Final Report – AI for Medical Imaging

Pathological complete response (pCR) classification: Implement and fine-tuning machine learning or deep learning model to predict pCR by using MRI_1 only

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Abstract

For project 1, there are two main targets: pathological complete response (pCR) prediction and recurrent free survival (RFS) prediction based on MRI_1 only by using deep learning and machine learning model. My goal is pCR prediction by using MRI_1 only. In this paper, I selected the T1-axial modalities at T_1 time point. After that, 3D Resnet is applied to predict the pCR status of patients. Because of lack of data, we apply augmentation and transfer learning to increase the number of samples, reduce the overfitting and get 69.23% on test dataset.

Introduction

Pathological complete response (pCR) is defined as disappearance of all invasive cancer in the breast after completion of neoadjuvant chemotherapy, although some authors require clearance of residual disease in axillary nodes as well (von Minckwitz et al., 2012). pCR can be used to evaluate the ability of response to treatment for breast cancer patient after surgical biopsy of patients. For this project, I will consider only MRI_1 in dataset (the MRI of patient starting anthracycline-cyclophosphamide chemotherapy described in Figure 1), which is the T1 magnetic resonance imaging (MRI) modality took from soonest date of each patient; after that, axial type of MRI of each patient are chosen for pCR prediction. The method for data selection will be described in the later section. For classification, 3D ResNet architecture is applied to predict the pCR status of each patient.

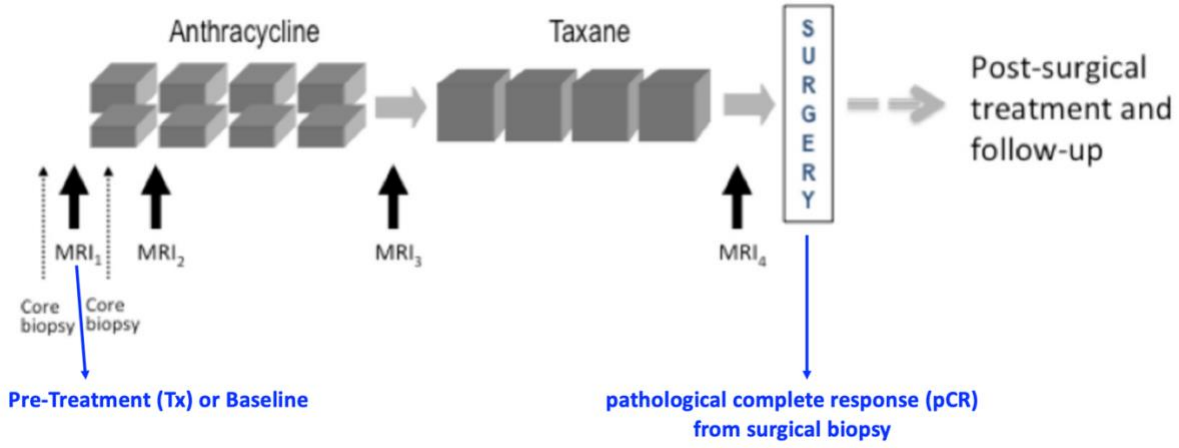

Figure 1: Pipeline for breast cancer treatment

Dataset

For this project, ISPY_1 dataset is used to predict pCR status for breast cancer patient. For original size of dataset, there 222 patients in total and each patient have MR image from different time point described in Figure 1. The total images of dataset are 386,528 images. Because of using only axial MRI_1, T1 modalities in dataset, I select 61 patients in total patients from original dataset to train and evaluate the model. T1 axial modalities are each for each patient. The pCR status of this task is binary classification containing 1 and 0 values for labeling. Furthermore, three of 61 selected patients (1078, 1094, 1152) has 2 axial MRI_1 in the T1 time point; therefore, I divide them in 6 different patients but having the original label. All the selected patients are saved on pCR_status_2.csv and df_final in attached file and source code file, respectively.

```
In [23]: df_final.head()
```

Out[23]:

	SUBJECTID	PCR	Paths
0	1001	0	/media/linh/hdd4TA/ISPY1/manifest-PyHQgfru6393...
1	1002	0	/media/linh/hdd4TA/ISPY1/manifest-PyHQgfru6393...
2	1003	0	/media/linh/hdd4TA/ISPY1/manifest-PyHQgfru6393...
3	1008	0	/media/linh/hdd4TA/ISPY1/manifest-PyHQgfru6393...
4	1009	0	/media/linh/hdd4TA/ISPY1/manifest-PyHQgfru6393...

Figure 2: Selected data for training and evaluating

Here is the example of some slices from MR image of axial T1 modality from ISPY_1 dataset. The example is shown below.

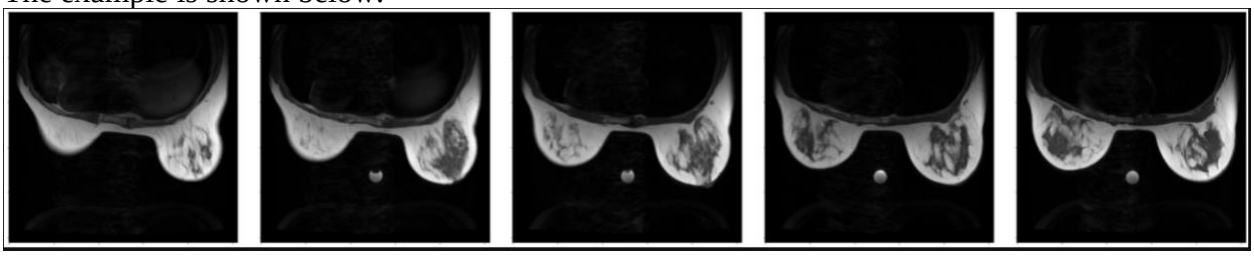

Figure 3: The example of axial MRI_1 T1 from ISPY_1 dataset

Method

Data selection and pre-processing data

Data selection

As I described in previous section, only MRI_1, T1 modalities are chosen for this task by using DICOM header. Pydicom package are used to read the DICOM header. Firstly, I only choose the first date of each patient. After that, depending on the DICOM header, tuple values are utilized to choose T1 time point, T1 modality and the axial type of MR images. All the tuple values are shown in the Figure 3 below.

```
2.000000-T1-axial-locator-51186
(0012, 0050) Clinical Trial Time Point ID        LO: 'T1'
(0018, 0080) Repetition Time                     DS: '500.0'
(0018, 0081) Echo Time                           DS: '14.0'
(0020, 0037) Image Orientation (Patient)         DS: [-1, 0, 0, 0, -1, 0]
(0020, 0032) Image Position (Patient)            DS: [160, 160, 80]
```

Figure 4: Tuple values for choosing data

In detail, the value of repetition time and echo time are used to choose the T1 modality because the value of T1 modality is much less than T2 modality, which could mainly be 500 and 14, respectively. Then, the axial type depends on the Image Orientation. The normal value for axial

type is [-1, 0, 0, 0, -1, 0] as shown in Figure 3. Based on these results we can choose 61 patients which satisfy all these requirements.

Pre-processing data
After selecting the data, I separate them into 3 sub-data: training data, valid data and test data as ratio shown in source code. The model is required input having the same dimension; therefore, I resize all the data samples to 15*256*256 for depth, height, width respectively.

Lack of data is critical problem in medical field, especially when only using MRI_1, T1 modality for prediction; therefore, augmentation is applied to increase the number of samples for training. In this project, some basics argumentation techniques such as adding noise or changing the affine in the original MR image.
All the MR images are standardized with mean, standard deviation and normalized in range of minimum and maximum of voxel values.

Training model
3D ResNet is applied to predict the pCR status of patients. In this project, I use 2 types of 3D ResNet: resnet18 and resnet34. For both of model, there are 4 layers but having different basic block of each layer. While Resnet18 has 2 basic blocks of each layer, the Resnet34 has [3, 4, 6, 3] blocks of each layer from 1 to 4, respectively. The detail of model is described in the source code. The model is pre-trained in ImageNet dataset. The resnet34 model is shown in Figure 4 as below.

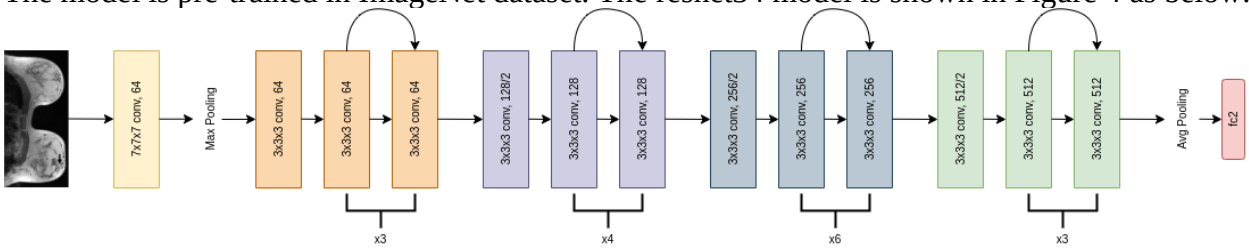

Figure 5: Architecture of 3D Resnet in this project. For each basic block, batch norm and ReLU activation function are used after each convolution block (3dconv)

Adam optimizer and cross entropy loss function is applied to train this model. Accuracy is the evaluation metrics to evaluate the effectiveness of the model. The accuracy is calculated by the number of correct predictions over total number of samples. The model is trained in 100 epochs on GTX 2080Ti.

Result

ResNet34 model predict the best result on validation and test dataset as shown in below table.
The result is evaluated on 11 and 13 samples on valid and test dataset respectively because lack of data sample for MRI_1, T1 modalities. The result is based on ResNet34 model.

Dataset	Loss	Accuracy
Valid dataset	0.293	81.82%
Test dataset	1.218	69.23%

Figure 6: Result table by ResNet34

Conclusion

Because the number of samples is too small, the model cannot be generalized and easy to get overfitting problem. In the future, more data samples need to be included for model to learn and we can apply more techniques to increase the number of samples. Lack of data is the critical problem for medical field. Through this project, I understand more about the MR image and how to read the DICOM header and metadata. Furthermore, I can build the simple model and know how to use the argumentation to handle with small number of data problem. I will develop this project more in the future with more complicate model and handle the data effectively.