SUPPLEMENTAL MATERIAL

Deep Learning for Automatically Predicting Early Hematoma Expansion in Chinese Patients

Image acquisition

The baseline CT images from our study were obtained with four CT scanners: GE Optima CT540, SIEMENS SOMATOM Definition Flash, SIEMENS SOMATOM Force, SIEMENS SOMATOM Perspective. The acquisition parameters were as follows: slice thickness, 5.0mm; axial slice number, 27-34; voxel size, 0.3906-0.5566×0.3906-0.5566×5.0mm; matrix size, 512×512; field of view, 200-285×200-285mm; window width, 90HU; window level, 35HU (**Supplemental Table1**).

Labeling and calculation of the hematoma volume

Manual segmentations for hematoma were performed on the CT scans by a single author with more than 10 years of experience. To assess interrater reliability, repeat manual segmentations in 20 randomly selected cases were performed after a minimal interval of 7 days. Labels were manually painted on each 2-dimensional slice of each CT image applying the open-source software ITK-SNAP[1] (http://www.itksnap.org/). Comparing to the contralateral hemisphere, intracerebral hemorrhage was differentiated from intraventricular hemorrhage or subarachnoid hemorrhage. Based on the binary label map, the hematoma volume was then calculated.

Data preprocessing

The CT images of our study were collected as a Digital Imaging and Communication in Medicine (DICOM) image series, and then were transformed to Neuroimaging Informatics Technology Initiative format. Each CT image was skull skipped by using Otsu`s method.[2] The CT images were resampling to a field of view of 112 × 112 × 160 mm and matrix size of 256 × 256 × 32 by applying a bicubic interpolation algorithm, and then the images were windowed with a threshold of 0 to 100 HU. After this, normalization was performed by subtracting the mean value within the skull-stripped brain region and dividing by the standard deviation of the signal intensity of the region, and negative values were set to zero.

Data augmentation

Data augmentation were performed by applying 3-dimensional image transformation with scaling, translation, and rotation. For the training dataset, each CT image was randomly transformed by applying these three transformations using a linear interpolation algorithm. The scaling and translation were performed between –10% and 10% of the image size and the rotation between –5 and 5 degrees. The size of the training dataset was increased 10 times with these techniques.

Model architecture

In this study, we build a two-task model based on a deep convolution neural network. The semantic segmentation of hematoma and the prediction of hematoma expansion were simultaneously working. Hematoma expansion outcome was binarized according to the volume of 24h follow-up CT image compared to the baseline CT image(⩾6 mL or ⩾33%). Detail of the model architecture is shown in **Supplemental Figure 1**.

Segmentation network

The segmentation network was based on U-Net[3], an encoder-decoder network for 3-dimentional image segmentation. Our network for segmentation had 4-level architecture with 2 down-sampling, 2 up-sampling and 1 convolution operation for bridging layer(Supplemental Figure 2): 32 × 256 × 256 (16 channels) → 16 × 128 × 128 (32 channels) → 8 × 64 × 64 (64 channels) → 8 × 64 × 64 (128 channels) → 16 × 128 × 128 (64 channels) → 32 × 256 × 256 (32 channels). The down-sampling of encoding path was performed by a 3 × 3 × 3 three-dimensional convolution layer with 2 × 2 × 2 strides, and the up-sampling of decoding path was performed with a size of 2 × 2 × 2. Padding was applied in steps above. The final output of segmentation was performed by applying 1 × 1 × 1 convolution with sigmoid function, reducing the channel number to one.

Classification network

The classification network was added to the bridging layer of the segmentation network (**Supplemental Figure 1**). Two 3 × 3 × 3(with 128 filters) three-dimensional convolution operations with padding were performed and then feature channels(size 128 × 8 × 64 × 64) were processed with three-dimensional global average pooling to be 128 units. The flattened features were connected to a unit of output applying the Sigmoid activation function for the binary classification work.

Training process

The deep neural network model had 3,802,578 parameters. The Adam optimizer was applied with back propagation. The loss function for segmentation was Dice loss (1 – Dice coefficient), and the loss function for classification was binary cross-entropy. The segmentation and classification were simultaneously trained with the cost function in the ratio 9:1 (segmentation: classification). The network was trained for 40 epochs totally with a batch size of 1. A multi-step learning rate schedule was performed with an initial learning rate of 1×10^{-4}, reduced by a factor of 10 at 20th and 30th epoch.

The training process was performed with an 11-GB graphics processing unit (NVIDIA GeForce RTX 2080Ti). Training process took about 14 hours. The code of convolution neural network was written in Python 3.7(https://www.python.org/) and implemented in open-source deep learning framework Pytorch 1.4.0(https://pytorch.org/).

Model evaluation

For the segmentation task, the Dice coefficient was calculated to evaluate the segmentation results.

For the classification task, the sensitivity, specificity, likelihood ratio weighted by prevalence, and area under the curve (AUC) were calculated based on receiver operating characteristic (ROC) curves (**Supplemental Figure 2**).

Figures and Tables

Supplemental Table1 Acquisition parameters for CT scanners

Scanner	GE Optima CT540	SIEMENS SOMATOM Definition Flash	SIEMENS SOMATOM Force	SIEMENS SOMATOM Perspective
Slice thickness, mm	5.0	5.0	5.0	5.0
Axial slice number	28~34	26~28	27	27
Voxel size, mm	0.4883×0.4883×5.0	0.3906~0.5566×0.3906~0.5566×5.0	0.3906~0.4453×0.3906~0.4453×5.0	0.4492×0.4492×5.0
Matrix size	512×512	512×512	512×512	512×512
Field of view, mm	250×250	200~285×200~285	200~228×200~228	230×230
Window width	90	90	90	90
Window level	35	35	35	35

CT indicates computed tomography.

Supplemental Table2 Diagnostic criteria for NCCT markers[4]

Marker	Criteria
Hypodensity	Any hypodense region strictly encapsulated within the hemorrhage with any shape, size, and density.
Black hole sign	Hypoattenuating area with a density difference >28HU compared with the surrounding hematoma. No connection with surface outside the hematoma.
Swirl sign	Rounded, streak-like, or irregular region of hypo- or isoattenuation compared with the brain parenchyma. Does not have to be encapsulated in the ICH.
Blend sign	Relatively hypoattenuating area next to a hyperattenuating area of the hematoma, with a well-defined margin and a density difference >18HU between the two areas.
Fluid level	Presence of an area hypodense to the brain above and one hyperattenuating area below a discrete straight line of separation, irrespective of its density appearance.
Irregular shape	Two or more focal hematoma margin irregularities, joined or separate from the hematoma edge on the axial NCCT slice with largest hematoma area.

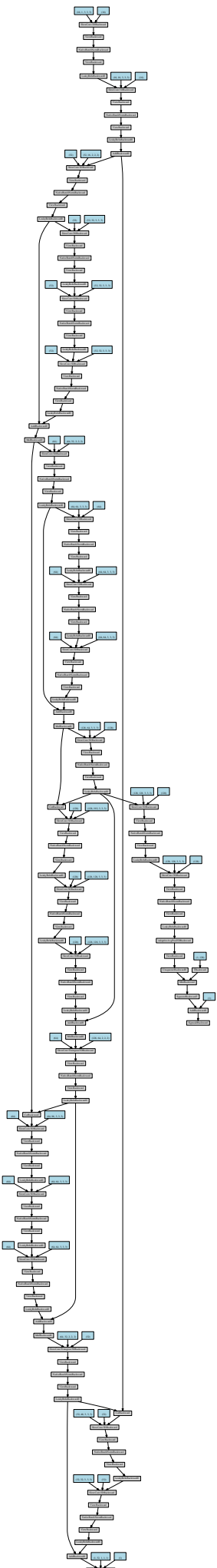
NCCT indicates non-contrast computed tomography.

Supplemental Table3 Criteria for the BAT score[5]

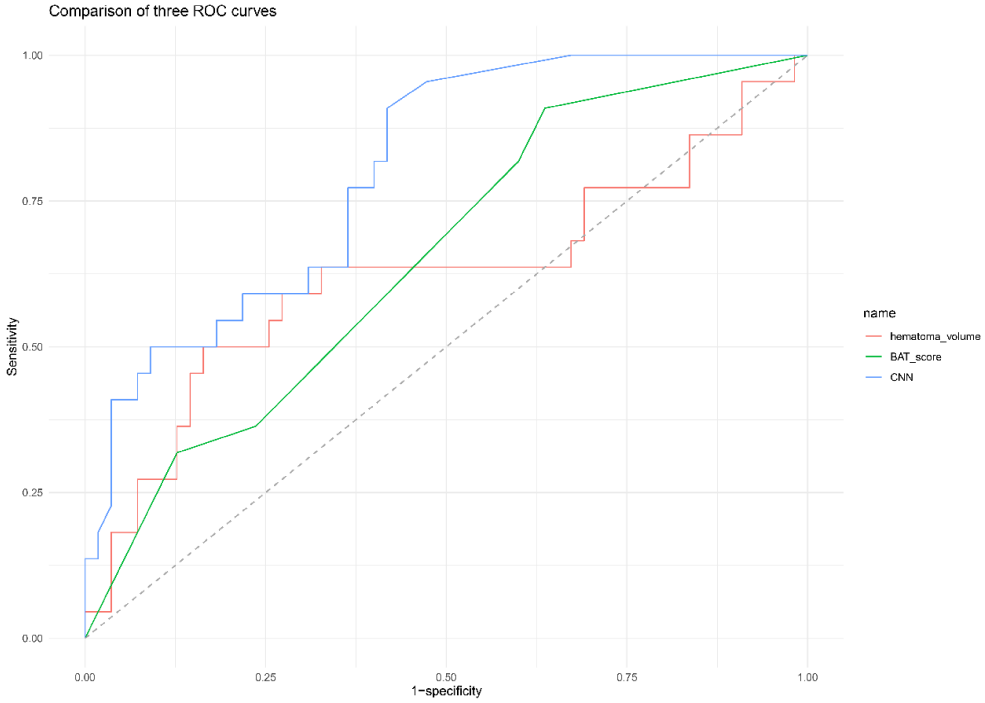
	Points
Blend sign	
Present	1
Absent	0
Any hypodensity	
Present	2
Absent	0
Time from onset to NCCT	
<2.5h	2
≥2.5h	0

NCCT indicates non-contrast computed tomography.

Supplemental Figure 1 The architecture of the model



Supplemental Figure 2 ROC curves of testing



The receiver operating characteristic curves of the CNN model, the hematoma volume model and the BAT score model were displayed.

References

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3. Ronneberger O, Fischer P, Brox T. U-Net: Convolutional Networks for Biomedical Image Segmentation. *Lect Notes Comput Sc*. 2015;9351:234-41.
4. Morotti A, Boulouis G, Dowlatshahi D, *et al.* Standards for Detecting, Interpreting, and Reporting Noncontrast Computed Tomographic Markers of Intracerebral Hemorrhage Expansion. *Ann Neurol*. 2019;86(4):480-92.
5. Morotti A, Dowlatshahi D, Boulouis G, *et al.* Predicting Intracerebral Hemorrhage Expansion With Noncontrast Computed Tomography: The BAT Score. *Stroke*. 2018;49(5):1163-9.