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A Dynamic Monitoring Method of DNA Synthesis Based on Electron Microscopy

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DNA synthesis is affected by many variables. The traditional dynamic monitoring method of DNA synthesis has a long response time, and the results of DNA synthesis can be seriously affected in the case of an abnormal situation. Therefore, a new design of the dynamic monitoring method of DNA synthesis based on electron microscopy is required. The dynamic monitoring data of DNA synthesis is collected, the dynamic monitoring indicator of DNA synthesis is established, the task of dynamic monitoring of DNA synthesis is divided, and then the matrix of dynamic monitoring characteristic co-efficient of DNA synthesis based on electron microscopy is constructed. The dynamic monitoring state of DNA synthesis is evaluated, and DNA synthesis is evaluated via the fault tree method. Finally, the dynamic monitoring database of DNA synthesis is established. The dynamic monitoring data of DNA synthesis is stored in the database, and the data of DNA synthesis is generated to analyze the dynamic synthesis of DNA, in order to complete the dynamic monitoring of DNA synthesis based on electronic microscopy. Experiments show that the designed dynamic monitoring method of DNA synthesis based on electron microscopy is shorter than that of the traditional monitoring method, which can detect the abnormal situation in DNA synthesis in a timely manner, in order to ensure the smooth progress of DNA synthesis tasks.

Keywords: Electron Microscopy, DNA Synthesis, Dynamic Monitoring, Task Division, Monitoring Blind Spot.

1. INTRODUCTION

DNA synthesis is a technology of synthesizing genes by artificial methods; this is one of the methods of gene acquisition. Compared with obtaining genes from existing organisms, DNA synthesis does not need templates, so it is not limited by gene sources. Through DNA synthesis, we can obtain genes that do not exist in nature, which can open up new directions for human beings to transform biology. DNA synthesis technology has important applications in the synthesis of genes and regulatory components, the redesign and assembly of gene circuits and biosynthetic pathways, and the artificial synthesis of genome. Since the 21st century, DNA synthesis technology has developed rapidly, and has been widely used in energy, diagnosis and treatment of major diseases, environment, medicine and other fields, with great social and economic benefits. At the same time, DNA synthesis has great flexibility, as it can modify the enzyme cutting sites and sequences of genes, facilitate downstream cloning and experiments, and researchers can design genes that are difficult to obtain or even do not exist in nature according to their own wishes. The genes synthesized by DNA can be optimized by Codon, so that the gene can be well expressed in various biological expression systems. However, DNA synthesis is impacted by multiple factors, which will have a certain impact on the results of DNA synthesis. At present, many scholars have studied the dynamic monitoring method of DNA synthesis, but there are some disadvantages in the research methods, such as large measurement error, low efficiency, and blind spots in monitoring. The traditional on-site monitoring methods cannot integrate the historical data to comprehensively evaluate the dynamic running state and measurement error of DNA synthesis, resulting in poor monitoring accuracy. The biggest problem is the long response

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time when DNA synthesis is abnormal and this research solves this issue. In order to solve this problem, a dynamic monitoring method of DNA synthesis based on electron microscopy is designed. Electron microscopy is a technology that uses high-resolution and magnification to analyze the characteristics of materials, such as morphology observation, energy dispersive X-ray analysis and so on. Electron microscopy is widely used in measurement, stereoscopic observation, image analysis, the electronics industry, defect detection and other fields. In recent years, with the rapid development and application of computer technology, the technology of image reception, transmission, processing and reproduction has been developed. At present, electron microscopy is moving towards a new scale of comprehensive microanalysis, and further towards electron microscopy control automation and electron micrograph analysis quantification. High resolution electron microscopy is also developing in a more accurate quantitative direction and has become one of the more attractive research fields. Therefore, the dynamic monitoring of DNA synthesis using electron microscopy technology can reduce the problem of long response times when the traditional monitoring methods have abnormal problems during DNA synthesis (Fayez et al., 2019; Somya and Shivani, 2019; Wanni and Fei, 2019).

The design method completes the dynamic monitoring of DNA synthesis based on electronic microscopy from four aspects: task division, status evaluation, real-time risk calculation and database establishment. The experimental results show that the dynamic monitoring method of DNA synthesis based on electron microscopy has a shorter response time than the traditional method when DNA synthesis is abnormal and can detect abnormal problems in DNA synthesis in a timely manner.

2. OVERALL FRAMEWORK OF DYNAMIC MONITORING OF DNA SYNTHESIS BASED ON ELECTRON MICROSCOPY

Using the design concept of front-end collection (Yat-Tung and Pang-Chui, 2017), back-end analysis and processing, the whole process of dynamic monitoring of DNA synthesis is divided into four steps: task division of dynamic monitoring of DNA synthesis, status evaluation of dynamic monitoring of DNA synthesis, dynamic real-time risk calculation of DNA synthesis and establishment of dynamic monitoring database of DNA synthesis. The interaction in the process of monitoring is through the data network. RMI / JMS mode is used to transmit and interact with the dynamic information of DNA synthesis. Among them, the dynamic monitoring task division of DNA synthesis includes the functions of data collection, monitoring indicator establishment and monitoring task weight determination. The dynamic monitoring state evaluation of DNA synthesis and the dynamic and real-time risk calculation of DNA synthesis are currently the main dynamic risk values of DNA synthesis. The establishment of a dynamic monitoring database of DNA synthesis provides the basis for DNA synthesis data analysis. The overall framework of dynamic monitoring of DNA synthesis based on electron microscopy is as follows:

According to Figure 1, the input layer is the initial operation data and state record during DNA synthesis. The data input matrix can be formed through fuzzy processing, and the fuzzy moment calculation of the evaluation indicator layer can then be used to get the evaluation results of the DNA synthesis state. As required, input layer data will be obfuscated, meaning that precise scripts cannot be used under certain obfuscated rules. The quantitative values presented by the generic relationship are subdivided to form a more practical state feature matrix (Ran and Reuven, 2017; Bettina and Nadezda, 2018). The criterion layer is the middle layer, which contains a variety of evaluation indicators that affect the running state of DNA. The target layer is the degree of recognition of the DNA abnormal state and the output result of online state monitoring. The data quantification is the key to affecting the dynamic monitoring accuracy of DNA synthesis. In the monitoring process, the fuzzy matrix can use the fuzzy function to quantify the logical relationship between various factors, that is to say, the fuzzy operation is used to get the fuzzy quantization value of each target in the layer, and then get the running state of DNA synthesis through the database.

3. DESIGN OF DYNAMIC MONITORING METHOD FOR DNA SYNTHESIS BASED ON ELECTRON MICROSCOPY

3.1 Dynamic Monitoring Task Division of DNA Synthesis

Before dividing the dynamic monitoring task of DNA synthesis, the dynamic monitoring data of DNA synthesis is collected (Kristijan et al., 2017; Lei et al., 2018; Christopher 2018; Cavanaugh and Bathrick, 2017). The execution process of the on-site sampling task is such that when the event of updating the sampling value triggers the interruption, the reading operation of some parameters needs to be carried out many times, the read results are then merged and the necessary conversion is made. Finally, the processed data values are put into the data buffer for waiting Ethernet control task processing. The following is the workflow of on-site sampling task service.

On this basis, the dynamic monitoring indicators of DNA synthesis are established. Indicators are a group of information reflecting the characteristics of the system or showing what has happened. The selection of indicators and the construction of the indicator system is one of the important components of DNA synthesis dynamic monitoring. Only by establishing a perfect indicator system and defining representative indicators can we achieve better dynamic monitoring of DNA synthesis and promote the progress of dynamic monitoring of DNA synthesis. The establishment principle of indicators is shown in Figure 3.

According to the actual dynamic monitoring of DNA synthesis, the monitoring indicators (Doan et al., 2017; Wu et al., 2018) are established, and the dynamic monitoring tasks of DNA synthesis are divided according to the importance

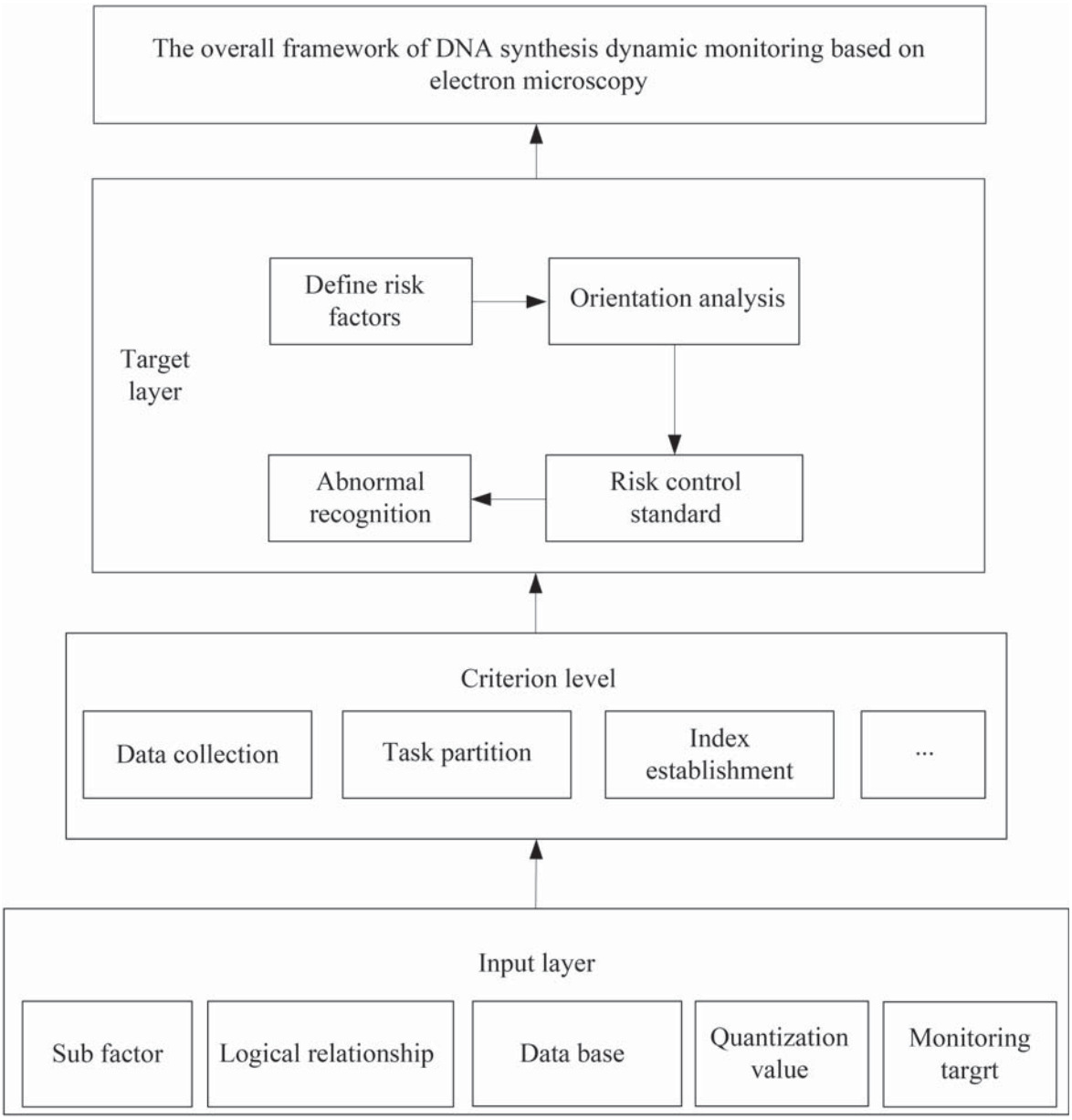

Figure 1 Overall framework of DNA synthesis dynamic monitoring based on electron microscopy.

of the monitoring indicators. Due to the different viewing formats of DNA synthesis data and data generated in the monitoring process, the calculation formula for the format conversion of monitoring data is as follows:

$$g = \frac{d}{\sum_{x} a * cm} \tag{1}$$

In Equation (1), g represents the dynamic monitoring information of DNA synthesis, $\sum_{x} a$ represents the data conversion factor, cm represents the conversion format, and d represents the initialization parameters of the dynamic monitoring of DNA synthesis based on electron microscopy.

On the basis of the format conversion of the above-mentioned monitoring data, the information fusion method is used to co-ordinate the monitoring tasks under the management, so the whole monitoring task division is designed based on the real-time DNA synthesis process. Therefore, it is necessary to divide the required tasks reasonably, assign an appropriate priority to each task, and specify the shared data transfer method used when calling between tasks. The task division and correlation of dynamic monitoring of DNA synthesis based on electron microscopy are shown in Figure 4.

According to the above principles, the dynamic monitoring data of DNA synthesis is divided, the threshold value is set, and the level of monitoring task is divided. The calculation formula is as follows:

$$Q|g| = l \Rightarrow \sqrt{C_f * va} \tag{2}$$

In Equation (2), $Q|H|$ represents the dynamic information of DNA synthesis, l is the set threshold value, C_f is the grade judgment parameter, and va represents the monitoring information.

In actual use, if $l \leq 1$, it means the monitoring task is important; if $l > 1$, it means the monitoring task is not very important. If the threshold value is exceeded, it will be divided

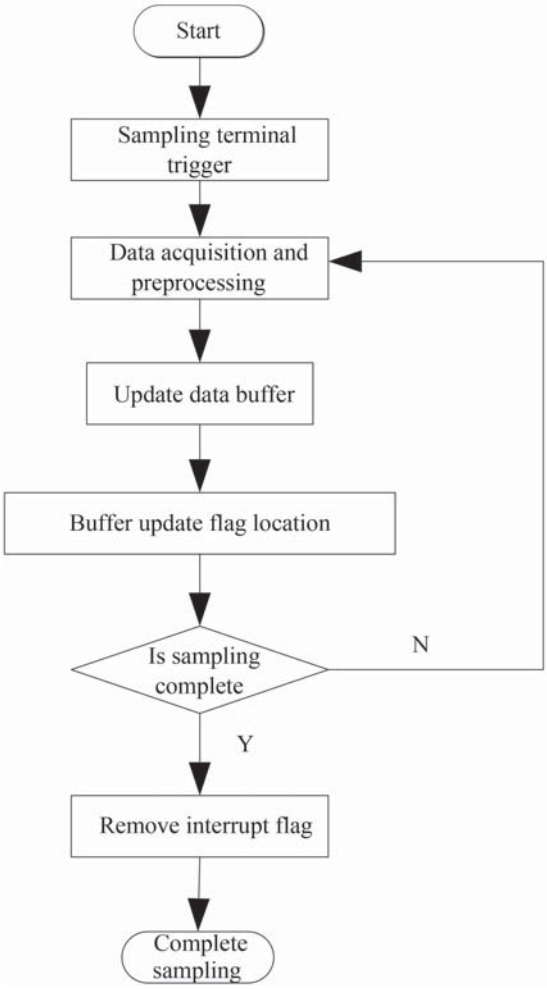

Figure 2 Sampling process of dynamic monitoring data of DNA synthesis.

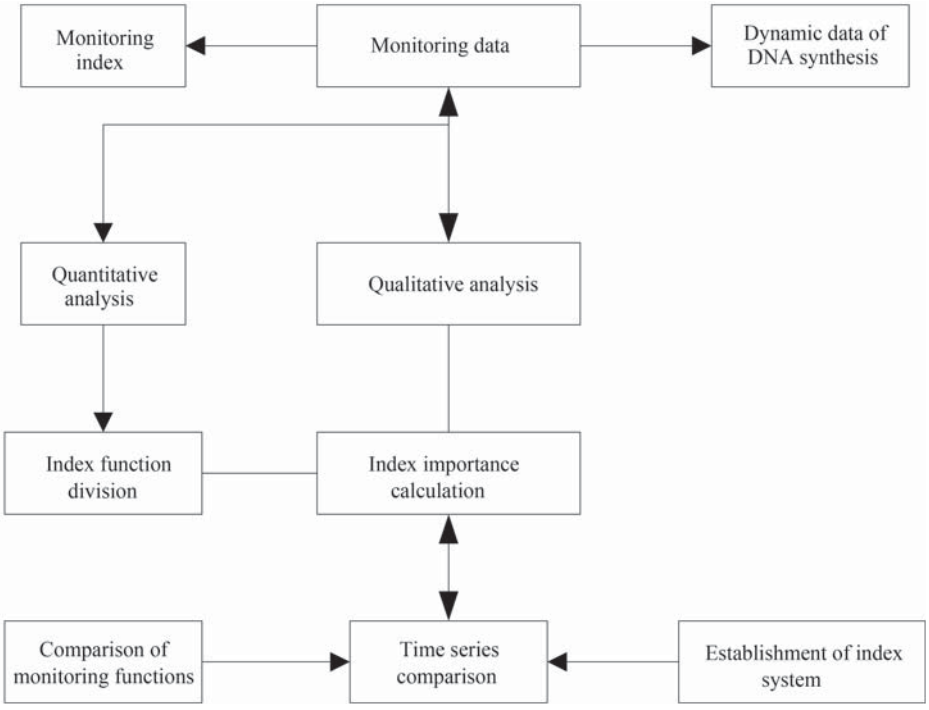

Figure 3 Establishment of dynamic monitoring indicators of DNA synthesis.

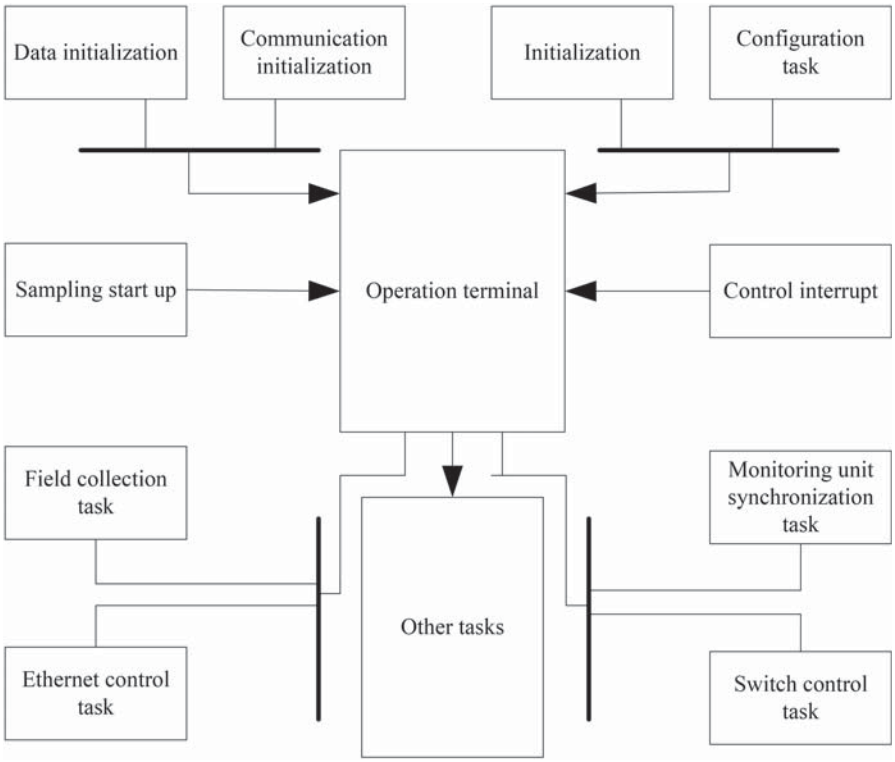

Figure 4 Task division and correlation diagram of DNA synthesis dynamic monitoring.

into the primary monitoring content, and a corresponding monitoring report will be generated in time to provide the basic inspection basis for dynamic monitoring of DNA synthesis.

3.2 Evaluation of Dynamic Monitoring of DNA Synthesis

According to the dynamic data of DNA synthesis collected above, the dynamic list of DNA synthesis is obtained, from which the characteristic co-efficients matrix of dynamic monitoring of DNA synthesis based on electronic microscopy is extracted and constructed (Siegel et al., 2018; He et al., 2018; Rykova et al., 2017). By using the 1–9 scale method, the dynamic judgment matrix of DNA synthesis is constructed, and the column vector R_1, R_2, R_3, R_4, R_5 of the fuzzy membership matrix of the sub factors in the input layer and the corresponding evaluation indicators in the criterion layer are obtained, and the consistency test of the evaluation matrix of DNA synthesis state is carried out to determine its rationality. Firstly, the collected data must be standardized, and the standardized processing process is as follows:

Where, the specific data specification processing formula is:

$$D = \frac{A|d * g.f|}{F * S} \tag{3}$$

In Equation (3), D is the weight value of each element in the collected data, F represents the influencing factors of the collected data, A is the target state parameter of DNA synthesis, and $d * g.f$ is the standardized parameter.

After the above calculation, the fuzzy quantized row vector of the DNA synthesis state is obtained, then the state evaluation coefficient matrix of the target layer is obtained by the combination operation, and its defuzzification. The calculation process of the DNA synthesis state evaluation is as follows:

$$G = \frac{R}{B}/K_i \tag{4}$$

In Equation (4), G is the fuzzy quantized value of each sub object in the input layer, B is the fuzzy quantized value of sub object, R is the evaluation parameter of the monitoring state, and K_i is the evaluation parameter of the operation state.

According to the above process, the state evaluation of dynamic monitoring of DNA synthesis is completed, which provides the basis for dynamic monitoring of DNA synthesis.

3.3 Dynamic and Real-Time Risk Calculation of DNA Synthesis

Due to the complexity of the DNA synthesis process, in order to improve the real-time performance of the dynamic monitoring of DNA synthesis, the purpose of dynamic and real-time risk calculation of DNA synthesis is to provide a timely reminder when there is abnormal situation in the dynamic rand real-time risk calculation of DNA synthesis (Yanf et al., 2018; Yan et al., 2018; Wang et al., 2019). Firstly, risk factors are defined, which are based on the development of probabilistic security technology. According to the risk factors, the process and real-time dynamics of DNA synthesis are determined to decide the real-time risk in the process of DNS synthesis. At any time of DNA synthesis, the current DNA synthesis process can be reflected according to the state of risk factors, so that the risk information of DNA synthesis

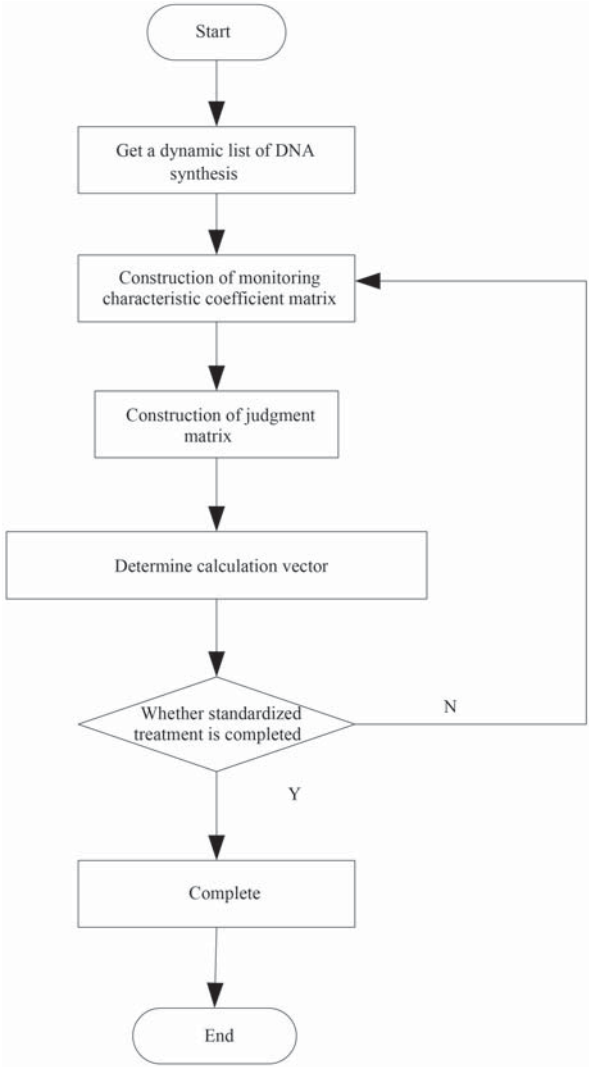

Figure 5 Data normalization process.

can be easily obtained in a timely manner, in order to achieve a targeted risk management of DNA synthesis, ensure that the risk of DNA synthesis is in a known and controllable state, and reduce the possibility of DNA synthesis errors. Therefore, in order to better evaluate the risks of DNA synthesis, a qualitative analysis of the fault tree is used to set the risk control standard. Qualitative analysis of the fault tree is the most critical step of risk factor analysis of DNA synthesis and the basis of quantitative analysis. The purpose of fault tree qualitative analysis is to find out the basic events or combinations of basic events that lead to top events, and to find out all the minimum cut sets of the fault tree. For a fault tree, it can be simplified to the form consisting of only logic and gate, logic or gate, logic non gate and bottom event. A fault tree consists of n independent bottom events, where x_i represents the state variable of the second event and φ represents the state variable of the top event. The structure function of fault tree can be expressed as $\varphi = \varphi(x_1, x_2, \ldots, x_n)$. The structure function of the fault tree reflects the functional relationship between DNA and each unit. Therefore, if the system structure function can be obtained, the relationship between the system and the unit will be clear. Figure 6 shows a simple fault tree:

As the fault tree in the DNA synthesis process is very complex, and the structural function φ of a boolean variable is also very complex, boolean algebra rules can be used to simplify, develop and absorb the expression in the form of the sum of product, which is convenient for analysis and calculation. The calculation formula is:

$$G = \phi * \frac{(x_1, x_2, x_3, \ldots, x_n)}{\sum_a q} \tag{5}$$

In Equation (5), $\sum_a q$ is the bottom event subset, x_1, x_2, x_3, x_n, etc. all represent the cut set corresponding to the fault tree, and ϕ is the minimum cut set judgment parameter.

One of the minimum cut sets represents a failure mode of the system, so the structure function of the fault tree can be represented by the minimum cut set. Based on this model, the DNA synthesis process was quantitatively analyzed, and the failure mode of the system was determined by qualitative analysis. In addition, the impact of each bottom event on the top event should be quantitatively analyzed. The purpose of the quantitative analysis of the fault tree is to calculate the probability and uncertainty of the top event and the importance

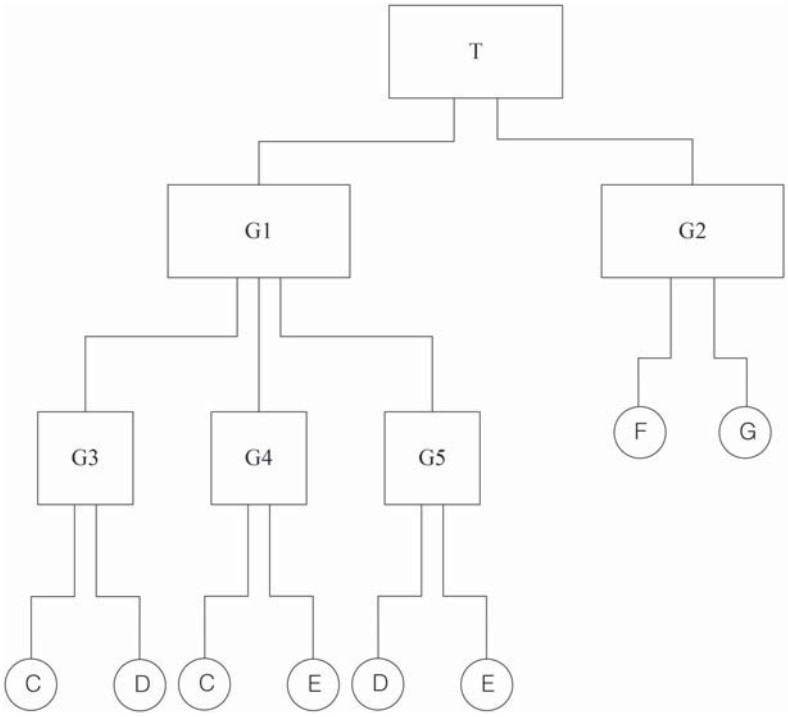

Figure 6 Schematic diagram of fault tree.

of the bottom event or cut set according to the minimum cut set (Rao et al., 2018; Liu and Wang, 2018). The calculation basis of the cut set method is the corresponding cut set file in the state of a power station. The following steps are required to complete the cut set method:

Step 1: Determine the room event value according to the condition of the standby column of DNA real-time synthesis, and find the corresponding cut set file through the room event value.

Step 2: Find out whether the cut set file exists, if it exists, proceed to the next step, if not, call the re-solution calculation core to generate the cut set file in the current DNA synthesis state.

Step 3: Read the cut set and basic events and their probability in the cut set file, and generate the structure.

Step 4: Import the corresponding basic events and delete, simplify and absorb the tree according to the outage events.

Step 5: Convert the tree to the minimum cut set.

Step 6: Calculate the value according to the minimum cut set and probability value.

The calculation process is as follows:

According to the above definition, the current risk monitoring of DNA synthesis is completed. This method is fast in calculation and easy to meet the real-time requirements of risk calculation, so as to reduce the occurrence of abnormal conditions in DNA synthesis.

3.4 Establishment of a Dynamic Monitoring Database of DNA Synthesis

In order to reduce the redundancy and calculation of the dynamic monitoring data of DNA synthesis a dynamic monitoring database of DNA synthesis is established, which is completed by table space partition and table partition.

Table space partition, which plays the role of the file system, can directly manage DNA synthesis data, reduce the generation of fragments, and improve the response speed of dynamic monitoring in the process of DNA synthesis. The user table space is established in the database and the data required by the electron microscope technology is stored in it. The partition of the table space affects the speed of data access. In the process of partitioning, the following principles are adopted: different data objects are set in the same table space, the load balancing of monitoring data is considered, and segments are stored in different folders separately. In principle, each table corresponds to a table space and a corresponding indicator table space; each large table under it corresponds to a separate table space and indicator table space. For large tables that need to be partitioned, each sub partition corresponds to a separate table space and indicator space. Therefore, this paper creates a table space and an indicator table space for DNA synthesis dynamic monitoring. In addition, different permission control schemes are used for different table spaces in the database, so workers have different permissions for different table spaces. Therefore, this paper improves the security of the database and the system to a certain extent by allocating specific table space to store data for the risk monitoring system and reasonably configuring the access rights of the table space for the users of the system.

Due to the requirement of the dynamic monitoring function of DNA synthesis, the structure of some tables is very

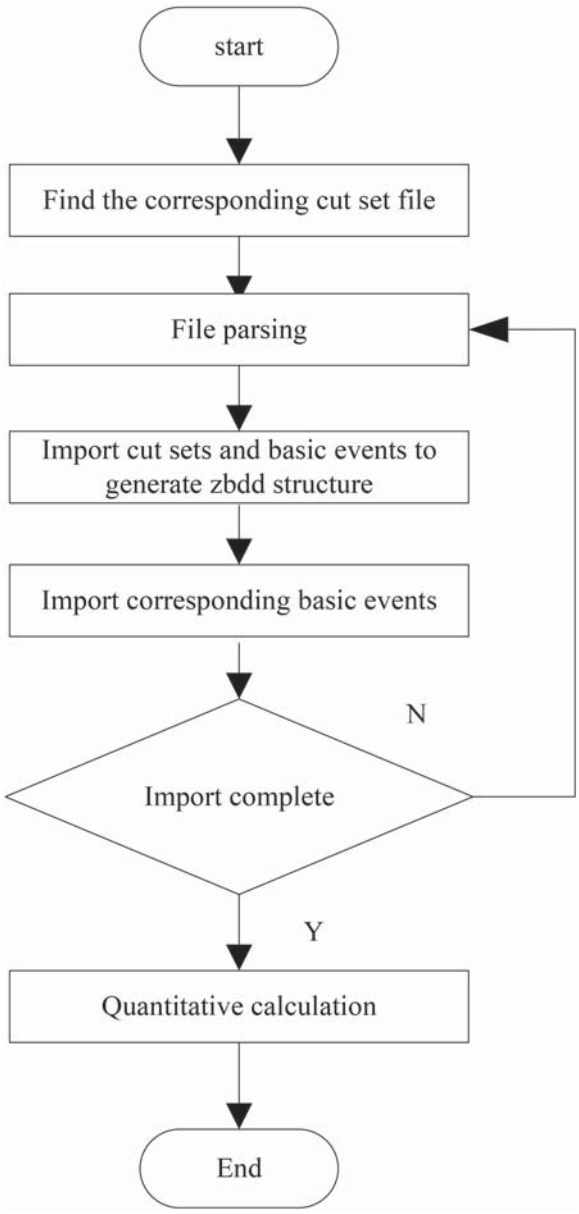

Figure 7 Calculation flow of minimum cut set.

complex, and there are many data columns or data types. Therefore, there are hundreds of different function points in the system, and the data information needed for each function point is different. Therefore, a large table can be divided into several small tables according to the actual needs in the design, so that each specific function application can only access the required information from its corresponding small table, so as to reduce the amount of data that all applications need to access in unit time, and improve database efficiency. The detailed division is shown in Figure 8.

Because of the frequent operation of the database in DNA synthesis dynamic monitoring, it takes more time to establish a database connection and dismantle a database connection. Therefore, it can be seen that the management of database connection directly affects the scalability and robustness of the whole dynamic monitoring process of DNA synthesis and the response speed of monitoring. If the management is not good, it will even lead to memory leakage and server collapse. Therefore, in order to improve the dynamic monitoring efficiency of DNA synthesis, there is a need to use database technology with a faster running speed and higher access efficiency. The database connection pool method is used to solve the above problems. After the initial connection to the database connection pool, when DNA synthesis needs to interact with the database it can obtain the database connection directly from the connection pool, and return the database connection to the connection pool after the interaction is completed, so as to realize the repeated use of the same database connection. The connection mode after the database connection pool is adopted is as shown in Figure 9.

Through the unified management of database connection pool, connections can frequently be established and released through the connection operation process, reducing the consumption of server resources, and improving the database operation performance, in order to complete the dynamic monitoring of DNA synthesis based on electronic microscopy.

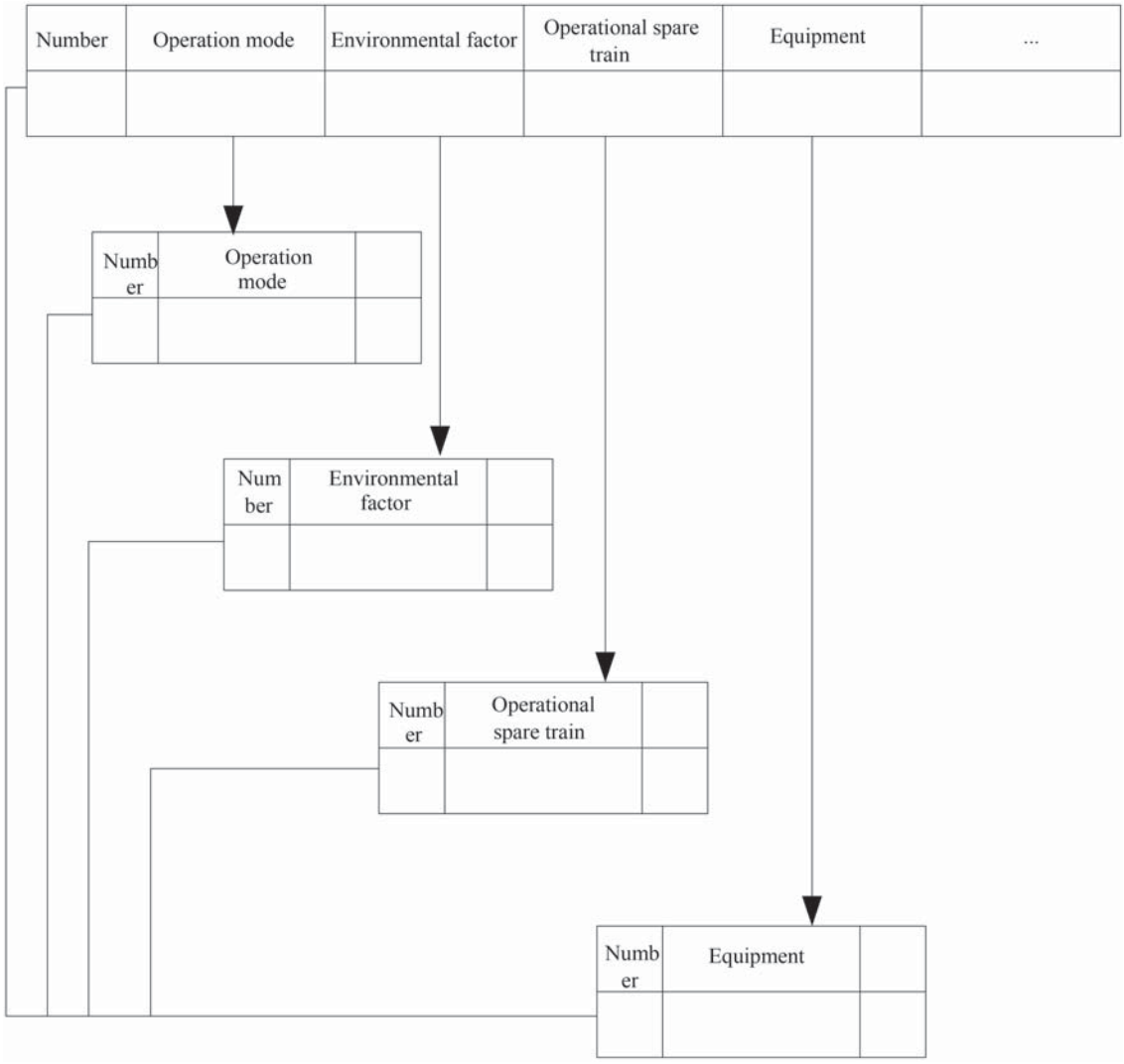

Figure 8 Principle of database partition.

4. EXPERIMENTAL COMPARISON

4.1 Experimental Platform

An experimental environment was built based on cloud computing platform. The cloud computing platform is composed of multiple computers. Through virtualization technology, the computing resources and storage resources of each machine are integrated to form a large-scale resource pool. This allows users to have convenient access through the Internet, and enables them to use computing resources, storage resources, software resources, data resources and other services on the cloud platform as required. The operating systems involved in the cloud platform are divided into two categories, the underlying operating system and the virtual machine operating system. The logical structure of the experimental platform is shown in Figure 10.

In the process of building the experimental platform, both the computing node and the management node use Intel Quad Core 2.66 GHz CPU, 4 GB memory and 500 GB hard disk, that can support virtualization of many nodes. Some of these virtual nodes are management nodes and the rest are calculation nodes. This experimental platform is a private cloud based on LAN, which has high security and reliability. The experimental platform can provide services to different types of users in different departments. Users are able to access the experimental platform from anywhere by accessing the LAN.

4.2 Experimental Scheme

The purpose of this experiment is to verify the practical performance of the dynamic monitoring method for DNA synthesis based on electron microscopy, and to ensure the preciseness of the experiment, therefore the traditional monitoring method is compared with the monitoring method designed in this paper.

In order to ensure the preciseness of the experiment, the experiment scheme is designed, the DNA data of a certain laboratory is selected, 10 DNA synthesis data are randomly selected as the experiment object, and interference factors are added in different synthesis data. The time to find the interference factors by the two methods is compared, and the experimental data is shown in Table 1.

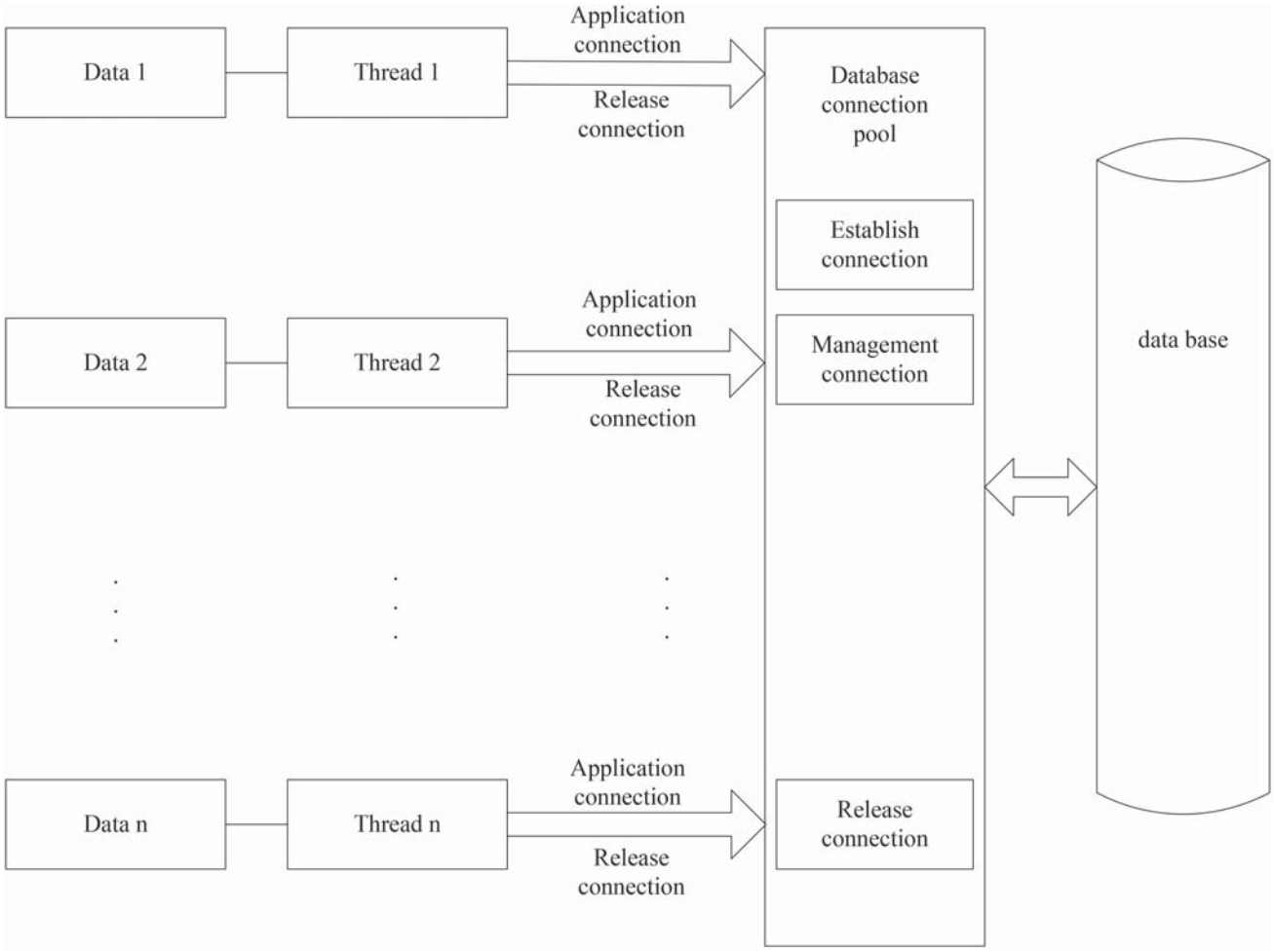

Figure 9 Database connection mode.

Table 1 Experimental Data.

Experiment Sample No.	Interference / Individual	Duration / S
1	1	22
2	2	50
3	3	15
4	2	22
5	3	12
6	4	9
7	6	56
8	5	120
9	10	63
10	12	45

The table is the experimental data support, and the specific experimental results are as follows.

4.3 Analysis of Experimental Results

The experimental platform is used to calculate the data generated in real time and generate the corresponding experimental results. The time comparison results of interference factors detected by the traditional monitoring method and the designed monitoring method are as follows:

It can be seen from the analysis of Figure 11 that in the first experiment, the interference factor is the least, the time difference between the traditional method and the designed method is small, while in the 10th experiment, where the interference factor is the highest, the time difference between the traditional method and the designed method is the largest, and the monitoring time of the traditional method is much longer. It shows that the traditional monitoring method is greatly affected by interference factors, and it cannot find the interference factors in time when there are more interference factors. However, the monitoring method designed in this paper is less affected by interference factors, and can ensure a faster recognition time when there are more interference factors.

In conclusion, the designed dynamic monitoring method of DNA synthesis based on electron microscopy is shorter

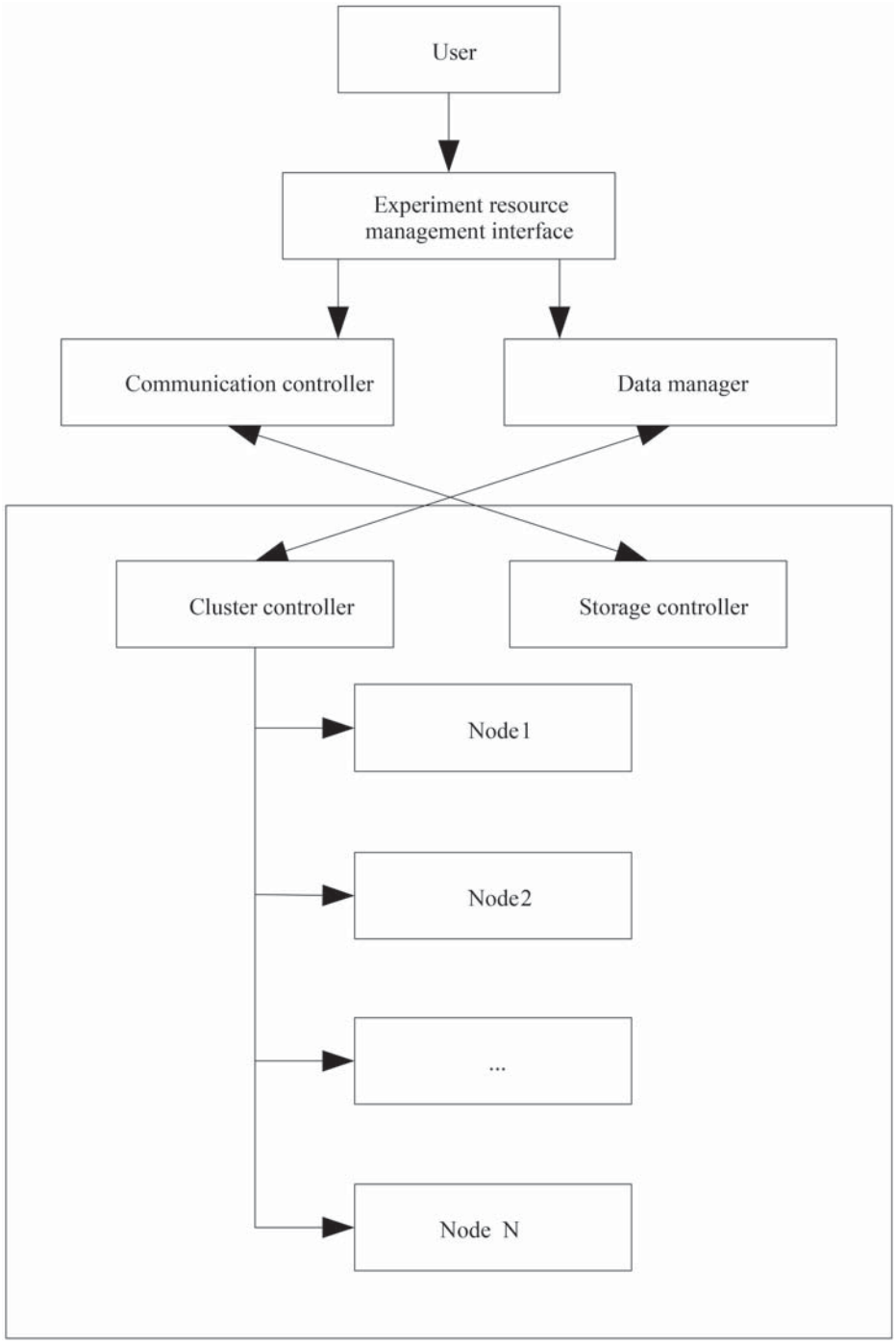

Figure 10 Logic architecture of the experimental platform.

than the traditional method in detecting abnormal conditions, which can meet the needs of dynamic monitoring of DNA synthesis.

5. CONCLUSION

A dynamic monitoring method of DNA synthesis based on electron microscopy is designed to solve the problem of traditional methods requiring a longer time to detect abnormal conditions. Experiments show that the designed method is faster than the traditional method when detecting abnormal conditions, which proves that the designed method can ensure the smooth progress of DNA synthesis, thus ensuring the accuracy of DNA synthesis and promoting the development of DNA synthesis in various fields.

However, there are still a series of deficiencies in this study. For example, when judging the risk attribute of the database, the establishment of the critical interface function does not combine with the complex characteristics of the Internet environment, resulting in some errors in the final dynamic monitoring results. Although it does not have a serious impact on the research results, it is hoped that in the next study, the above problems can be studied carefully to ensure that the final synthesis results are more illustrative, so as to maximize the smooth progress of DNA synthesis.

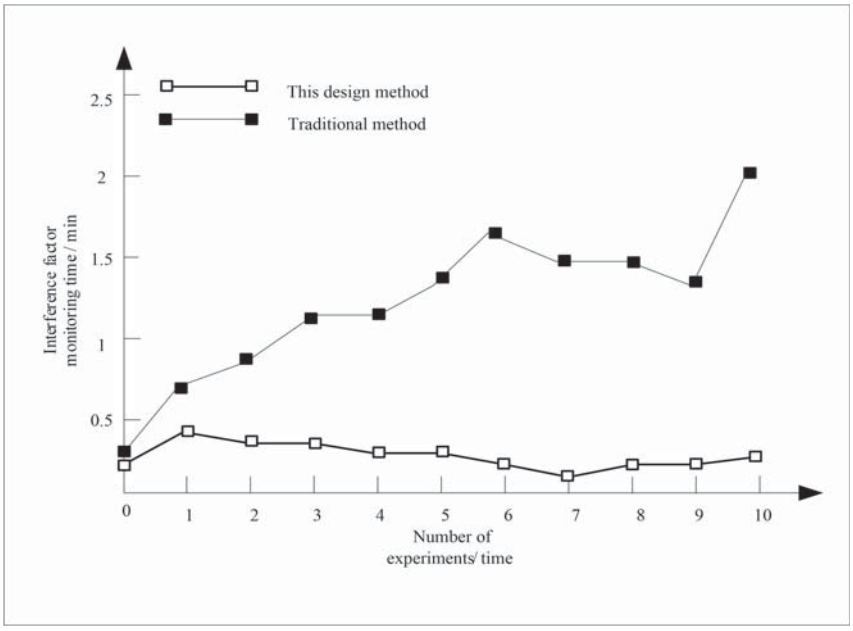

Figure 11 Experimental comparison results.

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