Molecular diagnosis: Drug target evaluation based on deep neural network prediction techniques

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Abstract

With the continuous improvement of computer performance and related technology, the combination of Artificial Intelligence (AI) and Bioinformatics can find new drugs more efficiently. However, most of the current researches focus on the prediction of drug target binding affinity and the determination of drug targets. In this work, the quantitative prediction model of drug target is established by combining of Network Bioinformatics and Deep Neural Network (DNN). It includes a regression model for predicting the strength of drug target binding affinity and a classification model for predicting the direction of drug target. After collecting, processing, and matching the data in the major bioinformatics databases, a classification and a regression model are built based on KERAS online library. Moreover, the performance of the model is verified by cross-validation techniques. Finally, the prediction of the strength and direction of binding affinity between drugs and targets is achieved

Keywords: Artificial Intelligence, Network Bioinformatics, biological.

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Introduction

In addition, to expand the application of the model, by combining Genetic Ontology Database, by combining medicine, a multi-layer network model is recognized. Our works aims to establish a drug target quantification model, in the future reveal the theoretical basis of medicine, and serve for drug screening, drug reorientation, drug development and other fields. After improving of model, the characteristics of data are analyzed, which is composed of similarity vector of 7306 - dimension and drug selection. The model is single output regression model, the partition ratio of data set is 98:1:1, the loss function is MSE, and the evaluation criteria are consistent with each other. The model in the performance of the test set is categorical-cross entropy = 0.2201categorical-accuracy = 0.9816, F1 score, precision and recall are 0.9648, 0.9646 and 0.9640respectively.

Drug targets are the core of drug research and development, and people have depended significantly on hundreds of drug targets to detect pharmaceuticals throughout the last few centuries. Despite the fact that the number of medications known to interact with target proteins is growing, the number of authorised therapeutic targets still represents a tiny portion of the human proteome. The discovery of drug-target interactions is the initial stage in the creation of novel medications, as well as one of the most important variables in drug screening and drug guided synthesis. With the help of high-throughput tests, researchers are learning more about the structural space of therapeutic compounds and the genetic space of target proteins. Unfortunately, our comprehension of the link between the two areas is still restricted due to the time-consuming and arduous experimental method. Researchers may systematically learn and evaluate diverse new data using computational approaches, and review drug-target interactions, thanks to the tremendous rise in publicly available biological and chemical data (DTIs). There are various free databases that focus on drug-target connections, including ChEMBL, DrugBank, and SuperTarget. These database contents serve as the gold standard datasets for the development of computer algorithms for predicting DTIs. Currently, there are three types of computational methods for DTI prediction: ligand-based approaches, docking approaches, and feature learning approaches. By comparing the chemical structural similarity of a particular medicine or substance to active compounds of known targets, ligand-based approaches are frequently employed to determine possible targets of action. Based on the chemical similarity of their ligands, Keiser et al. suggested a technique for inferring protein targets. Yamanishi et al. use a uniform space to integrate the chemical structure similarity of drugs and the amino acid sequence similarity of proteins to anticipate unknown drug-target interactions. By comparing phenotypic side effects, Campillos et al. anticipate likely target proteins. In the event of strong chemical structural similarity, this type of ligand-based technique is easy and effective, but it severely restricts the scope and precision of its use.

The docking approach infers prospective pharmacological targets of action by calculating the form and electrical matching of medicines and potential targets in a three-dimensional framework. The reverse docking approach is the most often used prediction method among them. This approach ranks drug targets by estimating the manner and affinity of interaction between a particular molecule and a target, hence identifying potential therapeutic targets. A structure-based maximum affinity model was created by Cheng et al. Li et al.created TarFisDock, a web service that employs docking algorithms to find drug targets. Although such methods fully consider the target protein's three-dimensional structural information, the molecular docking method itself still has some issues that have yet to be effectively resolved, such as protein flexibility, scoring function accuracy, and solvent water molecules, all of which lead to reverse docking. The method's prediction accuracy is modest. Another significant drawback of docking is that it cannot be used on proteins with uncertain three-dimensional structures. Proteins having a known three-dimensional structure make up a small percentage of all proteins. This drastically restricts the method's marketing and adoption. Drug target connections are treated as a two-class issue in a feature learning approach: interaction and non-interaction. Using machine learning algorithms, such approaches learn the probable patterns of known compound-target combinations, develop prediction models through iterative optimization, and then infer potential DTIs. A comprehensive strategy based on chemical, genetic, and pharmacological data was proposed by Yu et al. Using the signature molecular descriptor, Faulon et al. predicted therapeutic targets. Despite the fact that these strategies have sped up the finding of therapeutic targets, there is still a lot of potential for improvement.

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