Research Article

Machine Learning-Based Prediction Study of Hematoma Enlargement in Patients with Cerebral Hemorrhage

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The enlarged hematoma is closely related to the poor neurological prognosis of patients with cerebral hemorrhage (intracerebral hemorrhage, ICH). Therefore, it is of great clinical significance to accurately predict whether ICH patients. In this study, we explored the predictive ability of a two-model machine learning (ML) method to predict hematoma expansion. This method features nonenhanced CT (noncontrast computed tomography, NCCT) in ICH patients. The image information is combined with multiple clinical data for the prediction of hematoma enlargement. We retrospectively collected 140 ICH patients (including 58 patients with hematoma enlargement) from our hospital in 2021, and obtained a total of 5616 NCCT hematoma images (including 2635 images of hematoma enlargement) and 10 clinical data for each patient. The dual-model ML method used in this study contains 2 steps. The first step is to use a single-model predictor based on deep convolutional neural network (DCNN), which uses only the patients. The baseline NCCT images were performed for the prediction of hematoma enlargement. To select an appropriate DCNN model, we simultaneously compared the prediction performance of the three DCNN models, including ResNet34 (residual neural network with 34 layers), VGGNet (visual geometry group network), and GoogLeNet (Google inception network). In this step, we also explored whether the method of hematoma segmentation could improve the prediction outcome. The second step is to use the dual-model predictor based on multilayer perception (MLP), where the results of the single-model predictor in step 1 are combined with multiple clinical data of the patient to predict the final result. The sensitivity, specificity, positive predictive value, and negative predictive value were calculated for each model, and were predicted using the subject operating characteristic curve (the receiver operating characteristic, ROC) and area under curve (AUC) to evaluate prediction performance. The experimental results show that the ML method proposed in this study can comprehensively analyze the patient NCCT image information and clinical data, which can achieve 86.5% accuracy and have relatively equal sensitivity and specificity. Therefore, this ML method can be used as a predictive tool to effectively identify people at high risk of hematoma expansion. This study can make an effective prediction of hematoma expansion in patients with clinical cerebral hemorrhage, which can better treat patients, improve the doctor-patient relationship, reduce complications, etc.

1. Introduction

Intracerebral hemorrhage (ICH) is a fatal neurological disease, which accounts for about 10% to 30% of all strokes. It is one of the most dangerous subtypes of stroke, with a mortality rate of 30% to 50% within 30 days, and more than 75% of patients may have residual disability or death after 1 year [1]. The enlarged hematoma volume expansion occurs in 30% of ICH patients, which is an independent predictor of poor late functional prognosis and a key prevention and treatment target in clinical work [2]. However, the use of CTA is limited by multiple factors, such as patients with renal function impairment and elderly patients with poor peripheral vascular conditions unable to receive contrast agent injection. In contrast, nonenhanced computed tomography sweeps as the preferred diagnosis method, noncontrast computed
tomography (NCCT) is widely used in clinical work. For the above reasons, the use of NCCT to predict hematoma expansion has attracted more and more attention and research [3].

The prediction of hematoma enlargement has attracted more and more attention and research. At present, several predicted signs based on NCCT have been proposed, including hematoma irregular shape, heterogeneous density, “mixed sign”, “black hole sign” and “island sign”. Although the above signs can be relatively high specificity, but its sensitivity is only about 50%, which causes the above signs is difficult to accurately identify the hematoma expansion of high risk patients and difficult to be applied in clinical work, and the above prediction signs identification is difficult, especially for inexperienced doctors and basic hospital doctors is particularly difficult. The reason is that the above signs or for the lack of comparison. To define it accurately or to define it as cumbersome is difficult to remember. For the above reasons, we need to consider whether there is an insufficient prediction using only imaging information. Moreover, in addition to the above presented above, some clinical data, such as the time from onset to baseline NCCT, hematoma volume on baseline NCCT have been confirmed to be closely related to hematoma enlargement. Therefore, in this study, we tried to predict the risk of hematoma enlargement in patients with cerebral hemorrhage with 1 two-model prediction method, namely, combining imaging and clinical data.

If we consider the prediction of hematoma expansion as a classification task, which is divided into two categories of hematoma expansion and the other that does not expand, then, machine learning (ML) technology is the most effective tool to complete such tasks. Multiple studies have confirmed that ML can achieve good results in disease identification as well as prediction, with very good performance. However, ML-based model training usually requires a large number of patients to train neural networks to achieve satisfactory results. For example, pulmonary nodules and diabetic visual networks were detected. Membrane lesions require thousands of samples. Collecting such a large number of patients will be a very time-consuming process, and the time spent collecting patients can take years [4].

For the limited number of patients, this study chose a two-model ML method, through which we can combine NCCT images and patient clinical data together to predict the expansion of the hematoma, which can achieve good classification prediction effect with relatively small samples. Previous studies have also adopted the research method of combining images with clinical data and achieved good results.

2. Progress of NCCT in Predicting Hematoma Expansion and AI Machine Learning

Approximately 30% of patients with CH will experience hematoma enlargement, which is an independent predictor of poor neurological outcome, and is also a therapeutic focus in clinical work. In clinical work, identify high-risk patients with possible hematoma expansion in the early stage, and give early targeted treatment is critical to improve the treatment effect and prognosis of patients with cerebral hemorrhage [5]. NCCT is the most basic diagnosis and treatment method to diagnose cerebral hemorrhage, which is widely used in hospitals of all regions and levels [6]. Thus, the search for imaging predictors of an enlarged ICH hematoma in NCCT has been ongoing since the 1780s. So far, multiple imaging signs have been associated with hematoma enlargement. Compared with CTA, NCCT is easy to apply and cheap. However, the prediction accuracy of signs in NCCT is low and subjective. Moreover, for clinicians, it is very difficult to correctly identify signs in images, and manual identification is subjective and time-consuming [7].

Artificial intelligence belongs to the category of computer science; that is, we hope that computers have the same human intelligence and learning ability, to solve some practical problems [8]. Artificial intelligence technology can assist in early disease diagnosis by analyzing a large amount of medical data, so as to greatly improve the diagnosis efficiency of doctors, reduce the misdiagnosis rate, and alleviate the shortage of medical resources. In recent years, artificial intelligence technology has been applied to all walks of life, and the medical treatment aspect is no exception, and it has shown great application potential in disease identification, diagnosis, and risk prediction [9]. Studies have shown that it is of great significance in skin cancer diagnosis of skin cancer, imaging tuition judgment, diabetic membranopathy type II, breast cancer classification, and so on. NCCT and the current application of artificial intelligence (AI) in medical field has reached or even exceeded the average diagnosis level of doctors.

As an important part of artificial intelligence technology, ML belongs to the field of computer science and engineering together with artificial intelligence. Artificial intelligence is a big concept. The most ideal artificial intelligence is a machine with the human general intelligence and mind, but this kind of artificial intelligence is difficult to achieve at present. What we can do now is "weak artificial intelligence"; that is, the level of performing specific tasks is equivalent to human beings, or even beyond human technology [9]. The human-machine game that can be seen in real life, unmanned driving, and medical imaging interpretation belongs to this category. ML is currently the main method to implement artificial intelligence; it is to use algorithms to parse data, like people. A way to learn from the data, extracts the patterns in the data, and then makes analytical predictions about the real world. With the increasing computer performance and explosive data growth, ML can tirelessly and continuously analyze and refine the huge amount of data, so as to solve some problems that are too complex for humans. At present, ML Jing has been widely developed in the medical field, and it has shown great potential and even achieved good results in the risk prediction of disease, identification and classification, and medical image classification. Many studies have shown that ML in lung nodules, thyroid nodules vs the diagnosis of skin cancer, breast cancer, and diabetic retinopathy can be close to or even far beyond the accuracy of human experts [10].

At present, artificial intelligence has penetrated into various fields, such as driverless driving, medicine, finance and trade, and other fields. ML is the core of artificial intelligence. ML is about using algorithms that enable machines...
to learn rules from large amounts of historical data to intelligently identify new samples or make predictions about the future [11]. Deep learning is a new field in ML research. Deep learning methods simulate human neural networks, combine multiple nonlinear processing layer by layer, obtain different levels of abstract features from the data and use them for classification prediction. Many structural models of deep neural networks have been applied to medical imaging, such as convolutional neural networks, sparse coding networks, stack autoencoders, restricted Boltzmann machines, and deep belief networks. Convolutional neural network can extract the features of the images, and the relationship between the image features and the image labels can be found out very accurately and efficiently, so as to complete the effect of image recognition or classification. Compared with humans in big data operation, the neural network can maintain continuous high precision. At present, there have been many examples of deep learning applications in the medical field, such as the diagnosis of heart diseases, the diagnosis of respiratory diseases, the diagnosis and differentiation of retinal diseases, the classification and diagnosis of tumors, and skull shadow-like, the diagnosis and classification of epilepsy carbuncle, Parkinson’s diagnosis of hemorrhage after thrombolysis and so on.

3. Based on Machine Learning-Based Prediction of Hematoma Enlargement in Patients with Cerebral Hemorrhage

3.1. The ML Method for the Dual Model. Our ML method contains two predictive models. The first predictive model is a single-model predictor based on DCNN using the NCCCT skull images only. The purpose of this prediction model is to predict the chance of hematoma expansion in each NCCT image, and the image information is transformed into probabilistic information for the next step. The second prediction model is a dual-model predictor that combines the prediction results from the first prediction model with the patients’ clinical data, which is implemented through a neural network called multilayer perception (MLP). See the body steps in Figure 1.

3.1.1. First Prediction Model: Single Model Prediction Based on DCNN. The first model structure is shown in the upper half of the flow diagram. DCNN is one of the most successful deep learning technologies used for image recognition and classification, and a variety of DCNN models can achieve excellent image classification results, such as 34-layer Residual Network (ResNet34), Visual Geometry Group Network (VGGNet), and Google Inception Network (GoogLeNet). In this study, we used the ResNet34 to achieve single-model prediction trained using NCCT images, because it has the advantage of achieving deeper network training with limited data and achieving good performance. ResNet34 is invented based on the VGGNet network structure, contains 34-layer structure and uses a convolutional kernel of 3X3. Unlike in VGGNet, the ResNet34 downsampling method is done by using a convolutional layer of a step size of 2 rather than a pooling layer. The most prominent feature of ResNet is the insertion of a structure called a residual block based on the VGGNet network structure, where the output value of each two layers is added to the previous input value so that the network structure can become deeper, and caused by. This yields a better predictive performance. Stacking many residual blocks together constitutes the basic structure of the ResNet34.

To better validate the classification performance of ResNet34, we compared it with the prediction performance of two other neural networks, including VGGNet and GoogLeNet. We trained three DCNN using two NCCT brain images of DCNN network models to test the predictive performance of different network models. As previously introduced in “Preprocessing of Images,” we explored whether the image segmentation method that divides the hematoma part from the brain tissue background could improve the prediction performance, a step visible in the process graph. Each image was labeled, with hematoma enlargement labeled 1 and 0 without hematoma enlargement. The DCNN model was trained in 80 rounds, the initial learning rate was 10-3 (3 times lower per 20 rounds), the batch number of data was 60 images, and the optimizer was the Adam optimizer. A batch normalization method is used between each two convolution layers to prevent overfitting.

3.1.2. Second Prediction Model: Dual-Model Prediction Based on MLP. The second model is shown in the lower half of the flowchart. During the training process of the first prediction model, we obtained a single-model predictor (ResNet34) to predict the chance of hematoma expansion for each NCCT image. In this part, we will use a dual-model predictor based on the 1VB, P neural network, which combines the prediction results of ResNet34 with 10 patient clinical data to predict the chance of hematoma enlargement.

MLP is the most commonly used neural network model in ML. It consists of 1 input layer, 1 or more hidden layers, and 1 output layer 3 parts, to pass the input value from the input layer to the output layer and realize the mapping relationship between the input and the output. The first layer of the neural network is called the input layer, which is designed to receive various input data; the last layer of the neural network is called the output layer, which is the last result of the output network. Level 1 or more between the input and output layers is called hidden layers. Each layer is composed of neural nodes (or called neurons), and the points of the two adjacent segments are connected by the weights, referring to the first 1 nerve The magnitude of the effect value of the output of the element on the output of the next neuron. Values from each neuron in the first 1 layer were multiplied by 1 weight, and the resulting weighted values were then added together to obtain a combined value. The sum of the combined values is then entered into a transfer function whose output is passed to the next layer.

Due to the limited sample size data (140 patients), we chose to use a 3-layer MLP network with a relatively simple structure and a single hidden layer. The input values of MLP were predictive values from the single model predictor, age, gender, history of diabetes mellitus, coronary heart disease, smoking history, drinking history, hypertension history, baseline systolic BP value, time to the baseline NCCT, and
hematoma volume shown by the baseline NCCT. Notably, the ResNet34 predicts the chance of hematoma enlargement per NCCT cranial image, and in this part, we need the value of each predictive value of hematoma enlargement in 10 patients. Therefore, for each patient, we first use the first prediction model to predict the chance of each hematoma image, and then calculate the number of predicted positive images in the proportion of all images, so as the chance of the patient, namely the input value of the second prediction model.

The output values of the MLP network were predictive of hematoma enlargement in 1 patient. The number of nodes in the input and output layer is determined by the number of input and output variables, so that the input layer of the network consists of 11 neurons, and the output layer consists of 2 neurons. Neural networks optimize the best effect of classification by constantly adjusting the number of neurons and the number of hidden layers in the hidden layer. We tested the number of neurons ranging from two to eight in the hidden layer to determine the optimal number of neurons. During the course of training the MLP, we used the patients in the whole training set for batch training. The initial learning acquisition rate was 10-3, using the optimizer for the Adam optimizer.

3.2. Data Collection. Through retrospective analysis, ICH patients treated in our hospital in 2021 were selected as study subjects, and patients were complete and clear. According to the screening criteria, patients were adults, and patients gave informed consent to ensure baseline NCCT examination within 6 hours after ICH symptoms, and NCCT scan within 48 hours after baseline NCCT scan.

The hematoma volume was measured as follows: using the abc/2 formula, where $a$ is the maximum hematoma diameter of the NCCT, $b$ is the opposite diameter of $90^\circ$ from $a$, and $c$ is the approximate number of NCCT sections of the hematoma times the thickness of the section.

3.3. Preprocessing of the Images. Both baseline and review NCCT image scans were performed using standard clinical parameters with an axial thickness of 5 mm. NCCT images were acquired and saved in Medical Digital Imaging and Communication Format (digital imaging and communications in medicine) DICOM. To minimize the interference of irrelevant information, only the levels containing the hematoma images were selected from the NCCT images, and the levels without the hematoma images were discarded. To meet the image pixel values required for the subsequent ML analysis, the initially filtered NC was entered. The CT
images were centered at the image center of gravity and trimmed to a square of 227 × 227 pixels containing the hematoma area as an input image for further using ML analysis. In this step, we discarded images with trimmed hematoma areas of less than 200 pixels, because they were difficult to distinguish from the background brain tissue. To speed up NII, the efficiency of the analysis, we normalized and normalized all the trimmed images, with all the pixel values normalized to between 0 and 1.

Regarding the hematoma segmentation, here, we used a salient object detection method. This method is based on deep convolutional neural network (DCNN), which is fully called deep supervised saliency object detection with short connections. Unlike previous salient object detection methods, this new salient object detection system introduces a series of short connected structures into the original structure, characterized by combining the output of the deep structure of the prediction model and the output of the shallow structure. By combining different deep networks information about the structure, this short connection structure can provide more abundant information to each layer of the prediction model; that is, the image information extracted from multiple layers from deep structure to shallow structure. Unlike simple object edge detection, salient object detection methods can identify the most visually distinct objects and regions in an image and then segment them from the background. For the above reasons, we used this new significant object detection method for hematoma region segmentation. And in addition to extracting edge features, we expect that more details of the hematoma image can be extracted using this method.

### 3.4. Model Performance Evaluation.

Clinical variables included four continuous variables (age, baseline systolic blood pressure, time from onset to baseline NCCT, hematoma volume size at baseline NCCT) and six categorical variables (gender, alcohol consumption history, smoking history, hypertension, diabetes history, history of heart disease history). Categorical variables were expressed as percentage and continuous variables as mean standard deviation. The t-test was used for continuous variables and categorical variables using χ² test or Fisher test to compare differences in demographic characteristics, differences in clinical data, and imaging information between groups of patients with hematoma enlargement and patients without hematoma enlargement. In all statistical points, the analysis was performed using the SPSS software (version 25). A p value of <0.05 was considered statistically significant.

<table>
<thead>
<tr>
<th>Patient profile characteristics</th>
<th>Patients who have developed an enlarged hematoma (n = 114)</th>
<th>No patient developed a hematoma enlargement (n = 166)</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Average age (SD)</td>
<td>63.1 (12.5)</td>
<td>56.95 (11.8)</td>
<td>0.003</td>
</tr>
<tr>
<td>Gender (man)</td>
<td>40 (70.2%)</td>
<td>51 (61.4%)</td>
<td>0.287</td>
</tr>
<tr>
<td>History of drinking</td>
<td>21 (36.8%)</td>
<td>32 (38.6%)</td>
<td>0.837</td>
</tr>
<tr>
<td>History of smoking</td>
<td>25 (43.9%)</td>
<td>31 (37.3%)</td>
<td>0.440</td>
</tr>
<tr>
<td>Medical history of hypertension</td>
<td>46 (80.7%)</td>
<td>62 (74.7%)</td>
<td>0.406</td>
</tr>
<tr>
<td>History of diabetes</td>
<td>9 (15.8%)</td>
<td>8(9.6%)</td>
<td>0.274</td>
</tr>
<tr>
<td>HDH</td>
<td>12 (21.1%)</td>
<td>8(9.6%)</td>
<td>0.058</td>
</tr>
<tr>
<td>Baseline SBP value (SD)</td>
<td>171.9 (22.6)</td>
<td>153.6(21.1)</td>
<td>0.001</td>
</tr>
<tr>
<td>Time to baseline NCCT (SD)</td>
<td>2.9 (1.36)</td>
<td>4.1(1.28)</td>
<td>0.027</td>
</tr>
<tr>
<td>Hemoma volume at baseline NCCT</td>
<td>26.1 (15.57)</td>
<td>13.4 (12.40)</td>
<td>0.018</td>
</tr>
</tbody>
</table>

**Table 1: Comparison of the clinical characteristics of the patients with and without hematoma enlargement.**

**Figure 2: Example of the hematoma segmentation results.**
caused by 1 calculation. In the practice of this method, we ing the above prediction evaluation results to obtain more model predictions.

calculated separately to evaluate the performance of the accuracy of the DP and MCNN models predicted results were respectively, normalized to between [0,1].

Subjects’ operating characteristics curve (the receiver operating characteristic, ROC) and the area under the curve (AUC) value are depicted to evaluate the prediction performance of the above networks.

Two parameters were used to evaluate the segmentation effect of hematoma segmentation, including $F$ metric values and mean absolute error. For a given continuous significance map $S$, we converted the threshold to a binary mask $B$, and then calculated its precision and recall as

$$
\text{Precision} = \frac{|B \cap Z|}{|B|},
$$

$$
\text{Recall} = \frac{|B \cap Z|}{|Z|},
$$

where $Z$ represents the positive values in the binary atlas, and $|.|$ represents the nonzero entries in the cumulative mask. $F$ is used to comprehensively assess the quality of the explicit map, as defined as

$$
F = \frac{(1 + \beta^2) \text{Precision} \times \text{Recall}}{\beta^2 \text{Precision} + \text{Recall}},
$$

where $\beta^2$ sets it to 0.3 to indicate the importance of accuracy. The mean absolute error represents the average difference between the explicit map value and the label value, with the calculation formula:

$$
\text{MAE} = \frac{1}{H \times M} \sum_{i=1}^{H} \sum_{j=1}^{W} |\tilde{S}(i,j) - \hat{Z}(i,j)|.
$$

$S$ and $Z$ represent explicit map values and tag values, respectively, normalized to between [0,1].

The sensitivity, specificity, positive, negative, and accuracy of the DP and MCNN models predicted results were calculated separately to evaluate the performance of the model predictions.

We used the 10-fold cross-validation method in calculating the above prediction evaluation results to obtain more reasonable results and prevent the contingency of the results caused by 1 calculation. In the practice of this method, we conducted 10 training procedures and calculated predictors for DCNN and MLP. Before each training, the training set, test set, and validation set were randomly assigned again, using the average of 10 training results as the final model prediction results. During the training process, we used 75% of the data set as the training set, 15% as the test set, and 10% as the validation set.

### 4. Analysis of the Experimental Results

#### 4.1. Basic Patient Data

Of the 140 patients selected, male patients were relatively large, reaching 91, with an age range ranging from 30 to 85 years. The basic data of the patients are summarized as follows: the differences in the clinical data characteristics between the two groups with developed hematoma enlargement and no hematoma enlargement are shown in Table 1.

#### 4.2. Image Preprocessing Results

After image processing, a total of 5616 NCCT images in DICOM format were obtained from 140 patients with ICH, including 2635 hematoma images from 57 patients with hematoma enlargement and 2982 hematoma images from 83 patients without hematoma enlargement. The hematoma segmentation yielded good results, with an $F$ metric value of 0.96 and a mean absolute error of 0.0043. An example of the four hematoma segments is shown in Figure 2.

#### 4.3. Performance Evaluation of ML for Predicting Hematoma Enlargement

The results of the first prediction model, the comparison of the prediction performance of ResNet, VGGNet, and GoogLeNet 3 network models, and the results of using images with hematoma and image trained networks without hematoma segmentation are shown in Table 2. As we expected the results, the ResNet34 network model achieved the highest accuracy in predicting hematoma enlargement methods. However, unlike our previous expected results,
Table 3: Comparison of results for different numbers of neurons in the MLP hidden layer.

<table>
<thead>
<tr>
<th>No. of neurons in the hidden layer</th>
<th>Precision</th>
<th>Sensitivity</th>
<th>Specificity</th>
<th>AUC</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>71.4%</td>
<td>80.0%</td>
<td>68.8%</td>
<td>0.73</td>
</tr>
<tr>
<td>3</td>
<td>76.2%</td>
<td>77.8%</td>
<td>75.0%</td>
<td>0.79</td>
</tr>
<tr>
<td>4</td>
<td>81.0%</td>
<td>85.7%</td>
<td>78.6%</td>
<td>0.83</td>
</tr>
<tr>
<td>5</td>
<td>86.5%</td>
<td>82.6%</td>
<td>88.9%</td>
<td>0.93</td>
</tr>
<tr>
<td>6</td>
<td>81.0%</td>
<td>71.4%</td>
<td>85.7%</td>
<td>0.82</td>
</tr>
<tr>
<td>7</td>
<td>76.2%</td>
<td>77.8%</td>
<td>75.0%</td>
<td>0.79</td>
</tr>
<tr>
<td>8</td>
<td>71.4%</td>
<td>85.7%</td>
<td>64.3%</td>
<td>0.73</td>
</tr>
</tbody>
</table>

DCNN network models trained with images without hematoma segmentation have a prediction accuracy than trained with images without hematoma segmentation. The DCNN network model predicts 2%-3% more accuracy. The above situation is present in the 3 network models. Therefore, the model that achieves the best prediction results in the single-model prediction based on the DCNN is the ResNet34 model trained using the NCCT images without the hematoma segmentation. The prediction accuracy, sensitivity, specificity, positive predictive value, and negative predictive values were 69.5%, 75.4%, 64.9%, 62.6%, and 77.2%, respectively (as shown in the first column in Table 1). The AUC value is 0.68 and the ROC curve is shown in the red line in Figure 3.

The second prediction model is 1 two-model prediction based on MLP. To determine the number of neurons in the hidden layer in the MLP model, we tested the predictions for different numbers of neurons, as shown in Table 3. The MLP model with 1 hidden layer containing 5 neurons achieved the highest prediction accuracy in predicting hematoma enlargement. Happily, the two-model predictor is 17% more accurate than the single-model predictor. The prediction results of the dual-model predictor using NCCT images and clinical data are accuracy, sensitivity, specificity, positive predictive value, and negative predictive value are 86, respectively. 5%, 82.6%, 88.9%, 90.9%, and 80.0%. The AUC value is 0.91, and the ROC curve is shown in the blue line in Figure 3.

5. Conclusion

This paper is mainly based on machine-learning prediction study of hematoma expansion in patients with cerebral hemorrhage. By explaining the two-model ML method and combined with specific clinical case data, the ML method has certain advanced nature through experiments.

Only a single-model predictor trained using NCCT images has limited accuracy in predicting hematoma expansion. Image segmentation methods that separate the hematoma part from the brain tissue background fail not improve the predictor performance for hematoma enlargement.

The final ML method of dual-model prediction can comprehensively analyze the patient NCCT image information and clinical data, which can achieve 86.5% accuracy and have relatively equal sensitivity and specificity. Therefore, this ML method can be used as a predictive tool to effectively identify people at high risk of hematoma expansion.

Data Availability

The experimental data used to support the findings of this study are available from the corresponding author upon request.

Conflicts of Interest

The authors declared that they have no conflicts of interest regarding this work.

References