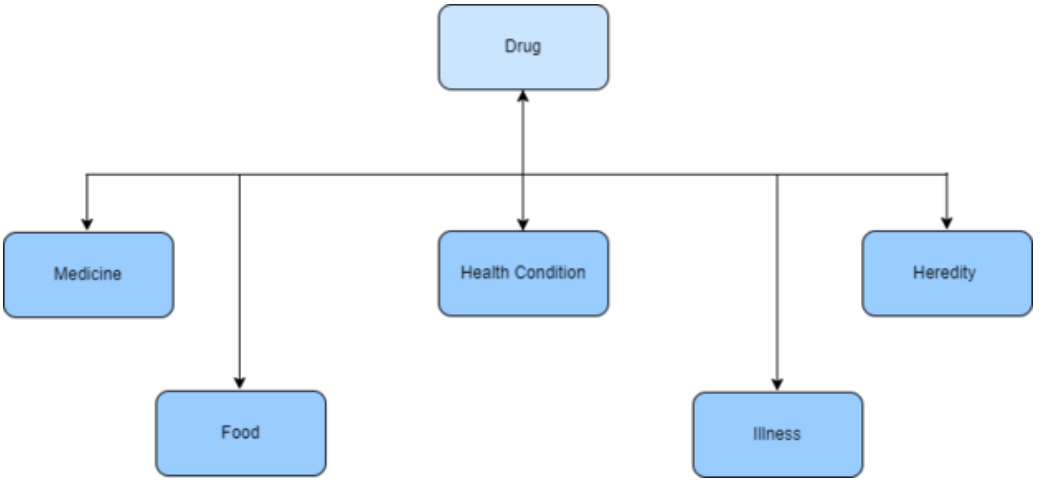
In this case, the pharmacokinetic (DDI) interaction is the most prevalent form of interaction, and it is the one responsible for the potentially lethal side effects. The process of taking many drugs increases the risk of making a serious mistake whenever one of those medications interacts with another. The primary goals of pharmacovigilance are to anticipate and evaluate the risks associated with the use of medications and to gain an understanding of the features of adverse drug reactions (ADRs). The pharmacokinetic and pharmacodynamic categorization systems are used for DDI prediction.

In order to discover medication groupings that are therapeutically useful for certain illnesses, a process based on networks is applied. In the human protein–protein interaction network, measuring the network-based relationship between drug targets and illness proteins revealed the presence of six distinct kinds of drug–drug–disease groupings (Cheng et al., 2019). These strategies, which were created on top of a network, are useful in elucidating the mechanism of action when a medication combination is utilised, and they also have the minimum adverse impact. CASTER is able to determine the chemical composition of the compounds, and the process that it uses to do so may be broken down into three distinct categories: sequential pattern mining, auto-encoding, and dictionary knowledge (Huang et al., 2020). LAGCN begins by integrating the known relationship between the compounds by using the graph convolution approach, then combines utilising the embedding techniques, and finally integrates the embedding layers by utilising the attention mechanism. In cases where the relationship cannot be determined, the embedding is used to determine the score. LAGCN is a method that may be used to make predictions about the associations between different chemicals (Yu et al., 2021).

A method that is based on probability and is used to mutually deduce undiscovered DDIs from a network that has a large number of drug-based similarities and known interactions. A framework for probabilistic programming that is both highly scalable and easily extensible The approach of probabilistic soft logic is utilized for the purpose of assessing the accuracy of discovering the interactions between the medications (Sridhar et al., 2016).

Another approach, known as deep DDI prediction, has been created, and it may be used to determine the sort of interaction that takes place between the medications and the food.

Figure 1. Classes of drug interactions



In addition to this, they built four apps that make use of deep DDI in order to comprehend the interaction in a more exact manner. The purpose of these applications is to reduce the number of negative effects brought on by drug-drug or drug-food interactions (Ryu et al., 2018). In order to provide an accurate prediction of the drug pair score, a relational machine learning model is utilized. It is concluded that the theoretical framework may unify interactions, pharmaceutical side effects, and compound synergy prediction by employing machine learning approaches (Rozemberczki et al., 2021).

A non-linear network-based approach that automatically learns topology-preserving representations of drugs and targets to make DTI prediction easier (Wan et al., 2019). This model incorporates the various data from mixed network statistics and uses machine learning to learn the depictions. using data on known interactions rather than a variety of organic or biotic data, which may not be collectible or may be difficult to ascertain. The K- clique approach is utilized for the patient's medical recommendation system, the monitoring of the patient's health state, and the provision of nutritional foods (Manoharan & Sathesh, 2020). The training model is used to gather the data sets, after which they are preprocessed and sorted on the basis of their similarities using the training model. The data sets are obtained from the network.

The matrix multiplication approach is used to generate a heterogeneous network that is made up of medications, proteins, and illnesses. The network is formed on the basis of an assumption, and its interactions are constructed using the method. With the help of this trustworthy negative data, we created the Random Forest classifier and made an accurate prediction regarding the possible drug-disease interactions (Liu et al., 2020). In order to explore the interactions between the medications, a feature set is taken from a dataset, and then the features are used to determine which adverse effects are related to the interactions (Yang & Yang, 2016).

(Jung & Cho, 2020) makes extensive use of machine learning algorithms, which, when applied to massive amounts of data, demonstrate superior performance. Since the size of the data has a direct impact on its accuracy, network-based techniques are utilized for the smaller amounts of data in order to improve its quality. These approaches are utilized to perform intelligently. In (Shi et al., 2019), a fundamentally mechanical association is carried out to solve two works, the first of which consists of the drug collaborative discovery as well as a full DDI prediction. This is done in the first phase. For the purpose of predicting the interaction, a method known as balance regularized semi-nonnegative matrix factorization (BRSNMF) is utilized. This method is well-balanced. This method is able to create better drug communities, and in addition, it offers a completely comprehensive DDI forecast.

3. CLASSES OF INTERACTIONS

The many distinct kinds of conceivable interactions are broken down into categories in Fig. 1. The interaction between two different drugs is the first and most common type. The interaction may be predicted using a variety of different methods, including the link prediction methodology, drug-target prediction, and protein prediction.

Another important factor that contributes to the intensification of the negative effects of pharmaceuticals is the interaction between medications and foods. It is possible to forecast how a medicine will react with food using any one of a number of different computer approaches. Certain chemicals are incompatible with the majority of foods. If, for instance, an ACE inhibitor is being taken as a compound, then eating bananas should be avoided in order to prevent an undesirable impact brought on by potassium. Before providing medication to a patient, it is necessary to take into account their past health state, namely whether or not they are allergic to any particular food or substance.

When pharmacotherapy intended to treat one disease in a patient result in the development of another disease or a worsening of the condition already being treated, this is an example of a drug-disease interaction. An interaction between drugs and genes takes place when a patient's genetic type is unable to clear the schedule of a certain medication type.

This may either improve the positive effects of the medicine or minimize the dangerous effects that it has.

2.1 Data Set

The acquisition of datasets is necessary in order to be adaptive for a variety of computational findings. In most cases, the data sets are employed for the goal of storing information on the medical history of a patient for the purpose of future reference or retrieval.

The patient's medical record is required to include specific information on the patient's prior diseases, treatments, laboratory histories, and allergy details, if there are any.

These records of medical care will also include the demographic information. Either physically collecting the data from the clinical trials or using internet data sets that are available are both viable options for extracting data sets. More than 3,450 data sets, organized into a wide variety of categories, are currently accessible over the internet within the field of healthcare. Instead of producing a new medicine, it is more vital to look at existing data to see how existing medications interact with one another and how existing medications might be repurposed to save money and time. A data set for health care is the compilation of information on the assessment, care, and treatment of a patient.

Table 1. Comparison between various methodology and the results

Reference	Data Set	Methodology	Result
CASTER: Predicting Drug Interactions with Chemical Substructure Representation (Huang et al., 2020)	BIOSNAP / DrugBank	CASTER	AUC - 0.910 ± 0.005
A probabilistic approach for collective similarity-based drug–drug interaction prediction (Sridhar et al., 2016)	Gottlieb – Pairwise interaction Fakhraei – Interactions from drug bank	INDI, NC-PSL	AUROC - 0.95 ± 0.003 F1 - 0.63 ± 0.01 (t ¼ 0.35)
Deep learning improves prediction of drug–drug and drug–food interactions (Ryu et al., 2018)	DrugBank	SMILES	Accuracy - 84.8–93.2%
Drug–drug interaction prediction with Wasserstein Adversarial Autoencoder-based knowledge graph Embeddings (Dai et al., 2021)	DeepDDI Decagon	Adversarial Autoencoders (AAEs)	PR-AUC - 0.7615, PR-AUC - 0.3568
A Drug-Target Interaction Prediction Based on GCN Learning (Wang et al., 2021)	DTI-net, HPRD, SIDER	GCN	AUC - 0.9186 AUPR - 0.9221

Even though there is an infinite amount of data sets accessible, the benchmark data sets are the most trustworthy. The following table provides details on the commonly utilized standard data set as well as the methodologies that were applied.

3. METHODS

Table 1 shows some of the evaluations that were done between the systems that were engaged in finding out how the chemicals interact with one another. The vast majority of the data sets come from the DrugBank data source. The data collection will include information about the end user's symptoms, previous medical records, allergies, and the substances that were delivered to them in the past. Using the feature selection techniques, several approaches are utilized in order to analyze both the symptoms and the medications.

The medications are evaluated and categorized based on the results of the feature selection's comparisons utilizing the link prediction methods. An end-to-end framework that contains a specific description for DDI prediction, interactions by the chemical processes may be found at site (Huang et al., 2020). They have also proven analytically that CASTER makes DDI predictions that are more accurate and explainable than the other techniques that have been evaluated previously. In reference to point (Sridhar et al., 2016), the issue with the collective DDI forecast has been fixed. This method is utilized to authenticate additional quantifiable data in order to better inform interaction prediction. See reference (Ryu et al., 2018) for predictions of interactions between drugs and between drugs and food using the keywords and the chemical formulations.

In the study referred to as (Dai et al., 2021), the primary objective was to locate an original approach that made use of negative sampling in order to improve the interaction prediction performance. Utilization of the learning framework results in an improvement in the performance of the baseline models.

4. CONCLUSION

According to the findings of these trials, it appears that an algorithm for interaction prediction that is based on machine learning and deep learning is a potential way to produce reliable forecasts. This study conducts a more in-depth investigation of the associated research and evaluations of the principal interaction mechanism. However, only a few studies have been conducted in this field; as a result, an extensive number of unanswered questions need to be resolved before the frequency of adverse medication interactions may be decreased. Recent research has focused on applying deep learning techniques and combining them with neural networks in order to uncover possible links between various prescriptions. This is being done in an effort to lessen the likelihood of harmful drug interactions occurring between different medications. We can mitigate the detrimental impact of DDI prediction on consumers if we increase both its speed and accuracy.

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