Brain Tumor Segmentation Using Convolutional Neural Networks by MRI Images

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Abstract: Among brain tumors, gliomas are the most common and aggressive, leading to a very short life expectancy in their highest grade. Thus, treatment planning is a key stage to improve the quality of life of oncological patients. Magnetic Resonance Imaging (MRI) is a widely used imaging technique to assess these tumors, but the large amount of data produced by MRI prevents manual segmentation in a reasonable time, limiting the use of precise quantitative measurements in the clinical practice. So, automatic and reliable segmentation methods are required; however, the large spatial and structural variability among brain tumors make automatic segmentation a challenging problem. The use of small kernels allows designing a deeper architecture, besides having a positive effect against over fitting, given the fewer number of weights in the network. To investigated the use of intensity normalization as a pre-processing step, which though not common in CNN-based segmentation methods, proved together with data augmentation to be very effective for brain tumor segmentation in MRI images. In addition to this tumor length, width and exact location is detected accurately. An extensive experimental evaluation on benchmark data demonstrates the effectiveness and efficiency of our approach.

Keywords: Image Segmentation, Brain tumors, Magnetic Resonance Imaging, Convolutional Neural Networks, Tumor segmentation etc.

I. INTRODUCTION

As a neurosurgical disease, the incidence of brain tumors is lower than that of stomach, breast, uterus, and esophageal tumors, but the mortality rate is much higher than other tumors. Brain tumors can be classified as benign tumors and malignant tumors. Benign tumors grow slowly and have no ability to infiltrate and metastasize. 80% of malignant tumors are gliomas and metastases, and gliomas [1] can be divided into Low-grade glioma cases (LGG) and High-grade glioma cases (HGG) according to their aggressiveness. In terms of composition, gliomas are generally divided into three parts: edema area, tumor enhancement necrosis area, and tumor core area. Magnetic Resonance Imaging (MRI) is an oninva - sive imaging technology [2], which is an effective means for the diagnosis and treatment of human tissues. Using the way of deep learning to process MRI images of brain tumors can provide a certain reference value for solving problems such as case analysis and intra operative localization. Image segmentation is a research hotspot in computer vision. Long et al [3] Proposed the networks of Full Convolutional Network (FCN). It adopts a deconvolution layer for up-sampling, avoiding the problems of repeated storage and the limits of the size of the image. Badrinarayan an et al [4] Proposed a pixel – level segmentation network, which considers spatial consistency and optimize training with stochastic gradient-decent, focusing on the advantages of memory usage and computational efficiency. He et al [5] proposed an adaptive pyramid context model, which adopts Global-guided Local Affinity to add all features from related pixels or regions to construct adaptively multi-scale context vector. Zhang et al [6] proposed a class-independent segmentation network. CANet uses the attention mechanism to fuse multiple supporting example information from K-shot learning settings and proposes an iterative optimization module to modify the prediction results. The complexity and objectivity of medical images have large limits on the development of image segmentation [7] As is known to all, medical image datasets face the following challenges: Firstly, the dataset is small. There are differences in image noise among images collected by different instruments and institutions, such as image resolution, tissue shape, and size, resulting in the difficulty in expanding the datasets. Secondly, the segmentation labeling of biomedical images requires considerable professional clinical knowledge. Thirdly, nearly 50% of human brains have developmental malformations, e.g., asymmetric and congenital cysts, which cause difficulties in image segmentation. In response to the above problems, we propose a multi- modal brain tumor image segmentation method based on the ACU-Net network. Our main contributions are summarized as:

1) We propose an ACU-Net network based on the frame- work of U-Net, set a deep separable convolution in the model to replace the ordinary convolution layer to solve the problem of network computing efficiency.

2) We use the Dense Residual block into the ACU-Net network, the full-scale jump connection method is adopted to realize flexible feature fusion and accelerate the speed of deep network convergence.

3) We insert the active contour model in the ACU-Net to ensure the fitting between the inside and outside of the boundary, to improve the accuracy of segmentation.

II. MEDICAL IMAGING

Medical imaging is the technique and procedure of creating visual demonstration of the internal of a body for experimental analysis and health intervention. Medical imaging seeks out to disclose internal structures hidden by the skin and bones, as well as to diagnose and treat disease. Medical imaging also establishes a database of normal anatomy and physiology to make it possible to identify abnormality. Although imaging of removed organs and tissues can be performed for medical reasons, such procedures are usually considered part of pathology instead of medical imaging.

Medical imaging is often perceived to designate the set of techniques that noninvasively produce images of the internal aspect of the body. In this restricted sense, medical imaging can be seen as the solution of mathematical inverse. This means that cause (the properties of living tissue) is inferred from effect (the observed signal). In the case of medical ultrasonography, the probe consists of ultrasonic pressure waves and echoes that go inside the tissue to show the internal structure. In the case of projection radiography, the probe uses X-ray radiation, which is absorbed at different rates by different tissue types such as bone, muscle and fat. The term noninvasive is used to denote a procedure where no instrument is introduced into a patient's body which is the case for most imaging techniques used. The MIPAV (Medical Image Processing, Analysis, and Visualization) application enables quantitative analysis and visualization of medical images of numerous modalities such as PET, MRI, CT, or microscopy. Using MIPAV's standard user-interface and analysis tools, researchers at remote sites (via the internet) can easily share research data and analyses, thereby enhancing their ability to research, diagnose, monitor, and treat medical disorders. MIPAV is a Java application and can be run on any Java-enabled platform such as Windows, UNIX, or Macintosh OS X.

A. Goal For MIPAV

MIPAV is to meet the following goals:

- To develop computational methods and algorithms to analyze and quantify biomedical data;
- To collaborate with NIH researchers and colleagues at other research centers in applying information analysis and visualization to biomedical research problems;
- To develop tools (in both hardware and software) to give our collaborators the ability to analyze biomedical data to support the discovery and advancement of biomedical knowledge.

B. Need For MIPAV

Imaging has become an essential component in many fields of bio-medical research and clinical practice. Biologists study cells and generate 3D confocal microscopy data sets, virologists generate 3D reconstructions of viruses from micrographs, radiologists identify and quantify tumors from MRI and CT scans, and neuroscientists detect regional metabolic brain activity from PET and functional MRI scans. Analysis of these diverse types of images requires sophisticated computerized quantification and visualization tools. To support scientific research in the NIH intramural program, CIT has made major progress in the development of a platform-independent, n-dimensional, general-purpose, extensible image processing and visualization program.

III. NEED FOR MACHINE LEARNING

Using machine learning techniques that learn the pattern of brain tumor is useful because manual segmentation is time consuming and being susceptible to human errors or mistakes. In general medical image segmentation is the process of automatic or semi-automatic detection of boundaries within a 2D or 3D images.
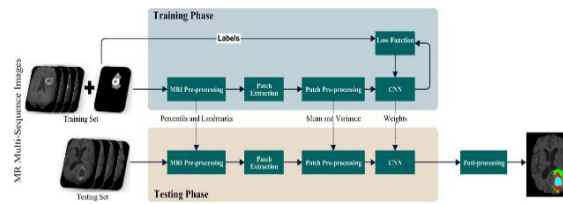
Fig. 1.Training and Testing phase

IV. SYSTEM ANALYSIS

The most difficult task in clustering time series is to find an appropriate similarity measure. Many approaches rely on feature transformation and dimensionality reduction. Features derived by Pearson correlation coefficient. Alternative approaches to feature extraction include e.g. the method of multi-resolution piecewise aggregate approximation presented. Recently, compression-based similarity measures have been proposed, e.g. Each time series is represented by a bit string indicating the intervals where the value of the time series is above the mean value of the time series. This representation is used to compute an approximate clustering. The bit level representations are compressed using standard compression algorithms in order to reduce the I/O cost and to speed-up the clustering task. A compression-based similarity measure is also proposed to compare long time series structure using co-compressibility as a dissimilarity measure. In the experimental section, we compare to the existing algorithms. Like RA, approach not an efficient clustering for brain region clustering. This approach is an iterative partitioning clustering method but it uses PCC to represent the cluster centers. And implement statistical merging algorithm to predict the diseases in brain regions.

A. Proposed System

Human brain activity is very complex and far from being fully understood. Many psychiatric disorders like Schizophrenia and Somatoform Pain Disorder can so far neither be identified by biomarkers, nor by physiological or histological abnormalities of the brain. Aberrant brain activity often is the only resource to understand psychiatric disorders. Functional magnetic resonance imaging (fMRI) opens up the opportunity to study human brain function in a noninvasive way. The basic signal of fMRI relies on the blood-oxygen-level-dependent (BOLD) effect, which allows indirectly imaging brain activity by changes in the blood flow related to the energy consumption of brain cells. Brain tissues are segmented using Conditional Random field approach. It presents a new CNN for segmenting SWI venography datasets.The CNN model aggregates multiple first- and second-order potentials. Specifically, appearance, shape, location, auto-logistic (Ising) interaction and data-dependent interaction potentials are combined to produce robust, complete and fully automated SWI venogram segmentation. This was inspired by the groundbreaking work of on deep CNNs, we investigate the potential of using deep architectures with small convolutional kernels for segmentation in MRI images proposed the use of small kernels we can stack more convolutional layers, while having the same receptive field of bigger kernels. For instance, two 3x3 cascaded convolutional layers have the same effective receptive field of one 5x5 layer, but fewer weights.

In a typical fMRI experiment, the subject to perform some cognitive task while in the scanner. And implement statistical region merging approach to group the similar regions. It is the reconstruction of regions on the observed image, based on an unknown theoretical (true) image on which the true regions we seek are statistical regions whose borders are defined from a simple axiom. Second, we show the existence of a particular blend of statistics and algorithmic to process observed images generated with this model, by region merging, with two statistical properties. With high probability, the algorithm suffers only one source of error for image segmentation: over merging, that is, the fact that some observed region may contain more than one true region. The algorithm does not suffer neither under merging, nor the most frequent hybrid cases where observed regions may partially span several true regions.
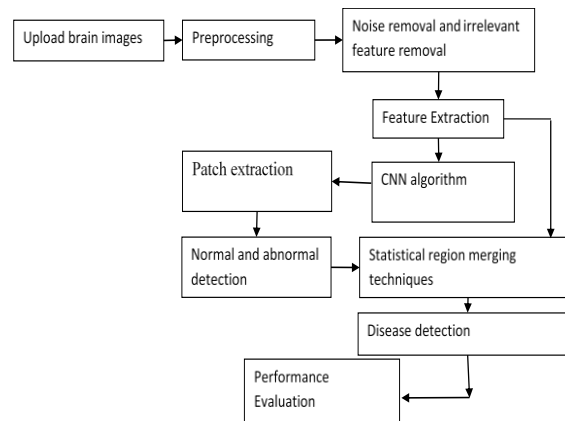
B. Proposed System Architecture

Fig. 2.Block Diagram

User can upload the images related to brain images. The data set contains MRI images. MRI images may be any time and any size. Type may be JPEG, PNG and so on. In the Pre-Processing step MRI images are altered by the bias field distortion. This makes the intensity of the same tissues to vary across the image. To correct it, we applied the N4TK method. This is not enough to ensure that the intensity distribution of a tissue type is in a similar intensity scale across different subjects for the same MRI sequence, which is an explicit or implicit assumption in most segmentation methods.

V. IMPLEMENTATION

A. Brain Image Acquisition

Functional magnetic resonance imaging or functional MRI (fMRI) is a functional neuroimaging procedure using MRI technology that measures brain activity by detecting changes associated with blood flow. This technique relies on the fact that cerebral blood flow and neuronal activation are coupled. When an area of the brain is in use, blood flow to that region also increase,[citation needed] The primary form of fMRI uses the blood-oxygen-level dependent (BOLD) contrast, discovered by Seiji Ogawa. This is a type of specialized brain and body scan used to map neural activity in the brain or spinal cord of humans or other animals by imaging the change in blood flow (hemodynamic response) related to energy use by brain cells. Since the early 1990s, fMRI has come to dominate brain mapping research because it does not require people to undergo shots, surgery, or to ingest substances, or be exposed to ionizing radiation, etc. Other methods of obtaining contrast are arterial spin labeling and diffusion MRI. The latter procedure is similar to MRI but uses the change in magnetization between oxygen-rich and oxygen-poor blood as its basic measure. This measure is frequently corrupted by noise from various sources and hence statistical procedures are used to extract the underlying signal. The resulting brain activation can be presented graphically by color-coding the strength of activation across the brain or the specific region studied. The technique can localize activity to within millimeters but, using standard techniques, no better than within a window of a few seconds. fMRI is used both in the research world, and to a lesser extent, in the clinical world. It can also be combined and complemented with other measures of brain physiology such as EEG and NIRS. Newer methods which improve both spatial and time resolution are being researched, and these largely use biomarkers other than the BOLD signal. Some companies have developed commercial products such as lie detectors based on fMRI techniques, but the research is not believed to be ripe enough for widespread commercialization. The fMRI concept builds on the earlier MRI scanning technology and the discovery of properties of oxygen-rich blood. MRI brain scans use a strong, permanent, static magnetic field to align nuclei in the brain region being studied. Another magnetic field, the gradient field, is then applied to spatially locate different nuclei. Finally, a radiofrequency (RF) pulse is played to kick the nuclei to higher magnetization levels, with the effect now depending on where they are located. When the RF field is removed, the nuclei go back to their original states, and the energy they emit is measured with a coil to recreate the positions of the nuclei. MRI thus provides a static structural view of brain matter. The central thrust behind fMRI was to extend MRI to capture functional changes in the brain caused by neuronal activity. Differences in magnetic properties between arterial (oxygen-rich) and venous (oxygen-poor) blood provided this link. Since the 1890s it has been known that changes in blood flow and blood oxygenation in the brain (collectively known as hemodynamics) are closely linked to neural activity. When neurons become active, local blood flow to those brain regions increases and oxygen-rich (oxygenated) blood displaces oxygen-depleted (deoxygenated) blood around 2 seconds later. This rises to a peak over 4–6 seconds, before falling back to the original level (and typically undershooting slightly). Oxygen is carried by the hemoglobin molecule in red blood cells.

Deoxygenated hemoglobin (dHb) is more magnetic (paramagnetic) than oxygenated hemoglobin (Hb), which is virtually resistant to magnetism (diamagnetic). This difference leads to an improved MR signal since the diamagnetic blood interferes with the magnetic MR signal less. This improvement can be mapped to show which neurons are active at a time. By improving the brain image. we can examine that with the patient effectively and efficiently with less time. With that we can face any tumor with the help of this fMRI image which is more useful in the medicine industry to overcome all the types of tumors effectively with the sample images. The rest is taken care by the doctors who takes of this in the further process. The sample fMRI images are:
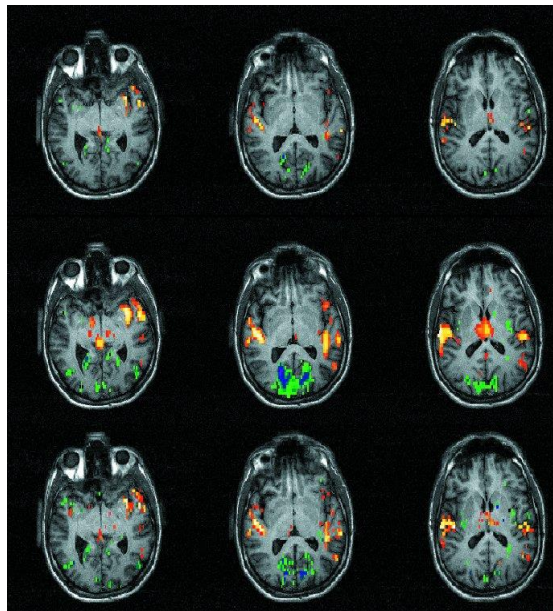

Fig. 3.fMRI Images

B. Preprocessing

In this module we convert the RGB image into gray scale images. The colors of leaves are always green shades and the variety of changes in atmosphere because the color features having low reliability. Therefore, to recognize various plants using their leaves, the obtained leaf image in RGB format will be converted to gray scale before pre-processing. The formula used for converting the RGB pixel value to its grey scale counterpart is given in Equation.

$$Gray = 0.2989 * R + 0.5870 * G + 0.1140 * B$$

where R, G, B correspond to the color of the pixel, respectively.

Then remove the noises from images by using filter techniques. The goal of the filter is to filter out noise that has corrupted image. In this phase using wiener filter to filter the noises in images. In image processing, the Wiener filter is a filter used to produce an estimate of a desired or target random process by linear time-invariant (LTI) filtering of an observed noisy process, assuming known stationary signal and noise spectra, and additive noise. The Wiener filter minimizes the mean square error between the estimated random process and the desired process. The process shown.
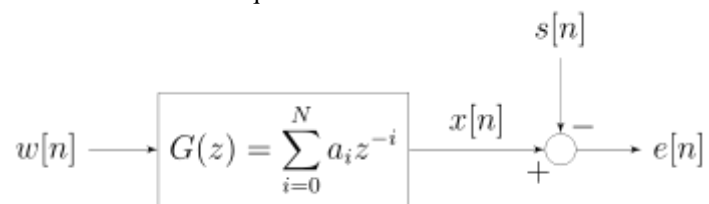
C. CNN Approach

Image segmentation is the process of partitioning a digital image into multiple segments (sets of pixels, also known as super pixels). The goal of segmentation is to simplify and/or change the representation of an image into something that is more meaningful and easier to analyze. Image segmentation is typically used to locate objects and boundaries (lines, curves, etc.) in images. More precisely, image segmentation is the process of assigning a label to every pixel in an image such that pixels with the same label share certain characteristics.

The result of image segmentation is a set of segments that collectively cover the entire image, or a set of contours extracted from the image (see edge detection). Each of the pixels in a region is similar with respect to some characteristic or computed property, such as color, intensity, or texture. Adjacent regions are significantly different with respect to the same characteristic.

- Image segmentation is the process of partitioning a digital image into multiple segments.
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Image segmentation is the process of assigning a label to every pixel in an image such that pixels with the same label share certain characteristics. CNN approaches are undirected graphical models that encode a conditional probability distribution using a given set of features. CNN are defined as follows Let G be an undirected model over sets of random variables y and x. As atypical special case y=$\{y_t\}$ and x=$\{x_t\}$ for t=1,…T, so that y is a labeling of an observed sequence x. If C=$\{y_c, x_c\}$ is the set of cliques in G, then CNN define the conditional probability of a state sequence give the observed sequence as:

$$P_\Lambda \left(\frac{y}{x} \right) = \frac{1}{Z(x)} \prod_{c \in C} \varphi(y_c, x_c)$$ Where φ is a potential function.

CNN approaches are a class of statistical modeling method often applied in pattern recognition and machine learning, where they are used for structured prediction. Whereas an ordinary classifier predicts a label for a single sample without regard to "neighboring" samples, a CNN can take context into account; e.g., the linear chain CNN approach popular in natural language processing predicts sequences of labels for sequences of input samples. CNN approaches the images with the great accuracy in area type of discriminative undirected probabilistic graphical model. It is used to encode known relationships between observations and construct consistent interpretations.
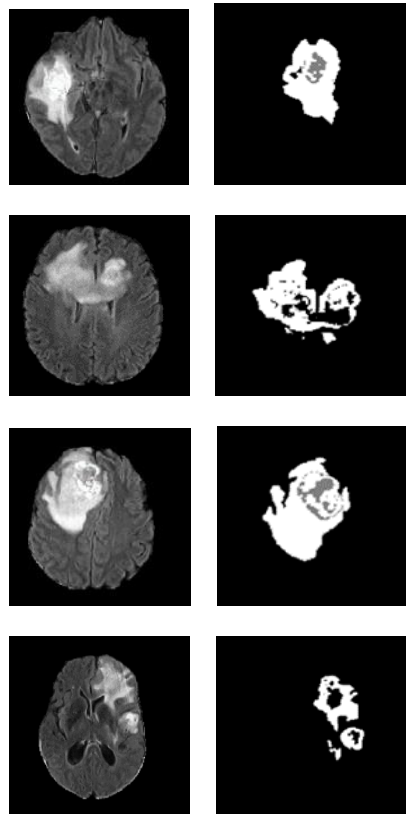

Fig. 4.Affected and the detected part

D. Patch Extraction and Regional Clustering

Statistical Region Merging (SRM) focuses on region merging techniques. It aims to propose a path and provide extensions to miscellaneous problems related to image segmentation. It considers different model for different region of time Series extension to miscellaneous problems related to image segmentation. The algorithm is used to evaluate the

values within a regional time and group them together based on the merging criteria, resulting in a smaller list and more number of information is collected and compared with the database and finally abnormality can be detected. Region based segmentation is a specific approach in which one seeks to construct surfaces by combining neighboring pixels according to a criterion of homogeneity.

E. Performance Evaluation

It can evaluate the performance to analyze the effectiveness of our proposed algorithm Accuracy metric is used to evaluate the performance of the system. It can be measured using truly classified pixels.
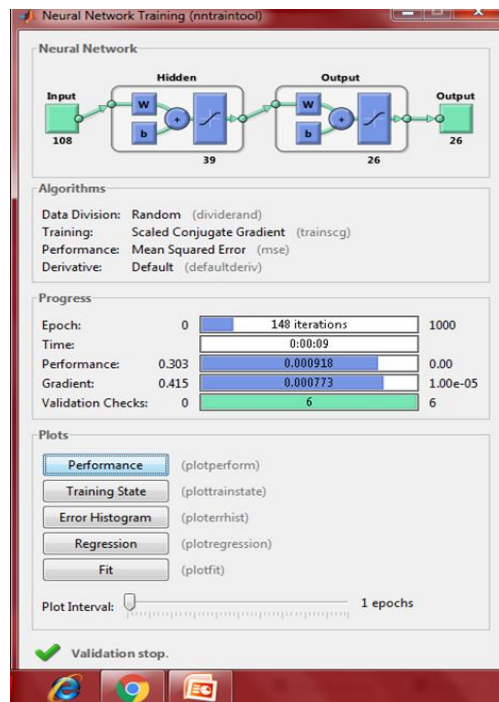
F. Testing

A test case is an asset of data that the system will process as normal input. The strategies that we have used in our project are, system testing, unit testing, integration testing, validation testing and acceptance testing.
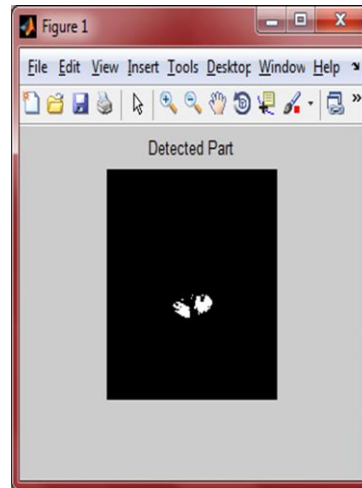
VII. Image Browsing
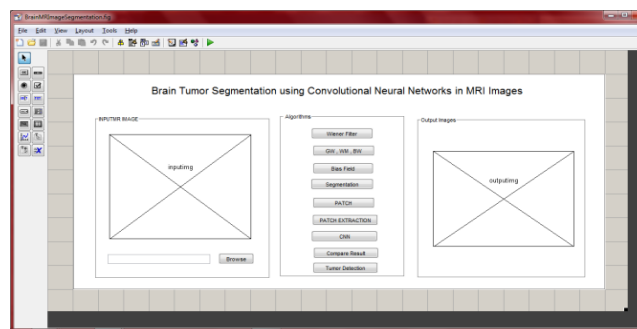
Fig. 5.Data Sheet Browsing

Fig. 6.Performance Sheet

Fig. 7.Detected Part

VIII. CONCLUSION

This project addresses few image processing methods for Brain Tumor by CNN algorithm. We define a segment as asset of objects sharing a specific interaction pattern among the dimensions. In addition, to propose CNN, an efficient algorithm for interaction-based segmentation. Our experimental evaluation demonstrates that the interaction-based cluster notion is a valuable complement to existing methods for clustering multivariate time series. CNN approach achieves good results on synthetic data and on real world data from various domains, but it cluster only the multivariate time series only so lot of in information loss and it not efficient to cluster the brain images especially results on EEG and fMRI data. So we propose to consider different models for different regions of the time series using statistical region clustering. We are also investigating in feature selection for interaction-based segmentation. By this experiment we finally compared our algorithm with the existing model's output to show our dominancy in our output. From segmentation with statistical region clustering can cluster the different brain region for gathering the more information. By comparing our final image with the numerous image which get involved in the data sheets for the exact location of the tumor detected part in the MRI image which we given. Here the statistical region clustering, it can be consider the different regions of brain and then cluster different brain region, and merging the cluster image with database image finally provide the result about the human being is normal or abnormal. Then provide diseases in brain images with improved accuracy rate.

IX. FUTURE WORK

In future work we can extend our work to implement this approach in advance 3D images and 4D images with improved segmentation algorithms to predict the neuron.

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