Screening of Tumor Markers and Targeted Therapy Strategy Based on Bioinformatics

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Abstract: This article mainly discusses the application of bioinformatics in tumor marker screening and targeted therapy strategy research, and provides theoretical support for precise tumor treatment. Methods Literature review and inductive deduction were used to systematically expound the basis of bioinformatics and sort out its application process and principle in tumor marker screening and targeted therapy strategy. In the screening of tumor markers, the process of data collection, differential expression and functional enrichment analysis based on bioinformatics is introduced. In the part of targeted therapy strategy, the strategy design based on tumor markers and the optimization function of bioinformatics are analyzed. It is clear that tumor markers can be divided into protein, carbohydrate antigens and other categories. Based on bioinformatics screening, differentially expressed genes such as cell proliferation and apoptosis regulation related pathways are found. In targeted therapy, there are effective targeted drugs for human epidermal growth factor receptor 2 (Her-2) positive breast cancer and epidermal growth factor receptor (EGFR) mutant non-small cell lung cancer. Bioinformatics is of great value in the screening of tumor markers and the study of targeted therapy strategies, which can efficiently mine potential markers and help design accurate targeted therapy schemes.

1. Introduction

Tumor, as one of the major diseases that seriously threaten human health today, its incidence and mortality are increasing year by year [1]. According to the relevant report of the World Health Organization, the number of new cancer patients in the world is huge every year, and the number of people who died of cancer is also high. The complexity and heterogeneity of tumors make traditional treatment methods, such as surgery, chemotherapy and radiotherapy, have many limitations in dealing with tumors [2]. Therefore, it is urgent to explore more accurate and effective tumor treatment strategies. Bioinformatics is playing an increasingly critical role in the field of life sciences [3]. With the help of advanced information technology, it efficiently stores, manages, analyzes and interprets massive biological data, such as gene sequence data and protein structure data. In the field of tumor research, the application of bioinformatics has opened a new perspective and approach for us.

Bioinformatics has shown unique advantages in screening tumor markers [4]. Tumor markers, as a kind of substance reflecting the existence and growth of tumors, are of great significance for early diagnosis, disease monitoring and prognosis evaluation of tumors [5]. Traditional screening methods for tumor markers have some problems, such as low efficiency and low flux, and it is difficult to comprehensively and systematically mine potential tumor markers. Bioinformatics, by integrating various biological database resources and using powerful data analysis algorithms, can quickly and accurately screen out potential markers such as genes or protein closely related to tumor occurrence and development [6]. Bioinformatics is also indispensable in the study of targeted therapy strategies. Targeted therapy, aiming at the specific molecular target of tumor cells, aims to design and use drugs to strike accurately, so as to achieve the purpose of treating tumors efficiently and reducing the damage to normal tissues [7]. Bioinformatics can deeply analyze the molecular

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biological characteristics of tumor cells, clarify the target of drug action, and assist in designing more accurate and effective targeted therapy programs. Bioinformatics can also predict the effect of targeted therapy and the emergence of drug resistance, providing an important basis for timely adjustment of clinical treatment programs.

At present, a lot of research has been carried out on bioinformatics in tumor marker screening and targeted therapy strategy. Some studies have successfully screened out a number of tumor markers with clinical application potential, and developed corresponding targeted therapeutic drugs based on these markers, which significantly improved the therapeutic effect and quality of life of some tumor patients. This study will systematically expound the application principles, methods and progress of bioinformatics in tumor marker screening and targeted therapy strategy, aiming at providing theoretical support and new ideas for accurate diagnosis and treatment of tumors.

2. Fundamentals of bioinformatics

The core of bioinformatics lies in the collection, storage, analysis and interpretation of massive biological data by using information technology to reveal the mystery behind life phenomena. Bioinformatics has abundant database resources, which provides massive data support for research. Among them, the gene database contains the gene sequence information of many organisms around the world [8]. Through this database, researchers can obtain detailed sequences of specific genes and understand their distribution and variation in different species. The protein database focuses on storing the three-dimensional structural data of protein. These data are very important for studying the function, mechanism of action and drug design of protein.

Sequence alignment technology is one of the commonly used data analysis methods in bioinformatics. By comparing the similarities between different biological sequences, it infers their evolutionary kinship and functional relevance. Another important technology is gene expression data analysis, which can detect the changes of gene expression level under different physiological or pathological conditions. By analyzing the gene expression data of tumor tissue and normal tissue, differentially expressed genes closely related to tumor occurrence and development can be screened out.

The application of bioinformatics in tumor research is based on the deep mining of tumor-related biomolecule data. The occurrence and development of tumor involves many genes and abnormal changes of protein [9]. Bioinformatics constructs tumor molecular maps by integrating genomics, transcriptomics, protein genomics and other omics data. Based on these data, bioinformatics can provide comprehensive and accurate information for early diagnosis, accurate classification, treatment target discovery and prognosis evaluation of tumors, and lay a solid foundation for individualized treatment of tumors.

3. Screening of tumor markers

3.1. Definition and classification of tumor markers

Table 1: Classification table of tumor markers

Category	For example	Characteristic
Protein tumor markers	Carcinoembryonic antigen (CEA) and alpha-fetoprotein (AFP)	Some of them are also expressed at a low level in normal people, but they are significantly increased when tumors occur.
Carbohydrate antigen tumor marker	Carbohydrate antigen 125(CA125) and carbohydrate antigen 19-9(CA19-9)	Most of them are produced by tumor cells, and their levels are related to tumor size and stage.
Enzyme tumor markers	Prostate specific antigen (PSA), neuron specific enolase (NSE)	Abnormal increase in activity in specific tumor tissues.
Gene tumor markers	Specific gene mutation sites, fusion genes	Directly reflecting the genetic variation of tumor cells has important guiding significance for targeted therapy of tumors.

Tumor markers refer to a class of substances synthesized and released by tumor cells themselves

or produced by the body's reaction to tumor cells during the process of tumor occurrence and proliferation. These substances can reflect the existence and growth of tumor and its influence on the body, which is of great significance in early diagnosis, disease monitoring, curative effect evaluation and prognosis judgment of tumor. According to the chemical properties and sources of tumor markers, they can be roughly divided into the following categories (see Table 1: Classification Table of Tumor Markers).

3.2. Process of screening tumor markers based on bioinformatics

The first step of screening tumor markers based on bioinformatics is comprehensive data collection. There are a wide range of data sources, including the public database (TCGA, The Cancer Genome Atlas, which contains genome and transcriptome data of various tumor types). When collecting data, strictly control the quality of data to ensure that the sample information is accurate and complete, covering the relevant data of tumor tissue and normal control tissue.

After data collection is completed, enter the critical data analysis stage. Firstly, the differential expression analysis was carried out, and the expression level of gene or protein in tumor tissue and normal tissue was compared by statistical method, and the molecules with significant differential expression between them were screened out. Then, functional enrichment analysis was carried out to explore the biological processes, cell components and signal pathways of differentially expressed molecules with the help of gene ontology and Kyoto encyclopedia database, so as to understand their potential functions. Studies have found that some differentially expressed genes are significantly enriched in the regulatory pathways of cell proliferation and apoptosis, suggesting that these genes may be closely related to the occurrence and development of tumors (see Table 2: Functional enrichment analysis of differentially expressed genes).

Table 2: Functional enrichment analysis of differentially expressed genes

Biological process of enrichment	Enriched signal pathway	Number of related differentially expressed genes
Cell proliferation regulation	PI3K-Akt signal path	15
Apoptosis regulation	P53 signaling pathway	10
Cell cycle regulation	Cell cycle signaling pathway	12

The preliminary screening of potential tumor markers needs further verification. Usually, experimental methods are used, real-time fluorescence quantitative PCR(qRT-PCR) is used to verify the expression level of genes, protein western blot is used to detect the expression of protein, and immunohistochemistry is used to determine the location and expression distribution of markers in tissues. Only the markers that have been strictly verified for many rounds have high credibility and potential clinical application value.

3.3. Advantages and challenges of screening tumor markers by bioinformatics

Advantages: Bioinformatics is efficient and comprehensive in screening tumor markers. It can process massive data at the same time, quickly screen a large number of potential markers, and greatly shorten the screening cycle. In addition, by integrating multiple omics data, we can understand the molecular characteristics of tumors from multiple levels, and mine more specific and sensitive markers to provide strong support for accurate diagnosis and treatment of tumors.

Challenges: This method also faces many challenges. On the one hand, the data quality is uneven, and the data generated by different databases and experimental platforms are different, which may lead to inaccurate results. On the other hand, there may be false positive or false negative results in data analysis. For example, in differential expression analysis, some molecules that are not truly differentially expressed may be misjudged as tumor markers due to the limitation of sample size or statistical methods.

4. Targeted therapy strategy

4.1. Design of targeted therapy strategy based on tumor markers

As an important breakthrough in the field of tumor therapy, the basic principle of targeted therapy is to accurately locate the specific molecular targets of tumor cells according to the differences between tumor cells and normal cells in molecular biology, and to design and use corresponding drugs for specific intervention. Its development has gone through exploration and innovation, and it relies on traditional chemotherapy in the early stage with great side effects. With the development of molecular biology, imatinib started a new era of targeted therapy. Since then, more targeted drugs have improved the therapeutic effect and quality of life of many cancer patients.

Tumor markers play a key guiding role in the design of targeted therapy strategies. Through the detection and analysis of tumor markers in tumor patients, the molecular characteristics of tumor cells in patients can be clarified, and then the most suitable targeted treatment scheme can be selected for them. For example, for HER-2 positive breast cancer patients, trastuzumab, as a monoclonal antibody against HER-2 receptor, can specifically bind to HER-2, block its downstream signal transduction and inhibit the growth of tumor cells. In practical clinical application, it is necessary to consider a variety of factors to optimize the targeted therapy strategy. In addition to the detection results of tumor markers, individual differences of patients, such as age, physical condition, genetic background, and tumor heterogeneity, may affect the curative effect of targeted therapy. Therefore, it is very important to make an individualized targeted treatment plan by multidisciplinary team cooperation and combining clinical, pathological, molecular biological and other information.

4.2. The role of bioinformatics in the optimization of targeted therapy strategy

Bioinformatics plays an indispensable role in the optimization of targeted therapy strategies. On the one hand, it can explore new potential drug targets by analyzing a large number of tumor genome data. On the other hand, bioinformatics can predict the efficacy and drug resistance of targeted therapy. By constructing a mathematical model and integrating multi-source information such as tumor marker data, gene expression profile data and clinical treatment results, patients' response to specific targeted drugs can be predicted, which can provide reference for doctors to adjust treatment plans in advance and avoid ineffective treatment and delay of illness. In addition, bioinformatics also helps to evaluate the feasibility of combined targeted therapy. By analyzing the interaction network between different targets, it provides a theoretical basis for designing a reasonable combined drug regimen and further improves the effect of targeted therapy.

5. Conclusions

This study systematically expounds the application of bioinformatics in tumor marker screening and targeted therapy strategy. In the field of tumor marker screening, by integrating multi-source data with bioinformatics, through differential expression and functional enrichment analysis, many potential markers closely related to tumor occurrence and development, such as differentially expressed genes enriched in cell proliferation and apoptosis regulation pathways, are found, which provides the possibility for early diagnosis and disease monitoring of tumors. In terms of targeted therapy strategy, based on the detection of tumor markers, effective targeted drugs have been successfully developed for tumors with different molecular characteristics, such as HER-2 positive breast cancer and EGFR mutation non-small cell lung cancer, which has significantly improved the therapeutic effect. At the same time, bioinformatics plays a key role in discovering new targets, predicting curative effect and drug resistance, and optimizing the combination treatment scheme. However, the application of bioinformatics also faces the problems of uneven data quality and false positive or false negative analysis results. In the future, it is necessary to further improve data quality control and optimize data analysis methods, so as to give full play to the potential of bioinformatics in precise tumor treatment and bring more benefits to tumor patients.

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