

Study on the Mechanism of Histone Methyltransferase G9a Inhibiting Liver Tumor Cell Proliferation based on Medical Big Data

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Abstract: While medical informatization has received unprecedented attention and development, there are also many problems in medical informatization due to the arrival of the big data era and the relatively backward development of traditional medical information technology. Medical big data will play a huge role in clinical decision-making assistance, medical quality supervision, disease prediction models, clinical trial analysis, personalized treatment and other medical services. This article investigates the mechanism of histone methyltransferase G9a inhibiting liver tumor cell proliferation based on medical big data. The occurrence of liver tumors was previously believed to be the result of mutations in tumor suppressor genes and oncogenes. Recently, more and more studies have shown that epigenetic regulatory mechanisms of gene expression, such as abnormal DNA and histone modifications, play a crucial role in tumor development. Compared with non cancerous tissues of liver cancer patients, the expression of G9a in liver cancer tissue is significantly increased, and knocking out the G9a gene can significantly inhibit the growth and invasion and metastasis of liver cancer cells, indicating a correlation between G9a and the occurrence of liver cancer.

1. Introduction

With the development of cloud computing, gene sequencing, modern clinical trials, targeted therapy and other technologies, big data and medicine will be highly integrated to achieve subversive medical care, and the medical and health industry will enter the era of big data. At the same time that medical informatization has received unprecedented attention and development, due to the arrival of the era of big data and the relatively backward development of traditional medical information technology, there are also many problems in medical informatization [1]. Applying and big data to hospital information construction is the only way to change the current situation of "chimney" hospital information system construction and application with high investment, low efficiency and difficult management, and to establish a new digital hospital information platform architecture system [2]. Autophagy of liver tumor cells plays a double-edged sword role in the development of tumor. On the one hand, when tumor cells are attacked by the outside world, such as the killing of tumor drugs and the existence of hypoxic environment, tumor autophagy, as a protective mechanism, can reuse macromolecular nutrients in tumor cells, which is a autophagy process that promotes cancer; On the other hand, when tumor cells are induced to autophagy deeply, the self-protection mechanism of tumor cells is not enough to resist the external pressure, and tumor cells will die of autophagy, which is a autophagy process to inhibit cancer. Based on medical big data, this paper studied the mechanism of histone methyltransferase G9a inhibiting the proliferation of liver tumor cells. In the past, the occurrence of liver tumors was thought to be the result of mutation of tumor suppressor genes and protooncogenes[3]. Recently, more and more studies have proved that the epigenetic regulation mechanism of gene expression, such as the abnormality of DNA and histone modification, plays a vital role in the occurrence of tumors [4]. The higher the expression of histone methyltransferase G9a, the shorter the survival time of patients with hepatocellular carcinoma and the worse the prognosis. At present, it is of great significance to find the specific target of each solid tumor in the treatment process. Compared with the application effect of CAR-T technology in hematological tumors, the effect of solid tumors is poor, which is caused by the complex microenvironment in solid tumors and

the lack of specific targets in solid tumors. At present, G9a inhibitors are mainly divided into two categories-natural product inhibitors and synthetic small molecule inhibitors. The structure of natural products is complex and the selectivity is low, while the chemical synthesis of small molecules has few structural types, lack of in vivo activity data, and they are all in the pre-clinical research stage, which limits their clinical development [5-6]. This paper mainly takes the demand analysis of medical big data as the main basis to complete the idea of related platform construction.

2. The application needs of medical big data

2.1 Support for the effectiveness of diagnosis and treatment plans

With the rapid expansion and geometric growth of medical and health data, how to fully utilize various data, including imaging data, medical record data, inspection results, diagnosis and treatment costs, and build a reasonable and advanced data cloud service platform based on cloud computing technology patient in a medical institution, the services provided by the hospital vary, resulting in different outcomes. Additionally, there are significant differences in the cost of many medical services provided by the hospital and once integrated through intelligent analysis and computer technology, secondary development of the data will generate great potential value[7-8].

Applying medical big data to a certain extent, for example, it can comprehensively analyze and compare many data of patients, and use many medical big data as the basis for comparison. The uncertainty in the interpretation of medical data can to some extent mislead and even cause unnecessary panic for patients [9]. As the American Society of Medical Genetics, through genetic testing, provides feedback on many genetic variations and says to participants, "We have found that these variations in your genes are important, but we don't know if they will make you sick or develop other diseases." Moreover, it is well known that if more sample data is collected, the final results will become more accurate, This is of great significance and role for both patients and medical service institutions [10].

2.2 Clinical assisted decision-making

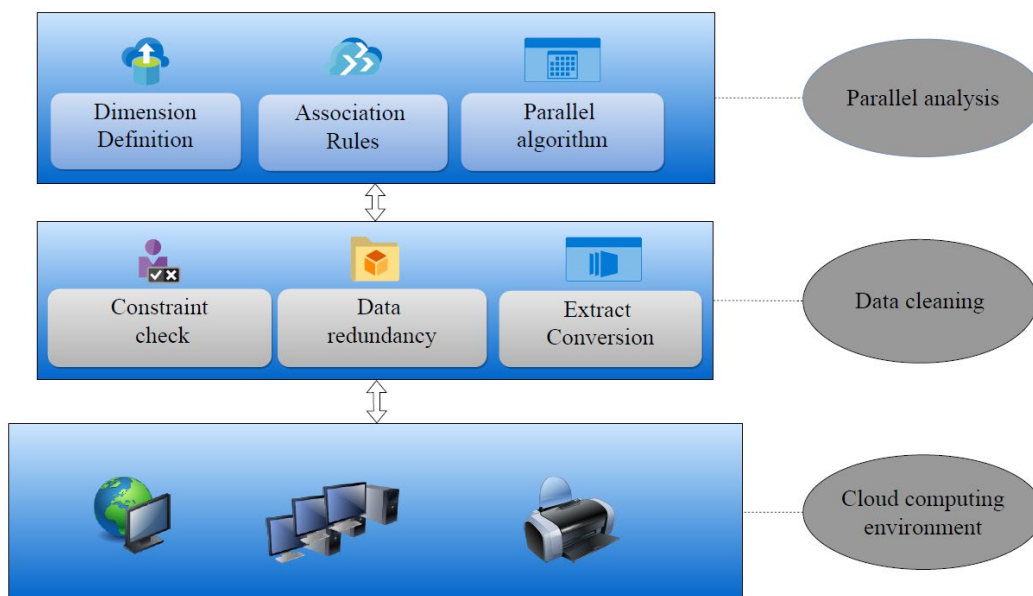


Figure 1 Architecture of a Distributed Data Mining Platform Based on Cloud Computing

It is common to use medication safely according to medical advice, as well as devise simple diagnosis and treatment plans. As shown in Figure 1, the distributed data mining architecture based on cloud computing is divided from bottom to top into cloud computing environment layers, including distributed file systems, parallel programming environments, distributed system management, data collection layer collecting data in parallel from various data sources, data cleaning layer including data constraint checking, redundancy processing, extraction transformation, and loading, and parallel

analysis layer mainly including dimension definition, association rule definition Parallel algorithms and report centers, etc.

According to the operation and performance data set set by medical service providers, data can be analyzed and visual flow charts and dashboards can be created to promote information transparency. With the development of the times, people's requirements for medical work have also improved significantly, and the application of medical big data in clinical auxiliary decision-making can make the decision-making more accurate. In every genetic electronic medical record, all potential diseases and drug sensitive information of individuals are recorded. According to the data in gene electronic medical records, combined with the patient's physiological indicators and medical intelligent decision support system, doctors conduct correlation analysis, simulate the effectiveness of clinical treatment, and finally form a personalized medical model.

3. Mechanism of histone methyltransferase G9a inhibiting liver tumor cell proliferation

3.1 Functions of G9a

G9a is the second histone methyltransferase discovered in mammals that catalyzes lysine methylation. Its main function is to participate in histone methylation, but it can also participate in DNA methylation and non histone methylation. The existing privacy protection technologies are mainly based on static datasets, and the typical features of massive, dynamic, shared, and cross retrieval of medical big data increase the risk of personal information leakage. Studies have shown that after knocking out G9a, the level of H3K9me2 in the perinuclear region is significantly reduced, and some genes in the promoter region that are suppressed by H3K9me2 can be restored to expression. Tumor stem cells are a small group of special cells in tumor tissues. Theoretically, all tumor cells can be developed from tumor stem cells. Tumor stem cells can be activated from dormant tumor stem cells and become self-replicating, or some ordinary tumor cells can be transformed into tumor stem cells through epithelial-mesenchymal transition. No matter which source, it is not the credit of one or two genes, and the larger-scale changes of chromatin modification at the genome level and its influence on transcription factors of "dry" genes may be the key molecular mechanism. The methylation of H3K9 inhibits gene transcription by recruiting transcription inhibitors, which tightly bind histones and DNA. The ultimate concern in medicine is a high recognition of the value of life, affirming that humans are a spiritual and cultural existence. Histone methyltransferase G9a is closely related to the autophagy process of cells. It is worth noting that different tumor cells and different degrees of autophagy will lead to different roles of G9a protein in killing tumor cells. As a mild attack, inducing tumor cells to autophagy in order to digest themselves through their own functions is a therapeutic direction worth exploring. However, "modern doctors focus on the instrumentalization, digitization, and computerization of diagnosis and treatment, while deviating from paying attention to the patient's psychology and spirit, thus separating the combination of medicine and humanities. In the era of medical big data, the potential value of data is mostly reflected in the secondary analysis of data. When collecting data, who will use this data and its purpose may be unknown, so users cannot be informed. In fact, G9a can also methylate its 239th lysine without changing its catalytic activity, thereby interacting with HP1, providing conditions for recruiting other regulatory factors such as HDAC1 and DNMT1.

3.2 The role of G9a in the occurrence of liver tumors

Under the framework of traditional medical system, there are many irrationalities in hospital informatization construction. First of all, the hospital internal information construction is unreasonable. For the hospital, the hospital information system is not the focus of its business, but a tool used by the hospital to realize its own medical business logic. In this paper, the mechanism of histone methyltransferase G9a inhibiting the proliferation of liver tumor cells was studied through medical big data. As shown in Figure 2, medical big data refers to the data set in the medical field that takes more than tolerable time to capture, manage and process data with conventional software tools. The typical characteristics of medical big data are mainly manifested in four aspects.

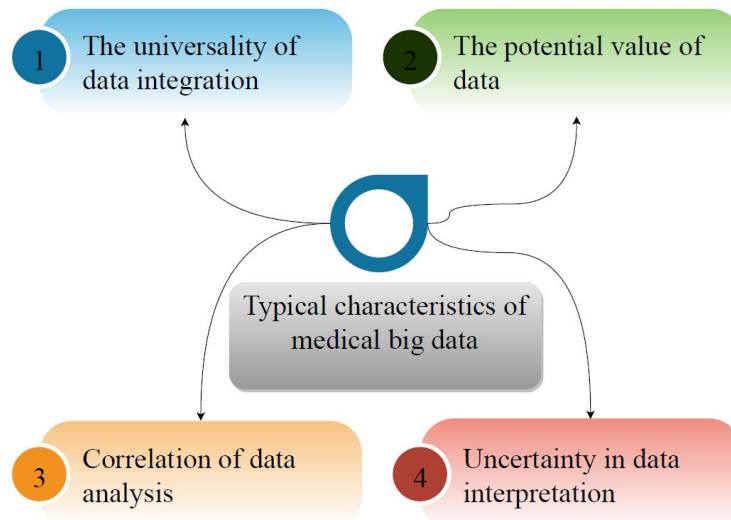


Figure 2 Typical characteristics of medical big data

Tumor is often regarded as a disease caused by genetic changes. More and more evidences show that the abnormal epigenetic modification of DNA and histone also affects the occurrence and development of liver tumors, and plays an important role in this process. Molecular markers of various tumors can be applied to clinical pathological classification, early diagnosis and prediction of tumor metastasis and recurrence. Epigenetic modification related to gene silencing can also be used as a marker for tumor pathological classification, early detection and prediction of tumor metastasis and recurrence. Patients are inevitably puzzled that doctors can see a doctor by tapping the keyboard and staring at the computer screen, and feel that they are not really listened to and understood. Then, the humanistic care such as contact and listening, patient communication, emotional comfort and value recognition between doctors and patients will be eroded. In the process of liver tumor, heterozygosity deletion and somatic mutation have higher genetic heterogeneity, and methylation of gene promoter region is common in all tumors. Cells with abnormal epigenetic modification have been found in many tumors such as breast cancer, lung cancer, head and neck cancer and ovarian cancer. At the same time, compared with the non-cancerous tissues of patients with liver cancer, the expression of G9a in liver cancer tissues is significantly increased, and the G9a gene knockout can significantly inhibit the growth and invasion and metastasis of liver cancer cells, indicating that G9a is related to the occurrence of liver cancer.

4. Conclusions

In summary, the application of medical big data conforms to the trend of the times and is a major system engineering. Therefore, while pursuing medical "technological goodness", we should also emphasize "ethical goodness", value human subjectivity, and respect the value of patients' lives. This article investigates the mechanism of histone methyltransferase G9a inhibiting liver tumor cell proliferation based on medical big data. Histone methyltransferase G9a is crucial in the growth and development of the body, and is closely related to the occurrence and development of tumors. It plays an important role in liver tumor cell proliferation, apoptosis, differentiation, and changes in motility. Explore the possibility of reversing epigenetic modifications and normalizing tumor cells by regulating the expression of G9a and other chromatin modified enzymes. Histone methyltransferase G9a is indeed highly expressed in liver tumor cell lines and does affect the proliferation and tumorigenesis process of tumor cells. Previous studies have shown that the proliferation ability of cells is related to cell dryness, while our research object, histone methyltransferase G9a, has been reported to be closely related to cell dryness. Therefore, there is still a considerable room for improvement in the utilization of medical big data in domestic medical institutions nowadays. Therefore, relevant staff need to continuously optimize and improve in the future work process, so that the domestic medical industry can continue to develop.

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