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Detecting Side Effects of Adverse Drug Reactions through Drug-Drug Interactions

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Abstract: Adverse drug reactions (ADRs) from drug-drug interactions (DDIs) are a major public health and healthcare cost problem worldwide. Increasing complexity of treatments and ageing populations make managing ADRs more challenging. Standard methods for predicting these reactions do not exist as ADRs are often not detected until reported post-market by patients. Here we present a novel framework using Graph Neural Networks (GNNs) with self-supervised learning to model and predict ADRs from DDIs. By representing drugs as molecular graphs we capture spatial and chemical properties of drug interactions. This research contributes to pharmacovigilance by providing a robust framework to identify potential DDIs and support clinical decision-making.

Keywords: Drug-Drug Interaction, Drug, graph neural network, side effect prediction, self-supervised learning, Adverse drug reaction.

I. INTRODUCTION

An ADR is the response to a medicine that is harmful or intolerable when used in their accepted application and whose prognosis requires therapy, a change in dosage, or withdrawal of the drug. These events again may present a problem to the healthcare system; they can lead to mortality, morbidity, prolonged hospitalizations, and increased costs of treatment. Most side effects happen after clinical trials, while very few are known after drug marketing. Some studies have also indicated that ADR reports are affected based on sex, geographic region, and country of origin. For example, at instance women are more prone to report serious reactions to medicines owing to differential pharmacokinetic and pharmacodynamic characteristics of the medicines and to a higher medication dose that women take when controlled for body weight. Access to healthcare, for instance, in such countries very often greatly varies due to availability of health systems and proper healthcare infrastructure. The chances that an ADR would turn out justifiable in between 71.6% and 59.6% were, respectively, above and below for developed and developing countries, with proportions of 1.7 % and 1.8% respectively for the ADRs associated with mortality. In both cases, the majority of those ADRs were preventable, which is a clear signal of the need of early prediction of this type of ADR in an effort to facilitate appropriate medical use in developing countries.

II. OBJECTIVE

The main goal for this study is to develop a solid methodology to predict Adverse Drug Reactions (ADRs) stemming from drug-drug interactions. Using a combination of algorithms such as K-Nearest Neighbors (KNN), Decision Tree and Graph Neural Network (GNN), the study aims at a front-running prediction of ADRs. This approach aims at an augmented detection of ADRs concerning the complexity of drug interactions and its related public health concern.

III. RESEARCH SURVEY

Paper [1] SSF-DDI: a deep learning method utilizing drug sequence and substructure features for drug-drug interaction prediction: [https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-024-05654-4#:~:text=In%20this%20paper,%20we%20propose%20](https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-024-05654-4#:~:text=In%20this%20paper,%20we%20propose%204#:~:text=In%20this%20paper,%20we%20propose%20)

4#:~:text=In%20this%20paper,%20we%20propose%20

Paper [2] Modular Multi-Source Prediction of Drug Side-Effects With DruGNN:

<https://pubmed.ncbi.nlm.nih.gov/35576419/#:~:text=Predicting%20the%20probability%20of%20side-effects,%20before>

Paper [3] Explainable Drug Repurposing Approach From Biased Random Walks:

<https://ieeexplore.ieee.org/document/9831014>

Paper [4] A Novel Drug-Drug Indicator Dataset and Ensemble Stacking Model for Detection and Classification of Drug-Drug Interaction Indicators:

<https://ieeexplore.ieee.org/stamp/stamp.jsp?tp=&arnumber=10250422>

Paper [5] NNDSVD-GRMF: A Graph Dual Regularization Matrix Factorization Method Using Non-Negative Initialization for Predicting Drug-Target Interactions:

<https://ieeexplore.ieee.org/document/9858885>

IV. METHODOLOGY

This work is aimed at a machine-learning-based approach to predicting ADRs arising from drug-drug interaction. Graph Neural Networks were used to model drug relationships in terms of their chemical structure, represented here as numerical vectors derived from SMILE strings. In other words, using GNN, nodes and edges capture the very complex interactions that exist between many different drugs. A Self-Supervised Variational Autoencoder is layered and integrated into the modeling in order to scale out learning while reducing the chances of overfitting since it can learn the distribution of what reactions are most likely to occur within a large dataset.

The system will also build in algorithms such as K-nearest neighbors and decision trees for comparative analysis. This will be a multi-altitudinal approach wherein a reliable predictive framework, which will enhance the measures of the defense towards the patients, will be developed by researching ways for professionals to proactively assess drug interactions in reducing the number of ADRs.

V. ALGORITHMS USED

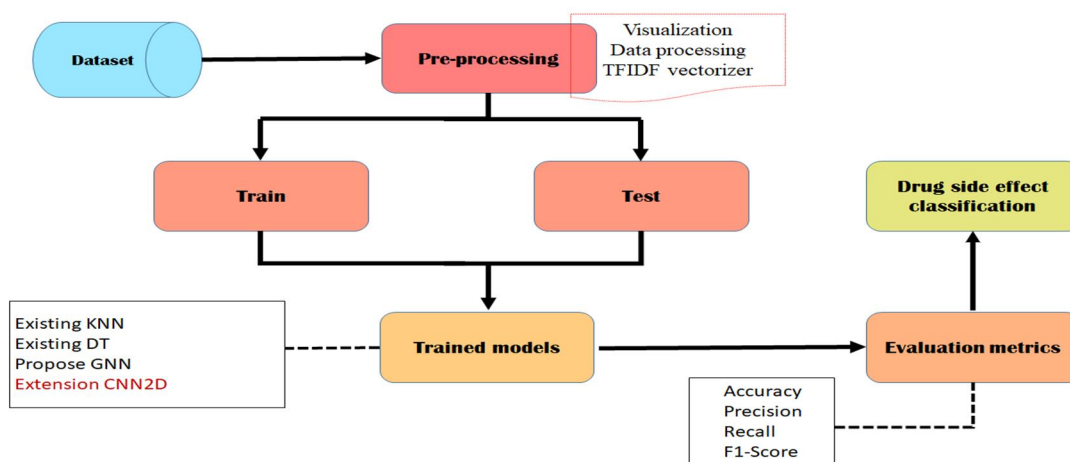
K-Nearest Neighbors (KNN) Algorithm: KNN is a simple, instance-based learning approach which performs a classification of a data point based on the majority class of its nearest neighbors. In our project, it will predict adverse drug reactions through the analysis of similarities in drug attributes and side effects previously recorded. Yet its simplicity of implementation makes KNN a good initial approach with which to get a comparison against more complex algorithms, setting a baseline for performance evaluation.

Decision Tree: The Decision Tree algorithm builds a model using a structure looking like a tree in order to make decisions based on the feature values. In our project, it is employed to classify drugs and predict side effects by creating branches, either by folding the branches equidistantly from each other on the splits made based on drug characteristics.

Graph Neural Network (GNN): The Graph Neural Network is designed as a GNN to model drug-drug interactions and predict adverse reactions by using graph structures. Drugs are represented as nodes, interactions as edges, and the GNN learns various complex relationships residing in the data. In our project, the GNN further processes drug attributes defined as numerical vectors in order to recognize patterns and associations that permit clear predictions of possible side effects. This modern approach solves some of the major limitations untraditional algorithms bring in to bear when trying to increase accuracy.

VI. SYSTEM DESIGN

A. System Architecture



The workflow for drug side effect classification using machine learning models is provided in this diagram. It begins from dataset input, moves on to pre-processing, such as visualization, data cleaning, and feature extraction with the TF-IDF vectorizer, and then proceeds to data splitting into training and testing data. Here, multiple models are trained, such as existing KNN and Decision Tree, a proposed Graph Neural Network GNN, and an extended CNN2D model. The trained model then classifies drug interactions to predict possible adverse effects. Finally, classification performance is evaluated via metrics of accuracy, precision, recall, and the F1-score in order to determine which model performs best.

VII. SNAPSHOTS

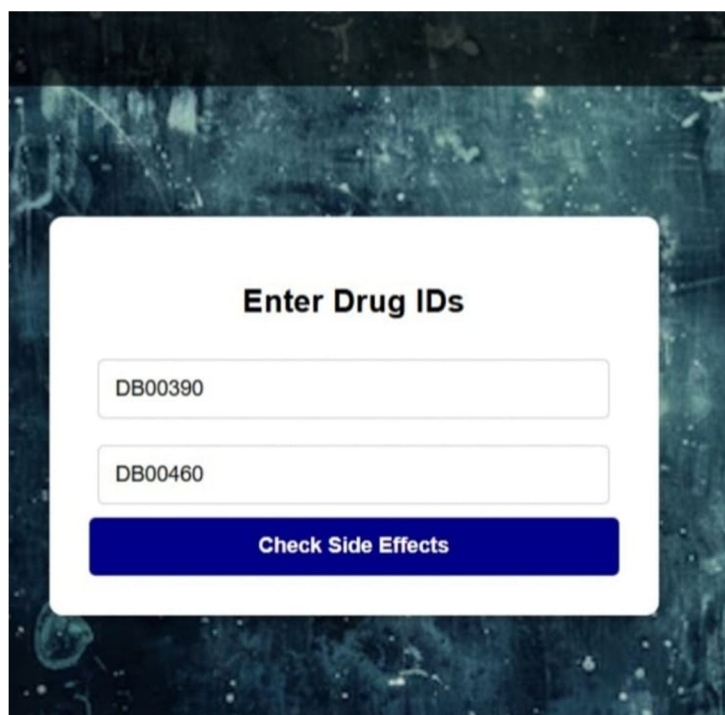


Figure 1 – Drug ID's input

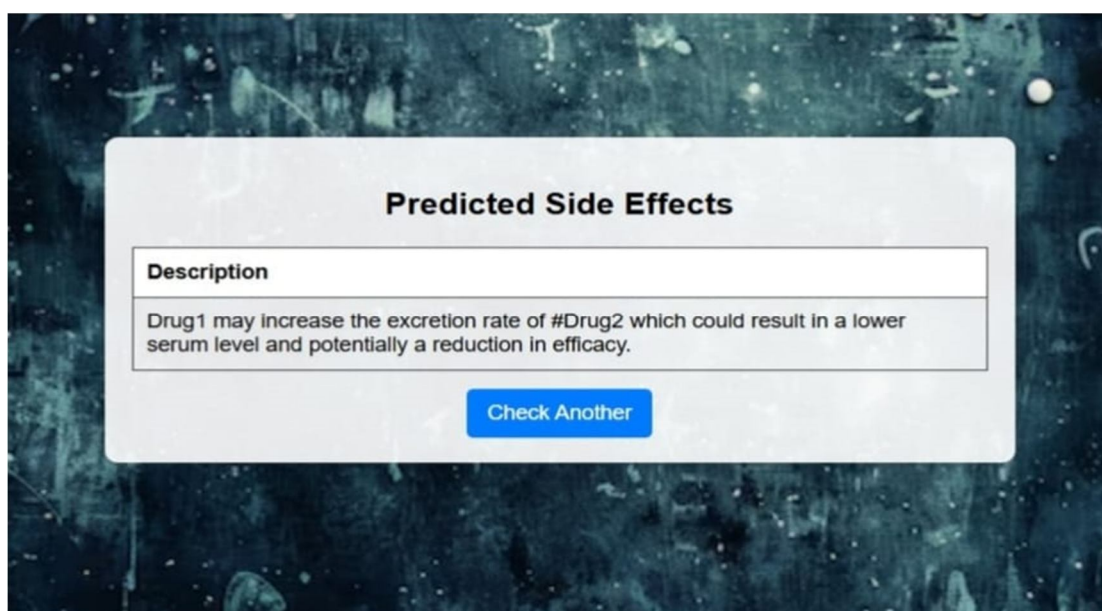


Figure 1.2 – Predicted Side effect

VIII. RESULTS

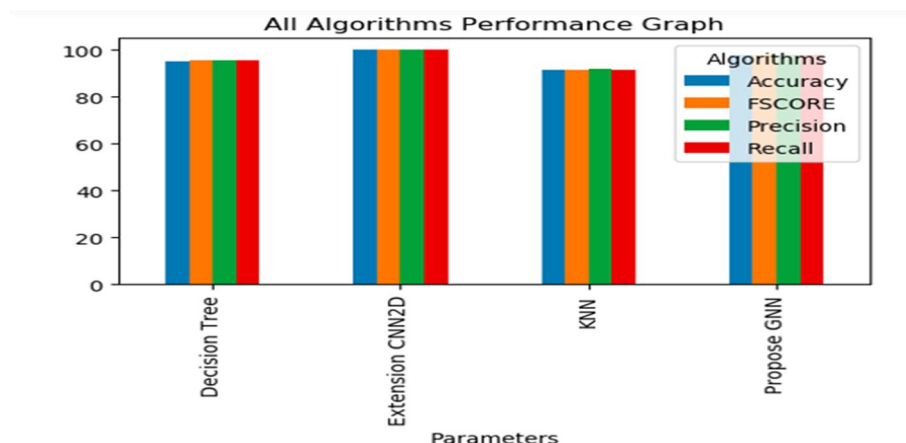


Figure - Evaluation of Algorithms Based on Accuracy, Precision, Recall, and F1-Score

The bar chart above visually represents the performance of different algorithms, with the x-axis displaying the algorithm names and the y-axis indicating key evaluation metrics, including accuracy, F1-score, precision, and recall, each represented by a different colored bar. Among all the algorithms compared, the Extension CNN2D and Proposed GNN models achieved the highest accuracy, demonstrating their superior effectiveness in the given task. This visualization provides a clear comparison of algorithmic performance, helping to identify the most efficient approach for predicting drug side effects.

Table - Comparison of Algorithm Performance on Drug Side Effect Prediction

Model	Accuracy	Precision	Recall	f1_score
K-Nearest Neighbors	91.56	91.92	91.30	91.32
Decision Tree	95.14	95.33	95.61	95.45
Graph Neural Network	97.69	97.88	97.70	97.72

IX. CONCLUSION

In conclusion, this study highlights the critical need for an efficient and reliable method to predict Adverse Drug Reactions (ADR) due to drug-drug interactions, since ADR itself is a risk for public health. This new system utilizes a Graph Neural Network (GNN) based on self-supervised learning, predicting ADRs from drug interactions far more skillfully than existing methods. GNN successfully describes the drug-drug relationship to enhance its prediction and improve the incidence of unusual interactions. The model performs better than other existing algorithms and predicts ADRs with an accuracy of approximately 97.69%.

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