

Under the Background of New Era, Computer Promotes the Deepening and Development of Biomedical Industry

Jinsong Zhang, Yuting Zhang, Dingchen Wei, Xinyan Xie, Hailin Lu, Xinyi Wang

School of medicine, Soochow University, Suzhou 215000, China.

Abstract

In recent years, computer increasingly significant role in the biological medicine industry, computer technology continues to boost the continuous deepening and development of modern biological medicine industry from the early stage of the computer for high-throughput target selection, the pharmacokinetic experiment platform with the help of computer, the computer has greatly increased the current biomedical research and development efficiency. This paper will introduce the application and development of computer technology in the field of biomedicine under the background of new era from three important links in biomedical research and development.

Keywords

Computer; Biological Medicine Industry; Drug Target Screening; Protein; Pharmacokinetic Monitoring.

1. Introduction

With the continuous development of information technology and the continuous improvement of scientific and technological innovation ability, the computer gradually integrates into all fields of modern society. The development of biomedicine, physics, mathematics, engineering and other directions can not be separated from the continuous progress and breakthrough of computer technology. With the development of computer technology, the traditional drug development of each link are constantly breakthroughs, from the early stage of the drug targets screening, drug design, the pharmacokinetics experiment, drug toxicity experiment, and the late period, phase ii, phase iii clinical trials, the computer will undoubtedly greatly promotes the current drug development progress, shortening the period of the drug development, significantly improve the efficiency of drug development, and to a large extent save experimental expenditure and avoid for early screening of error later capital investment losses. This article, from the computer technology to promote drug targets screening, computer-aided protein structure prediction of protein ligand interactions, and computer aided pharmacokinetic monitoring three important link in drug research and development, to introduce in the new era background, the computer technology to promote biological medicine industry deepening and sustainable development

2. Computer technology advances drug target screening

With the development of AI technology and the popularization of big data, artificial intelligence technology has achieved great deepening and development in the field of biomedicine in the past two years [1] in terms of scientific research and even application.[2] Artificial intelligence technology has played a huge role in assisting disease diagnosis, new drug research and development, and assisting gene data analysis [3].Among them, AI is involved in the upstream to downstream of new drug development in the following aspects: drug target identification [4], lead compound screening, lead compound optimization, and final clinical trials.[5] With

reference to the advances in computer technology in advancing drug target screening [6-7], it is important to understand that the discovery of molecules often requires it to be combined with the desired drug delivery characteristics in an appropriate dosage form. Artificial intelligence has replaced the traditional trial-and-error approach, which is cumbersome and error-prone. Therefore, finding, determining and preparing target molecular drug targets for drug screening [8] is the most critical point in the research and development of new drugs. Targets for drugs [9] refers to the binding sites in the body, including biological macromolecules, such as loci, receptor and nucleic acids, enzymes, ion channels, etc., and to identify new drug targets effectively is the key of the new drug development, so the discovery and validation of molecular targets involved in work greatly increased the burden of drug development. The deep knowledge of coding through combinatorial design and evaluation can be realized by machine learning algorithms [10]. It greatly lightened the burden of work. The researchers first investigated the possibility of the target selectively binding to equilibrium small molecules to determine which targets are most readily chemically treatable. For bispecific small molecules, the design process is similar to that of a single target drug. The key difference is that efficacy must simultaneously meet two different goals. In terms of drug target screening, the startup ExScientia is a typical example of AI companies. ExScientia develops innovative small molecule drugs for 10 disease targets of GSK through the AI drug discovery platform [11] to discover clinical candidates for a new drug. Computer technology is also used in oncology drug development [12] [13]. At a time when malignancy has become the second leading cause of death worldwide, we are constantly trying to find ways to treat it. While medication therapy is one of the important means of [14]. Philosophy and clinical practice in tumor treatment [15], under the rapid advance of oncology has not only confined to the traditional cytotoxic drugs [16], cell receptors, key gene regulation in [17] as the targets for new antitumor drugs has been applied in clinic, and the development and achievements and computer technology are inseparable. Traditional drug screening methods adopt pharmacological experimental methods, and molecular or cell-level experimental methods (or screening models) are the technical basis for achieving high-throughput drug screening [18]. Automatic operating system is a fully automatic experimental operating equipment controlled by a computer. With the help of computers, we can define the target molecular structure of drug action through organic chemistry, quantum chemistry and stereochemistry calculation, and find out the optimal drug molecular structure combining with target molecule [19]. Compared with traditional drug target screening, the advantage of computer technology is that the screening of drug activity by computer technology is carried out on a large scale, with tens of millions of compounds screened, which can truly realize multiple screening of one drug. The activity data screened by different models of the same compound and the structure-activity relationships derived from the activity data of different compounds in the same model can provide valuable information for drug discovery. In high-throughput drug screening [20], activity data processing processes are used to determine the drug activity of compounds and prepare accurate and rich data for information-based drug discovery processes.

3. Computer aided prediction of protein structure and protein ligand interaction

3.1. Study the role of proteins

Proteins are important nutrients in organisms and play an important role in the life activities of organisms [21]. The study of the biological function of proteins helps to understand the mechanism of individual life activities and plays an important role in medical research, pathological analysis and pharmacological effects [22]. In addition, the discovery of drug targets is the basis of new drug research and drug analysis. At present, most drug targets are

proteins [23]. Understanding the function of proteins is conducive to in-depth understanding of the characteristics of drug targets, improving the efficiency of searching for drug targets, and facilitating the screening of required molecular action proteins [24]. However, the variety, quantity and arrangement of amino acids vary greatly, and the structure and morphology of the peptide chain vary, leading to the diversity of protein functions [25]. With the development of genomics, more and more protein sequences have been sequenced, but less than one percent of proteins can be annotated [26]. Therefore, it is urgent to solve the problems of protein structure annotation and functional protein screening in the field of medical research.

3.2. Comparison between traditional methods and computer methods

The traditional way is by biochemical experiments, the design process, to experiment, to get the data, processing data, prediction study of unknown protein, mainly to compare the unknown protein with known protein, according to the sequence and the structure and function of active sites to infer unknown protein, screening can be protein [27]. However, there is a certain connection between function and structure but no direct relationship, and the protein that has been annotated is less than 1% of the sequenced protein [28]. Therefore, the blank database makes the calculation and prediction engineering with high labor cost, time consuming and energy consuming, and cannot meet the needs of a large number of protein structure and function classification studies to help the discovery of drug targets [29]. Therefore, with the development of computer technology and artificial intelligence, computer technology and artificial intelligence have been gradually developed and utilized for making protein structure model, selecting function and affected protein, screening protein function, etc. [30]. Computer aided protein research improves the efficiency of protein function annotation and prediction of protein ligand interactions, and makes the screening of the affected protein more accurate, which is of great help to the new drug research and medical development field.

3.3. Computer-aided protein research

3.3.1. Computer-assisted protein prediction

At present, there are about three mainstream strategies for protein function prediction [31]. First, the similarity of protein sequences was compared. During the evolutionary process, the homologous proteins changed, but the sequences still had some similarity. Proteins with high homologous similarity were found in the database through screening software for function comparison [32]. Secondly, based on the prediction function of structural similarity, the arrangement of amino acids has changed after cumulative evolution and sequence similarity method has become ineffective. We can use the three-dimensional structure of proteins to find similar proteins and predict the function of proteins [33]. The most reliable method is to screen proteins through local structural overlap, that is, the similarity of the evolved residues around the active site, so as to narrow the screening range, reduce the amount of calculation and reduce the false positive rate [34]. Thirdly, the machine learning method of artificial intelligence is used to implant the discrete vector of the measured sequence and put it into the computer algorithm to judge the subcellular localization of proteins [35], which is mostly used to capture proteins that have not obtained the sequence or have similar functions [36].

In the study of the structure and function of novel coronavirusM protein and the prediction of the dominant epitope of B cell [37], a computer-assisted method was used. The base sequence of M protein was found in NCBL GenBank database [38], and the physicochemical properties were analyzed by ExPASy online soft [39] ProtParam. The secondary structure of M cells was predicted in SPOMA of ExPASy [40], and its tertiary structure was predicted by GOR. The M protein parameters were measured by ExPASy, and the dominant epitope of M protein B cell was predicted by antigenicity index. Finally, the novel coronavirusM protein was compared

with other coronavirus proteins in Vector NTI [41]. From this, we can determine the dominant epitope of B cells, immune recognition, and help vaccine development.

3.3.2. Computer-assisted protein screening

Virtual screening technology is mainly used for protein screening [42]. Clark first proposed computer virtual screening technology in 1994. Screening technology is to screen molecules based on computer methods based on the analysis of biological structure. At present, it is mainly used for the discovery of protein targets, that is, to search for the unknown molecules that can act through known proteins, namely, reverse screening [43]. This is now the dominant strategy for finding targets based on proteins.

In traditional Chinese medicine, the process of exploring the active components of traditional Chinese medicine on target protein relies on computer virtual screening technology. According to the clinical reactions of COVID-19, part of the traditional Chinese medicine used to treat the disease and the molecular components that may play a role were selected [44]. In order to study the treatment will be coronavirus (SARS - CoV - 2) active ingredients of traditional Chinese medicine [45], extract the SARS - CoV - 2 to reproduce the key proteins in the process of 3 cl hydrolysis enzyme protein as a target protein, select three ye qing Chinese native medicine ingredient, using Vina software [46] screening of amt has affinity with its target protein of the three molecules, molecular docking, find and 3 cl protein has good combining ability of the compound (flavonoid, phenolic acid and styrene glycosides compounds) [47]. PyMoL and LigPlot software were used to discover the binding mechanism between protein and molecule and the action mechanism of amino acids, which provided a direction for the research of new drugs for the prevention and treatment of SARS-CoV-2 [48]. At present, some prescriptions, such as Qingjie Anti-Infectious Mixture and Jinlian Disinfecting Decoction, have been used for clinical prevention and treatment of COVID-19 [49]. Computer virtual screening facilitates the reverse screening of target proteins, accelerates the rate of compound discovery, and enables the high-throughput screening of traditional Chinese medicines with large quantities and complex active components [50], greatly improving the efficiency.

4. Computer aided pharmacokinetic monitoring

Drug metabolism [51] refers to the process in which the chemical structure of a drug is changed by a variety of biochemical reactions after entering the organism [52], which plays an important role in drug research and development. The development of computer programs for the study of pharmacokinetics [53-54] can be traced back to the 1960s. The applications of these programs are mainly to calculate pharmacokinetic parameters by using the nonlinear least two percent method [55] and to simulate the dynamics of drug processes in vivo. With the rapid development of computer technology, computer program software plays a more and more important role in the experimental study of drug metabolism.

Drug metabolism detection by traditional experimental methods [56] consumes time and materials, and preliminary results can only be obtained at the later stage of the experiment [57-58]. In contrast, the application of computer programs to predict drug metabolism in vivo saves time and effort. While saving time and cost, preliminary data can be obtained in the early stage of drug development [59] so as to provide guidance and evaluation for further drug development. At the same time, in the traditional process of new drug development, there is a large span between the two steps of in vitro, animal experiment and in vivo experiment, and the intermediate links are miscellany and the influencing factors are complex [60-63]. In the evaluation experiments on efficacy and safety, in vitro experimental materials are mostly used. Although humanoid materials or animals close to human are selected as experimental objects, sometimes they still fall far short of clinical efficacy and safety detection requirements [64-65]. Social factors, such as the unique ethical attributes of human society, the size of drug samples,

age and gender limitations, also greatly affect the effect of human drug research experiments. However, through the computer technology is based on the experimental model of human body in vitro prediction can be used as a bridge to better join in vitro [66], and in vivo animal experiment, more realistic simulation of drug metabolism in human body [67], simplifying the development step, overcome all kinds of social ethical reality factors, thus reducing the elimination rate of clinical experiment.

Simcyp is in the late ninety s at the university of Sheffield Geoff Tucker [69], a professor of waiting by the target population variability and pharmacokinetic behavior of whole integrate to write prediction software, the principle of which is combined with the target groups of various kinds of feature information, through the monte carlo method to simulate the virtual crowd's pharmacokinetic behavior, estimate the clearance rate of drug in the body [70]. The calculation contents mainly include three aspects: prediction of liver clearance rate, prediction of intestinal clearance rate, and plasma clearance rate after intravenous and oral administration. The benefits of using this software, can more fully in the case of considering the variation in the process of evaluation [71-72], can reduce the limitation of the age, clinical trial subjects size can better given by the body of children of drug metabolism and organ tolerance and adult differences due to different experimental results and predicted more in line with the experimental results of children, can better consider due to the different ethnic influence on drug clearance [73-74]. The shortcomings of this software are as follows: the workload of obtaining external parameters is very large and the software cannot provide convenient ways for it; the simulation and information integration of the software itself are not perfect either.

However, it is worth mentioning that it has been 20 years since the software came into being. During this period of time, computer technology and artificial intelligence have developed rapidly, and its application in pharmacokinetics has been comprehensively deepened, and its development potential has also been increasingly recognized. It can be predicted that in the future development, they will also increasingly become the mainstay of pharmacokinetic research [75]. Although the computer simulation of drug metabolism model cannot completely replace the real clinical trial, it plays an important role in saving time and cost, improving the safety of clinical trial and weakening the limitations of clinical trial in the process of research and development.

5. Conclusion

The application of computer technology in the biomedical industry has become a research hotspot in the biomedical field in recent years. A series of problems, such as how to design a more accurate drug prediction platform and how to design a more efficient drug design software, have attracted a number of researchers to devote themselves to the field of computer biomedical. In some aspects, computer technology still has some aspects that cannot go beyond animal experiments and clinical experiments, and computer technology still has considerable limitations in the process of biomedical research and development. However, there is no doubt that computer technology is an important method of innovation and development in the field of biomedicine in the future, and it is a hot direction in the field of biotechnology. In the next few years, we hope to hear about computer technology in many other areas of the biomedical field, not just oncology medicine.

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