Editorial

The Computational Methods in Drug Targets Discovery

With the development of high-throughput sequencing techniques, more and more sequencing data is available, including genomics reads, transcriptomes data, and proteomics sequences, which provide us an opportunity for disease treatment and prevention that takes into account individual variability in environment, lifestyle and genes for each person. Thus, it is critical to develop various methods in the identification of drug targets. Application of computational methods in drugs targets discovery is more and more popular because these techniques can extract the essential characteristics of research object and improve accuracies of models, which is needed by all biological scholars. This special issue focused on various aspects of the development and application of computational techniques in drug targets recognition analysis.

In this special issue, nine papers were published. As the major drug targets, membrane proteins have been wildly concerned in the researching field for many decades, especially in recent, more and more computational methods appeared to help us understanding the membrane proteins, including the structural biology and system biology approaches. No doubt, those research achievements opened a new sight of drug target researching in computational perspective. Gong et al. firstly introduce the basic knowledge of drug-related membrane proteins, including G-protein coupled receptors (GPCRs), transporters and ion channels. Then, the infrastructure researchings are list, including structural and systemic data sources of the membrane protein, and many practical applications. The major part of this review is discussing a series of state-of-the-art computational methods, which improve the membrane protein drug target researching, respectively from drug-target interactions, network-based and machine-learning-based targets discovering. All the evidence discussed strongly indicates that the computational approach offers a promising improvement for understanding membrane protein drug targets.

GPCRs are the largest family of drug targets. About 34% of FDA approved drugs act on 108 unique GPCRs. The growing impact of polypharmacology for complex diseases requires novel targets from the proteins. Saikia et al. reviewed the establishment and in-trials of GPCRs along with the genetic basis for some failures of existing therapies. Ion channels are also associated with diseases. It has been reported that they are targets for over 700 drugs. Many computational methods have been proposed to identity ion channel and their types. However, there is no comparison these methods. Gao et. al. gave us a comprehensive review about the ion channels predictors, and evaluate these methods on a new benchmarked dataset. They also point out that there is no method can predict ion channels that are classified into multiple ion channel types. Their work can help the biologist to choose the proper method to identify ion channels which are target for drug.

Enzymes are well-known proteins which are in charge of various of biological function and process. Thus, they are also important drug targets. Correct identification of their types could provide important clues for enzyme function study and relevant drug design. Tan et al. reviewed the development of enzyme type classification by using machine learning methods. This review mainly focused six types of enzymes. The benchmark datasets, feature extraction, machine learning approaches and published results were summarized. The review could provide guide for enzyme classification study. Xanthine oxidase (XO) is an enzyme which can catalyze the oxidation of hypoxanthine to xanthine and can further catalyze the oxidation of xanthine to uric acid. These enzymes play an important role in the catabolism of purines. As a well-known pharmacophore, some of curcumin derivatives could target XO to alleviate disorders caused by the excess production of uric acid. Ailik et al. designed and synthesized two series of curcumin derivatives along with good antioxidant potential.

Cancer is one of the worlds’ highest causes of morbidity and mortality. The study of anticancer drugs has become one of the most popular medical topics. Hu and co-authors introduced the application of machine learning in predicting anticancer drugs activity including Linear Discriminant Analysis (LDA), Principal components analysis (PCA), Support Vector Machine (SVM), Random forest (RF), k-Nearest Neighbor (kNN), and Naive Bayes (NB). Feng and Wang focused on the development of anticancer peptides identification by using machine learning methods. The challenges and future perspectives in developing reliable methods for identification of ACPs were also discussed. This review could provide novel insights into future researches on anticancer peptides.

Ubiquitination is an important post-translational modification process for the regulation of protein functions, which is associated with cancer, cardiovascular and other diseases. Computational methods play pivotal roles in identifying the ubiquitination sites for their effectiveness and timesaving than the traditional experimental verification approaches. A variety of computational methods and tools have been reported in recent publications. Wang and Zhang mainly summarized the construction of benchmark datasets, together with feature representation methods, feature selection approaches and the classification algorithms involved in predicting protein ubiquitination sites. In addition, they constructed an independent test dataset to compare the performance among the current available webservers and delivered some suggestions to explore pertinent development.
trends. Their work can not only help us understand the main research methods and latest research progress about ubiquitination sites more conveniently, but also conducive to the research of identifying ubiquitination sites in pertinent therapeutic strategies and drugs.

Molecular docking is an important field to investigate the interaction between two molecules by using computational methods. Saikia reviewed the challenges of docking and troubleshooters in existing programs including their algorithmic background and preferences. They also compared the performance for existing tools and algorithms. The review would be an asset to the bioinformatics and drug designing communities.

In summary, it is more and more popular for us to utilize computational methods in drug target analysis and prediction because of their high-performance and resource-saving characteristics. These compositional methods will be widely applied in more fields.

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