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Clinical intelligent diagnosis and treatment analysis of hemorrhagic stroke

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Abstract: With the continuous progress and development of artificial intelligence, it has been widely applied in many fields. In the current stage of rapid development of medical technology, many medical technologies need to analyze complex basic data based on artificial intelligence to provide further treatment plans or predict and analyze patient conditions. This article focuses on the risk factors of hematoma after hemorrhagic stroke in patients, and combines the patient's personal information, treatment plans, and other data provided. Based on factor analysis, a quantitative data dimensionality reduction model is established using BP neural network, GABP neural network, and other related models to achieve accurate and personalized prognosis prediction, treatment evaluation, and opinions. To predict the probability of hematoma expansion in patients, complex patient information is first dimensionally reduced based on factor analysis. Then, the personal history and disease history of the top 100 patients, as well as relevant treatment plans, are used as input features, and the prediction probability of hematoma expansion is used as output. BP neural network is used to predict the probability of hematoma expansion in patients.

1. Background

With the rise and development of technologies such as artificial intelligence, machine learning, and big data in recent years, artificial intelligence is increasingly being used in the field of smart healthcare. Among them, the causes of hemorrhagic stroke are relatively complex and rapid, with poor prognosis and consistently high mortality rates. After the onset of hemorrhagic stroke, some patients may experience enlarged hematoma due to brain tissue damage or inflammatory edema, which seriously affects the continuous deterioration of the patient's brain nerves. In severe cases, it can endanger the patient's life and bring great impact to the patient and their family, It also seriously hinders the pace of exploration and construction of smart healthcare in society. This topic aims to establish a relevant mathematical model, hoping to accurately predict the incidence and probability of hematoma expansion and surrounding edema after hemorrhagic stroke based on the background knowledge provided in this competition, combined with the patient's personal information and corresponding specific treatment plans and prognosis. Through accurate identification and prediction, the patient's prognosis and quality of life can be improved[1].

2. Analysis of Risk Identification for Hematoma Expansion

2.1. Analysis of the basis for the occurrence of hematoma expansion

Based on the collected information, determine whether all patients have experienced hematoma expansion events within 48 hours of onset and record them. Based on the patient's first imaging examination serial number upon admission and the time interval between the patient's first imaging examination, it can be basically determined whether the top 100 patients will experience hematoma expansion within 48 hours after onset. The judgment is based on whether the absolute increase in hematoma volume from subsequent examinations to the patient's first examination exceeds 6mL, or whether the relative increase in volume exceeds 33%. The first step is to preprocess the data provided by the question, screen out the required data, screen out abnormal or missing data in the table, and calculate the time difference between each time point and the onset of the disease; Afterwards, the data required for the problem, such as the serial number of the first imaging examination, the time interval from onset to the first imaging examination, the serial number at each time point, and the corresponding HM volume, will be filtered and extracted, and a new table will be established. Then, the volume change value before and after the hematoma will be calculated as the basis for determining whether hematoma expansion has occurred. If edema expansion occurs, the time of hematoma expansion will be recorded.

2.2. Calculation and analysis of the probability of hematoma expansion

Secondly, a quantitative data dimensionality reduction model based on factor analysis is needed to categorize a large number of complex relationships into a small number of comprehensive factors based on the personal history, disease history, disease-related information of the first 100 patients, as well as the imaging examination results in the data. By constructing a BP neural network, the top 100 patient data are used as input features, and the output results are used as the probability of hematoma expansion for each patient. Using the collected information, a model is developed to estimate the likelihood of hematoma expansion for all patients and recorded.

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3. Model establishment and solution

3.1. Establishment of a risk identification model for hematoma expansion

Based on relevant information points, we determine whether the top 100 patients will experience hematoma expansion events[4]. If so, we need to record the time of hematoma expansion. According to the given conditions, if the volume of hematoma in subsequent examinations increases by $\geq$ 6mL or $\geq$ 33% compared to the first examination, it is determined that hematoma expansion has occurred. By analyzing the content, specific judgment steps were listed:

We need to filter and extract the serial number of each patient's first imaging examination upon admission, as well as the time interval between the onset of the patient and the first imaging examination, from the patient's data. The serial number of each time point in the data and its

corresponding HM_ The volume of hematoma has also been extracted as the basic data for determining whether hematoma expansion has occurred;

Based on the given judgment basis, if the calculated change in hematoma volume is ≥ 6mL or the change percentage is ≥ 33%, it is marked as hematoma expansion, the field is marked as 1, and the time point of hematoma expansion is recorded.

The second step involves calculating the time difference between the onset of the disease and the onset of the disease. Subsequently, the data provided in the attached table is divided into two parts: time point information and the date of the day. The format of the collected time point information is "hour: minute: second". To further calculate the time difference, we directly refine the time point information to the format of only hours. The specific calculation method is:

$$\min = \min + 1, \text{ if } \sec \geq 30, \min < 59\min$$

$$\min = 0, h = h + 1, \text{ if } \sec \geq 30, \min = 59$$

$$h = h + 1, \min > 30$$

In the formula, h represents the "hour" part of the time point, similarly, min represents the "minute" part of the time point, and s represents the "second" part of the time point. By using the formula, precise time points can be calculated, making it convenient to calculate the time difference. We did not consider the upper limit of time h here, as obtaining an accurate value will directly subtract it from the onset time calculation and will not affect the final result. The flowchart is as follows:

Start: The process begins.

Input: Table 1, Table 2, Appendix Table 1: The required tables are inputted.

Record the time of the first imaging examination: The date and time (year, month, day, hour, minute, second) of the first imaging examination are recorded.

Seconds > 30? Check if the seconds are greater than 30. Yes: Add 1 to the minutes.

No: Proceed to round the minutes.

Minutes > 59? Check if the minutes are greater than 59 after addition. Yes: Set minutes to 0, add 1 to the hours.

No: Proceed to round the minutes.

Minutes > 30? Check if the minutes are greater than 30. Yes: Add 1 to the hours.

No: Proceed to iterate through each follow-up.

Iterate through each follow-up: For each follow-up, record the date and time of the imaging examination.

Round the hours: Perform rounding on the hours.

Calculate the time difference: Are the months the same? Yes:Are the dates the same?Yes: Time difference = Hour difference.

No: Time difference = New hour difference - Original hours.

No: Calculate the day difference, then calculate the time difference.

The flowchart is shown in Figure 1:

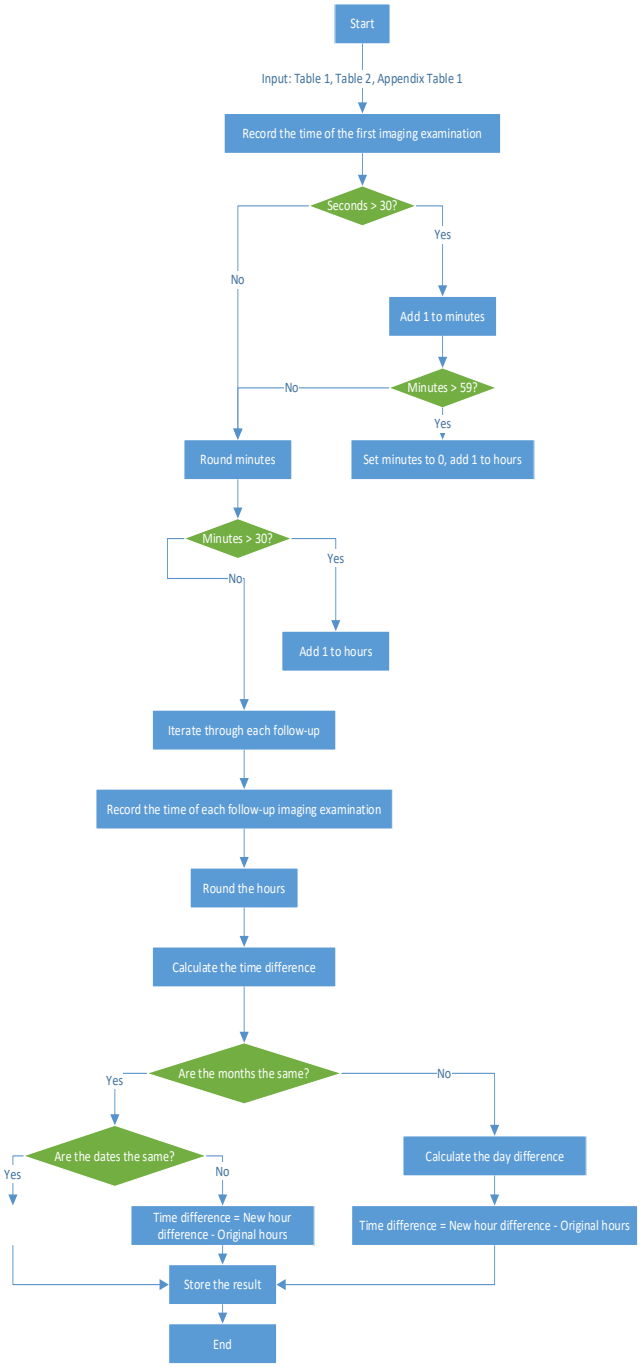

Figure 1: Calculation time flowchart

Store the result: Add the time interval from the onset to the first imaging examination to the table and store the result.

End: The process ends.

After calculating the date interval, events can be identified based on the extent of hematoma expansion [5]. Under the premise of satisfying formula 2, and meeting both conditions of formula 3 and formula 4, it is determined that a hematoma expansion event will occur, and the result is determined. Expansion time.

$$h\mathrm{h}_{\mathrm{gap}} \leq 48$$

$$HV_{gap} \geq 6$$

$$\varphi_{gap} \geq 33\%$$

Record the results of the final model operation, for example, if the judgment result of individual patients is 1, it represents the occurrence of hematoma expansion event, and the expansion time is 39.67 (unit hour).

3.2 Quantitative data dimensionality reduction model using factor analysis

In order to classify complex data information into more representative factors, factor analysis [6] is used to analyze and process the degree of dependency between related attributes. Multiple complex related attributes are reduced to a small number of feature factors, and are divided based on the variance contribution effect between each attribute. More and more complex attributes are represented by new small number of comprehensive factors to represent the internal connections of the original system. The structural model is as follows:

$$x_1 = a_{11}F_1 + a_{12}F_2 + \ldots + a_{1m}F_m + e_1$$

$$x_2 = a_{21}F_1 + a_{22}F_2 + \ldots + a_{2m}F_m + e_2$$

.....

$$x_p = a_{p1}F_1 + a_{p2}F_2 + \ldots + a_{pm}F_m + e_p$$

Among them, X=(x1, x2... xp)Tis the relevant continuous attribute of the data, which is an observable random vector and satisfies that the E (X) mean vector is zero, and Cov (x)=∑;

F=(F1, F2... Fm) T (m<p) represents the common factor, which must satisfy that the mean vector of E (F) is zero, Cov (F)=1, and each vector is independent of each other[7];

Ɛ=(e1, e2... ep) T and F are independent of each other, satisfying E (e)=0, where each element e is independent of each other. It can be expressed as a matrix form X=AF+Ɛ, where is the factor load matrix. The obtained factor model can be expressed as:

$$F_1 = \omega_{11}x_1 + \omega_{12}x_2 + \ldots + \omega_{1p}x_p$$

$$F_2 = \omega_{21}x_1 + \omega_{22}x_2 + \ldots + \omega_{2p}x_p$$

.....

$$F_m = \omega_{m1}x_1 + \omega_{m2}x_2 + \ldots + \omega_{mp}x_p$$

Model solving:

After calculating the variance of the factors, it can be concluded that there are 13 factors with eigenvalues greater than 1, with a cumulative interpretability of 84.267%. Through intuitive comparison, it can be concluded that before the 13th component, it is the main factor, and after the 13th component, the trend of changes in eigenvalues gradually stabilizes, that is, the components after the 13th component are all secondary factors, as shown in Figure 2:

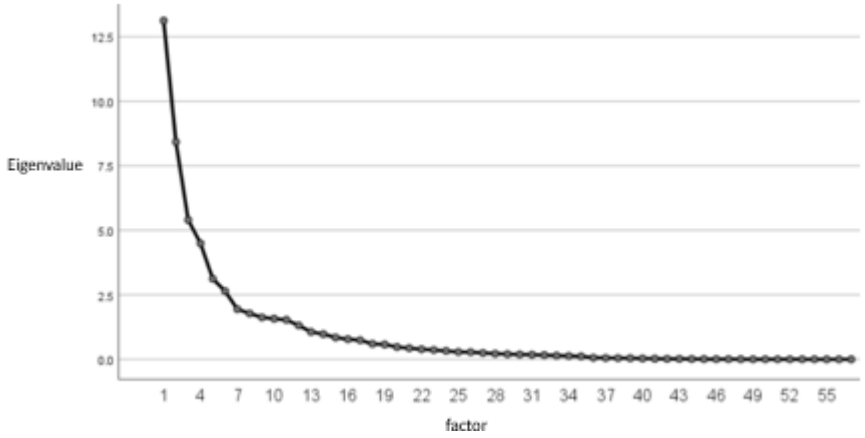

Figure 2: Calculating factors

Based on the analysis of factor extraction and information content, it can be seen from the above figure that a total of 13 factors were extracted through factor analysis, with feature root values greater than 1. The variance interpretation rates of these 13 factors after rotation were 20.490%, 9.813%, 7.831%, 7.503%, 4.775%, 4.433%, 4.386%, 4.104%, 3.984%, 3.516%, 3.293%, 2.309%, and the cumulative variance interpretation rate after rotation was 85.948%[8].

4. Prospect

Looking ahead, GABP neural network is first used to continuously optimize and adjust parameters to achieve a high prediction rate.

Secondly, the parameter search performance based on differential evolution algorithm is better.

In predicting the probability of patient hematoma volume and discussing the changes in hematoma volume caused by treatment plans, it can be extended to other disease prediction and treatment suggestions in the medical field.

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