

Brain Stroke Analysis from Non-Contrast Brain CT and Path-planning for Robot-assisted Thrombectomy

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Source Code: <https://github.com/karthik-d/Vision-For-Robot-Path-Planning>

1 Abstract

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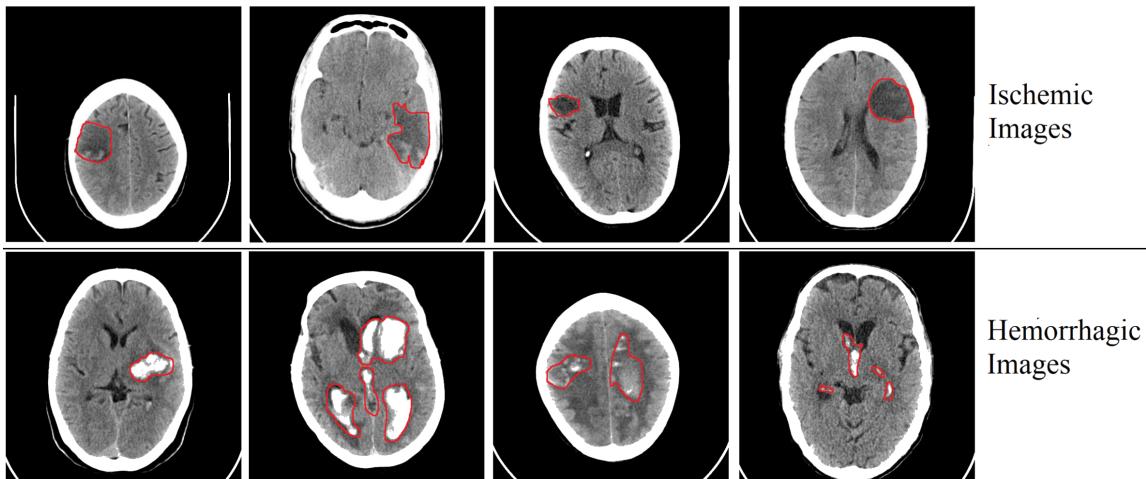


Figure 1: Samples of CT slices to depict the infarcts arising from *Ischemic* and *Hemorrhagic* strokes.

2 Problem statement

To this end, this research proposes to achieve the following objectives through data-driven computational modeling and analysis. The approach and methods that will be

adopted in meeting these objectives is detailed in the subsequent section. An overview of the workflow finalized for the current timeline is presented in Figure 2. Furthermore, a high-level overview of the complete clinical workflow of the proposed system is presented in Figure 3. The specific objectives that we sought to achieve in this project are as follows,

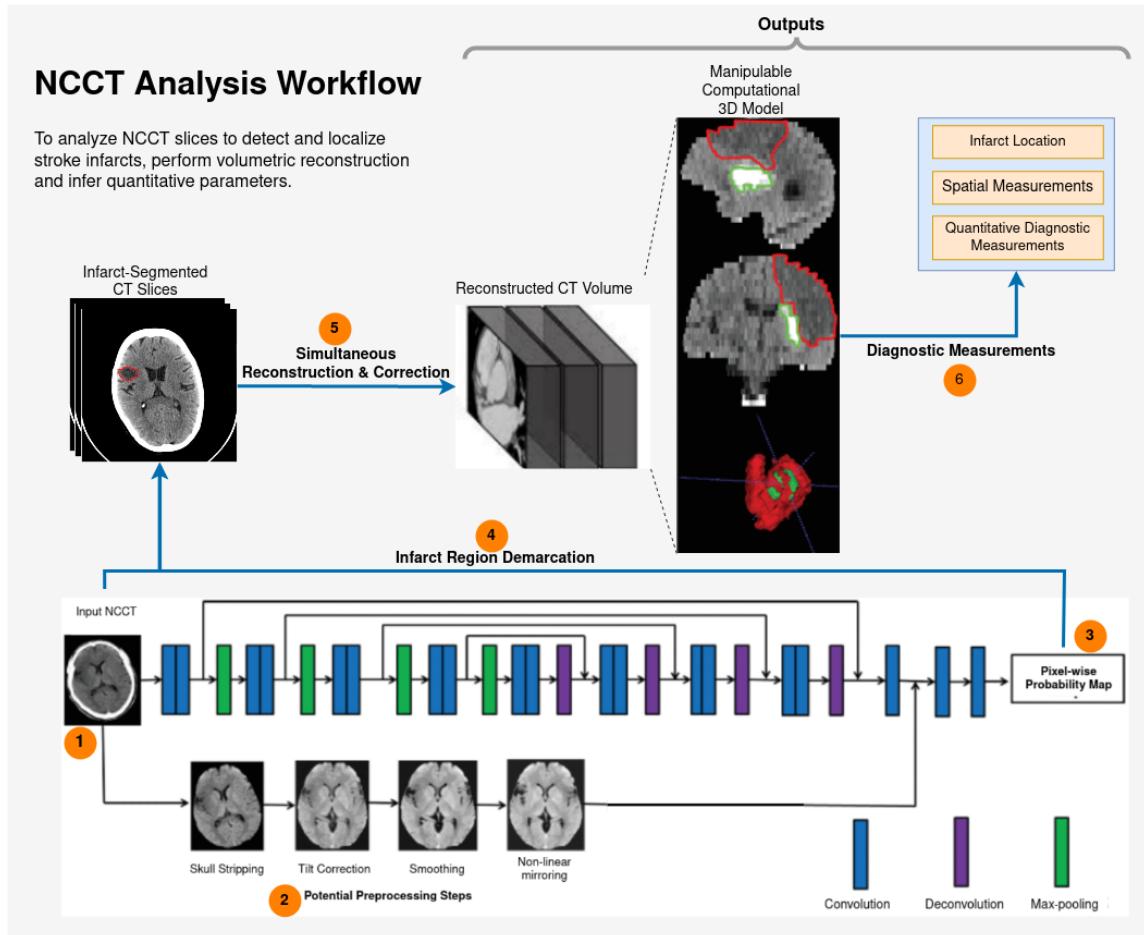


Figure 2: Overview of the NCCT analysis workflow following steps 1 through 6.

- To detect the presence of and differentiate between ischemic and hemorrhagic infarcts from non-contrast CT (NCCT) slices of the brain.
- To localize and segment the regions representing normal, ischemic infarcts, and hemorrhagic infarcts from the NCCT slice images.
- To reconstruct the volumetric NCCT image of the brain from the processed slices while simultaneously extrapolating and correcting infarct segmentation demarcations based on geometric constraints.

- To infer location information and other quantitative diagnostic measures from the reconstructed volumes to assess the condition such as cerebral infarct volume (CIT).
- To fuse patient-specific details into a computational model that will integrate the quantitative measures and parameters describing the infarct location with a generalized structural model of the brain.
- To transfer the structural model parameters to a robotic simulation environment constructed using a '*robot visualization gym*'.
- To devise a suitable path-planning strategy to perform autonomous thrombectomy using a robotic arm in the simulation environment with support for manual intervention in case of emergencies.

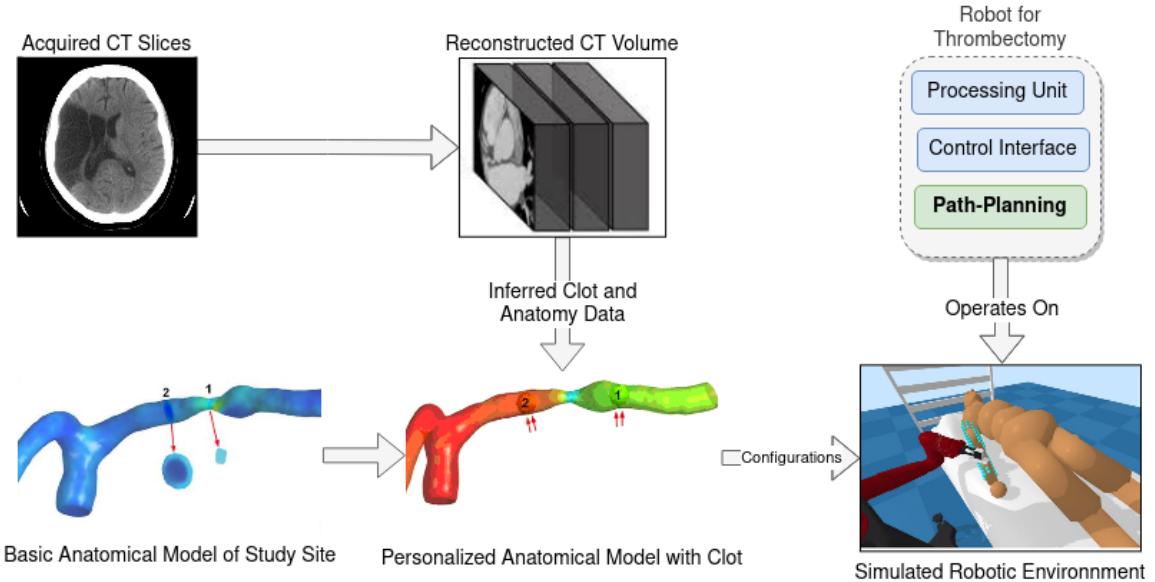


Figure 3: Overview of the NCCT analysis workflow following steps 1 through 6.

3 Literature survey

In general, processing and analysis of medical images using computer-aided diagnosis (CAD) systems can help physicians in early identification of diseases [24, 11, 16, 39]. Herein, the proposal briefly describe some important image preprocessing and classification methods used so far in order to analyze brain strokes from medical images.

Saatman et al. [29] have discussed various classification techniques for traumatic brain injury so that proper treatment can be provided for that targeted injury. They

discussed classification based on the severity of brain injury where various parameters which include Glasgow Coma Scale (GCS) have been used to identify the severity, however these procedures require many clinical trials. Other techniques which they have discussed are pathoanatomic classification, classification by physical mechanism, pathophysiology and prognostic modeling. According to them, for avoiding several clinical trials of patients new tools can be developed like dataset development, data sharing, data mining, and bioinformatics, etc. In 2008, Mozqueda et al. [36] have tested the hypothesis on clinical data of patients that acute ischemic stroke classification from CT or MR angiography images into major and minor stroke can be done by using Boston Acute Stroke Imaging Scale (BASIS) instrument. They have proved that BASIS classification instrument is better than Alberta Stroke Program Early CT Score (ASPECTS) in predicting stroke.

Chawla et al. [2] presented an automatic method for the detection and classification of an abnormality from low-contrast CT images into three categories — hemorrhage, chronic and acute infarct. Their proposed technique comprises of three steps: enhancement of the image, recognition of mid-line symmetry and classification of abnormal slices. The main limitation of their work is that they have just shown results on the dataset and have not compared their results with any of the previous state-of-the-art methods by generating their results on their dataset. The accuracy obtained by them on their dataset was also not given and have just shown precision and recall values for the experiments. Griffis et al. [10] have also worked on ischemic stroke lesions identification where they utilized the T1-weighted MRI scans and predict the stroke region using Gaussian naïve Bayes classification method. Limitations of their method was that they were unable to detect very subtle WM lesions with very small extents. Shahangian and Pourghassem [31] proposed a method to segment and classify hemorrhage, where segmentation was based on a modified version of distance regularized level set evolution (MDRLSE). Thereafter, SVM classifier was used to classify images by extracting weighted grayscale histogram features where they achieved an accuracy of 94.13%. However, the complete dataset information is not given like under what parameters images have been acquired and the details of CT scanner. The other limitation is that, the number of images which they have used for classification were also very less for 5 different categories i.e. only 627 images. The segmentation of hemorrhagic stroke from CT scan images was proposed by Gautam et al. [8] using variant of fuzzy clustering named as modified robust fuzzy c-means clustering (MRFCM) and used it with distance regularization level set evolution (DRLSE) method for the segmentation. However, their method was not able to identify very small lesions from the images. They have also proposed the method for the classification of a brain CT scan

images into hemorrhagic, ischemic and normal [7]. A new feature descriptor known as the local gradient of gradient pattern (LG2P) descriptor has been proposed by them. The highest classification accuracy achieved by them on 900 image dataset is 83.11% and 86.11% using fine NN and cubic SVM. However, this accuracy is very less and for better results it must be improved. Incremental gradient descent decision boundary feature extraction method was proposed by Woo et al. [38] for the classification of UCI dataset where they have shown results on Parkinson speech, chess, molecular biology, gas sensor, and array drift datasets of UCI. Recently, some researchers have published a literature survey on feature extraction methods and they can be found in [30, 3], so readers are referred to these papers for more methods.

Subudhi et al. [33] have proposed a new method for the segmentation and classification of brain stroke from MR images where they used expectation–maximization and random forest classifier. The accuracy achieved by them was 93.4% on the dataset of 192 brain images. The limitation of this paper is that they do not have any discussion of the dataset like from where they collected it and how. Ortiz-Ramón et al. [25] also worked on MR images where they proposed a texture analysis method to identify whether the patient has a stroke or not and also identify whether that stroke is lacunar or cortical. In this paper, they have used various methods proposed by different researchers in order to carry out their work and references for them can be found in [33]. According to them the limitation of their work is inability to combine stroke and aging (old stroke lesion) datasets for the analysis of images showing recent cortical or lacunar strokes. However, image normalization techniques can solve this issue by improving the image qualities.

Apart from the conventional machine learning methods which have been used very widely for the identification of diseases from the medical images, deep learning approaches are gaining attention because of the accurate diagnosis results. In 2012, Krizhevsky et al. proposed AlexNet as the CNN architecture and won the most difficult ImageNet large-scale visual recognition challenge (ILSVRC) [17]. Thereafter, it emerged as the revolution in the field of computer vision and machine learning. AlexNet has 5 convolutional and 3 fully connected layers where 2 dropout layers have been used with 0.5 probability. The best classification prediction with it can be achieved when the softmax layer is fed with the result of the last fully connected layer. In this architecture, the input image size should be $224 \times 224 \times 3$. However, in order to improve the accuracy many researchers have tried to develop new architectures. In 2014, VGG16 has come into existence, proposed by Simonyan and Zisserman [32]. The main contribution of their network is that they have made a very deep CNN architecture for the recognition of very large image dataset by increasing the network depth

to 16–19 layers with 3×3 convolution filter. VGG16 consists of five batches of 13–16 convolutional layers and 3 fully connected layers. In the first layer the number of filters starts from 64 and increases by a factor of 2 for each layer after the max-pooling till it becomes 512. The input image size for this architecture remains the same as that of AlexNet i.e $224 \times 224 \times 3$. The other CNN architecture ResNet50 proposed by He et al. [12] is a very deep residual network and it won the first place in ILSVRC 2015. It is a 50 layer architecture instead of 16–19 layers, which was trained on the 1.28 million training images. The input image size for this architecture is $224 \times 224 \times 3$. After that, many variants of CNN architectures have come into existence in order to provide better results for the diagnosis of the patients. Recently, deep learning has shown good classification accuracy on both training and testing datasets of breast cancer histopathology images [11]. The other work on the detection and classification of breast cancer makes use of four fully convolutional networks (FCN) [9]. CNN has also been used to detect colorectal cancer from the histology images [40]. Gao et al. [6] used deep CNNs to classify interstitial lung diseases (ILD) from CT images by using the entire image as a holistic input.

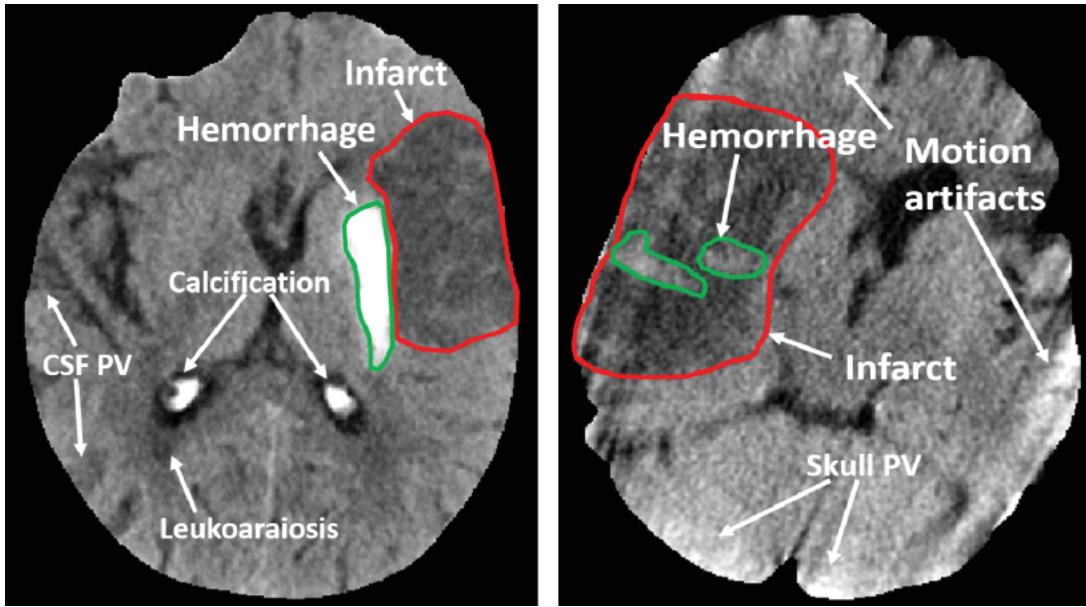


Figure 4: Samples of CT slices to depict *overlapping infarcts* – infarcts of multiple types at the same image region.

However, the work on the classification and localization of origin of brain strokes from CT/MR images still requires improvements for clinical applicability. Furthermore, the presence of overlapping infarcts of the two types – ischemic and hemorrhagic – on the CT slides, as depicted in Figure 4 gives rise to a *multi-label* segmentation problem, where each image pixel may belong to more than one class. Therefore, in

this research, we propose to develop a new deep learning -based processing pipeline to classify brain stroke from CT scan images, and further localize the infarct through volumetric reconstruction. Moreover, to the best of the authors' knowledge, this work is the first attempt to implement simultaneous volumetric reconstruction and correction of segmentation to improve demarcation performance and evolve a pliable computational model that can be used to infer quantitative diagnostic measures and with further extensions, for simulating surgical procedures as well.

4 Proposed Solution Architecture

In recent years, research in deep learning has demonstrated successful application of deep learning and convolutional neural networks for image classification, including medical image analysis. In this study, we propose to develop a deep neural network -based processing pipeline for classifying different stroke patterns on NCCT images, and localizing the infarct for downstream treatment formulation.

Toward solving the problem, we will collect NCCT imaging slides of study patients. Following this, the digital images will be randomly partitioned into two sets, one for model training and another as an independent test set for the final evaluation of the model. Care will be taken to avoid overlapping slides from a given patient across the training and test sets. Each slice will be manually assessed and its regions will be labeled as either *normal* (0), *ischemic infarction* (1), *hemorrhagic infarction* (2) by a trained cardiovascular radiologist. Thus, labeled slice image will form the input for training the deep learning -based computational pipeline. The model will be developed to take in square patches or tiles as inputs and output a prediction probability for each of the three classes: 0, 1, and 2 in a multi-label setting. Different model parameters including network weights, test for multiple network layers, learning rates, loss functions will be considered to fine-tune the model and formulate a model with optimal parameter settings. An unseen held-out subset of the slices data will be used for independently validating and evaluating performance and accuracy of the trained model. Finally, the models' ability to recognize the individual segmentation classes will be analyzed. As a final step, the processed image slides with infarct region annotations, as predicted by the developed computational model, will be used to perform volumetric reconstruction and infarct region correction. Furthermore, we will visualize the model's predictions overlaying color-coded dots on patches for which the model predicted patterns. This will aid in quickly identifying regions of the slice(s) from a given patient containing abnormal tissue.

4.1 Scan Processing Module

Data Collection. To develop and evaluate our computational model for detecting distinctive infarct patterns in CTs, we will acquire volumetric NCCT slices in a digital image format, typically DICOM or NIFTI. Following this, the images will be randomly partitioned into two sets: (a) one for *model building* – i.e., training and validation (about three-fourths of the dataset), and (b) for *model evaluation* (about one-fourth of the dataset).

Slice-level Annotation to Establish Ground Truth. All NCCT slice images will be manually labeled by one or more medical experts. Each image corresponding to the model building dataset will be annotated with scan regions as either one of the two patterns or normal/non-applicable. These are: *normal* (0), *ischemic infarction* (1), *hemorrhagic infarction* (2). Ideally, we would resort to multiple independent annotation results by the experts and correct for inter-rater biases to ensure high quality of the ground truth. For the purpose of annotations, a granulated user-friendly tool will be provided to the medical expert(s) to perform manual annotation at the super-pixel image region level, with the ability to select large regions of the image at a time and label them. This will save time and effort on their part. In addition, case-specific comments will be collected for downstream evaluation and analysis of the developed processing framework. The test set will be used, once the model development is complete, to evaluate its performance and compare it against that of expert annotators.

Data Pre-processing The input data in the form of CT slices will be processed by a computation processing pipeline that comprise deep learning network to analyze images and draw inferences. Initially, basic pre-processing methods to ensure consistency of image quality and exposure statistics across the dataset will adopted, and further pre-processing workflows may be integrated at a later stage during model building by empirically determining the specific image artifacts to be managed and the method required to do so. Some of the basic methods include: automatic resizing of training images to contain a fixed dimension of pixels; apply color jittering on the brightness, contrast, saturation, and hue of each image to neutralize the differences across the dataset; and augmentation of image data to randomly flip and rotate them along the horizontal and vertical axes to obtain variability in the training data, and to ensure robust model development, among others. Some more potential pre-processing methods that may be employed, should the need arise, are depicted in Figure 5.

Detection and Segmentation Model Building. Before training the classification and segmentation models, 90% of the model building data will be randomly selected for training and 10% for internal validation. The models will be implemented using the deep learning library Torch available for Python. Torch is a high-level neural net-

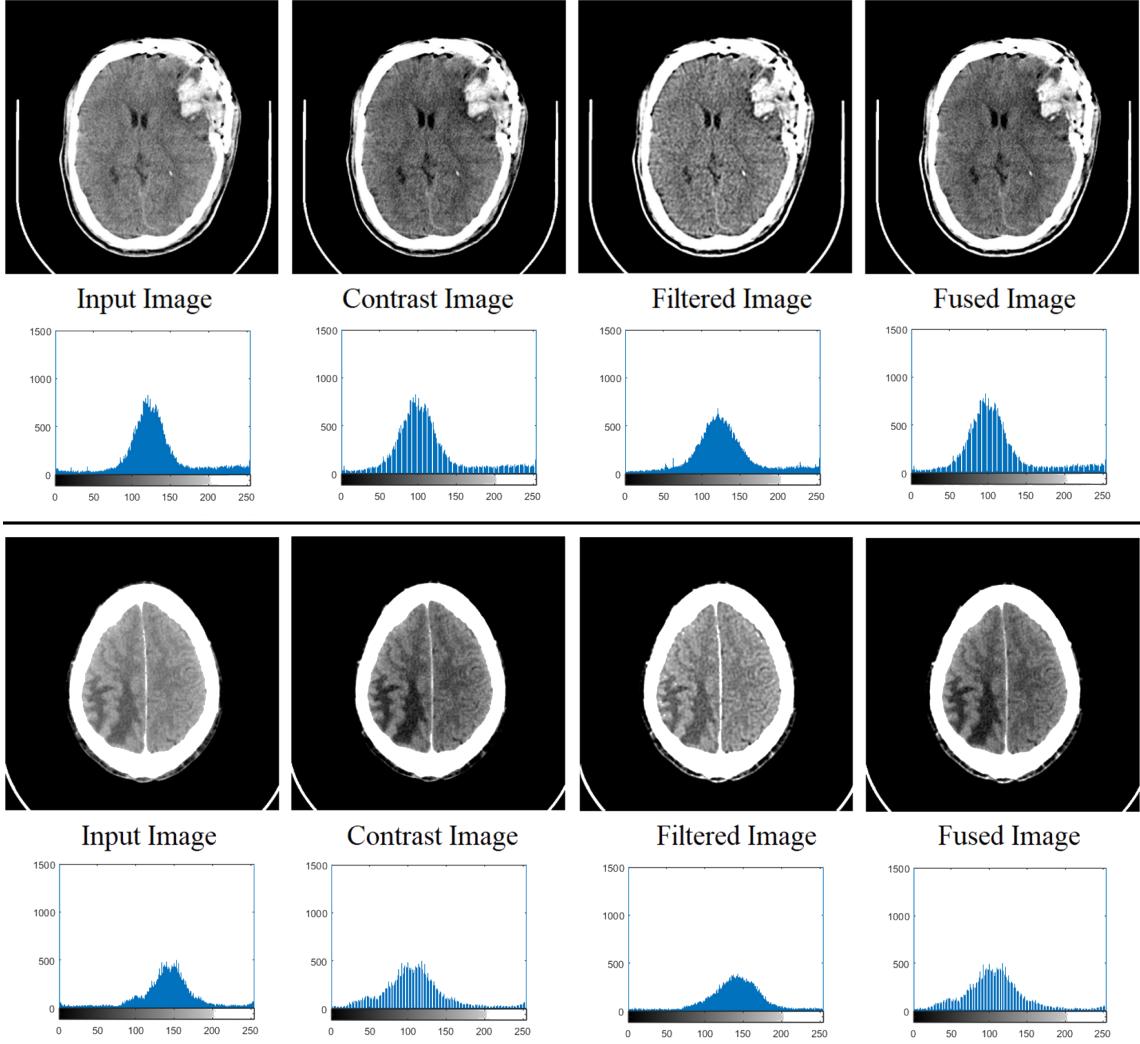


Figure 5: Potential pre-processing methods to apply on the NCCT slices before passing them to the neural network and computational analysis pipeline to correct artifacts.

works API, capable of running on top of various backend architectures. The models will be trained under a supervised setting, with NCCT slices fed as input, and outputs corrected against their corresponding expert-annotated and inter-rater corrected NCCT slices. Different tests will be conducted to optimize for the number of epochs, initial learning rates as well as the optimal depth of the neural network and other functionally configurable portions of the computational pipeline. The output of the models will be configured to output probability vectors p per stroke type, normalized to 1. Finally, the learning curves (accuracy vs. no. of iterations) for both training and testing will be plotted to determine if there is a generalization of the deep learning network model(s) to the unseen validation/test data i.e., no over-fitting has occurred.

Visualization of Predicted Patterns on the TAB sections. The processed and region-predicted NCCT slices will be visualized by overlaying color-coded dots on patches

for which our model predicted a stroke infarct pattern, or each type of the stroke. This visualization will allow us to the decisions generated by the model and further aid to gain insights into the model’s classification method.

Volumetric Reconstruction and Correction. With the infarct segmentation workflows in place, the subsequent steps involve reconstructing the volumetric CT of the patient’s brain with annotated infarct regions, labeled by type – ischemic and hemorrhagic. This process will involve stacking the processed NCCT slides whilst simultaneously correcting the neighbors for potential errors in region segmentation. These corrections will be automated based on geometric, spatial, and shape-based constraints of adjacent slides such as contour evolution methods [18], depicted in Figure 6. The correction strategy will not only improve the overall localization accuracy of the ischemic strokes facilitating subsequent use of the reconstructed volume, but will save compute time due to simultaneous reconstruction and correction and improve model inference through a more interpretable basis for reconstruction. Ultimately, this step yields an annotated volumetric model of the brain region that is pliable for exploratory analysis on a computer.

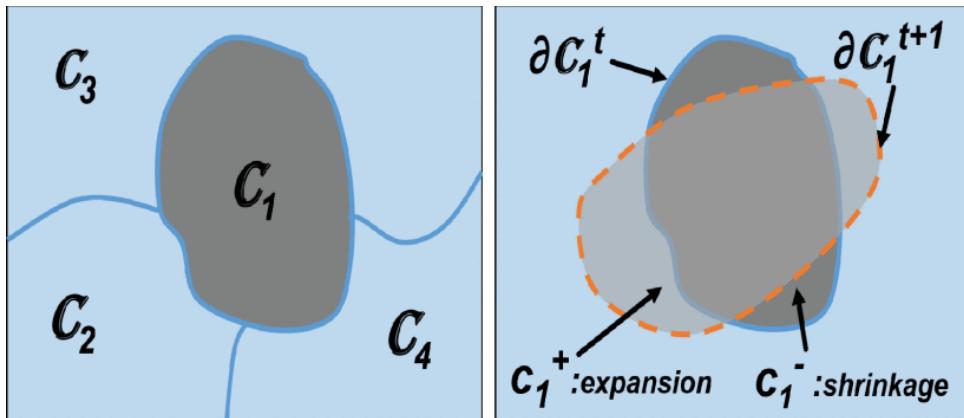


Figure 6: An abstract depiction of the *contour evolution* method, as an example of the correction methods that can be applied during volumetric reconstruction.

Diagnostic Inference from Volumes. The ultimate goal is to localize infarct types and locations in the spatial context. In addition, we also propose to estimate quantitative diagnostic measures. The annotated volume of the patient’s brain can be easily exploited to draw out any form of geometric, spatial, or structural measurements, and even a combination thereof. Furthermore, the presence of each type of infarct can be individually quantified to present summary inferences of the patient diagnosis to help clinicians devise an ideal treatment strategy.

Validation from Radiologists. At the completion of the complete processing pipeline, two sets of validations will be performed to ensure correctness of the overall computa-

tional pipeline – (1) *the volume-level annotations* will be validated by radiologists, and (2) *the slice-level annotations* of the held-out test-set will be compared to the model predictions. *Evaluation 1* will be qualitative in nature, owing to the tediousness of manually annotating volumetric regions. However, this evaluation will be supported by *evaluation 2*. In conjunction, the two sets of validations will provide sufficient evidence to verify the complete proposed computational pipeline. To evaluate the slide-level performance, the model’s labels will be compared against those of the radiologists’ by calculating an inter-rater reliability metric called Cohen’s kappa score [21], as it has been adapted as a standard metric when it comes to annotation of medical images. Thus, between every two sets of annotations from radiologists and/or the computational pipeline, both p_d scores and kappa score per class will be computed. K_{pd} refers to the percentage of NCCT slices in which two annotators agreed on the same annotation. Kappa scores per infarct class, on the other hand, estimates the detection of a given infarct pattern or type between two sets of annotations. The annotations will be quantified using a suitable metric as deemed suitable during discussions with the experts.

Anticipated Results, Potential Pitfalls, and Alternatives. We anticipate that the predictive model developed as part of this study will be able to accurately predict all stroke infarct features associated with patterns specific and non-specific to ischemic and hemorrhagic strokes. If this is not the case and/or model tends to accurately predict only the class labels having majority instances/samples, the authors will generate image slices with different overlapping areas for each class to accommodate for a *uniform distribution* through augmentation techniques across all classes (0-2) defined in this study. Further, we envision that there will be a good agreement i.e., 75% or higher, between the internal radiologist and the deep learning pipeline annotations. If it is less than what is expected, randomly selected image tiles annotated by the annotators will be cross-compared for their mutual agreement. This will allow us to reflect on whether the developed predictive models are capable of learning from a given training dataset provided by a single study radiologist. If the models perform worse in agreement compared to the two human experts themselves, then the models will be re-trained using the curated inputs from different radiologists on the whole training dataset. It is very important to provide high quality gold standard data set for training a deep learning network.

4.2 Robotic Path Planning Module

5 Proofs of Hypotheses Used

Portions of the adopted methodology in the proposed solution was designed based on two hypotheses. Specifically, a slice-wise segmentation approach was used amidst several other approaches in literature owing to its advantages in model inference time in the context of deep learning models and spatial context awareness, among others. In addition, to facilitate easy manual annotation of NCCT volumes by experts, an approximate unsupervised segmentation algorithm was designed. A primitive proof of the feasibility and applicability of these methods is presented in this section.

5.1 On the effectiveness of slice-wise segmentation

Statement. *Slice-wise segmentation is at least as effective as global volumetric segmentation of the CT slices to identify infarct regions.*

Explanation. We begin by noting that many structures in medical imaging are naturally represented as a stack of 2D images, with the relevant features of the structure spread out across multiple slices. For example, the edges of the lungs are often visible on multiple slices, and may be difficult to identify on any individual slice. By examining the entire stack of slices, we can identify the edges more easily and accurately. Therefore, slice-by-slice segmentation can be an effective way to segment these structures.

To make this more concrete, let's consider a simplified example of a 3D CT image of a cube. Suppose we wish to segment the cube from the background. We could apply a thresholding algorithm to the entire 3D volume at once, but this may not be effective if the cube is not easily distinguishable from the background. Instead, we could use slice-by-slice segmentation. We begin by segmenting the first slice using a thresholding algorithm. We then move on to the second slice, and use the segmentation of the first slice as a prior to guide the segmentation of the second slice. Specifically, we can use the segmentation of the first slice to identify a range of intensity values that are likely to correspond to the cube, and then apply a threshold within this range to the second slice. We repeat this process for each subsequent slice, using the previous segmentations as priors to guide the segmentation of the current slice.

The key advantage of this approach is that it can be more robust to noise and other artifacts that may be present in the image. If we were to apply a global thresholding algorithm to the entire 3D volume at once, we may include or exclude voxels that should

be part of the cube due to variations in the intensity values across the volume. However, by segmenting each slice individually and using the previous segmentations as priors, we can incorporate more information about the structure into the segmentation process, and potentially achieve better results.

Therefore, we conclude that slice-by-slice segmentation can be an effective way to segment 3D CT images, particularly for structures that are naturally represented as a stack of 2D images. By segmenting each slice individually and using the previous segmentations as priors, we can incorporate more information about the structure into the segmentation process and potentially achieve better results than by applying a global thresholding algorithm to the entire 3D volume at once.

Proof 1

Assumptions

1. The CT scan is of a single anatomical structure, such as a lung, liver, or kidney.
2. The structure is contiguous, meaning that there are no gaps or holes in the 3D volume.
3. The structure has a consistent appearance across all slices, meaning that it looks the same in each 2D image.

Definitions

1. A voxel is a 3D pixel in the CT image, with a certain intensity value.
2. A segmentation is a labeling of voxels as belonging to either the structure of interest or the background.

Let $I(x, y, z)$ be a 3D CT image, where x, y, z denote the spatial coordinates. Our goal is to segment a target structure S from the background. We assume that S is connected and has a reasonably smooth boundary in the image.

Suppose we apply a global thresholding algorithm to the entire 3D volume at once, using a threshold value T . Let S_T be the resulting segmentation, defined as:

$$S_T(x, y, z) = \begin{cases} 1 & \text{if } I(x, y, z) > T \\ 0 & \text{otherwise} \end{cases}$$

Note that S_T is a binary image that indicates which voxels belong to the target structure.

Now, let us consider slice-by-slice segmentation. We begin by segmenting the first slice, which we assume is parallel to the xy plane. Let $S_1(x, y)$ be the resulting segmentation of the first slice, defined as:

$$S_1(x, y) = \begin{cases} 1 & \text{if } I(x, y, 1) > T \\ 0 & \text{otherwise} \end{cases}$$

Note that S_1 is a binary image that indicates which pixels in the first slice belong to the target structure.

Next, we move on to the second slice, and use the segmentation of the first slice as a prior to guide the segmentation of the second slice. Specifically, we define a prior probability map $P(x, y)$, where $P(x, y)$ is proportional to the probability that a voxel with spatial coordinates $(x, y, 1)$ belongs to the target structure. We can define $P(x, y)$ as:

$$P(x, y) = \frac{1}{Z_1} \sum_{i,j} S_1(i, j) \exp\left(-\alpha(x - i)^2 - \beta(y - j)^2\right)$$

where Z is a normalization constant, α and β are parameters that control the spatial smoothness of the prior, and the sum is taken over all pixels (i, j) in the first slice. Note that the prior probability map is essentially a smoothed version of the segmentation of the first slice, with the smoothing controlled by the parameters α and β .

We can then use the prior probability map to guide the segmentation of the second slice. Specifically, we define the segmentation of the second slice, $S_2(x, y)$, as:

$$S_2(x, y) = \begin{cases} 1 & \text{if } I(x, y, 2) > TP(x, y) \\ 0 & \text{otherwise} \end{cases}$$

Note that we have used the prior probability map $P(x, y)$ to define a local threshold value $TP(x, y)$ for each voxel in the second slice.

We can repeat this process for each subsequent slice, using the previous segmentations as priors to guide the segmentation of the current slice. Specifically, for the k th slice, we define the prior probability map $P(x, y)$ as:

$$P(x, y) = \frac{1}{Z_{k-1}} \sum_{i,j} S_{k-1}(i, j) \exp\left(-\alpha(x - i)^2 - \beta(y - j)^2\right)$$

and the segmentation of the k th slice, $S_k(x, y)$, as:

$$S_k(x, y) = \begin{cases} 1 & \text{if } I(x, y, k) > TP(x, y) \\ 0 & \text{otherwise} \end{cases}$$

The final segmentation of the target structure, $S_{final}(x, y, z)$, is the union of all slice segmentations:

$$S_{final}(x, y, z) = \bigcup_{k=1}^n S_k(x, y) \delta_{z,k}$$

where $\delta_{z,k}$ is the Kronecker delta function that equals 1 if $z = k$ and 0 otherwise.

We claim that this slice-by-slice segmentation algorithm is equivalent to the global thresholding algorithm. To prove this, we need to show that $S_{final}(x, y, z)$ is equal to $S_T(x, y, z)$ for all voxels (x, y, z) .

First, note that by construction, $S_1(x, y)$ is a subset of $S_T(x, y, 1)$ for all (x, y) . That is, the pixels that are classified as belonging to the target structure in the first slice using the slice-by-slice algorithm are a subset of the pixels that are classified as belonging to the target structure using the global thresholding algorithm.

Now, suppose that for some $k > 1$, $S_{k-1}(x, y)$ is a subset of $S_T(x, y, k-1)$ for all (x, y) . We claim that this implies that $S_k(x, y)$ is a subset of $S_T(x, y, k)$ for all (x, y) .

To see why, consider a voxel (x, y, k) that belongs to the target structure. By definition of S_T , we have $I(x, y, k) > T$. Also, by assumption, $S_{k-1}(i, j) = 1$ for all (i, j) such that $(i, j, k-1)$ belongs to the target structure. Therefore, the prior probability map $P(x, y)$ is nonzero in a neighborhood of (x, y) , and the local threshold value $TP(x, y)$ is greater than T . Hence, $S_k(x, y) = 1$ for this voxel.

Conversely, suppose that for some (x, y, k) , $S_k(x, y) = 1$ but $S_T(x, y, k) = 0$. Then, by definition of S_T , we have $I(x, y, k) \leq T$. But this means that the local threshold value $TP(x, y)$ is also less than or equal to T , since $P(x, y) \leq 1$. Hence, we should have $S_k(x, y) = 0$, a contradiction.

Therefore, we have shown that for all k , $S_k(x, y)$ is a subset of $S_T(x, y, k)$ for all (x, y) . Hence, the final segmentation $S_{final}(x, y, z)$ is a subset of $S_T(x, y, z)$ for all voxels (x, y, z) . By a similar argument, we can show that $S_T(x, y, z)$ is a subset of $S_{final}(x, y, z)$, so the two segmentations are equal.

This completes the proof that the slice-by-slice segmentation algorithm is equivalent to the global thresholding algorithm.

Proof 2 – By contradiction

We will prove this theorem by contradiction. Suppose that slice-by-slice segmentation does not work, i.e., that it produces an invalid segmentation of the entire struc-

ture. Then, there must be at least one voxel in the structure that is mislabeled by the segmentation. Let v be such a voxel.

Consider the slice that contains v . Since the structure is contiguous, there must be some neighboring voxels in the same slice that are also part of the structure. Let w be one of these voxels.

Case 1. The voxel v is mislabeled as background, but it should be part of the structure. In this case, the intensity value of v must be similar to the intensity value of w , since they are both part of the same structure. Therefore, if we were to use a global thresholding method to segment the entire 3D volume at once, both v and w would be labeled as part of the structure. However, since we are doing slice-by-slice segmentation, v is mislabeled because the threshold used on that particular slice was not appropriate. Therefore, this case contradicts our assumption that the structure has a consistent appearance across all slices.

Case 2. The voxel v is mislabeled as part of the structure, but it should be background. In this case, the intensity value of v must be different from the intensity value of w , since w is part of the structure and v is not. Therefore, if we were to use a global thresholding method to segment the entire 3D volume at once, v would be correctly labeled as background. However, since we are doing slice-by-slice segmentation, v is mislabeled because the threshold used on that particular slice was not appropriate. Therefore, this case contradicts our assumption that the structure is contiguous.

Since both cases lead to a contradiction, we have shown that slice-by-slice segmentation of a contiguous anatomical structure in a 3D CT scan works, given the assumptions above.

5.2 On the feasibility of dimensionality reduction for segmentation

Statement. *Unsupervised segmentation with dimensionality reduction applied to encoded image features is a feasible approach to segment stroke infarcts from NCCT volumes.*

Proof. To prove why unsupervised learning with dimensionality reduction will work for stroke infarct segmentation, we need to consider the following assumptions,

1. The data is high-dimensional, meaning it has a large number of features.
2. The stroke infarcts differ from healthy tissue in some measurable way, even in a reduced feature space.

3. The algorithm is able to capture the underlying structure of the data in a reduced feature space without the need for explicit supervision.

Let us consider the first assumption. Medical images such as MRI and CT scans are typically high-dimensional, with thousands or even millions of voxels or pixels, each with multiple intensity values across different modalities or time points. High-dimensional data can be difficult to process and analyze, and may suffer from the curse of dimensionality.

Now let us consider the second assumption. As previously stated, stroke infarcts differ from healthy tissue in terms of their intensity values on medical images. However, even in a reduced feature space, where only a subset of the original features are retained, the stroke infarcts may still have a distinct pattern that can be captured by an unsupervised learning algorithm.

Dimensionality reduction techniques such as principal component analysis (PCA) and t-distributed stochastic neighbor embedding (t-SNE) can be used to reduce the dimensionality of the data while preserving the most relevant information. These techniques transform the original high-dimensional data into a lower-dimensional space, where the most important features or patterns are retained.

Let X be the set of all medical images that can be used for stroke infarct segmentation, and let x_i be an image in X . Each image x_i can be represented as a set of N pixels/voxels, where pixel/voxel j in image x_i is denoted by x_{ij} . Let $F = f_1, f_2, \dots, f_k$ be the set of k features, where each feature f_j is a linear combination of the original intensity values of x_{ij} . We can assume that the stroke infarcts have a distinct pattern in this reduced feature space, which can be used to identify them as a separate cluster.

To formalize this argument, let Y be the set of all possible segmentations of the images into infarct and non-infarct regions. Let g be an unsupervised learning algorithm that takes an image x_i as input and produces a segmentation $y_i \in Y$ as output, using dimensionality reduction. This can be written as,

$$g : X \rightarrow Y \quad (1)$$

To prove that g is effective for stroke infarct segmentation, we need to show that g produces accurate segmentations of infarct regions in the reduced feature space. We can do this by showing that g is able to identify the stroke infarcts as a separate cluster in this space.

Let Z_i be the set of reduced feature vectors of the pixels/voxels in image x_i , obtained using PCA or t-SNE. Let C_i be the cluster corresponding to the stroke infarcts

in the reduced feature space. This can be written as,

$$C_i = \{z_j \in Z_i | z_j \text{ is in the stroke infarct cluster}\} \quad (2)$$

To show that g is effective, we need to show that C_i is a distinct cluster that can be separated from the healthy tissue in the reduced feature space. This means that there exists a decision boundary that can be used to classify the pixels/voxels in Z_i as belonging to either the infarct or non-infarct region.

We can formalize this argument as follows:

$$\exists(\phi : Z_i \rightarrow \{0, 1\}) \forall z_j \in Z_i \quad (3)$$

where ϕ is defined as,

$$\phi(z_j) = 1 \text{ iff } z_j \in C_i \quad (4)$$

This means that there exists a decision function that can classify each feature vector z_j in Z_i as belonging to the infarct region ($(z_j) = 1$) or the healthy tissue region ($(z_j) = 0$). This decision boundary can be learned using an unsupervised learning algorithm such as clustering, which groups similar feature vectors together.

Let K be the number of clusters in the reduced feature space. The unsupervised learning algorithm can partition the feature vectors into K clusters, where K is typically determined using heuristics such as the elbow method or silhouette score. One of these clusters corresponds to the stroke infarcts, and the rest correspond to healthy tissue.

We can write the unsupervised learning algorithm as,

$$C = \{C_1, C_2, \dots, C_K\} = g(Z_i) \quad (5)$$

where C is the set of K clusters produced by the unsupervised learning algorithm. We can assume that C_1 corresponds to the stroke infarcts, since this cluster should have a distinct pattern that separates it from the healthy tissue.

To show that the unsupervised learning algorithm is effective, we need to show that C_1 is a distinct cluster that contains most of the infarct pixels/voxels in the image. This means that C_1 has a high purity or accuracy, and a low overlap with the other clusters.

We can formalize this argument as follows,

$$\forall z_j \in C_i \exists C_k \in C : z_j \in C_k \quad (6)$$

This means that each feature vector z_j in the infarct cluster C_i should be assigned to

one of the K clusters produced by the unsupervised learning algorithm. This implies that C1 contains most of the infarct pixels/voxels in the image, and has a high purity.

In conclusion, we have shown that an unsupervised learning algorithm that uses dimensionality reduction can effectively segment stroke infarcts in medical images. This is achieved by reducing the dimensionality of the data to a lower-dimensional space where the stroke infarcts have a distinct pattern that can be captured by an unsupervised learning algorithm. The algorithm can then learn a decision boundary that separates the infarct and non-infarct regions in the reduced feature space. The effectiveness of the algorithm can be measured by the purity or accuracy of the infarct cluster produced by the algorithm.

6 Results

An overview of the proposed timeline and progress thereof is presented in Figure 7.

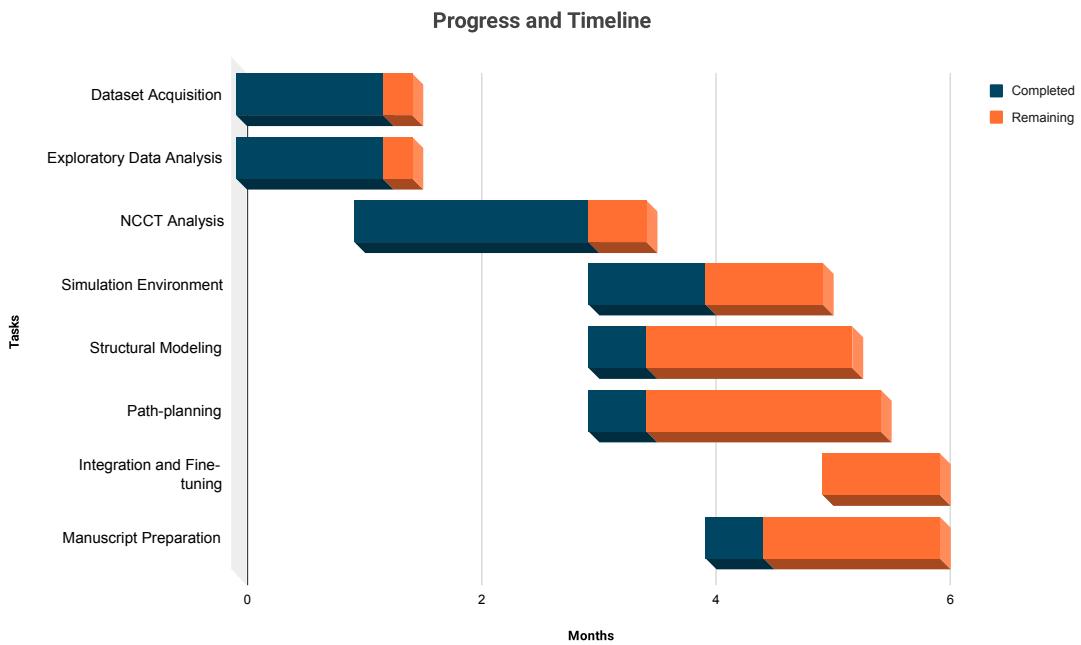


Figure 7: Tentative project timeline and progress made.

Exploratory Data Analysis. To prepare our processing and experimentation pipeline for the proprietary data we expect to acquire from *Chettinad Academy for Research and Education*, we reviewed closely-related NCCT datasets. To analyze the applicability of this data to our problem statement, and to ensure translation of developed methods to the proprietary dataset, we performed EDA to analyze these datasets.

Based on these analyses, we chose to benchmark our experiments using two representative datasets. These analyses are available in our project codebase at: <https://github.com/karthik-d/Vision-For-Robot-Path-Planning>.

- A *Brain Tumor Classification* dataset sourced from [Kaggle](#) comprising over 3,000 scan slices of the brain, classified into four tumor types. The dataset is sourced from multiple patients, across multiple medical centers.
- A peer-reviewed *intracranial hemorrhage dataset* [15] comprising 2500 brain window images and 2500 bone window images collected from 82 patient samples. This dataset provides annotations indicating the location of the hemorrhage on each slice.

Classification Models. We performed classification experiments using state-of-the-art deep-learning approaches on open-access datasets, particularly a well-established and widely-adopted brain tumor dataset sourced from [\[Kaggle\]](#), to assess the suitability and viability of these methods and to arrive upon a suitable course of action for the proprietary dataset. These experiments are summarized in Table 1.

Table 1: Comparison of classification approaches on open-access datasets.

Approach	Dataset	Accuracy
SVM		96.73%
Five-layer CNN		94.62%
ResNet-152		93.86%
GoogLeNet		85.13%
MobileNet		88.45%
EfficientNet-B0	Open-Access Brain Tumor Dataset [Kaggle]	98.71%
EfficientNet-B1		98.37%

Segmentation Models. For segmentation, we again performed experiments using state-of-the-art deep-learning approaches on open-access datasets, particularly a peer-reviewed intracranial hemorrhage dataset [15], to assess the suitability and viability of these methods and to arrive upon a suitable course of action for the proprietary dataset. Furthermore, we explored the possibility of adopting an *unsupervised* approach for segmentation to minimize, or even eliminate the need for time-consuming manual annotation of stroke infarcts by expert radiologists. These experiments are summarized in Table 2. In addition to the most commonly used supervised deep-learning methods, we also experimented with an unsupervised clustering-based approach to deal with sparse availability of lesion annotation masks. This workflow is presented in Figure 6. *The approach can be further improved, for the proprietary dataset if*

appropriate, by integrating a high-performing pre-trained deep-learning backbone model as an autoencoder, or even in the few-shot learning regime.

Table 2: Comparison of segmentation approaches on open-access datasets.

Approach	Backbone	Dataset	MeanIoU	AuROC
FPN	DenseNet121	Licensed Open-Access Intracranial Hemorrhage Dataset [15]	85.34%	78.07%
FPN	EffNet-B0		86.42%	87.07%
FPN	ResNet-152		51.18%	78.20%
UNet	DenseNet121		89.94%	95.02%
UNet	EffNet-B0		92.90%	91.68%
UNet	ResNet-152		97.26%	66.01%
M Net			92.76%	90.61%
Slice-Aware Net			89.14%	88.04%
Clustering Analysis			82.72%	82.09%

Path Planning for Thrombectomy. To model robotic environments based on quantitative parameters measured from the proposed NCCT analysis pipeline, we conducted experiments to determine the most feasible simulation workflows and perform path-planning for a 6-DOF arm. Based on this review, we have found the following *simulation gyms* most suitable for this project.

- *OpenAI Gym* is a comprehensive collection of environments to train and test reinforcement learning algorithms. We particularly intend to use its “pusher” environment that simulates a robotic arm pushing an object towards a target position.
- *Panda Gym* [5] provides a set of RL environments integrated with the OpenAI Gym. It provisions five tasks, namely reach, push, slide, pick place, and stack.
- *Robo Gym* [19] is a unified setup for simulation and real environments, allowing seamless transfer from training to application. Particularly known for its distributive capabilities, it provides further scope for extension.

When performing experiments to evaluate the proposed path-planning strategies, the following parameters were used,

$$\begin{aligned}
 & initial_temp = 1.0; \\
 & cooling_rate = 0.005; \\
 & episode = 1; \\
 & finite_states = 100000; \\
 & iterations = 5;
 \end{aligned} \tag{7}$$

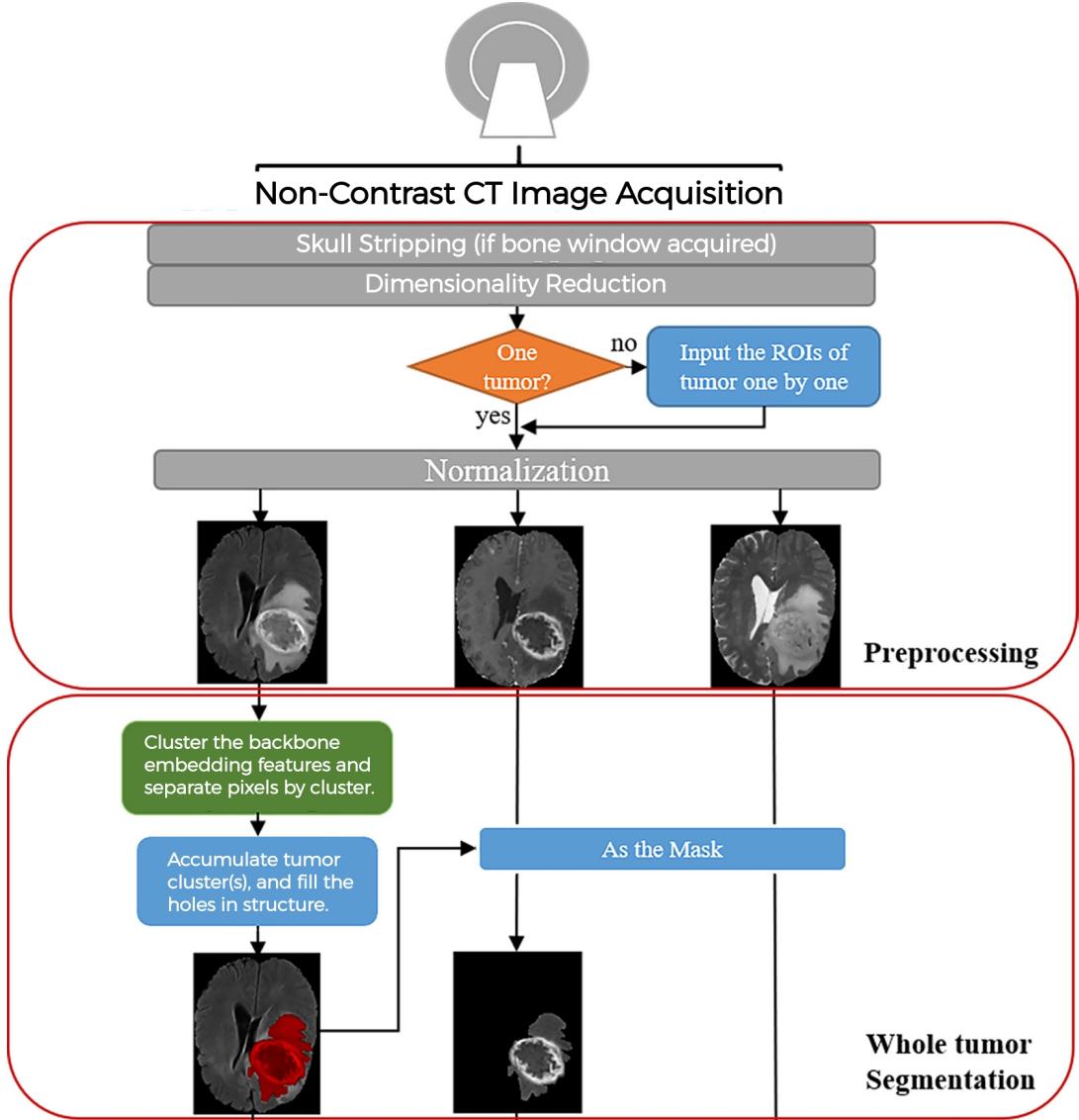


Figure 8: An unsupervised approach to segment hemorrhagic infarcts from brain CTs.

Qualitative results on one simulation environment is presented in Figure 6. It is worth noting that the proposed changes to the path-planning algorithm was able to improve the comparative baseline by successfully completing 6 of 7 target positions, as opposed to the baseline's 4 of 7.

The results show that the assisted learning strategies efficiently speed up the learning process and the mechanical arm can successfully avoid obstacles and reach the target point safely, even when limited by safe distance constraints. The proposed approach has potential applications in industries such as manufacturing, warehousing, and transportation.

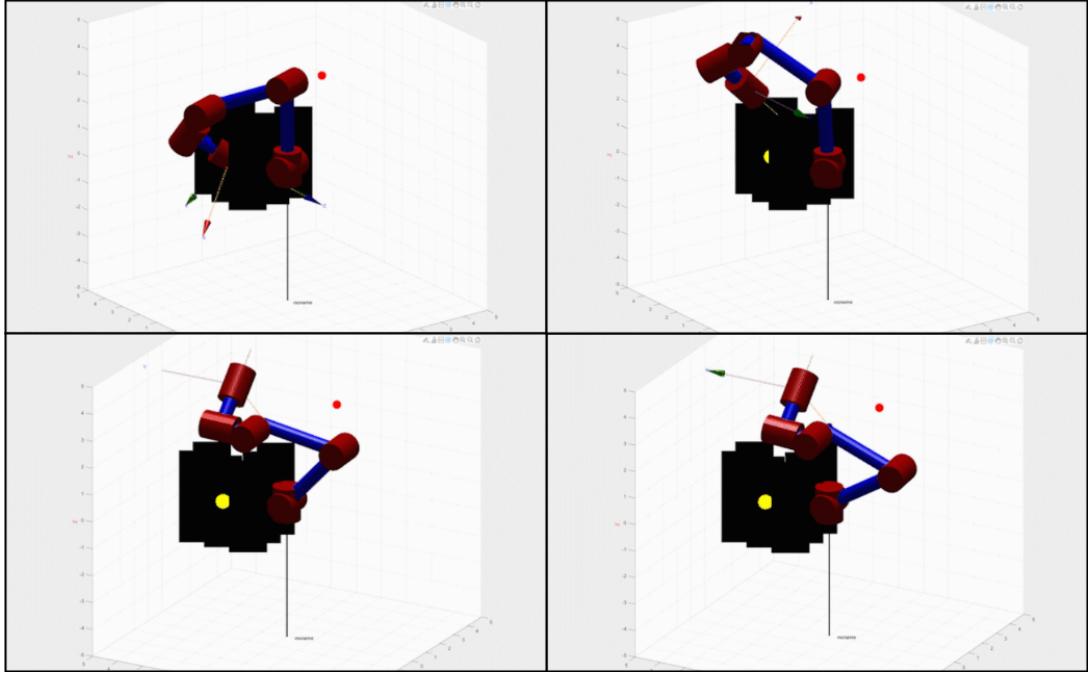


Figure 9: Intermediate states of the 6-DOF robotic arm when implementing the planned path in one of the six successful environments successfully planned by the proposed algorithm.

7 Motivation and Relevance in Healthcare

After heart disease, brain stroke is the most common reason for death around the world [22]. Due to which the majority of survivors need to live with changeless or long-term injury. Brain imaging methods like magnetic resonance imaging (MRI) and CT are quite helpful for a doctor in order to start the initial screening of the patient. There are also many imaging modalities for the analysis of brain, which may include X-ray imaging, diffuse optical imaging, magnetoencephalography, functional MRI and positron emission tomography [4, 41]. However, all these imaging techniques require high operating cost and well-trained operator, hence most of these imaging methods may not be available in all the clinics and hospitals.

Image classification is widely used in medical imaging [28]. However, for better accuracy of the classification system, results should be close to the manual diagnosis. Nowadays, deep learning has been extensively used as a classification method because it automatically calculates features within the convolutional layers of the deep system [23, 1]. The main advantage of using deep learning is that it outperforms other conventional methods for image classification [34]. Many deep learning methods have come into existence such as recurrent neural networks, long short-term memory (LSTM) [14], CNNs [26], deep belief nets (DBN) [13], etc. Among these methods, CNN has

been generally utilized in computer vision and medical image processing problems like ImageNet, face recognition, house numbers digit classification, patch classification from medical images etc. Classification methods other than deep learning methods are random forest (RF), -nearest neighbors (NN), decision tree (DT), multilayer perceptron (MLP), support vector machine (SVM) and many more [37, 33, 35].

In this research, an automatic classification method has been proposed to predict the category to which brain CT scan image belongs, along with the locations of the stroke infarcts for hemorrhagic and ischemic stroke types, and normal tissue. *Hemorrhagic stroke* occurs due to fragile blood vessel which burst and drains into the neighboring brain tissues. On the other side, *ischemic stroke* occurs when blood supply in the brain stops due to the presence of blood clots. Brain hemorrhage can also occur after ischemic stroke which results in a serious complication [20]. Sample images of the two types of stroke on CT slices are depicted in Figure 1, with infarct regions demarcated in red.

Towards the diagnosis of stroke, doctors first confirm symptoms from the patient or family members. The most important thing which will help in accurate identification is the stroke history. This is usually followed by neuroimaging of the patient. The most commonly used neuroimaging method used by experts is CT scan for diagnosing brain strokes, on account of their greater affordability. The prediction of stroke from CT scan images serve as the initial step towards the proper diagnosis of a patient. These images are then sent to a cardiovascular radiologist to identify the stroke type. Thereafter, physical and manual examination of the patient is performed to determine an appropriate course of treatment. However, this manual diagnosis procedure is extremely time-consuming for the already overburdened radiologist, and is prone to human-error. Many researchers have worked in this area for providing a computer-aided diagnosis (CAD) system, in spite of the significant requirement, there is no clinically accepted CAD system for stroke [24, 27]. The system proposed by [24] was not automated and requires significant performance improvements to warrant automation. Peixoto and Filho [27] have worked on the classification of hemorrhagic and ischemic stroke CT scan images. Their method was developed for small dataset where each case had 100 images and for future work they have to test their method on large datasets. Thus, there is a need for an effective automated system for diagnosing strokes that can help physicians quickly start treatment after stroke onset. Hence, in this work, we proposed to develop a deep learning -based computation pipeline to process CT slices to detect stroke type and localize infarct location. Furthermore, we propose to reconstruct the CT slices into volumetric models while correcting errors in infarct localization, and cast the volume into a computationally pliable 3D model that

can be used to draw out diagnostic measurements as well as for treatment simulations.

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