**Deep learning for survival time prediction of brain tumor**

**Introduction**

Medical images are one of the most important resources used by doctors to diagnose brain tumors, and a tool with high accuracy to automate this process can be extremely valuable. In recent years, interest in designing tools for diagnosing brain tumors has been increasing. However, past research on brain tumor were focusing on using the image processing and machine learning techniques to extract features from MRI records to diagnose the tumor itself. For example, Evangelia and colleagues conducted a machine learning scheme study to classify brain tumor type and grade [1], and [Lavneet](http://link.springer.com/search?facet-author=%22Lavneet+Singh%22) *etc.* studied the early detection of brain abnormalities based on machine learning [2]. Few studies have been conducted in relation to assessment of the potential association between clinical data, DNA mutations and the extracted features. In the United States the average 5-year survival rate is 33%, which is relatively low compared to other common cancers such as colon cancer (61.7%), rectum cancer (62.6%), ovary cancer (55.0%) and kidney and renal cancer (61.8%) *etc.* In addition, past research have found that some DNA mutations (EGFR, IDH1, IDH2, PTEN, PT 53 *etc.*)are positively related to brain tumor. Actually these associations above are important because they can not only reflect the effects of therapy, but also provide directions and inspiration of future diagnosis and treatment.

In our project we extracted the most important and discriminating features from the preprocessed images and then predicted the survival time and gene mutation of patients with brain tumor. To investigate the association, we used deep learning, specifically, convolutional neural network as our primary method. A convolutional neural network is a type of feed-forward artificial neural network where the individual neurons are tiled in such a way that they respond to overlapping regions in the visual field. It is inspired by biological processes and variations of multilayer perceptrons, which are designed to use minimal amounts of preprocessing. Such architecture allows it to take advantage of the 2D structure of input data. Thus in comparison with other deep architectures, convolutional neural networks have superior results in image analysis, so we decided to apply it to our project. In the following sections we first introduce our data source and pre-processing, and then describe the method and data analysis we conducted. Then we present our results and related graphs in the results section. In the last part we discuss our advantages and several limitations of our project, and describe some our thoughts about this project.

[1] Zacharaki EI, Wang S, Chawla S, et al. Classification of brain tumor type and grade using MRI texture and shape in a machine learning scheme. *Magnetic resonance in medicine : official journal of the Society of Magnetic Resonance in Medicine / Society of Magnetic Resonance in Medicine* 2009;62(6):1609-1618. doi:10.1002/mrm.22147.

[2] Singh, L, Chetty, G, Sharma D et al. A novel machine learning approach for detecting the brain abnormalities from MRI structural images. 7th IAPR International Conference, PRIB 2012, Tokyo, Japan, November 8-10, 2012.

**Results**

After data cleaning, in the survival prediction model 133 cases were applied to the analysis. We then randomly chose 90 from them as our training data, 20 as validation data, and 23 as test data. In the construction of convolutional neural network, we tested several parameters, and in the final model we chose 4 as our model layers size, 100 as epoch number, [40, 100] as kernels number, [16, 16] as kernel size, and [4, 4] as pooling size. The validation errors and test errors results of our convolutional neural network model are 35.0% and 40.0%, respectively. To compare the speed of CPU and GPU, we also produced a chart that is shown below.

**Comparison of calculation Speed between CPU and GPU**

Likewise, in the gene mutation prediction model 59 cases were applied to the analysis. We then randomly chose 40 as our training data, 9 as validation data, and 10 as test. In the final model we chose 4 as our model layers size, 100 as epoch number, [10, 30] as kernels number, [16, 16] as kernel size, and [4, 4] as pooling size. The validation errors and test errors results of our convolutional neural network model for EGFR mutation are 12.5% and 30.0%, and for IDH1 mutation are 12.5% and 10.0%, respectively. However, for the three other gene mutations, we found that the validation error and test error were close to 0, which implied that we might have some bias or errors on the choose of parameters in the analysis, and in the future work we may consider to explore such effects on our results.