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Application of Genetic Algorithm-Optimized BP Neural Network in Prognosis Prediction of Hemorrhagic Stroke

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Abstract: Clinical intelligent diagnosis and treatment of hemorrhagic stroke, as a combination of artificial intelligence and intelligent medical treatment, is more conducive to perfectly monitoring the pathological cycle changes of patients through data flow. Based on the BP neural network model, this paper constructs a neural network model based on GABP to predict the 90-day mRS Score of patients, and successfully accurately predicts the prognosis of patients with hemorrhagic stroke. Based on the relationship between the patient's prognosis and personal history, disease history, treatment methods and imaging features, the recommendations for clinical decision-making were made. In order to test the distribution of the data, a Shapiro-Wilk distribution test model was constructed to test whether there were significant differences in the distribution of multiple populations, and finally a conclusion was reached that 90-day mRS Was not related to gender. The GABP neural network model constructed in this paper overcomes the limitation of BP neural network in complex problems, and uses genetic algorithm to optimize the weight and threshold, which improves the performance and optimization efficiency of the model. Overall, the GABP-based neural network model represents an approach that integrates neural networks and genetic algorithms and has the potential to solve complex problems. Future research and development will help to further improve the performance, interpretability and applicability of the model, thus promoting its wide application in different fields.

Keywords: Genetic Algorithm; Backpropagation Neural Network; Hemorrhagic Stroke Prognosis; Modified Rankin Scale Score; Correlation Analysis.

1. Introduction

As one of the leading causes of death and disability worldwide, the clinical treatment and prognosis assessment of hemorrhagic stroke has been a major challenge in the medical field [1]. With the rapid development of artificial intelligence technology, intelligent medical treatment has gradually become an important means to improve patient diagnosis and treatment experience and improve medical efficiency. Especially in the clinical management of hemorrhagic stroke, how to accurately predict the prognosis of patients and develop personalized treatment plans has become a hot topic in current research.

The purpose of this study was to explore the application of BP neural network (GABP) optimized by genetic algorithm in prognosis prediction of hemorrhagic stroke [2]. Although the traditional BP neural network is widely used in the field of pattern recognition and prediction, it is easy to fall into the local optimal solution, which limits the performance of the model in complex problems. To overcome this limitation, we introduce genetic algorithms [3], a global optimization algorithm that simulates natural selection and genetic mechanisms, to optimize the weights and thresholds of BP neural networks to build more accurate GABP neural network models [4].

By comprehensively considering various factors such as patients' personal history, disease history, treatment methods and image characteristics, the GABP model constructed in this study can not only accurately predict the 90-day mRS Score of patients with hemorrhagic stroke [5], but also provide scientific basis for clinical decision-making according to the predicted results. In addition, statistical methods such as Shapiro-Wilk distribution test are used to verify the predictive performance of the model [6].

The structure of this paper is as follows: Firstly, the construction process and optimization strategy of GABP neural network are introduced; Then the methods of data preprocessing, model training and prediction evaluation are described in detail. Then, the relationship between different clinical features and prognosis was discussed by correlation analysis. Finally, the potential and future research direction of GABP model in prognosis prediction of hemorrhagic stroke were summarized.

2. Model Building

2.1. GABP Neural Network

The problem of predicting 90-day mRS Scores in patients with hemorrhagic stroke has multiple input features, including personal history, disease history, treatment, and imaging features, and the complex relationship between these features needs to be modeled. Although traditional BP neural network [4] can be used to solve this problem, its training process may be affected by local optimal solutions, resulting in degraded model performance.

In order to cope with the limitations of BP neural network in dealing with complex problems, this study introduced genetic algorithm [3] to optimize the neural network model. Genetic algorithm is a kind of natural heuristic algorithm, which can be used for global optimization problems and help to jump out of the local optimal solution, thus improving the performance of the model. In order to enhance the optimization efficiency of the algorithm, the forward propagation mechanism of BP neural network is also fully

used to evaluate the fitness of each individual genetic algorithm, so as to guide the search path of the genetic algorithm more effectively.

Therefore, through the combination of genetic algorithm and BP neural network [4], a method named GABP (Global balanced backpropagation) was proposed in this study to deal with this complex prediction problem [7], so as to further improve model performance and optimization efficiency. This approach has potential when dealing with complex problems and can be used effectively in multiple application areas such as the medical field. The GABP flow chart designed in this paper is shown in Fig. 1.

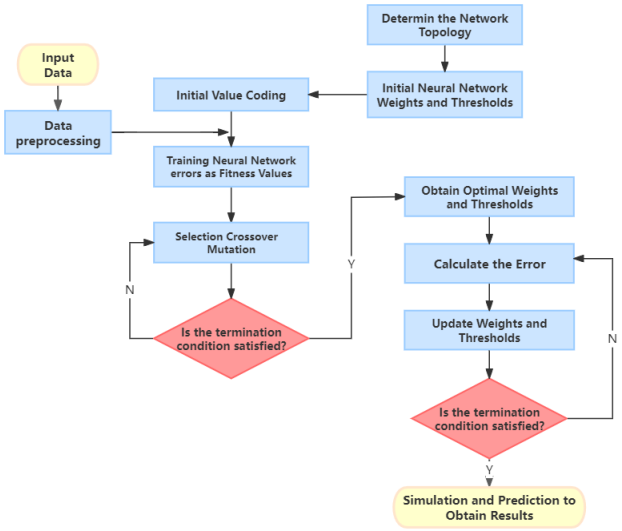

Fig 1. The overall process of GABP

In the process of GABP model construction, we first applied min-max normalization to the training data set and the test data set to ensure the consistency and stability of the model training. Then, we set the number of hidden layer neurons of BP neural network, and defined the key parameters such as population size, iteration number, crossover probability and mutation probability according to the requirement of genetic algorithm. We then initialized the population, generating a set of initial populations with multiple individuals, each representing a set of possible weights and thresholds in the neural network. Using the forward propagation mechanism of the neural network, we calculate the fitness of each individual, in which the mean square error (MSE) is used as the fitness evaluation criterion.

In the operation stage of genetic algorithm, a new population is generated through crossover and mutation operations, and individuals with higher fitness are screened out through selection operations. The optimized weights and thresholds are applied to the training process of BP neural network to build and train GABP model. Finally, the resulting GABP model was used to predict 90-day mRS Scores in patients with hemorrhagic stroke. In addition, in order to evaluate the predictive performance of the model, we also de-normalized the output of the model in order to convert it back to the original data range for comparison and analysis with the actual mRS Score. This complete normalization and de-normalization process ensures the accuracy of GABP model training and prediction, while also improving the robustness of the model to different feature scales.

2.2. Encoding and Decoding

Suppose that the neural network structure adopted in BAGP is shown in Fig. 2.

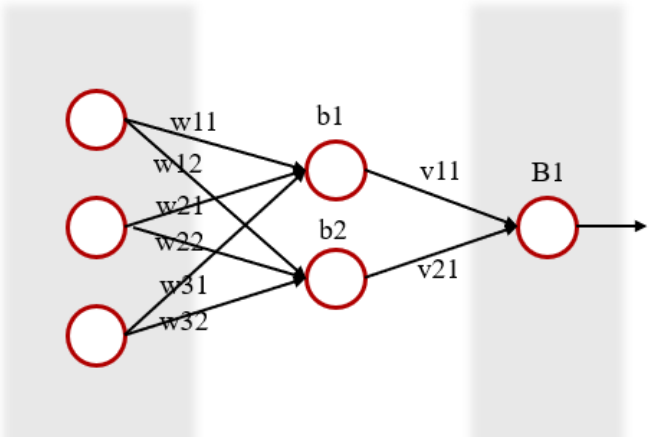

Fig 2. Neural network based on RBP

Then, when determining the weight and threshold of the network, the coding structure can be designed, as shown in Fig. 3.

w11	w12	w21	w22	w31	w32	b1	b1	v11	v21	B1

Fig 3. A diagram of the encoded structure

In the chromosome we designed, the sequence of gene locations represents each component of the neural network, including the weight between the input layer and the hidden layer, the threshold value of the hidden layer, the weight between the hidden layer and the output layer, and the weight of the output layer. This arrangement can uniquely determine the complete structure of a neural network, including the topology and parameter Settings of the network. This enables genetic algorithms to efficiently search and optimize the structure and parameters of neural networks.

3. Correlation Analysis

3.1. Distribution Test Model

The Kolmogorov-Smirnov (KS) distribution test is a statistical test used to test whether data obeys a specific probability distribution (usually a normal distribution) [8]. The null hypothesis (H0) of this test is that the data fits a particular probability distribution, and the alternative hypothesis (H1) is that the data does not.

Let the distribution function of the population be X, where $F(x)$ is a continuous function of X, and $X_1, X_2, \ldots, X_n$ is the sample from X. Then its cumulative distribution function can be written as follows.

$$F_n(x) = \frac{1}{n}\sum_{i=1}^{n} I_{[-\infty,x]}(X_i) \tag{1}$$

Where $I_{[-\inf,x]}$ is the indicator function, its value is as follows.

$$I_{[-inf,x]}(X_i) = \begin{cases} 1, X_i \le x \\ 0, X_i > x \end{cases} \quad (2)$$

At this point, the Kolmogorov-Smirnov statistic can be expressed as:

$$D_n = \sup_x |F_n(x) - F(x)| \quad (3)$$

Where $F_n(x)$ is the cumulative distribution function and $F(x)$ is a hypothetical theoretical distribution. In this paper, we assume that it follows a normal distribution. sup is the upper bound of distance, based on Glivenko-Cantell quantification, and if X_i follows the theoretical distribution $F(x)$, then approaches 0 as n approaches infinity D_n. In general, 0.05 was chosen for significance. That is, if the test value P is less than 0.05, then the null hypothesis H_0 is rejected and the indicator does not obey the normal distribution.

The Shapiro-Wilk distribution test model can be described as follows:

The zero test of this test is that the sample x comes from a normally distributed population. The statistics for this test are as follows.

$$W = \frac{\left(\sum_{i=1}^{n} a_i x_{(i)}\right)^2}{\sum_{i-1}^{n} (x_i - \bar{x})^2} \quad (4)$$

Where $x_{(i)}$ contains the subscript index i in parentheses;

Not to be confused with i, it is the i th order statistic, i.e. the i th smallest number in the sample. $\bar{x}$ is the average of the sample. Constant a_i is calculated by the following formula:

$$(a_1, ..., a_n) = \frac{m^\top V^{-1}}{(m^\top V^{-1} V^{-1} m)^{1/2}} \quad (5)$$

3.2. Correlation Model

For normally distributed ordered variables, we can use the Pearson correlation coefficient to analyze the correlation between them. The Pearson correlation coefficient is the product of the covariance divided by the standard deviation of two variables and indicates the degree of linear relationship between them.

$$\rho_{X,Y} = \frac{\operatorname{cov}(X,Y)}{\sigma_X \sigma_Y} = \frac{E[(X - \mu_X)(Y - \mu_Y)]}{\sigma_X \sigma_Y} \quad (6)$$

The above formula describes the correlation coefficient of the population and is usually expressed in Greek lowercase letters. By estimating the covariance and standard deviation of the sample, we can calculate the Pearson correlation coefficient, which is usually indicated by the lowercase letter "r" in English. This coefficient measures the linear relationship between two variables.

$$r = \frac{\sum_{i=1}^{n} (X_i - \bar{X})(Y_i - \bar{Y})}{\sqrt{\sum_{i=1}^{n} (X_i - \bar{X})^2} \sqrt{\sum_{i=1}^{n} (Y_i - \bar{Y})^2}} \quad (7)$$

r can also be estimated by the mean of the standard scores of the sample points (X_i, Y_i) to obtain an expression equivalent to the above:

$$r = \frac{1}{n-1} \sum_{i=1}^{n} \left(\frac{X_i - \bar{X}}{\sigma_X}\right)\left(\frac{Y_i - \bar{Y}}{\sigma_Y}\right) \quad (8)$$

Where $\bar{X}$, and σ_X are the sample mean, and sample standard deviation of sample x, respectively.

For ordered variables that do not obey normal distribution, it is necessary to conduct correlation analysis based on Spearman correlation model. Spearman's correlation coefficient can be expressed as floows.

$$r_s = 1 - \frac{6 \sum_{i=1}^{n} d_i^2}{n(n^2 - 1)} \quad (9)$$

Where n is the number of samples and d represents the grade difference between data x and y.

Before performing the Kruskal-Wallis H test, we need to perform a homogeneity test of variances to ensure that the variances between different groups are equal. This helps to verify whether the variance of the groups can be assumed to be equal when the Kruskal-Wallis H test is performed. The procedure for testing the homogeneity of variance is as follows.

Hypothesis H_0 is made first, that is, homogeneity of variance is satisfied. When the number of test repeats at each level is equal, that is:

$$m_1 = m_2 = \cdots = m_r = m \quad (10)$$

m is the number of repetitions at each level, which is the ratio of the maximum and minimum variances of r samples. Under the condition that the differences are equal, the quantile of H distribution can be obtained by random simulation method. The distribution depends on the level number r and the degree of freedom f=m-1 of the sample variance, so the distribution can be recorded as H(r,f). When H_0 is established, there are:

$$\sigma_1^2 = \sigma_2^2 = \cdots = \sigma_r^2 \quad (11)$$

The value of H should be close to 1, when the value of H is large, the difference between the differences between the various approaches will be large, the larger the value of H, the greater the difference between the differences between the approaches, then reject the original hypothesis H_0. It follows that for a given significance level α, the rejection domain of test H_0 is:

$$W_1 = \{H > H_{1-\alpha}(r, f)\} \tag{12}$$

Where $H_{1-\alpha}(r, f)$ is the $1-\alpha$ quantile of the H distribution.

If the data for an unordered variable does not conform to either a normal distribution or the assumption of homogeneity of variance, then consider using the Kruskal-Wallis H test to assess whether there is a significant difference between them. The basic idea of Kruskal-Wallis H test is to combine multiple groups of sample data, arrange them in ascending order, calculate the rank of each data point, and then check whether there are significant differences in the average rank of each group of data points. In conducting this test, we need to establish the following assumptions:

$$H_0: \mu_1 = \mu_2 = \cdots \mu_k \tag{13}$$

The alternative assumption is that H_1 exists at least one pair $\mu_i \neq \mu_j$ .Build test statistics as shown below.

$$H = \frac{12}{N(N+1)} \sum_{i=1}^{k} n_i (\overline{R}_i - \overline{R})^2 = \frac{12}{N(N+1)} \sum_{i=1}^{k} n_i \overline{R}_i^2 - 3(N+1) \sim \chi^2(k-1) \tag{14}$$

4. Results

4.1. Forecast Result

The predicted value of the first 100 patients was compared with the ground truth value, and the drawing error was shown in Fig. 4. Fig. 4 shows the predicted versus actual 90-day mRS Scores for the top 100 hemorrhagic stroke patients. With an intuitive graphical presentation, we can assess the predictive accuracy and reliability of the GABP neural network model. High consistency between predicted and actual values can be observed in the figure, indicating that the GABP model can capture the dynamic changes in prognosis of patients with hemorrhagic stroke. Most of the data points are concentrated near the 45-degree line, which indicates that the model's predictions are very close to the actual observations, thus verifying the validity of the model.

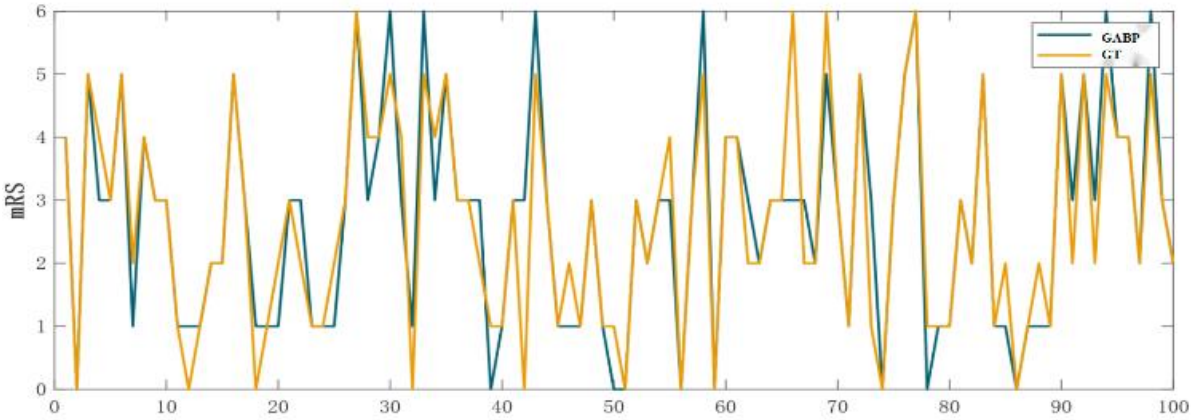

Fig 4. Comparison of predicted values in 100 patients

4.2. Analysis of Correlation between Disordered Variables and 90-day mRS

There are disordered variables in the features to be analyzed, so this part of variables needs to be discussed separately. In general, Kolmogorov-Smirnov chose 0.05 for significance. That is, if the test P-value is less than 0.05, then the null hypothesis H_0 is rejected and the indicator does not obey the normal distribution. The following takes the relationship with gender as an example.

The results of the normality test are shown in Table 1.

Table 1. Normality test

Index	Significance
90-day mRS	2.5293E-19

If the values of *P* are all less than 0.05, then the null hypothesis *H*0 is rejected, and the 90-day mRS Does not obey the normal distribution. The test results of homogeneity of variance are shown in Table 2.

Table 2. Test results of homogeneity of variance

	Levin Statistics	Significance
90-day mRS	289.119480	5.2904E-280

By calculating Levin statistics based on the mean, we find that the significance level is less than 0.1, which indicates that the variance of the data is not uniform. To sum up, for the data of disordered variables, neither the normal distribution nor the hypothesis of homogeneity of variance is satisfied. Therefore, it is appropriate to consider using the Kruskal-Wallis H test to assess the correlation between them.

The analysis results of Kruskal-Wallis H test are shown in Table 3.

Table 3. Kruskal-Wallis H test results

Index	Value	Daily Sales
Sex	H	3893.258556
	P	0.655502

The results showed that the significance of disorder index was less than 0.05. Therefore, there is no significant correlation between gender and 90-day mRS, that is, gender is not an important factor affecting the 90-day prognosis score of stroke patients. There are several possible explanations and important perspectives for this finding:

(1) Individual differences: Although gender has been recognized as an important predictor in many medical studies, gender does not appear to significantly affect 90-day mRS Scores in this specific population of stroke patients. This suggests that the prognostic score may be influenced by other more important factors, such as age, previous medical history, and severity of disease.

(2) Disease complexity: Stroke is a complex disease, and its prognosis is affected by many factors. While gender can have an impact on the prognosis of stroke patients in some cases, this does not necessarily apply in all cases. Therefore, a comprehensive assessment of prognosis requires a comprehensive consideration of multiple factors.

(3) Statistical methods: Appropriate statistical methods, including Kruskal-Wallis H test, are used to deal with data that do not follow normal distribution and have uneven variance. Such methods allow for more accurate detection of relationships between variables, independent of data distribution.

4.3. Analysis of Correlation between Ordered Variables and 90-day mRS

Table 4. Normality test results

Variable	Significance
Age	0.072
HM_volume	0
HM_ACA_R_Ratio	0
original_shape_Elongation	0.32
original_shape_Flatness	0.426
original_shape_LeastAxisLength	0.039
NCCT_original_firstorder_RobustMeanAbsoluteDeviation	0.056
NCCT_original_firstorder_RootMeanSquared	0.581
NCCT_original_firstorder_Skewness	0
NCCT_original_firstorder_Uniformity	0
NCCT_original_firstorder_Variance	0.549
90-day mRS	0

Given that the features required for the analysis include ordered variables, and given that our data set is relatively small, we performed the Shapiro-Wilk test to determine whether these variables conform to a normal distribution. The results of normality test are shown in Table 4. Due to space limitation, only the normality test results of some variables are shown.

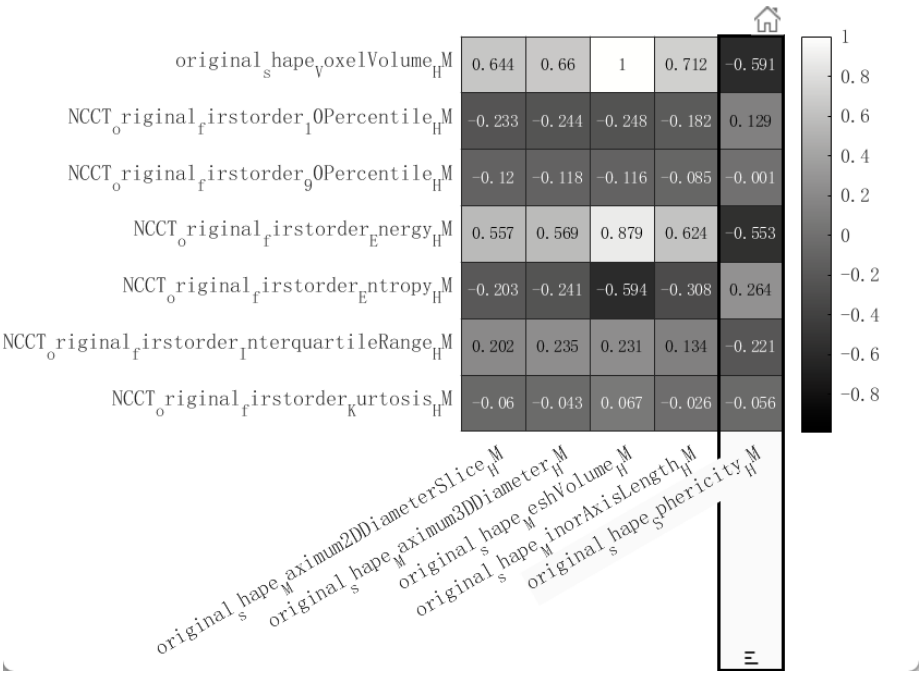

Fig 5. Normality test results

Since the P-value in the test result is less than 0.05, we reject the null hypothesis H0, which means that the data does not meet the requirements of a normal distribution. Therefore, in the subsequent analysis, we will use Spearman correlation coefficient to study the correlation between these variables. The analysis results are shown in Fig. 5.

When analyzing the relationship between 90-day mRS Scores and different variables, a significant negative correlation was found between diastolic blood pressure and 90-day mRS Scores, suggesting that higher diastolic blood pressure may be associated with poorer 90-day mRS Scores. However, HM_volume in the brain showed a small positive correlation with 90-day mRS Score, suggesting that brain volume may be associated with better 90-day mRS Score. The correlation between age and the time interval between onset and first imaging examination and the 90-day mRS Score was almost zero, suggesting that these factors had no significant linear relationship with the 90-day mRS Score. In addition, the correlation between shape features such as Elongation and Flatness of the original shape and the 90-day mRS Score was also close to zero, indicating a weak linear relationship between these shape features and the score. The volume and ratio of most other brain regions were similarly less correlated with the 90-day mRS Score. However, some variables such as the InterquartileRange, Skewness, and Variance of the NCCT original image were positively correlated with the 90-day

mRS Score, and although these correlations were relatively high, they still indicated some positive association with the 90-day mRS Score.

5. Conclusion

By constructing a BP neural network (GABP) model optimized based on genetic algorithm, this study successfully accurately predicted the 90-day mRS Score of patients with hemorrhagic stroke. By using genetic algorithm to globally optimize the weights and thresholds of BP neural network, we overcome the problem that traditional BP neural network is prone to falling into local optimal, and significantly improve the prediction performance and generalization ability of the model. In the process of model construction, we adopted min-max standardization to ensure the consistency and stability of training and test data sets. In addition, the fitness of each individual genetic algorithm is evaluated by the forward propagation mechanism of the neural network, which effectively guides the search path of the genetic algorithm and further enhances the optimization efficiency of the model. By analyzing the model prediction results, we found a significant negative correlation between diastolic blood pressure and 90-day mRS Score, and a small positive correlation between brain volume and 90-day mRS Score. These findings provide clinicians with important prognostic indicators and help to develop more personalized and precise treatment plans.

Although this study has achieved certain results, there are still some limitations. First, the relatively limited size of the data set may affect the generalization ability of the model. Second, the interpretability of the model needs to be further improved in order to better understand the influence of different features on the prognostic score. Future studies could explore larger data sets, as well as consider more clinical features and biomarkers, to further improve the model's predictive accuracy and interpretability. In conclusion, this study demonstrates the potential of GABP neural network models in predicting prognosis of hemorrhagic stroke. With the continuous progress of artificial intelligence technology, we believe that GABP model will play an increasingly important role in the field of intelligent medicine, providing more scientific and accurate decision support for the clinical diagnosis and treatment of hemorrhagic stroke patients.

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