

Automatic Thrombus Localization on Patient with Ischemic Stroke on Non-contrast CT Using MCA Location Filter

Donlawit Beesomboon[†], Natsuda Kaothanthong[†], Tanapon Chansumpao[§], and Dittapong Songsaeng[§]

[†]Sirindhorn International Institute of Technology, Thammasat University, Pathum Thani, Thailand
donlawit.bees@gmail.com, natsuda@siit.tu.ac.th*

[§]Department of Radiology, Faculty of Medicine Siriraj Hospital Mahidol University, Bangkok, Thailand
bah_paw@hotmail.com, dsongsaeng@gmail.com

Abstract—Acute Ischemic Stroke (AIS) is commonly caused by thrombus in the middle cerebral artery (MCA). The localization of the thrombus on non-contrast computerized tomography (ncCT) images of an AIS patient is subtle. Additional imaging such as a computed tomography angiography (CTA) is required to locate the thrombus, which results in a delay of the treatment and affects the damage of patient’s brain. This work presents an algorithm to locate an MCA region to improve the computation time of the thrombus segmentation of our previous work. Given a brain region of the input ncCT image, an MCA is found by a summation of pixels’ weight in the interested region. The MCA is used as a reference for computing thrombus candidates using k -mean clustering. The located thrombus is selected from the candidate regions that are closer to the MCA region. Experiment is conducted on 1154 ncCT images of 10 patients. The result shows that the proposed thrombus localization algorithm is able to locate the thrombus with accuracy 99.93 %, precision 1.76 %, sensitivity 62.54 % and specificity 99.93 %. The computation time is averagely improved from 2536.18 second per patient to 305.58 seconds.

I. INTRODUCTION

The Acute Ischemic Stroke (AIS) is a neurovascular disease, which is a cause of death and disability of approximately 10% of the world population [5]. More than 75% of death are from underdeveloped and developing countries [10]. In Thailand, the stroke is a leading cause of death [1]. The AIS are the common stroke [11], which commonly caused by a clot, also known as *thrombus*, in a blood vessel. The thrombus prevents the blood flow and oxygen that rapidly results in neuronal death/necrosis from occlusion of the vessel [12]. The most common location of the AIS are in the middle cerebral artery (MCA). The time interval from the stroke onset until receiving a proper treatment directly affects the chance of survival and recovery [3], since the brain damage becomes irreversible and cause permanent brain damage for a long interval [13].

To locate thrombus, a computed tomography angiography (CTA) images are used in addition to the ncCT to locate a precise location of the thrombus. The CTA improves the clot visibility by applying a contrast medium, but the image acquisition process requires an experts and not suitable for allergic patients. Moreover, the additional process taking long time for a patient to receive a treatment. This work presents an

image segmentation algorithm that is able to assist radiologists in locating a tiny thrombus directly on the ncCT images of AIS patient. The outcome of the proposed method is able to shorten the diagnosing time for radiologist to analyze the thrombus and be able perform the treatment after the ncCT images has been received.

The thrombus segmentation has been studied in several works. Machine-learning techniques are applied to classify the composite of thrombus for predicting the outcome of alteplase treatments using a number of radiomics features [7]. Given a ncCT and a CTA images, a thrombus was segmented manually by an expert. The result shows that utilizing 12 features from both types of images can predict the outcome of the alteplase. One limitation of this method is a requirement of both ncCT and CTA for making a prediction. MCA dot sign, which indicates the chance of stroke, are automatically detected on ncCT [6]. Since the MCA dot sign are only occurred inside the lentiform nuclei region, a region growing in the three-dimensional space is employed for a region segmentation. The support vector machine (SVM) is used to classify the MCA dot sign from the segmented region inside the lentiform nuclei region. In our previous work [14], a k -mean clustering is applied for separating a brain region on the ncCT image into small groups. An MCA is found by using one of the small groups to refine the thrombus candidates. The limitation is a number of false positive candidates due to a low quality of the located MCA. Moreover, the computation time is long .

This work proposes an improved algorithm for automatically locating thrombus on ncCT images using an MCA region as a reference that can be computed faster and gives lower false positives. A more precise MCA region is obtained using a proposed MCA reference windows and the pixels’ weight in each window. The candidates, which are lying in the MCA area, are refined using the distance to the center to each candidate. The detail of the proposed method can be found in Section 3 and the experimental results are reported in Section 4.

II. PREVIOUS WORK

A. Salient Regions Segmentation on CT Image

Takahashi N [7] proposed an automated detection method for the MCA dot sign of acute stroke in unenhanced CT. 3D region growing are used on the left and right lentiform nuclei with seeds given by Statistical Parametric Mapping 8 (SPM8) program. Because the MCA dot sign did not appear outside the lentiform nucleus. The candidate regions are selected if it was inside of lentiform nucleus region. Then, a support vector machine (SVM) is applied with four feature; maximum and an average pixel value within a region, the number of pixels within a region and the number of connections of the region. The localization results are compared with the manually located boundary by the neuroradiologists. This method gave 0.975 accuracy. Jonas J. Schöttler [2] proposed an automatic thrombus segmentation on CT image using a cascaded convolutional neural network (CNN). Two CNN networks were applied for candidates segmentation and classifying thrombus region. The candidate regions also contain the information i.e., location, shape, density, and volume of each region. Then, the regions are classified whether or not it is a thrombus by using the second CNN network. This method gave 0.99 accuracy on prediction of the existence of the thrombus and its location. However, the authors mentioned that it could be worthwhile to evaluate simpler and more efficient approaches without using the CNN network for segmentation.

B. Intervention Outcome Prediction

W. Qiu.[7] proposed a method for predicting the recanalization with intravenous alteplase using radiomics-based features. A thrombus is manually segmented by neuroradiologists. The linear discriminative and receiver operating characteristic were used for feature selection. The multivariable SVM is used to predict the outcome of the recanalization with intravenous alteplase. The best accuracy is 0.85 ± 0.03 on selected 12 features from the combination group of NCCT, CTA, and radiomics.

C. Image Segmentation

The k-mean clustering method is a widely used for separating interested region from its background. J. Macqueen.[4] describe the k-mean method to be a process for partitioning an N-dimensional population into k sets. The method find the k amount of center in the data that represent each data group.

The Otsu's threshold method is a segmentation method that propose by N. Otsu [5]. The separate the front-ground from the back-ground using a threshold values that calculate from intensity of the image. This method can separate really well when the front-ground and back-ground have a high different in intensity value.

Canny is an edge detection method proposed by Canny. J.[1]. Edges in an image are found using; Gaussian filter for noise reduction, find intensity gradients and Apply non-maximum suppression to select only the maximal intensity gradients value. Then double threshold weak edge to reduce false detection.

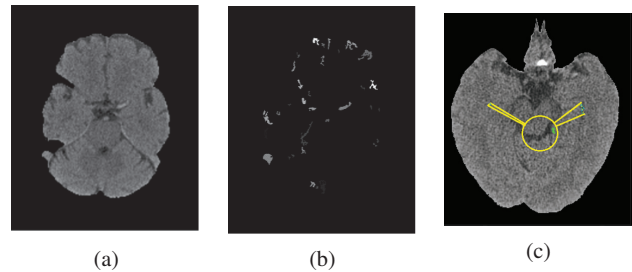


Fig. 1: Output of our previous work. (a) Brain region. (b) Thrombus candidates obtained using the clusters' center of k -mean clustering as seeds and segmented using a region growing method. (c) An example of a wrong MCA reference region that is used as a reference for refining candidates in (b).

D. Our previous work

While our previous work is able to find thrombus location automatically[14], it is less efficient in terms of a computation time and prone to high intensity value, which leads to a high false positives. Given an ncCT image, the brain region is extracted using a region growing method using the clusters' center computed by k -mean clustering as depicted in Fig.1(a). The thrombus candidate segmentation in Fig. 1(b) also applies k -means clustering to find seeds for proceeding with a region growing. The reference MCA is obtained similarly using different cluster's center as a seed. Since the intensity values of each component on each ncCT image are varied, the selection of seed and a region growing criteria cannot give a correct location of MCA as shown in Fig. 1 (c) and too many candidates are selected.

III. PROPOSED METHOD

Our improved thrombus segmentation has 2 main parts. Given a segmented brain region on an ncCT slice as an input, an intended MCA frame is placed. The windows of the frame are selected and the enclosing brain area is used for finding thrombus in the second part as shown in Fig. 2 (a). Given the brain area in the enclosing MCA region, it is used to find thrombus candidates and refine them as the output as shown in Fig. 2 (b). By locating MCA region prior to the candidate detection, the number of pixels is greatly reduced and results in a shorter computation time.

A. Middle Cerebral Artery (MCA) Detection

To detect the MCA of each ncCT slice, let I be an image of a brain region of size $n \times m$. Let $p(i, j)$ be a pixel in I , where $1 \leq i \leq n$ and $1 \leq j \leq m$, and $p(i, j)$ is a Hounsfield value in the range $[-2000, 2000]$. The MCA is found by locating the brain's center point and it is used for drawing referenced windows to a weight of each pixel within each window for selecting reference windows.

Given a slice I , let $c(x, y)$ be the brain's center point at c_x and c_y coordinate, where c_x is the half of the image width and c_y is the point above the center of the height. The coordinate

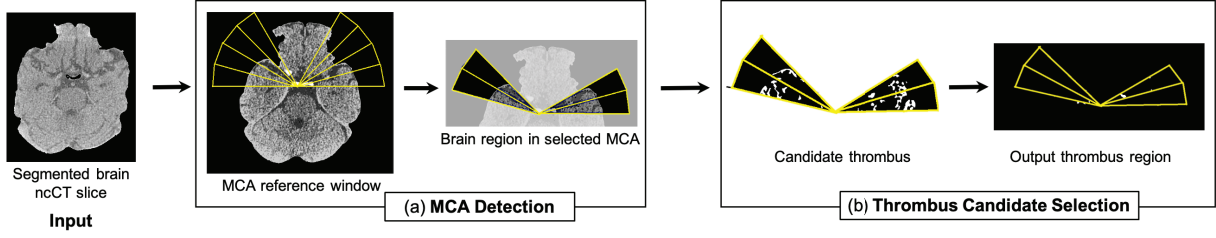


Fig. 2: Our proposed the thrombus segmentation has two parts: a) Finding MCA region and b) Finding thrombus from the brain region enclosing in the MCA.

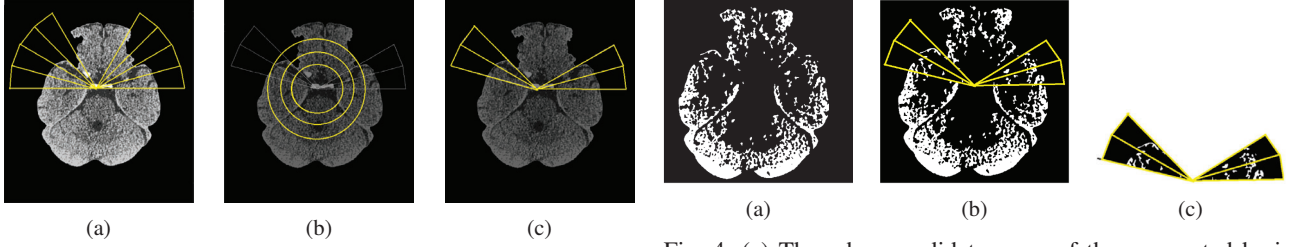


Fig. 3: (a) The output of the MCA reference windows computed from the center point $c(x, y)$. (b) The distance from the center point used for assigning weights to each pixel. (c) The selected windows computed using pixels' weight summation of (b) to each window of (a).

c_x and c_y are defined as follow: $c_x = \lfloor (n/2) \rfloor$ and $c_y = \lfloor (m/2) \rfloor - \lfloor (m \times 0.05) \rfloor$

The obtained center point $c(x, y)$ is used to compute MCA reference windows by drawing 10 lines, denoted by $l(c(x, y), s(x, y))$, to the point $s(x, y)$. The point $s(x, y)$ is a point with the distance $\lfloor (n/2) \rfloor$ away from $c(x, y)$. The coordinate s_x and s_y of the point $s_{x,y}$ is defined as

$$\begin{aligned} s_x &= \lfloor (n/2) \rfloor \times \cos(\theta), \\ s_y &= \lfloor (n/2) \rfloor \times \sin(\theta) \end{aligned} \quad (1)$$

where $\theta_L = \{0, -15, -30, -45, -60\}$ for the windows on the left side and $\theta_R = \{180, 195, 210, 225, 240\}$ for the right side. Let $M_L = \{m_1, \dots, m_4\}$, be a set of windows obtained from the two adjacent lines $l(c(x, y), s(x, y))$ computed from θ_L , where m_1 is the lower left-most window and clock-wise increment until m_4 . A set of windows $M_R = \{m_5, \dots, m_8\}$ on the right side are obtained using θ_R and can be defined analogously. The reference window of the left- and the right-side of the center point are shown in Fig. 3 (a).

Since the MCA is darker than the brain tissue, the dark pixels that are closed to the center of the brain are more likely to be an MCA area. Let $p^k = (p_x^k, p_y^k)$ be a dark pixel in the window m_k . Let $v(p^k)$ be a weight of p^k that is assigned according to the distance $d(c, p^k)$ from the center point. The distance, $d(c, p^k)$ is defined as:

$$d(c, p^k) = \sqrt{(c_x - p_x^k)^2 + (c_y - p_y^k)^2} \quad (2)$$

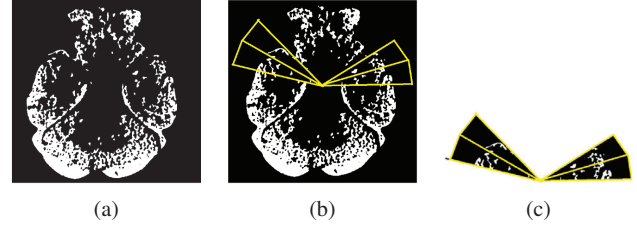


Fig. 4: (a) Thrombus candidates area of the segmented brain region. (b) An overlay of the selected MCA on the thrombus candidates (a). (c) The selected MCA and the enclosing thrombus candidates.

The weight $v(p^k)$ is varied by $d(c, p^k)$, which is,

$$v(p^k) = \begin{cases} 100 & \text{if } d(c, p^k) < 0.4 \times \lfloor (n/2) \rfloor, \\ 80 & \text{if } d(c, p^k) < 0.6 \times \lfloor (n/2) \rfloor, \\ 60 & \text{if } d(c, p^k) < 0.8 \times \lfloor (n/2) \rfloor, \\ 0 & \text{Otherwise} \end{cases} \quad (3)$$

Let $M_L = \{m_1, m_2\}$ be the selected MCA windows on the left side of the center point, where m_1 is the windows m_i with the highest summation of the weights $v(p^k)$, while m_2 has the highest weight among the adjacent windows of m_1 . They are defined as:

$$\begin{aligned} m_1 &= \max_{1 \leq i \leq 4} (\sum v(p^i)) \\ m_2 &= \max_{j \in \{i-1, i+1\}} (\sum v(p^j)) \end{aligned} \quad (4)$$

Let $M_R = \{m_1, m_2\}$ be the selected MCA windows on the right side and it is defined analogously as follow:

$$\begin{aligned} m_1 &= \max_{5 \leq i \leq 8} (\sum v(p^i)) \\ m_2 &= \max_{j \in \{i-1, i+1\}} (\sum v(p^j)) \end{aligned} \quad (5)$$

Let $W = M_L \cup M_R$ be the selected MCA window on the left- and the right- side of the center point. An example of the selected MCA windows is shown in Fig. 3 (c).

B. Thrombus Candidate Segmentation

The limitation of our previous thrombus segmentation algorithm is the scattered candidates, since the whole segmented brain region is used for detecting candidates as shown in Fig. 4 (a). It results in a long computation time. In this work, only the pixels in the selected MCA that are M_L and M_R are used for selecting candidates as shown in Fig. 4 (b) and (c).

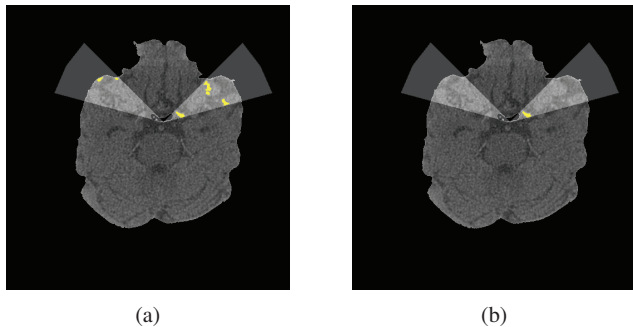


Fig. 5: (a) The candidate regions obtained from a region-growing method. (b) The refined candidates obtained from (a).

Given the selected MCA windows W , the pixels are clustered using k -mean clustering, where $k = 8$. The clustered pixels in the eighth group have the highest pixel values, while the first one is the lowest. Only the pixels in the eighth, the seventh, the sixth, and the fifth clusters, denoted as Q are employed for segmenting the thrombus candidate regions.

The candidates are obtained using a region-growing method, where the pixels in the eighth cluster are considered as the seeds. The pixels are included in the candidates if they are in Q as shown in Fig. 5 (a).

Since thrombus is tiny and often locates nearby the MCA, the size of the segmented region from the region-growing and the distance from the center point c is used to refined the candidate. The size of the thrombus candidates must not be larger than 0.4% of the brain’s area. The distance from the center point must be less than $0.25 \times n$. The thrombus candidate of Fig. 5 (a) after refining using the size and the distance are shown in Fig. 5 (b).

IV. RESULT

Institutional review board approval was obtained for this study (COA no. SI 984/2020) from Siriraj Hospital, Thailand. In this work, a total of 10 sets of ncCT slices, which has 1154 slices, from Siriraj Hospital were used to measure the performance of the proposed method. All included patients underwent 1.25 mm (GE Discovery; GE Healthcare, Little Chalfont, UK) or 1.50 mm (GE Light Speed VCT; GE Healthcare) axial NCCT and CTA (acquired at 0.625 mm and reformatted to 1.25 mm). Among the obtained 1154 slices, only 32 contains ground truth that were labeled by a radiologist.

The proposed algorithm was implemented in Python programming language and the experiments were conducted on a Window 10 64bits, CPU Intel(R) Core(TM) i7-8700K CPU @ 3.70GHz, RAM 16 GB, NVIDIA GeForce GTX 1080 8192MB machine.

The aims of this experiment was to measure the segmentation performance and the computation time of the proposed method. The segmentation performance was measured using accuracy, precision, sensitivity, and specificity. The computation time was captured from the detection of MCA until the segmented thrombus regions were found.

TABLE I: Segmentation performance of 32 ncCT images, which have ground truth provided by the radiologist.

Method	Accuracy	Precision	Sensitivity	Specificity
Previous work [14]	53.55%	0.17%	91.57%	53.52%
This paper	99.92%	23.90%	53.03%	99.94%

TABLE II: Segmentation performance of 1154 images, where only 32 images have thrombus labeled by the radiologist.

Method	Accuracy	Precision	Sensitivity	Specificity
Previous work [14]	98.64%	0.17%	3.64%	98.69%
This paper	99.93%	1.76%	62.54%	99.93%

A. Segmentation Performance

The comparison of the result between the previous work and the segmentation algorithm proposed in this paper are shown in Table I and Table II and their corresponding confusion matrix in Table III and Table IV. The former compares the segmentation among 32 ncCT slice with ground truth. The proposed algorithm in this paper achieves 99.92% accuracy, 23.90% precision, 53.03% sensitivity, and 99.94% specificity. Compared to the previous work in [14], the number of false positive greatly reduces as evidence in an improve in the specificity from 53.25% to 99.94%. However, the sensitivity of this method is lower because the thrombus on one patient as shown in Fig. 7 cannot be detected.

The result shown in Table II also demonstrates that the method in this work is able to perform better. The sensitivity has been better than the previous work, which reflects a lower false negative. The specificity of the two method are similar.

B. Computation Time

One of the objectives in this work is to decrease the computation time for localizing thrombus on a set of ncCT slices have been obtained from one patient. The result is shown in Table V for the thrombus localization and Table VI for the whole process starting from the brain region segmentation.

The proposed MCA reference location averagely required 1.607 seconds for locating thrombus in the interested region. While our previous method took 11.775 seconds to find clots. The method presented in this work was able to perform about 6 times faster than the previous method. For finding thrombus for one patient, the time is about 7 times faster as shown in Table V.

TABLE III: The confusion matrix of previous work [14] with the number of pixels

	Ground truth positive	Ground truth negative
Predicted positive	607.5	15455.7
Predicted negative	388720.3	29728580

TABLE IV: The confusion matrix of proposed work with the number of pixels

	Ground truth positive	Ground truth negative
Predicted positive	167.2	148.1
Predicted negative	19402	30113646

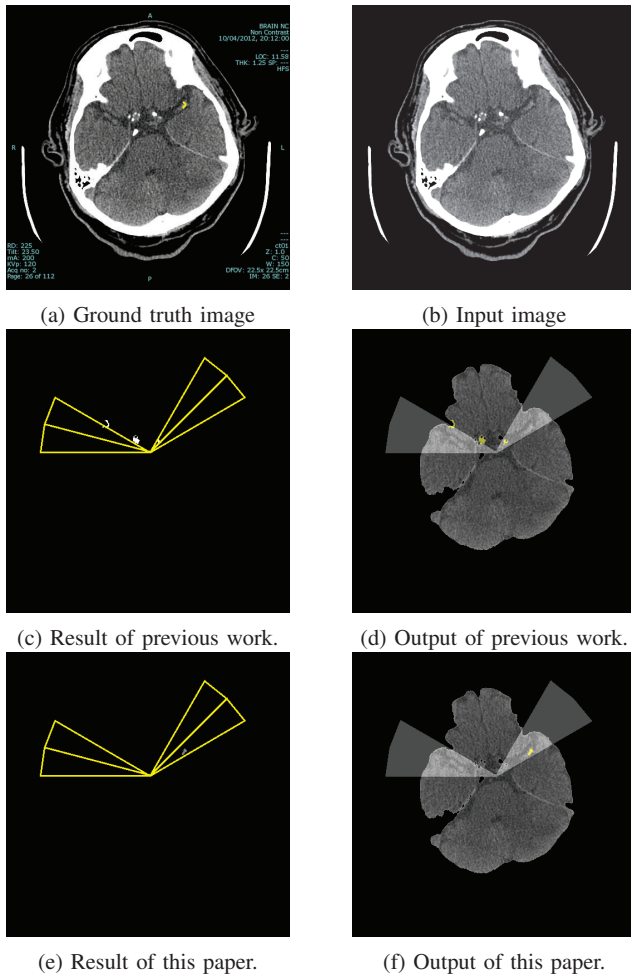


Fig. 6: Examples of the segmentation results presented in our previous work in [14] (c) and (d). The segmented result of the method presented in this work is shown in (e) and (f).

TABLE V: Comparison of the average computation time to detect thrombus of all 1154 slices using the previous method [14] and the algorithm proposed in this paper.

	Average per Slice (sec.)	Average per Head (sec.)
Previous work [14]	11.775	1327.008
This paper	1.607	184.868
Different ratio	6.884	7.178

For the overall computation time from segmenting brain region on each ncCT slice, the average time was 2.655 seconds, which is about 8 times faster than the previous method. The average computation time for one patient was 305.578 seconds, while the previous work required 2536.184 seconds. From Table VI, it showed that our improved algorithm could be completed about 8 times faster for each slice and each patient.

TABLE VI: Comparison of the average computation time starting from segmenting brain region until detecting thrombus of all 1154 slices. The result shows the time of previous method [14] and the algorithm proposed in this paper.

	Average per Slice (sec.)	Average per Head (sec.)
Previous work [14]	22.328	2536.184
This paper	2.655	305.578
Different ratio	8.110	8.300

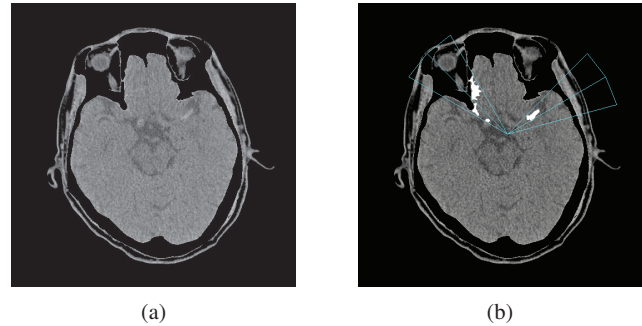


Fig. 7: (a) The Brain region segmentation segment incorrectly and did not remove non brain area. (b) The Thrombus segmentation that incorrectly locate the wrong MCA region because of (a).

C. Qualitative Analysis

Examples of the segmented thrombus can be found in Fig. 8 and Fig. 9. The segmented outputs in Fig. 8 (b) and (d) showed the different result. Our previous work cannot locate the thrombus, however, the method in this paper did. The results in Fig. 9 (b) and (c) are the same for the large region on the left, but an additionally wrong detection was found in the current method as depict in the small ersion on the left of Fig. 9 (c).

V. CONCLUSIONS

This paper presents a thrombus segmentation algorithm which is an extended version of our previous algorithm in [14]. A new algorithm for finding MCA is presented to limit the area for computing thrombus candidates and excludes the ones that are not in the interested area as much as possible.

Experiments have been conducted and demonstrated the improvement in reducing the number of false positive using the new MCA area localization method. Moreover, the computation time have been greatly decreased as the area to be applied for computing thrombus candidates is much smaller than our previous work.

To further reduce the false positive, we aim to remove unrelated organ on the ncCT such as eyes and mouth in our future work by applying an a slice classification model to select of slices in the brain's MCA.

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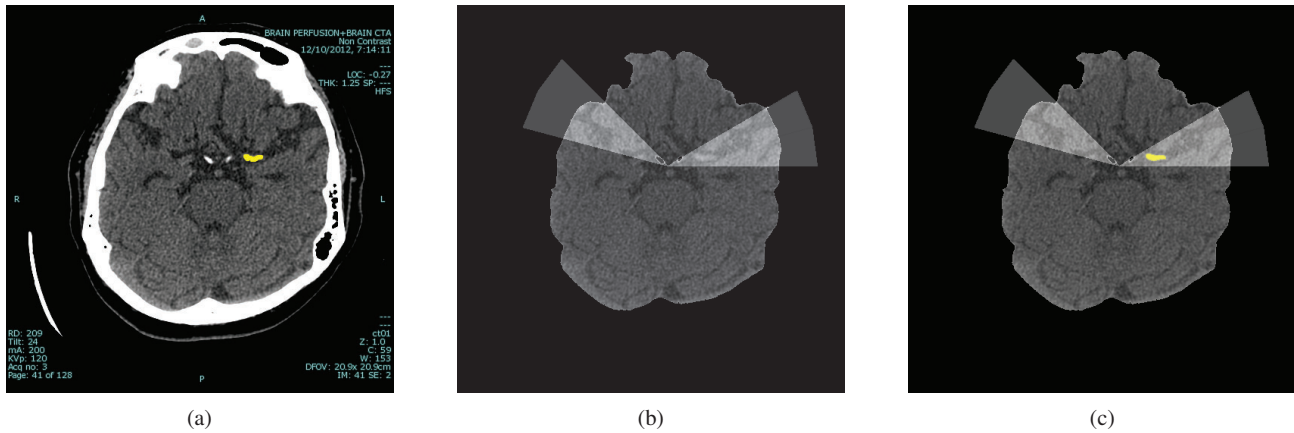


Fig. 8: Example of the thrombus that cannot be detected by the previous work, but it can be segmented in this paper. (a) Ground truth image. (b) Output of the previous method. (c) Output of this paper.

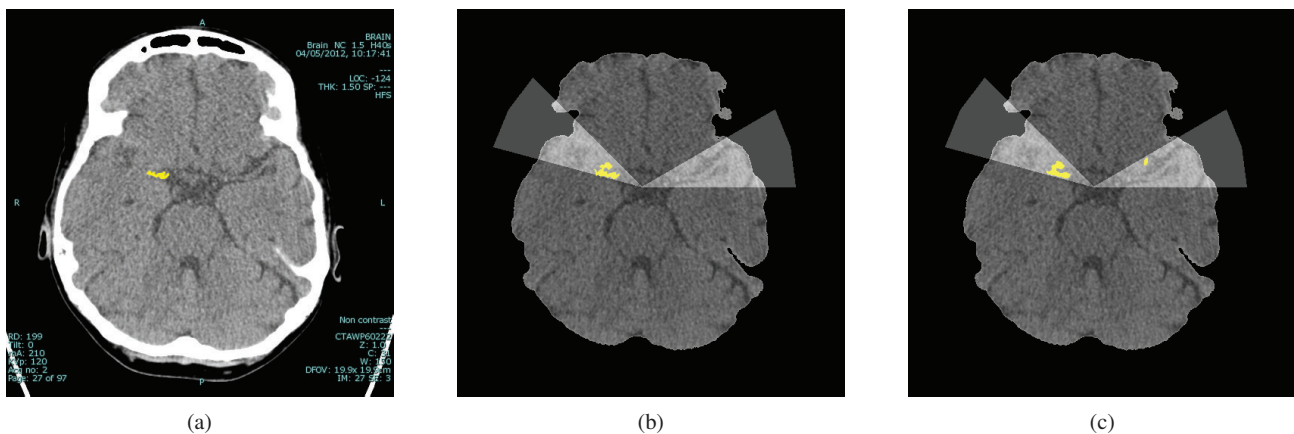


Fig. 9: A comparison of the segmented result of our previous work and this paper. (a) Ground truth image. (b) Output of the previous method. (c) Output of this paper.

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