

RSNA-MICCAI Brain Tumor Radiogenomic Classification Review

1. Introduction

This project is about the classification and prediction of Gliomas, which is a really vital task in the process of tumor treatment. As we all know, malignant tumors in the brain are a life-threatening condition. Glioblastoma is the most common form of brain cancer in adults and the worst prognosis, which patients only can survive less than one year. Glioma is the most common and aggressive malignant primary tumor of the central nervous system in adults. Therefore, accurate classification of gliomas is of great significance for treatment. However, manually detecting and tracking tumor sub-regions is verbose, time-costing, and subjective. In a clinical setting, this manual process is performed by the radiologist in a high-quality visual process, so it becomes less practical when dealing with a large number of patients. For example, radiologists may make some wrong decisions when classify so many real patients' samples. These wrong decisions may have terrible effects on patients and even lose their lives. This situation highlights the need for automated segmentation solutions that can benefit in this process.

Recently, the appearance of a specific genetic sequence in the tumor known as MGMT promoter methylation has been shown to be a favorable prognostic factor and a predictor of responsiveness to chemotherapy. What's more, genetic analysis of cancer requires surgery to extract a tissue sample. Then it can take several weeks to determine the genetic characterization of the tumor. Depending on the results and type of initial therapy recommended, a subsequent surgery may be necessary. If an accurate method to predict the genetics of the cancer through imaging alone could be developed, this would minimize the number of surgeries and perfectly refine the type of therapy required.

The Radiological Society of North America (RSNA) and the Medical Image Computing and Computer Assisted Intervention Society (the MICCAI Society) has improved diagnosis and treatment planning for patients with glioblastoma. In this project I will predict the genetic subtype of glioblastoma using MRI (magnetic resonance imaging) scans

to train and test Neural Networking model to detect for the presence of MGMT promoter methylation.

From this project, I will learn how to use Machine Learning to help brain cancer patients receive less invasive diagnoses and treatments. The introduction of new treatment strategies before surgery has the potential to improve the management, survival, and prospects of patients with brain cancer. Maybe this method is not always perfectly useful in clinical situation, but it must promote the tumor diagnoses and treatments. What's more, it will bring more courage and hope to patients to support to overcome the Grim Reaper-Gliomas. Of course I know that I cannot heal whole world. However, if I can put what I have learned from books into real world and make some difference for tumor patients, I would feel comfortable. This is the most meaningful part of this project.

2. Method

In my opinion, this project is a Computer Vision Problem, which is my favorite aspect in Machine Learning. We need data to train our model and load model on test data to make sure that our model is useful in real situations. And after searching on Internet, now I have a outline of this project.

2.1 Data processing

Firstly, for Image-data, we should remove some noise data that we don't need to deal with. If so, our workload would be reduced and the model we trained would be more pervasive and universal for more patients. There are some ways to do that, filtering algorithm, sparse representations algorithm, Low-rank clustering and so on. Here, I will use some filtering algorithms. Before noise data reduction, we also need to crop and resize these image-data. That's because sometimes we don't need to analyze whole picture, just the core picture is enough. In this project, we only need to analyze the location where tumors are, which means we can cut off edges of images to focus on core pixels that represent all tumors. And then resize the cropped image, now we get a enlarged image data that is convenient for us to analyze.

2.2 Neural Network Choosing

In CV problems, researchers often choose CNN to work. Here, I will also choose CNN as my Neural Networking. For CNN, there are some key

parameters that we need to consider and choose carefully. For example, if epoch and learning rate are too small, the results would be too terrible to use for classify or prediction. Other parameters are also very important. We need to set and choose them properly. Luckily, with the help of Keras.applications, we can load pre-trained model with pre-trained weights on ImageNet. This will reduce our workload. Because so much data that we need to deal with, ResNet will bring us a lot of convenience. And ResNet50 is a proper model.

2.3 Key Matrix Creating

In the Transfer Learning part, we will not train the ResNet50 model, but will only calculate the prediction for each image of each patient sequence. Therefore, we will obtain the model weight matrix for each image. Finally, we will create a global matrix that combines the ResNet50 sequences that predict all patient matrices.

2.4 Classification Choosing

Long short term memory (LSTM) is a recurrent neural network (RNN) architecture (an artificial neural network). Unlike traditional RNNs, a LSTM network is well-suited to learn from experience to classify, process and predict time series when there are very long time lags of unknown size between important events. This is one of the main reasons why LSTM outperforms alternative RNNs and Hidden Markov Models and other sequence learning methods in numerous applications. Hence, LSTM is widely used for data involved in time series.

2.5 Test and Predict

After all the pre-work has been done, now we can create matrices for the test set and make predictions on the test patients.

Reference

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