Tissue Fate Prediction in Acute Stroke based on MRI

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I. Method

A. Materials

The medical department of University of California, Los Angeles provided us with the anonymous perfusion and FLAIR imaging data. In this project, 18 patients who suffer from ischemic stroke were studied. 14 of these patients have lesions shown in their perfusion and FLAIR image. 4 of the patients do not possess lesion in their brain, and their images are considered as control group. For each patient, approximately two thousand perfusion images of his/her brain were obtained. More than 20 FLAIR images taken three days after patients' admission were used. All images contain unique timestamps and location information that separate them from one another. The dcm files also contain the thickness and size of images. Images are read into Jupyter Notebook using python pydicom package for future process. The label images are binary images, where ones indicate the area of lesions.

B. Image Process

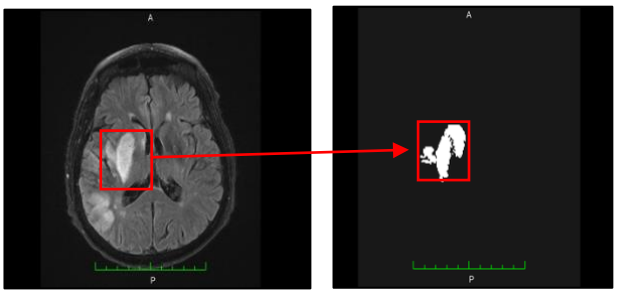

Fig. 1. One slice of sample brain FLAIR and label image (left) and ROI (right)

As a first step, we manually segmented the region of interest (ROI) to create 3D labels of the lesion regions in FLAIR images of all 18 patients using Horos, a DICOM medical image viewer computer software. Figure 1 is a sample of a slice of the FLAIR image of patient's brain, and the corresponding slice of label. The image on the right is a slice of the 3D ROI generated with Horos. By clicking on any pixel of an identified lesion region and adjusting the range of ROI, Horos automatically create 3D labels. Since FLAIR image removes cerebrospinal fluid signals, regions of lesion are much easier to identify. According to our online research and help from Dr. Scalzo, Fabien, we concluded that lesion labels are identifies based on mainly two characteristics: firstly, images of brains that suffer from lesion show asymmetrical white images. As shown in the sample figure, lesion regions are the white areas. Furthermore, lesion areas, in light grey or white, are in large contrast with other healthy parts of the brain which are in dark grey. For those patients who do not suffer from lesion, we created all black 3D images to conform with the others. The outputs of all labelling are series of dcm format images.

To process the image more easily, we first changed all dcm files to numpy arrays, and each cell in the array is either 0 or 1. Then we encountered a problem that the sizes of all images and labels generated from Horos do not conform in shape. It was an obstacle because in order to use Convolutional Neural Network (CNN) to train and predict the outcomes, we have to have inputs of same shapes, otherwise CNN will not work. So we firstly tried to fix the size of labels in Horos, yet this approach did not seem to be possible due to different shapes of the flair image. As a second approach, we used opencv package in python to resize all numpy arrays to 128 * 128. The shape of some slices is not square, so the slices are padded with zeros to be square shape. Also, the slices that are not in shape 128 * 128 are reshaped to 128 * 128. Since all images are of different number of slices, we chose to first test on four series of

images that have the same number of slices using Convolutional Neural Network (CNN) with package keras via Sequential form. Keras is a neural network library written in python that runs on top of TensorFlow, and allows fast experimentation with deep neural networks, which is exactly what we needed.

After testing four series of images that have the same dimensions, in order to achieve better results, we have also tried to utilize all the data, since the number of patients is quite small. So as a second approach to fix the problem of differently sized images, in particular, we compressed and reshaped all 18 patient's perfusion data into 18 tensors, each has a size 45 * 12 * 92 * 92. For the shapes that are multiples of 45, we compress the images directly; for those that are of shape 90, we took the average of two slices to downsize to 45; as for those of shape 50, we directly removed the first three slices and the last two slices. This should not affect the content itself since the affected areas are around center of the brain. So the labels and brains are centered in the middle as well. However, this approach is proven to be unsuccessful since loading the datasets of all 18 patients at once requires too much RAM, so we decided to go with the previous approach.

C. Methods

1) Classification & Segmentation

In the first approach, we tried to use machine learning methods to classify the patients based on the perfusion images to two categories: having lesions (marked as 1) and not having lesions (marked as 2). More specifically, the image classification methods we have used include: Neural Networks, Random Forests, Decision Trees, Multivariable Regression, and Support Vector Machine. After the classification, for those patients that are classified as having lesions, we use the active contour methods to segment out the lesion region on their flair images. Segmentation is the process of separation of required information from a data for future processing. In this case, we are separating the lesion region to mark them. To realize the classification methods, we used the scikit learn package and the keras package. And, to realize the active contour methods, we used the active contour functions from the scikit image package.

2) Convolutional Neural Networks

The second approach is to use Convolutional Neural Networks (CNN) to output the lesion region directly. The CNN is constructed by Keras Sequential model. The model layers and parameters are shown in TABLE I.

TABLE I. CNN LAYERS AND PARAMETERS

Layer (type)	Output Shape	Param #
conv3d_1 (Conv3D)	(None, 15, 26, 128, 128)	6015
max_pooling3d_1 (MaxPooling3	(None, 15, 26, 64, 64)	0
conv3d_2 (Conv3D)	(None, 25, 26, 64, 64)	3025
dropout_1 (Dropout)	(None, 25, 26, 64, 64)	0
up_sampling3d_1 (UpSampling3	(None, 25, 26, 128, 128)	0
conv3d_3 (Conv3D)	(None, 1, 26, 128, 128)	26

Total params: 9,066
Trainable params: 9,066
Non-trainable params: 0

The model is complied with optimizer: Adam, loss function: binary cross entropy and metrics: accuracy. The accuracy of the final model achieved 99.10% after 6 epochs training with random seed set to 1337. The input of the model is a 4D numpy array (time*height*length*width), and the output of the model is a 3D numpy array (height*length*width). Then the model is used to predict the ROI by using the Perfusion imaging data from patients.

II. RESULTS/EXPERIMENTS

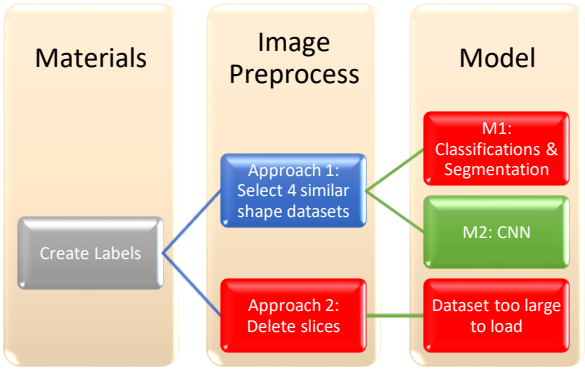

Fig. 2. Experiments and final design

A. Testing Result

Figure 2 shows all approaches that we took and experiments we tested. Red blocks mark the approaches that did not work as expected. All the results for classification methods are not very good. The accuracy was indeed nearly 0. We suspect that this is due to the fact that the number of patients is very small, but general machine learning classification models are only more practical for larger datasets. Therefore, the first approach (classification first, then apply active contour method for lesion segmentation) fails to achieve the ideal result.

In the second approach, where we use Convolutional Neural Networks to find the lesion's region of interest directly, the result of experiment with data of only four patients indeed provides the highest accuracy of 99.10%. Then, we used matplotlib to plot a predicted output 3D numpy arrays, and the sample result and labeled data are shown in Fig. 2 below.

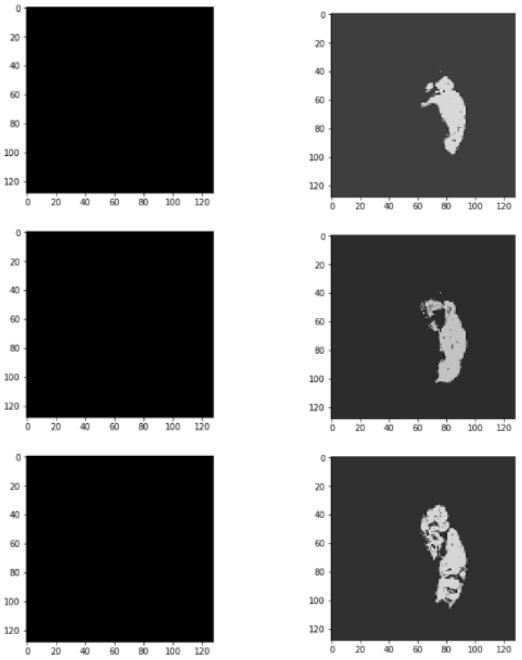

Fig. 3. Predicted output (left) with accuracy 99.10% model and labeled data (right)

B. Evaluation

Overall, our result is not as good as we expected. For the first approach where we used various machine learning methods to predict the result and then try to segment lesion regions, we aborted this approach due to extremely low prediction accuracy of the outcomes.

Although the accuracy of the model is high, the best evaluation method is to output the predicted result image and compare it with the corresponding label image in the dataset.

We noticed that although the accuracy of the model is very high, the predicted output image is almost black, which means that the real accuracy is very low, shown in figure 2 above. We consider that it is caused by too many black pixels in the labeled image. However, when the accuracy of the model is low, some pixel segments appear in the predicted output image. We consider that when the accuracy is low, the ROI can be retained more because the model does not fit the black pixels sufficiently, but the prediction results with smaller actual bias are obtained. On the other hand, although the predicted labels seem too small compared to the real ones, these outputs show potential locations where lesions are most likely to occur.

C. Conclusion

The data of four patients are still too small to generalize the model. However, the bigger problem is that the black area of the labeled image is too large for the model, although the accuracy measurement of the model is very high.

III. Discussion And Future Work

When we found that the output is large black area, we tried to track the performance changes of the model training, so the model of first epoch with accuracy 96.67% was used to predict the data. The sample result and labeled data are shown in Fig. 3 below.

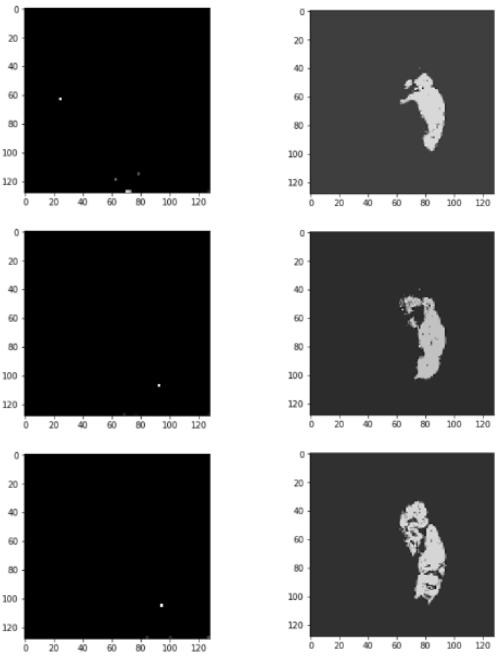

Fig. 4. Predicted output (left) with accuracy 96.67% model and labeled data (right)

Therefore, from the output, we can reasonably suspect that the model fits too many black pixels. Because when the model is not fully fitted, the model can output some white pixel fragments instead.

From the evaluation and observation above, we noticed the accuracy of the model cannot properly indicate the actual accuracy of the prediction results. Considering the characteristics of the labeled image, that is, it contains a large number of black pixels, which has a great misleading effect on the training of the model. The large number of black pixels in the labeled image makes the model tend to predict more

black pixels, which results in a large bias of the model prediction.

Moreover, the convolution and pooling in CNN will further increase the number of black pixels, which may lead to a large loss of ROI information. Therefore, when using CNN, we should consider that the convolutional kernel should not be too large and the pooling size should not be too large to retain more information of ROI.

Considering that there are too many black pixels in the labeled image, large bias may be avoided if the white pixels in the labeled image have higher weights than the black pixels or add penalty weight to black pixels while training the model.

ACKNOWLEDGMENT

Thanks to Dr. Scalzo, Fabien for his help with ideas on preprocessing the imaging data and his teaching of deep learning algorithms, especially on Convolutional Neural Network. We also want to pay special thanks to medical department of University of California, Los Angeles for providing us with the anonymous perfusion and FLAIR MRI images.

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