

Retraction

Retracted: The Design of Critical Care Information System Supporting Clinical Decision Based on Deep Learning Recognition Method

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This article has been retracted by Hindawi following an investigation undertaken by the publisher [1]. This investigation has uncovered evidence of one or more of the following indicators of systematic manipulation of the publication process:

- (1) Discrepancies in scope
- (2) Discrepancies in the description of the research reported
- (3) Discrepancies between the availability of data and the research described
- (4) Inappropriate citations
- (5) Incoherent, meaningless and/or irrelevant content included in the article
- (6) Peer-review manipulation

The presence of these indicators undermines our confidence in the integrity of the article's content and we cannot, therefore, vouch for its reliability. Please note that this notice is intended solely to alert readers that the content of this article is unreliable. We have not investigated whether authors were aware of or involved in the systematic manipulation of the publication process.

Wiley and Hindawi regrets that the usual quality checks did not identify these issues before publication and have since put additional measures in place to safeguard research integrity.

We wish to credit our own Research Integrity and Research Publishing teams and anonymous and named external researchers and research integrity experts for contributing to this investigation. The corresponding author, as the representative of all authors, has been given the opportunity to register their agreement or disagreement to this retraction. We have kept a record of any response received.

References

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WILEY WINDOw

Research Article

The Design of Critical Care Information System Supporting Clinical Decision Based on Deep Learning Recognition Method

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In recent years, the clinical decision support system (CDSS) has been gradually improved, which effectively reduces the probability of doctors' misdiagnosis or missed diagnosis. Therefore, the clinical decision support system has always been a research hotspot, deep learning and collaborative filtering technologies are developing rapidly, and more and more are applied to different fields. Based on the deep learning technology, this paper conducts in-depth research on the methods of assisted diagnosis of clinical diseases and prediction of clinical high-risk diseases in the field of CDSS. Aiming at the problem of clinical decision support system, this article analyzes the deep learning identification method in depth and is committed to applying machine deep learning to clinical decision-making, changing the lack of information and its challenges to clinical decision-making. Based on previous studies, two unsupervised learning methods based on machine learning are proposed, namely user collaborative filtering and RBM, to improve CDSS. The experimental results show that the overall performance of the RBM-based method is the best. When the missing degree of the two data sets is 30.6%, the classification accuracy rate is still more than 92.8%.

1. Introduction

With the outline of the "Healthy China 2030" plan, the country and society pay more attention to physical health, and a health trend is set off for the whole people. After the 21st century, with the development of science and technology, especially artificial intelligence, medical innovation and improvement of medical standards based on deep learning cognitive techniques have become the consensus of the people. The decision of critically ill patients must be made in a short period of time. If the decision is wrong, the serious loss faced will be at the cost of life. In this case, the clinical decision support system can put aside past experience and deviations to make rational judgments, which also pave the way for the development and wide application of the clinical decision support system.

The research and development of emergency information systems that support clinical decision-making are very important to ensure the safety of critically ill patients. This article mainly focuses on the research and development team and application platform of the emergency information system. The basic patient information source is the only one that can be extracted automatically, and the bedside monitoring information has intelligent error correction and tendency. In terms of analysis function, the closed-loop management of the clinical decision information system can form early warnings, nursing observation records and other information, and the systems are linked to each other to realize the sharing of medical resources and ensure the consistency of information. Therefore, a comprehensive introduction to the important technical points of the research and development of critical illness information systems will help the overall promotion of intelligent medical treatment.

Nowadays, with the continuous update and iterative development of big data technology, the field of symptomatic medicine has gradually begun to pay attention to the construction of informatization. For the diagnosis and treatment of critically ill patients and subsequent care, doctors need to quickly determine the actual situation of the patient and relieve the patient from the danger. The proposal of the clinical decision support system based on big data technology greatly reduces the blindness of doctors in judging the condition of the disease and provides a reference for rationally judging the actual situation of the patient. Therefore, increasing the research on critical illness information systems that support clinical decision-making and the treatment of critically ill patients can bring significant progress and development. Charalampous and Gasteratos proposed an unsupervised online deep learning algorithm for action recognition in video sequences. In the past, deep learning models that can derive spatiotemporal data have been proposed, and significant results have been achieved, but most of them are limited to constructing features from shorter window lengths. On the other hand, the model they introduced considers the entire sequence of samples and extracts descriptions on a frame-by-frame basis. Each computing node of the proposed paradigm forms a cluster that computes point representatives. Subsequently, the firstorder transition matrix stores and continuously updates the successive transitions between clusters. Both spatial and temporal information is processed simultaneously by the Viterbi algorithm, which maximizes the criteria based on (a) time conversion and (b) the similarity between the corresponding input sequence and the cluster representative. The derived Viterbi path is the output of the node, and the concatenation of nine such adjacent paths constitutes the input of the corresponding upper node [1]. Luo and others have done research on the identification of Alzheimer's disease. This neurological disease is currently incurable and can lead to progressive mental deterioration. Although the definitive diagnosis of AD is difficult, in practice, the diagnosis of AD is mainly based on the clinical history and neuropsychological data, including magnetic resource imaging (MRI). In recent years, there have been more and more research on the application of machine learning to AD recognition. It describes an automatic AD recognition algorithm based on 3D brain MRI deep learning. This algorithm uses Convolutional Neural Network (CNN) to realize AD recognition. The unique feature is that it takes into account the three-dimensional topological structure of the brain as a whole in AD recognition, thereby producing accurate recognition. Experiments show that the algorithm has a high AD recognition accuracy, with a sensitivity of 1 and a specificity of 10.94 [2]. In terms of clinical decisionmaking, Klein and others aim to evaluate the influence of the ratio of soluble fms-like tyrosine kinase 1/placental growth factor on doctors' decision-making in pregnant women with symptoms and signs of preeclampsia in routine clinical practice. The results indicate that the use of the soluble fmslike tyrosine kinase 1/placental growth factor test affects the clinical decision-making of a significant proportion of women with suspected preeclampsia in order to make appropriate hospitalizations. This is the first study to demonstrate the impact of angiogenesis biomarkers on decisionmaking in routine clinical practice [3]. Horng and others demonstrated the incremental benefit of using free text data in addition to vital signs and demographic data to identify patients with suspected infections in the emergency department. This is a retrospective, observational cohort study conducted in a tertiary academic teaching hospital, including all consecutive ED patient visits between 12/17/08 and 2/17/13. No patients were excluded. Therefore, the use

of free text greatly improves the ability to identify infections (AUC increased from 0.67 to 0.86) [4]. Ali and others have done research on chronic disease care, such as diabetes, in clinical decision-making. They believe that there has been a gap between current diabetes care practices and recommended diabetes care standards reported in the literature. Many IT-based interventions have been developed to improve compliance with quality standards of care for chronic diseases such as diabetes. The research design should be improved, especially in terms of baseline characteristics, sample size, and research period. Regarding the implementation of CDSS, it is not a sudden change in clinical work practice but a gradual adoption of technology to minimize interference with clinical work processes [5]. Stokes and others took the frequently occurring disease as a major problem in primary care as a breakthrough, aiming to explore the description of the management of frequently occurring diseases by primary care professionals and its impact on clinical decision-making and regional health care provision. The method is to conduct qualitative interviews with 12 general practitioners and 4 primary care nurses in Otago, New Zealand, and use the constant comparison method for thematic analysis. As a result, primary care professionals encounter challenges in clinical decision-making and healthcare services when providing care for patients with multiple diseases. Clinical decision-making occurs in timelimited consultations, where the challenge of the complexity and insufficiency of single-disease guidelines is managed through the use of "satisfaction" (satisfactory and adequate care for a given patient) and sequential consultations using relationship continuity care. The New Zealand primary care copayment funding model is seen as an obstacle to the provision of care because it does not encourage sequential consultations. This problem can only be partially solved by using Care Plus's additional per capita funding stream. Fragmentation of care has also occurred in general practice and the primary/secondary care interface. The conclusions indicate that these findings highlight specific barriers to providing primary care to patients with multiple diseases in New Zealand. Therefore, it is necessary to develop, implement, and evaluate a revised version of Care Plus that takes these barriers into account on a nationwide scale [6]. System design based on clinical decision-making is also the focus of modern society. Puthucheary and others considered that patients who survived a critical illness have severe physical disabilities. The effects of rehabilitation strategies on healthrelated quality of life are inconsistent, and population heterogeneity is considered a potential confounding factor. Their experiments showed that in sepsis survivors, there are two different recovery trajectories for physical recovery. Elderly patients with more comorbidities and lower educational achievement are more likely to have sustained physical injury trajectories. The response ratio of PF score to SF-36 in trajectory prediction is PCS, which can be considered the main result. Future trials should consider adaptive trial design to more effectively deal with nonresponders or subgroup specific outcome measures [7]. Qin and others took a third-class hospital in Beijing as the object, taking into account the continuous development of the

Intensive Care Information System (ICIS) to meet the changing information needs of the Intensive Care Unit (ICU); it provides the backbone for a safe, intelligent, and efficient patient care environment. This greatly helps the application development of ICIS. The result is to measure the improvement of ward nursing performance through ward management, routine nursing practices, disinfection and isolation, infection rate, and mortality. Nurses from this ICU unit in Beijing actively participate in the development of ICIS and make full use of the system to record nursing care. The introduction of ICIS has significantly improved the quality and efficiency of nursing documentation, transcription, and management of drug orders. It allows nurses to spend more time with patients to improve the quality of care, which leads to an improvement in overall nursing performance. Further research should investigate how the ICIS system can help improve the decision-making of ICU nurses and intensive care doctors [8]. Clinical research in China is more in the design stage. The top three hospitals in China rely little on such systems, and there are not many related applications.

This article pays more attention to the design of the bottom of the system. Different from previous studies, it has the following innovations. (1) For the first time, the participation of the algorithm in this paper in the deep learning framework has led to a completely different method of action recognition. Compared with other deep learning methods, it performs better than others in classification accuracy in most cases. (2) Based on the collaborative filtering method and the deep learning method, this paper focuses on the two systems, respectively, and tests and compares them separately. The comparison shows that the RBM-based method has the best overall performance. (3) In system design, this article digs deep into the field of system learning, which is of great significance to medical clinical decision-making.

2. System Design Method

2.1. Deep Learning. Deep learning is a hot topic in the field of machine learning in recent years [9, 10]. This is a collection of modeling methods that use a complex model structure (multilayer nonlinear transformation) to extract and summarize the high-level information hidden in the data [11]. Generally speaking, deep learning algorithms are developed based on the decentralized representation of data. In a distributed representation, the observable data is generally considered to be produced by the interaction of various factors at different layers [12, 13]. Based on this, deep learning is based on the premise that these factors are composed of different levels of structure, and these different levels of data correspond to various concepts or components of observable data. The number of layers is different, the model scale of each layer is different, and the abstract information provided is also different. The deep learning algorithm uses this level concept and adopts the modeling techniques of each level to construct the deep structure of the model. In this structure, high-level concepts or abstract information can be obtained from low-level abstract

information. Because in clinical decision-making, the introduction of big data algorithms and machine learning technology can make use of the powerful data processing capabilities and analytical modeling functions of the cloud computing platform to make use of existing data and use model algorithms to fill in missing values to help the doctor make a decision [14, 15]. When making a diagnosis for a new patient, it is possible to make a rational decision regardless of past experience or external interference combined with the plan given by the system [16]. It is precisely because of its powerful functions and practicality that for patients and doctors, such a platform is very eager to be widely used. The overall design is divided into several parts, which will be expanded in detail in the system design part.

Based on the deep learning system, the design diagram of the critical illness information system design supporting clinical decision-making is shown in Figure 1.

2.1.1. Resampling. Resampling is often used to process onedimensional signals such as audio, which is the combination of continuous signals in time or space [17]. Specifically, suppose that the original sample sequence for resampling is A[n], and it satisfies the formula:

$$A[n] = a_c (nT). \tag{1}$$

The target sequence of resampling is $\overline{A}[n]$ and satisfies the formula

$$\overline{A}[n] = a_c (n\overline{T}). \tag{2}$$

If the signal is assumed to be periodic, the Fourier transform method can be used to resample the original analog signal.

2.1.2. Discrete Fourier Transform. The Fourier transform is a chemical analysis that determines the basic composition of a substance. The signal is generated from nature, and the basic composition can also be determined through analysis [18, 19]. To put it simply, the Fourier transform is an extension of the Fourier series, and the function period represented by this is close to infinity. The complex periodic function signal can be represented by the sum of many simple sine waves and cosine waves. In signal processing, the most important use of Fourier transform is to decompose the signal into frequency components and amplitude components [20].

For the sampled signal sequence $\{a[k]\}, 0 \le k \le N$ with equal time interval, its discrete Fourier transform expresses it as frequency f_k , formula

$$f_k = \frac{k}{n}.$$
 (3)

And the corresponding coefficient A_k , as shown in the formula:





$$X_k = \sum_{n=0}^{N-1} a[k] e^{-2\pi i (n/N)k}.$$
 (4)

The discrete Fourier transform represents the sum of f_k and A_k complex sinusoids.

2.1.3. Data Standardization Method. The standard deviation standardization method is used more in the experiments in this article. The data after using the *z*-score method needs to conform to the standard normal distribution. The conversion function is as follows:

$$a^* = \frac{a - \mu}{\sigma}.$$
 (5)

In formula (5), a is the original feature data value, u is the average of all feature data values, and 6 is the standard deviation of all feature data values.

2.1.4. Data Preprocessing Steps. EEG data preprocessing generally has four steps, namely resampling, filtering, Fourier transform, and z-score standardization [21], as shown in Figure 2.



FIGURE 2: EEG data preprocessing steps.

2.2. Brief Description of System-Related Algorithms

2.2.1. GSV-SVM Identification Method. Due to the hierarchical information extraction process of neural networks, researchers apply it to the field of feature learning to extract a nonlinear feature of the underlying input. A large number of studies have shown that the use of neural networks as a nonlinear transformation of features can obtain more effective feature expressions [22–25]. The Gaussian components of each language GMM model adaptively obtained from the UBM model are comparable. Generally speaking, KL divergence (Kullback Leibler divergence) can be used to define the degree of similarity between two probability models. The formulas are as follows:

$$KL(A_{sa}||A_{sb}) = -\int A_{sa} \ln \frac{A_{sb}}{A_{sa}} dx,$$

$$KL(A_{sa}||A_{sb}) = \int \sum_{m=1}^{M} \pi_m N(x|\mu_{a,m}).$$
(6)

Unfortunately, the KL divergence does not satisfy the kernel function of the SVM model. For this reason, the upper limit of the KL function is considered. The specific steps are as in the following formula:

$$\mathrm{KL}(A_{\mathrm{sa}} \| A_{\mathrm{sb}}) = \int \sum_{m=1}^{M} \pi_m N(x | \mu_{a,m}) \ln \frac{\sum_{m=1}^{M} \pi_m N(x | \mu_{a,m}, \sum_m)}{\sum_{m=1}^{M} \pi_m N(x | \mu_{a,m}, \sum_m)} \mathrm{d}x, \tag{7}$$

$$\mathrm{KL}(A_{\mathrm{sa}} \| A_{\mathrm{sb}}) \leq \sum_{m=1}^{M} \pi_m \mathrm{KL}\left(N\left(x | \mu_{a,m,\sum_m}\right) \| N\left(x | \mu_{a,m,\sum_m}\right)\right), \quad (8)$$

$$\mathrm{KL}(A_{\mathrm{sa}} \| A_{\mathrm{sb}}) \approx \frac{1}{2} \sum_{m=1}^{M} \pi_m (\mu_{a,m}, \mu_{b,m})^T \sum_{m=1}^{-1} (\mu_{a,m} - \mu_{b,m}).$$
(9)

In formual (7), Equation (8) and Equation (9), Asa represents the data set; due to the relationship between formula (7), formula (7), and formula (7), it is obvious that the KL divergence between the two GMM models satisfies the following inequality:

$$0 \le \mathrm{KL}\left(A_{sa} \| A_{sb}\right) \le d\left(A_{sa} \| A_{sb}\right). \tag{10}$$

In this way, it is easy to derive the form of the corresponding kernel function, as shown in the following:

$$K(s_a, s_b) = \sum_{m=1}^{M} \pi_m \mu_{a,m}^T \sum_m^{-1} \mu_{b,m},$$
(11)

$$K(s_a, s_b) = \sum_{m=1}^{M} \left(\sqrt{\pi_m} \sum_{m=1}^{-1/2} \mu_{a,m} \right)^T \left(\sqrt{\pi_m} \sum_{m=1}^{-1/2} \mu_{b,m} \right).$$
(12)

Since formula (11) and formula (12) are typical linear forms, they satisfy the Mercer condition of the SVM kernel function. In this way, under the definition of the above kernel function, an SVM classifier can be constructed, as shown in the formula:

$$M_{a} = \begin{bmatrix} \sqrt{\pi_{1} \sum_{1}^{-1/2} \mu_{a,1}} \\ \sqrt{\pi_{2} \sum_{2}^{-1/2} \mu_{a,2}} \\ \dots \\ \sqrt{\pi_{M} \sum_{M}^{-1/2} \mu_{a,M}} \end{bmatrix}.$$
 (13)

Obviously, it is a high-dimensional vector with dimension $(D \times M)$.

The following picture shows the difference between the three language recognition methods when modeling.

As can be seen from Figure 3, GMM, the UBM model is a typical generative model, which is only responsible for fitting the distribution of the given data. It can be found that the degree of the fitting is relatively high, 95% of the data points are inside the model, and the correct rate can almost reach more than 95% [26].

As shown in Figure 4, specifically, under the GMM and MMI methods, the collection of data uses the MMI criteria to select the most easily missing information so that the model can describe the most confusing data more accurately, and those data that can easily be missed are weakened in MMI training [27]. After transforming the above-mentioned entity-relationship model into a relational model, and according to the connections between entities, gradually eliminate the transitive dependence and functional dependence candidate keys in the relational model so that the relational model can be mapped to a table structure that can be realized. The following lists the structure of several main database tables in the clinical safety medication decision support system, including detailed definitions such as field names, data items, length, whether it is empty, and value range [28].

In Figure 5, GSV-SVM tries to find the support vector f with the smallest distance from the classification surface in the training set and then determines the classification surface by maximizing the distance from the support vector to the classification surface. In this way, the incorrect assignment of uncertain values can be minimized [29]. In terms of big data learning, machine learning model methods have relatively strong functions. This type of method is based on big data analysis for model training and feature learning, the training results are recalculated, and the powerful modeling function is used for intelligent decision-making [30]. In Figure 5, the solid black dots are the training data, and the hollow dots are the input data set.

3. Platform System Design

3.1. Design Based on RBM Model. Nowadays, there are many deep learning algorithms, but due to the complexity of medicine and the uncertainty of practical problems, although the amount of funds required for the development of a rational drug use decision support system is much lower than that of the system, it has considerable economic and



FIGURE 3: Generative model GMM-UBM.



FIGURE 4: Discrimination training process.

social benefits. Therefore, the development of this system is bound to be the inevitable trend in future hospital development [31].

RBM is a special form of logarithmic, linear Markov random field. That is, its energy function has a linear relationship with free parameters, as shown in the left part of Figure 6. Under normal circumstances, RBM is a neural network model with a two-layer structure, including a display layer and a hidden layer. The reason why it is called "restricted" is that its connection relationship only exists between hidden layer nodes h = [h1, h2, ..., hi] and explicit layer nodes v = [V1, V2,..., Vn]. Later, a deep information extraction relationship is established between the underlying input features and the output phoneme state. The phonemerelated information in the underlying acoustic features is abstracted layer by layer, while the phoneme-independent information is gradually suppressed [32].

The parameter training process is as follows.



FIGURE 5: Differential model SVM.

Due to the existence of the partition function Z in the objective function, the optimal solution of the parameters does not have a closed solution form, so the gradient descent method is often used for iterative optimization. However, the partition function is a summation of all hidden and explicit variables, and the estimation of its gradient cannot be accurately given. This makes the parameter optimization of RBM a difficult problem. At present, the parameter estimation of RBM generally uses the classic contrast divergence algorithm, which approximates the gradient of the partition function based on random sampling so as to realize the RBM parameter update process based on the gradient descent method.

Under the above-mentioned RBM parameter training method, it can use the layer-by-layer training method to perform the RBM pre-training of the DNN network parameters. As shown in the left part of Figure 6, the lowestlevel Gauss Bernoulli RBM is trained first, given the input observation features. After the parameter training is completed, its output value is used as the next layer of Bernoulli's assignment as the RBM's explicit layer output, and then the second layer of RBM is obtained through training. By analogy, the output of the hidden layer of the current layer of RBM is used as the input of the explicit layer of the next layer of RBM to complete the training of all RBMs. After the RBM training is completed, the parameters of each RBM are stacked according to the hierarchical relationship to form a deep confidence network (DBN), as shown in the middle part of Figure 6, which constitutes the initial value of the network parameters under the DNN fine adjustment step. The right part of Figure 6 is the subsequent feature extraction.

Finally, the extraction of deep bottleneck features is performed and can be combined with the deep learning DNN network model, and the principle is as follows.

After completing the above training, as shown in Figure 6, the extraction form can be expressed as follows:



FIGURE 6: DNN structure training process and structure diagram with 5 hidden layers and a Bottleneck layer.

$$y = h(x).$$
 (14) Among them, $y \in \mathbb{R}^{D' \times 1} = [y_1, \dots, y_{D_l}]^T$, D' represents the number of nodes in the bottleneck layer, and the input feature vector is $x = [x_1, \dots, x_D]^T$.

$$y_{d_{l}} = h(x|\theta) = \sum_{j} w_{d_{l},j}^{i} f\left(\sum_{j} w_{d_{l},j}^{i} f\left(\dots + f\left(\sum_{j} w_{d_{l},j}^{i} + b_{i}^{1}\right)\dots\right)\right) + b_{d}^{t}.$$
 (15)

In formula (15), the extraction of yd is completed, and the DBF extraction process is completed at this point.

3.2. Related Module Design

3.2.1. Prescription Safety Monitoring and Early Warning Module. During the development of the PDSS system, the greatest difficulty in demand analysis was that system users could not fully and accurately describe their business needs. After comprehensively analyzing the characteristics, limitations, and difficulties of the system in the design, using the prototype method, combined with drawing business use case diagrams, functional diagrams and other means, completed the system requirements analysis.

The prescription safety monitoring and early warning module extracts prescriptions and medication-related information in medical orders from the system so as to perform prescription evaluation and prescription early warning, and realize the basic review statistical function. The principle is shown in Figure 7.

In Figure 7, the hospital leader is in the terminal authority position of the platform, and the output of doctors, departments, and the whole hospital all received and are given feedback by the hospital leader. This not only reasonably solves the improper handling of the decisionmaking problems but also enables the hospital leaders to take into account the suggestions of various relevant departments and doctors and finally make a quick decision.

3.2.2. Rational Drug Use Monitoring and Management Module. This module counts the problems examined by the PDSS system from multiple perspectives such as departments, doctors, and hospitals, statistics of doctors' adoption, statistics of doctor's orders, statistics of all diseases, abnormal signal monitoring, monitoring data reporting, and central pharmacy for statistics and analysis, provides a basis for hospital leaders and deans to evaluate doctors' work and medical treatment effects, and realizes the informatization of hospital management, as shown in Figure 8.

In Figure 8, the medication module is similar to the detection, early warning, and decision-making module, but the medication issues are not handled so flexibly. It only needs to determine more variables, considering important antibiotic drugs, which can largely avoid problems in decision-making. Considering that there are four levels of feedback levels, you can contact the following middle-level design to make quick feedback.

3.2.3. PDSS Middle Layer Design. The middle layer mainly includes the following aspects, such as a rational drug use plan, antibiotic review, "individualized" window,



FIGURE 7: Use case diagram of prescription safety monitoring and early warning module.

"standardized" window, warning window, and other functions, as shown in Figure 9.

The core of the middle layer is to give a reasonable medication plan during the diagnosis on the first page of the diagnosis page. On the doctor's order page, every drug entered by the doctor, if it is an antibiotic, is also reviewed for antibiotics and made "individualized" instructions. If the medicine is in a group, display all medicines in the same group and review the different effects of this medical order list with other medicines. The specific design table is shown in Table 1.

As the core output layer, the middle layer undertakes more important tasks. As shown in Table 1, most of the operations are provided by the big data platform. In view of the above requirements, this paper has carried out research on data standardization in a distributed clinical decisionmaking environment. In this paper, based on the FHIR medical data exchange standard organized by HL7, combined with a multiagent clinical decision-making system based on a rule knowledge base, a multiagent clinical decision support system based on the FHIR data exchange standard is researched and designed. This article analyzes and determines the structure and requirements of the FHIR standard. Through the comparison with the data in the hospital information system database, the mapping between the database and the FHIR is completed, and the reversible process of FHIR generation and analysis is realized. After

completing the reciprocal mapping between FHIR and the database, starting from the decision-making level, the use of FHIR by decision-making agents in the decision-making process is studied. When designing the framework of the multiagent clinical decision support system, the XML-based expression of the agent decision rule knowledge was studied, and the structure and parsing method of the XML rule were clarified.

3.3. CDSS Method Testing and Evaluation

3.3.1. Clinical Disease Diagnosis Results Based on User-Based Collaborative Filtering. This experiment focuses on comparing the pros and cons of the two models. In the processing of data, the complexity of clinical cases determines that the similarity calculation is also very complicated, and similarity calculation methods need to be designed separately for different situations. Different similarity calculation methods and calculation formulas are given below for different attribute values. On this basis, the comprehensive similarity of clinical cases is calculated by attribute weights, item weights, and comprehensive weights, and the CDSS method is used for evaluation. In the case treatment analysis of critically ill patients, the experimental results are shown in Figure 10.

It can be seen from Figure 10 that the accuracy rate of the clinical decision support platform based on the collaborative



FIGURE 8: Diagram of rational drug use monitoring and management system.

filtering model designed by the PDSS middle layer is above 85%, and the highest rate reaches 98%. There is little difference in each part, and the fluctuation range is well controlled, especially since the fit of the model is not low. On the other hand, it can be seen that the higher the missing degree of the data set, the overall downward trend of the model's prediction accuracy, which explains the importance of the data set in the model. The best results of the model under each data set are sorted out, as shown in Table 2. From the statistical results in Table 2, it can be seen that in the decision-making of critical diseases, when the degree of missing is not very large, the fewer similar patients are referred to, the more accurate the result will be. The abovementioned experimental results show that in the case of a serious lack of clinical medical data, the collaborative filtering method based on DRBM is the best method to assist disease diagnosis. This method informs the complex relationship with the medical inquiry information and infers



FIGURE 9: PDSS middle layer module relationship diagram.

TABLE 1: PDSS middle layer module design table.

Diagnose				
Module name Function brief				
Rational drug use Judgment function on the first page of the doctor's of	Judgment function on the first page of the doctor's order			
Antibiotic review The function of judging whether the medicine is antibiot	The function of judging whether the medicine is antibiotics or not			
Drugdictform				
Module name Function brief				
Warning window The display window for judging the interaction between all medicines on the e medical order page	ntire medical order page on the			
Individual window At the end of the doctor's advice page, the page for judging the different	ent effects of each drug			
Standardized when entering a new medicine on the doctor's order page, judge whether oth	er medicines are used together			

hidden features. In addition, it can also learn about the diagnosis of disease physiology to improve the accuracy of disease diagnosis.

3.3.2. Based on RBM Model Test. The experimental results based on the RBM clinical decision support system model are shown in Table 3.

It can be found from Table 3 that the overall classification performance of the RBM-based model is good. An analysis of the training process is shown in Figure 11.

It can be seen from Figure 11 that only 5 iterations are required, and the cost function of the RBM model has been optimized to a very small value, but the average error of the visual layer is indeed very high, and the RBM model has a large prediction error for missing values [33]. After analyzing the reasons, the data set is too small to be the main key. The data set provides too little information, and it is difficult to extract enough feature information from the visible layer to construct the hidden vector through multiple iterations. And thus, it is impossible to construct a reasonable joint probability distribution. It is clear that the collaborative filtering method based on DRBM is the best method to assist in disease diagnosis. This method has complex associations with medical inquiry information and infers hidden features [34, 35]. It is possible to learn disease physiological detection information to improve the accuracy of disease diagnosis. When the missing degree of the two data sets is 30.6%, there is still a classification accuracy of more than 92.8%.

4. Discussion

Participatory design is a method for ICU nurses, hospital IT departments, and software companies to jointly develop Intensive Care systems (ICIS) [36]. Conducting focus group discussions to understand nurses' subjective views on ICIS and compare the time and quality of nursing documents before and after the implementation of the system. ICU



TABLE 2: The best results of each data set of the user-based collaborative filtering model.

Missing	Raw data	10%	20%	30%
Accuracy of skin disease data set	$0.96894 \ (k=1)$	$0.96382 \ (k=1)$	$0.92764 \ (k=1)$	$0.82814 \ (k=8)$
Skin disease data set F 1-S core	$0.96787 \ (k=1)$	$0.96313 \ (k=1)$	0.8937 (k=1)	$0.7251 \ (k=8)$
Chronic nephritis accuracy rate	$0.97183 \ (k=4)$	$0.96894 \ (k=6)$	$0.97041 \ (k=7)$	$0.95275 \ (k=6)$
Chronic nephritis F 1-S core	$0.97019 \ (k=4)$	$0.96894 \ (k=6)$	$0.96894 \ (k=7)$	$0.95077 \ (k=6)$

nursing performance is extracted from the annual nursing performance data collected by the hospital. ICU nurses, hospital IT staff, and company software engineers follow a participatory design process to develop and implement very useful ICIS [37]. Nursing documents are fully digitized, quality and efficiency are significantly improved, and

TABLE 3: Results of auxiliary diagnosis of clinical diseases based on the RB M model.



FIGURE 11: Changes in cost and error during RBM training.

incorrect data, missing data items, and calculation errors are significantly reduced. After the introduction of ICIS, nurses spend more time on direct patient care, and the accuracy and efficiency of medication administration have also been improved [38].

In recent years, deep learning technology and collaborative filtering technology have continued to become one of the fastest growing fields on the global stage, and more and more services and products are based on them. CDSS, artificial intelligence that supports doctors in decision-making, has obvious advantages over doctors in some aspects.

At the same time, the experiment has many shortcomings. (1) The lack of depth of the experiment. The design of the system includes a complicated and long process. Due to external and internal factors such as time and equipment, this article does not discuss this in depth. For example, in the system model setting, the collaborative filtering method is used, and other methods can be considered for comparison. (2) The unity of data, the main data in this article are the skin disease data set and the chronic nephritis data set. There is not much data acquisition and analysis. After all, the individual differences of critically ill patients are large, and the single data may lead to system errors that cannot be accurately judged. (3) Lacking applicability, the design of the system does not fully investigate hospitals, clinics, and other laboratories that use this type of system. In the future, hoping that there will be more opportunities for applications, inspections, and upgrades.

5. Conclusions

The design research of critical illness information systems based on the deep learning recognition method to support clinical decision-making has been a hot research topic in recent years. With the rapid development of deep learning theory, many fields of artificial intelligence have made new milestones, pointing out a new direction for the development of artificial intelligence. The system mentioned in this article can provide accurate judgments in the absence of data. After comparison and screening of models, the accuracy of filling in missing data can reach more than 95% after analysis. For this reason, hoping that this article can be used as a reference for follow-up development, and the follow-up scientific development of clinical support decision-making system will be more applied to medical places. Due to limited knowledge, there are still many areas for improvement in research, hoping that this system can contribute a little to follow-up research.

Data Availability

The data of this paper can be obtained from the corresponding author upon request.

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this work.

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