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Analysis of the application of bioinformatics in the medicine

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Abstract. As humans develop, science is also rapidly evolving, and biological science and medical support are vital for humans need. The development of biology has been particularly important. It stretches from the initial understanding of plants and animals to human biology and micro molecular biology, from macro understanding of life to micro molecular biology. Although it has accumulated a lot of knowledge about biology, it still has many unknowns about this giant and precise system. However, in recent years, a new interdisciplinary and emerging discipline has greatly opened up people's understanding about biological information-bioinformatics. The most fundamental research target of bioinformatics is different sequences. The most important is the amino acid sequence of proteins and the base sequence of DNA. To study sequences and their constituent components, bioinformatics has another major research target - the biological database. This involves analysing the structure, connotation, and function of biological information through basic protein and nucleic acid sequences. Therefore, bioinformatics has made tremendous applications in the medical field. This research mainly analyzes and discusses the advantages and disadvantages of the application of bioinformatics in the medical field.

Keywords: bioinformatics, medicine, application.

1. Introduction

Bioinformatics combines computer science and mathematics to study the storage and connotation of information in biological systems and organisms. It is a relatively novel discipline that contains a wide range of knowledge and applications. Bioinformatics originated in the early stage of the development of computers, and in the 20th century, as the storage of computers and informatics rapidly developed, bioinformatics also made rapid progress. From the initial acquisition of all the gene sequences of a bacterium to the current acquisition of gene sequences of hundreds of species, humans have more and more biological information. The need to utilise them, analyse them, and understand them has become urgent. The emergence of this discipline has made it possible to collect transcriptional information from many complex systems and tissues. The concept of bioinformatics is to collect, analyse, and manage a large amount of biomolecular data, enable biological researchers in different fields to quickly and efficiently obtain the relevant information they need for research. It also expand people's understanding of this very complex biological system by sorting, processing, and mining this vast amount of biomolecular information.

Bioinformatics has many applications in bioscience, and its application in medicine is particularly important. Bioinformatics can greatly improve the efficiency of research and development in the medical field. The application of biological sciences in medicine is very extensive. It mainly includes genomics,

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transcriptome, drug development, clinical genomics, proteomics, metabolomics, and cancer research. In addition to the above, bioinformatics has many expanded applications, such as discovering disease genes, researching new disease genes, forming and analysing new drugs, and inferring personalised treatment of diseases. Overall, the development of bioinformatics has greatly expanded the scope of the medical field by the improve of medical accuracy and the research on new drugs [1].

The most widespread and fundamental application of bioinformatics is to determine and compare the similarities between gene sequences and amino acid residue sequences in order to determine homology. By comparing gene sequences with amino acid residue sequences, another application is to measure and compare the homology between gene sequences and protein primary structural sequences. As the DNA of different species are collected, information database gradually expands. The database of base sequences and protein primary structural sequences is also increasing. With the continuous filling of these databases, cloning and identifying homology have become more convenient. To this end, this research will analyze the different applications of bioinformatics analysis methods in the medical field.

2. Analysis of the application performance of bioinformatics

Nowadays, people can clone new gene sequences through computer calculations and analysing them. The comparison of homology can also further determine the specific position of chromosomes in new genes. People no longer need to use fluorescence in situ hybridization to determine the precise location of chromosomes. The source of chromosomes in DNA sequences is very clear in the HTGS database. This shows how important bioinformatics is in the process of locating chromosomes. The analysis of homology in biological structures does not only exist through pairwise comparisons. In recent years, the technology of comparing multiple sequences with each other is also developing. The comparison of homology of multiple sequences can be used to efficiently identify the source of infection, as well as to compare particularly significant sequence features in different organisms and perform cloning analysis to determine their kin relationship. Furthermore, the expansion of biological databases can also accurately predict virus transmission pathways and analyse and understand viruses in order to conquer them [2]. For example, in the case of Severe Acute Respiratory Syndrome (SARS) in 2003, computer software was used to locate and analyse the sequencing of its genome and the frequency of the occurrence of a certain gene. It was found that a complementary palindrome sequence with a length of 6 bp in the SARS virus was particularly rare when compared with other virus sequences. Therefore, the conclusion is that the rarity of this 6-bp complementary palindrome sequence may effectively help the virus to avoid the host's immune system, that is used for disease defencing, and improve its lifespan and vitality. Moreover, gene analysis and homology judgment can determine the transmission route and source of the virus. First, by analysing the gene and protein sequences of the virus and then comparing multiple sequences from the database, the final analysis concludes that the transmission route of SARS virus is from bats to civets and then to humans [3].

Bioinformatics also has a wide range of applications in the field of drug research. Bioinformatics is a very convenient and accessible tool for analysing the impact of drugs on the genome. Many studies are now devoted to explaining how drug molecules indirectly affect the organisation and the transcription of downstream genes after binding to target proteins' upstream, as well as how these affected downstream genes' operation to form new systems and interact with each other. However, it is difficult to refine this analysis accurately through charts and data. Because the relationship between a particular genome within an organism and other genomes are interconnected. When the first batch of drug molecules bind to the target protein upstream, the second batch of genes will also be affected. The affected gene will be passed down layer by layer, ultimately affecting all the genes in the second and third batches. The expansionary effects may be positive or negative, but there is a high probability that they will eventually have an overall impact on the whole body. For very complex drug systems and molecular genes' interactions, identifying each gene one by one and analysing it will consume a lot of time and effort.

It is very difficult to operate and requires a lot of resources. In current development conditions, the Bioinformatics Society is a very good tool to validate this research. There are many genes and the

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expressions they carry in the bioinformatics database, and such a platform can quickly and efficiently detect the expression of the entire genome. The Board Research Institute of the United States published a large number of databases and related research about analysing the impact and of drugs on human cells. This database is called Connectivity Map (CMAP). In this platform, it is possible to measure clearly whether each cell group undergoes upregulation or downregulation under the effect of certain drugs. It provides a solution to the two difficulties mentioned above. In the study of treating genomes of this drug, 1309 drugs were used to treat 6100 human cells. After processing, we can see the impact of these drugs on the human genome and on corresponding cells. It was found that the effects of some drugs not only affect their target cells, but also indirectly affect adjacent or partially overlapping downstream genes. For example, if a drug used to treat coronary heart disease has a significant positive correlation characteristic with some anticancer drugs in the genome expression profile of CMAP, it is likely that the drug to treat coronary heart disease has an impact on the cancer cells. This indicates that it may regulate cancer related genes and reflect some anticancer characteristics [4].

Bioinformatics also makes a significant contribution in integrating traditional Chinese and Western medicine. Traditional Chinese medicine is good at distinguishing symptoms and diagnosing sickness through the four diagnostic methods: looking, smelling, asking, and touching. The information process through the four diagnostic methods and herbs are used to mobilise the body's immune system and enhance the body's ability to resist diseases. The main treatment of traditional Chinese medicine is to achieve recovery by balancing the body's pathology with one's mental state. However, the development of traditional Chinese medicine still maintains a pre-scientific state. It analyzes pathology and regulating one's own mental state through the method of drug testing to alleviate diseases. The advantage of this is that from a macro perspective, it analyzes the human body as a whole instead of analyse a specific functional system. The downside is that many small system errors may lead to symptoms that cannot be detected. This results in making unstable and subjective judgments. In comparison, western medicine is good at distinguishing diseases. To achieve this, it starts from a subtle aspect to understand organisms, biomolecules, system structures, and other data then analyse the causes. Both specific systemic issues and micro treatment plans are highly effective without inconsistency. Nowadays, medicine is constantly refining research from the whole to organs, cells, and molecular biology. It processes from layer to layer, and it continuously analyse detailed information. Although basic medical theory is advancing, the perspective of body as a whole is constantly regressing. Ignoring the macro research direction has the opposite effect of increasingly focusing on small issues. From this perspective, the shortcomings of traditional Chinese medicine lie in insufficient reductionist thinking and research, while Western medicine lacks macro and holistic thinking. This is when bioinformatics comes into the play. Bioinformatics effectively combines the strengths of the two distinct type of medicines. Making it possible for medicine from different backgrounds to combine.

The study of the application of syndrome differentiation to the kidneys is a method of inferring internal symptoms of the body through external physical manifestations and reactions to pathogens. Therefore, in specific medical applications, there is a high probability of subjective judgment from both medical practitioners and patients, making syndrome differentiation difficult to be evaluated objectively and quantitatively. The information can be obtained through the four diagnostic methods, quantitative data and information can be analysed based on experience and research on the symptoms. Using the macroscopic network hypothesis proposed by Besedovsky in 1977 in Western medicine: a bidirectional information transmission system of the formation of neural endocrine immune. The three can be identical and mutually regulated because they share a common chemical information molecule and receptor, forming a multi-dimensional network like connection. It can be asserted that the human body is composed of countless networks of various sizes and links between functional organisms. These networks and functions will also be considered as the foundation of self-regulation. The normal expression function and the function of the human body are an ordered gene expression. Symptoms only occur when gene expression is imbalanced. To treat diseases, it is necessary to start with regulating gene expressions and use microscopic information and techniques to slightly improve imbalanced gene expressions and result they cause. To understand the causes and pathology, it is necessary to create

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interference in order to see changes, and this is where the application of traditional Chinese medicine is used. Traditional Chinese medicine meticulously observes changes in the human body by observing application systems, while the previously mentioned "measuring symptoms with drugs" can effectively construct a dynamic intervention method to improve system analysis and research [5].

Bioinformatics is also widely used to study the nervous system and its related diseases, as well as target genes for drug dependence. This study is about using bioinformatics to study the key genes that lead to opioid dependence in humans. Long term use of opioid drugs can cause atrophy of some brain functional areas and mental disorders. However, there is still no clear answer to the study of dependence on opioid drugs. By using bioinformatics to analyse what factors lead to dependencies, the result shows that all data is very discrete without any aggregation inference. The opioid dependence is closely related to inheritance, gender, and the genes present in the drug.

The function of GO is to upregulate or downregulate DECs. Upregulation of DECs and such materials mainly leads to neural development, apoptosis, and 27 other biological processes. Downregulation of DECs and such materials plays a significant role in cell development, apoptosis, and 36 other biological processes. The difference between upregulation and downregulation of DECs is that upregulation of DECs mainly exists in six similar parts of the cell exterior and nervous system, while downregulation of DECs exists in nine similar parts of the cell interior, even within the nucleus and blood granules. Functional differences are also slightly different between the two. The function of upregulation DECs molecules includes transcriptional activation activity, hormonal effects, and many others. The downregulated DECs has a slightly different molecular effect. The downregulation of DECs involves the binding of proteins and integrins. The two DECs have different positions, resulting in their different functions. Upregulation of DECs mainly occurs in the cancer signalling pathway and other 11 signalling pathways such as glioma. Downregulation of DECs mainly occurs in six signalling pathways, including insulin secretion and gastric acid secretion. Among them, P13K/Akt is a common signalling pathway that upregulates and downregulates DECs [6].

Bioinformatics can also serve as a commonly used tool for identifying and analysing the function and mechanism of Hub genes. This can be concluded by analysing the damage of kidney mitochondria in mice under hypoxic conditions. Oxygen is very important for living organisms. Oxygen can keep the oxygen metabolism in the human or mammalian body in a normal state. Oxygen can also promote the metabolism of mitochondrial cells, thereby maintaining a stable state of cellular energy. Mitochondria are primarily responsible for regulating cell viability (including apoptosis and ferroptosis) and it is a highly active organelle responsible for regulating inflammation. If the body is in a state of hypoxia, the fusion and fission of mitochondria in the body will change, which can lead to mitochondrial autophagy and oxidative phosphorylation. This leads to overall mitochondrial dysfunction. Mitochondrial dysfunction can ultimately lead to a series of related diseases, such as Parkinson's disease and other neurological disorders.

The kidney plays a significant role in regulating the state and balance of water and salt, and it is also an organ in the body that requires a large amount of energy to operate. Most mitochondria in the kidneys are produced by ATP. The clearance and production of ATP are directly related to the health of kidney mitochondria. Hypoxia is a major factor in renal ischemia-reperfusion (RIRI) injury. When RIRI is damaged. 1 α- BNIP3 mediated renal tubular cell mitochondria inhibit apoptosis and oxidative stress in RIRI cells through autophagy, thereby providing protection. The results showed that compared with the normoxia group at normal altitude, the glomeruli of mice at high altitude shows the characteristic of atrophy, and the surface cells of renal tubules increase in volume, leading to swelling and rupture. Analysis of KEGG pathway enrichment reveals that the DECs are highly enriched in Parkinson's disease signalling pathways, ribosomal signalling pathways, and other pathways related to mitochondrial function. This analysis indicates that high-altitude hypoxia environment induces some changes in the kidneys of mice by altering the function and mechanism of mitochondria [7]. In addition, such as vaccine candidate's discovery [8], drug-screening [9] and disease treatment [10]. As shown in Figure 1, bioinformatics can also be used to analyze the correlation between genetic variables and disease symptoms.

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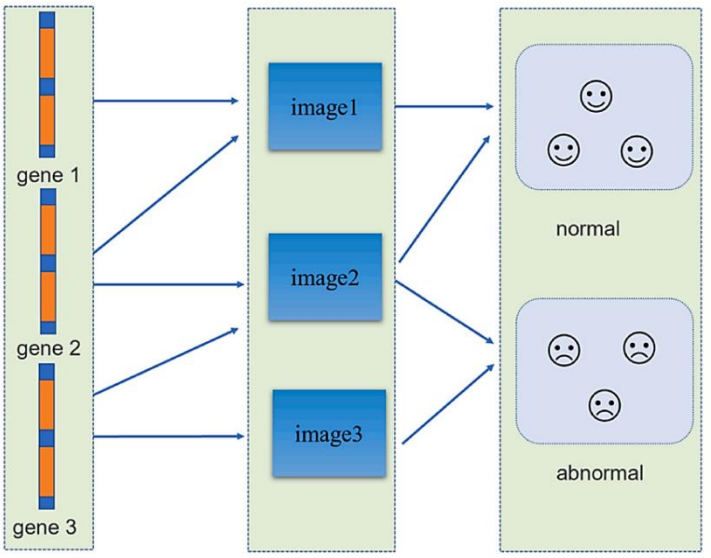

Figure 1. The correlation between genetic variables and disease symptoms [10].

3. Conclusion

Bioinformatics has a great role in contributing it the application of medicine science. This includes the comparing of similarities between gene sequences and amino acid residue sequences to determine homology and the transmission pathways of diseases, analysing the impact of drugs on the genome, combining the traditional Chinese and Western medicine, studying the nervous system, related diseases of the nervous system, and target genes for drug dependence, as well as identifying and analysing the function and mechanism of the Hub gene. In addition to these, bioinformatics also has many applications in other fields. By collecting more biological information and DNA sequences can be very effective in helping people to understand more human functions and mechanisms. Also, it can further improve our research on this huge and precise system. This new interdisciplinary field integrates two rapidly developing disciplines together. As the discipline of bioinformatics becomes more mature, this tool can also enable many diseases that biologists cannot solve or understand yet to be explored and treated in the future. This means that bioinformatics can greatly help people to treat some incurable diseases at current stage of development. Although bioinformatics still faces some controversy opinions, as this system is further improved and advanced, the more reliable data presents to the public will gain more trust and support from the people.

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