Radiogenomic Analysis of Glioblastoma with Deep learning Techniques

Progress Report 2

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1 Brief Overview

1.1 Basic Glioblastoma Information

Glioblastoma (GBM) is a highly aggressive adult brain tumor and the deadliest brain tumor that originates in glial cells, and in some rare cases intracranial glioblastomas have very small chance of transfer to the spine via cerebrospinal fluid. Gliomas such as glioblastoma have long been thought to originate in glial cells due to the similarities in the immunostaining of glioblastomas and glioblastomas. Recent studies have shown that astrocytes, oligodendrocyte progenitor cells and neural stem cells can also serve as cells of origin. In addition, several studies have shown that specific patterns of genetic alterations shape the clinical features of brain tumors, leading to a rapid increase in the use of these patterns for classification and diagnostic purposes in recent years. Gliomas are characterized by uncontrolled cell proliferation, diffuse infiltration, resistance to apoptosis, and genomic instability. The tumorigenesis mechanism of glioblastoma remains unclear, and many patients relapse due to ineffective treatment options. Clinical data suggest that glioblastoma has a poor prognosis, with less than 5 percent of patients surviving five years after diagnosis.

1.2 Subtypes of Glioblastoma

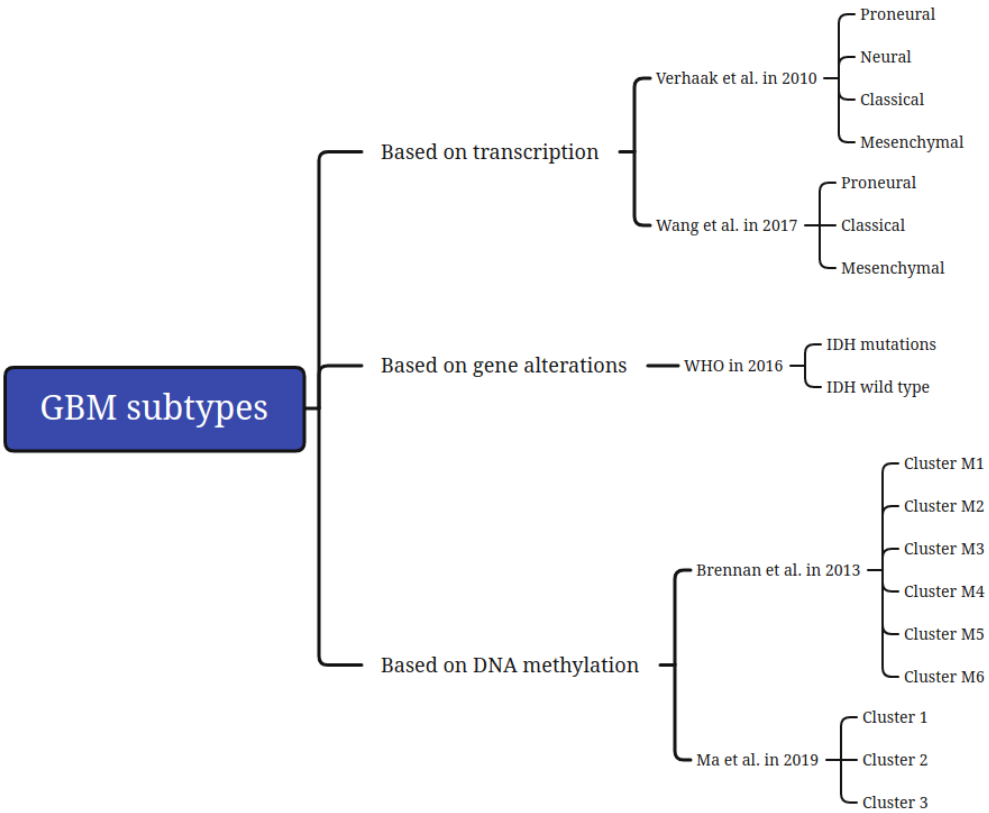


Figure 1: GBM Subtypes

Glioblastoma can be divided into different groups in the molecular level by three main methods, based on the transcription, based on the gene alterations and based on the DNA methylation. Different subtypes will have really different features. Furthermore, due to glioblastomas exhibit a high degree of heterogeneity in both space and time, molecular-level diagnosis, patient stratification, and personalized treatment are increasingly important.

1.3 Why Radiogenomic Analysis is Important for Glioblastoma

Glioblastomas exhibit a high degree of heterogeneity in both space and time. The presence of distinct genetic subgroups in glioblastoma enables this tumor to adapt to environmental forces. As a result, glioblastoma patients do not respond well to prescribed therapy because therapy targets the entire tumor rather than specific genetic sub-regions. Genomic alterations within tumors produce distinct radiographic phenotypes. In this regard, magnetic resonance imaging plays a key role in characterizing the molecular features of glioblastomas according to the regional variation and phenotypic presentation of the tumor. Radiogenomics has emerged as a new area of research to explore links between genetic alterations and imaging features. Radiogenomics offers many advantages, including non-invasive and holistic assessment of tumors and their response to therapy.

1.4 Radiogenomic Research Typical Workflow

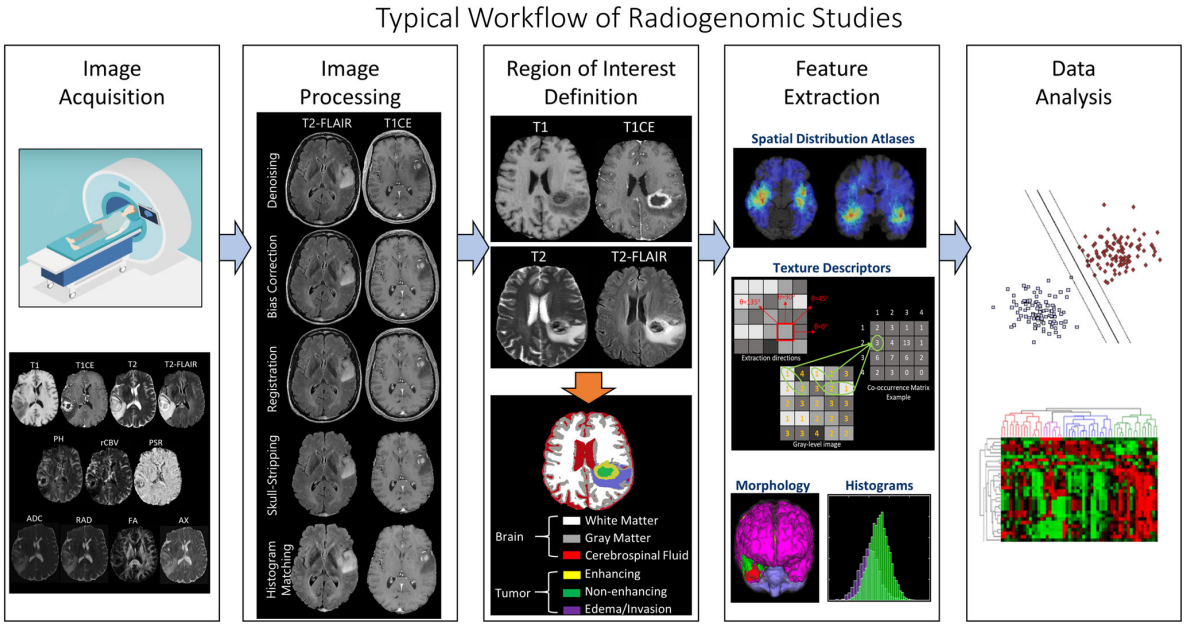


Figure 2: : Typical Workflow of Radiogenomics Research

Most existing radiogenomics studies aim to establish the relationship between tumor radiographic features (eg, tumor enhancement volume, degree of necrosis) and gene expression profiles or pathways. These exploratory studies are designed to lay

the groundwork for optimal study design, data collection, and analysis to help formulate relevant hypotheses for future research. Exploratory studies are aimed at finding relevant mutations that may give rise to unique radio logical phenotypes. Ideally, radiogenomics studies are designed based on the following systematic approach:1) image acquisition; 2)image processing, including noise/artifact reduction, intensity and/or orientation standardization, coregistration of the multiparametric MRI scans; 3) ROI definition using manual annotation or (semi-)automatic segmentation; 4) feature extraction based on human-engineered (conventional radiomics) or deep-learning approaches; and 5) data analysis, involving machine/deep-learning methods for feature selection, classification, and cross-validation. This project focus on last three steps, including ROI definition, also known as image segmentation, feature extraction and data analysis.

2 Current Progress

2.1 ROI Definition/Image Segmentation

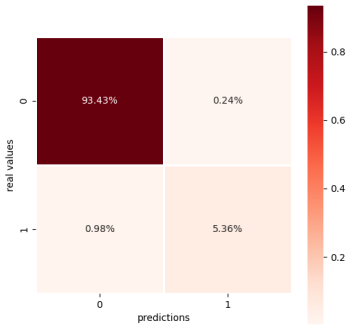
For GBM segmentation, there are four main types of methods, region-based approaches, edge-based approaches, classification approaches, altas-based approaches.

Both of them have typical and famous algorithms such as watershed segmentation is a famous region-based approaches, Fuzzy C-means is a famous unsupervised classification approaches and U-net is a famous supervised classification approaches. Meanwhile, absolutely, both of them have pros and cons, such as edge-based regions approaches are not suitable for automatic tasks, altas is not good for GBM because different GBM will be much different, the altas will be not very match-able to every patients' MRI.

For this procedure, we choose U-net to do the segmentation. We apply U-net to dataset from Ivy Glioblastoma Atlas Project. This dataset have 39 patients coding from W! to W2, each patients have different MRI series MRI images, such as T1, T2, T1Gd, FLAIR and so on. Case Western Reserve University (CWRU) make every patients' T1, T2, FLAIR MRI images into MNI standard and make annotations for them. Due to that, this prepossessing dataset made by CWRU will be used for our research.

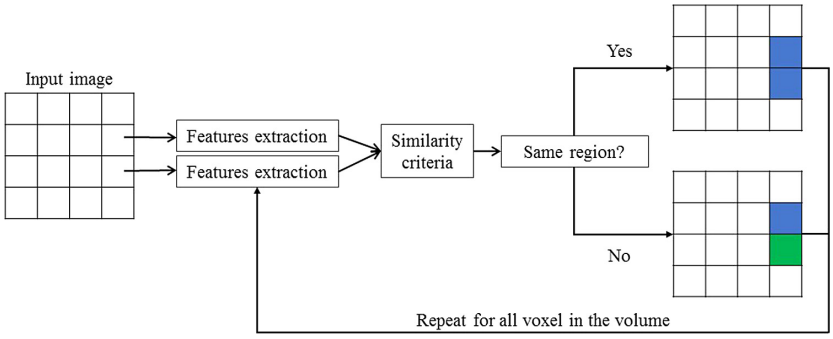
Till now, we apply all different MRI series image as single input into U-net, we get the results like that:

(a) Left: MRI Image, Middle: Ground Truth, Right: Predict Result

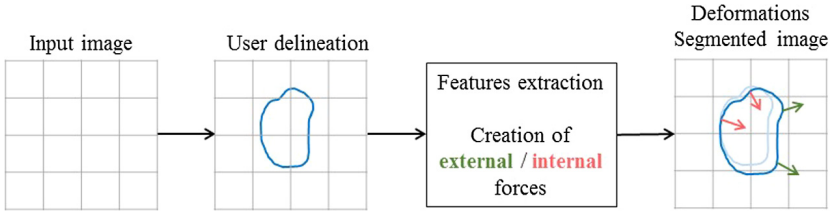


(b) ConfusionMatrix of Segmentation

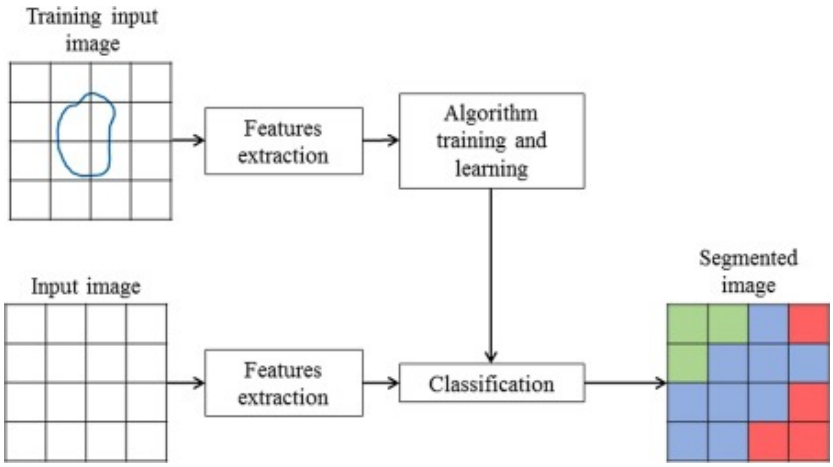
Figure 4: Segmentation Assessment



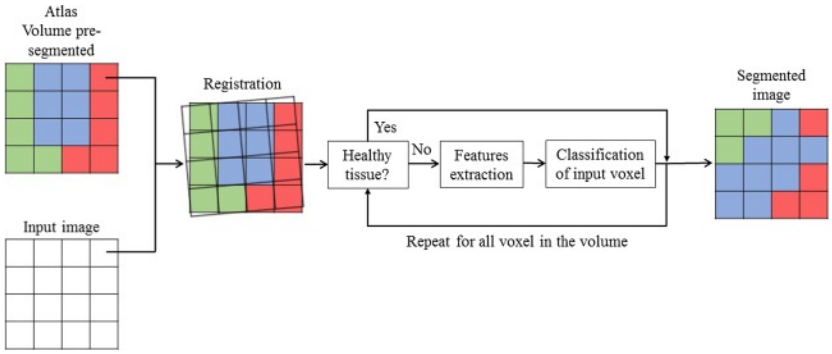
(a) Region-based Approaches



(b) Edge-Based Approaches



(c) Classification approaches



(d) Altas-based approcahes

Figure 3: Four main segmentation approaches for Glioblastoma

$$sensitivity = \frac{TruePositive}{TruePositive + FalseNegative}$$

The sensitivity of test dataset above 98%

On training processing, I don's store the sensitivity changing processing, so I can not generate the train processing monitor graph.

2.2 Feature Extraction

There are two main approaches for feature extraction: deterministic and nondeterministic extraction. For deterministic feature extraction, it is the most common method where a mathematical formula is employed to extract features relating to imaging features such as texture, intensity or shape(Figure 4). Currently, based on the literature review, texture features are one of the most important imaging features for the field of radiomics.

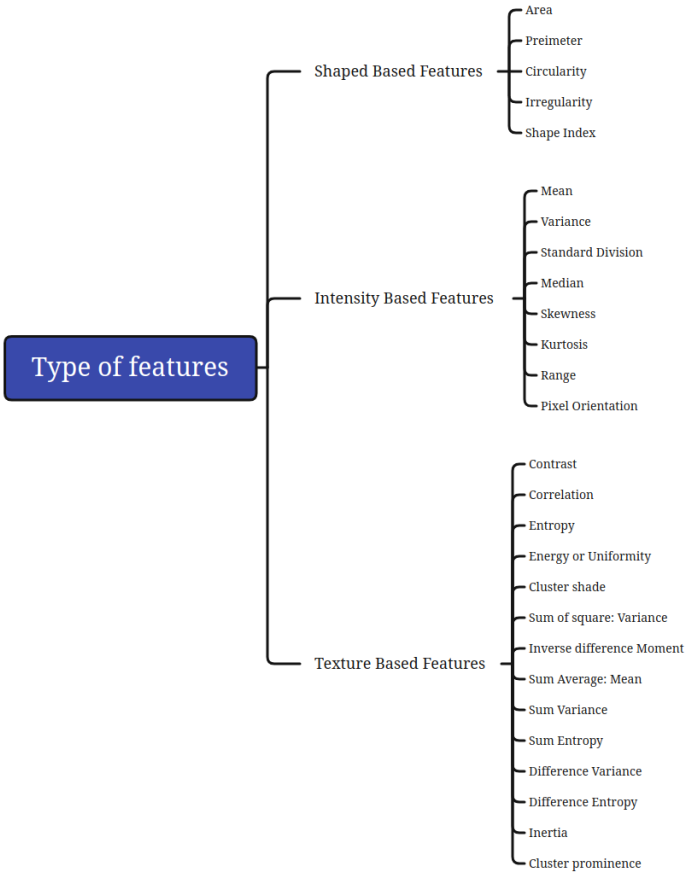


Figure 5: : Basic Classification of Features

In the beginning, I designed the image feature by coding by myself, you can see the code here:https://github.com/PinkR1ver/Image-Feature-Extraction. But design by own, the calculation speed is very low, we find the python module pyradiomics meant to do the feature extraction in the ROI.

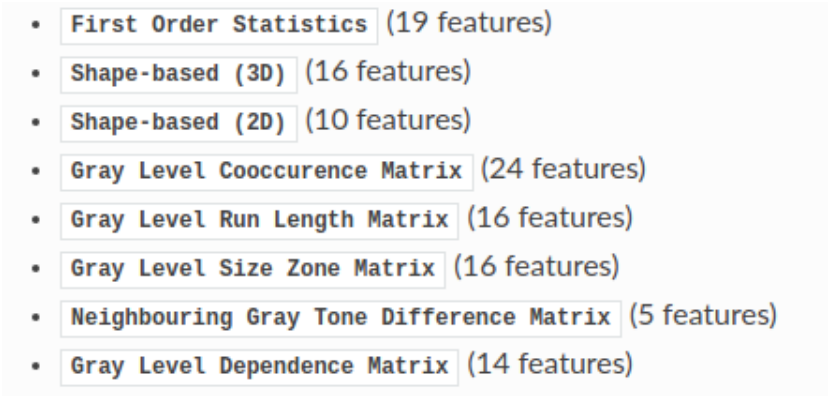


Figure 6: : Features in Pyradiomics

There are totally 120 features in Pyradiomics module, including intensity based features, shape based features and Texture based features. Texture features occupying the most features in the Pyradiomics module. The calculate texture features from gray level matrix(GLCM) and its advanced maatrix, such as GLRLM, GLSZM, GLDM and so on. GLCM is the most famous tool designed to calculate texture features, which is proven be useful.

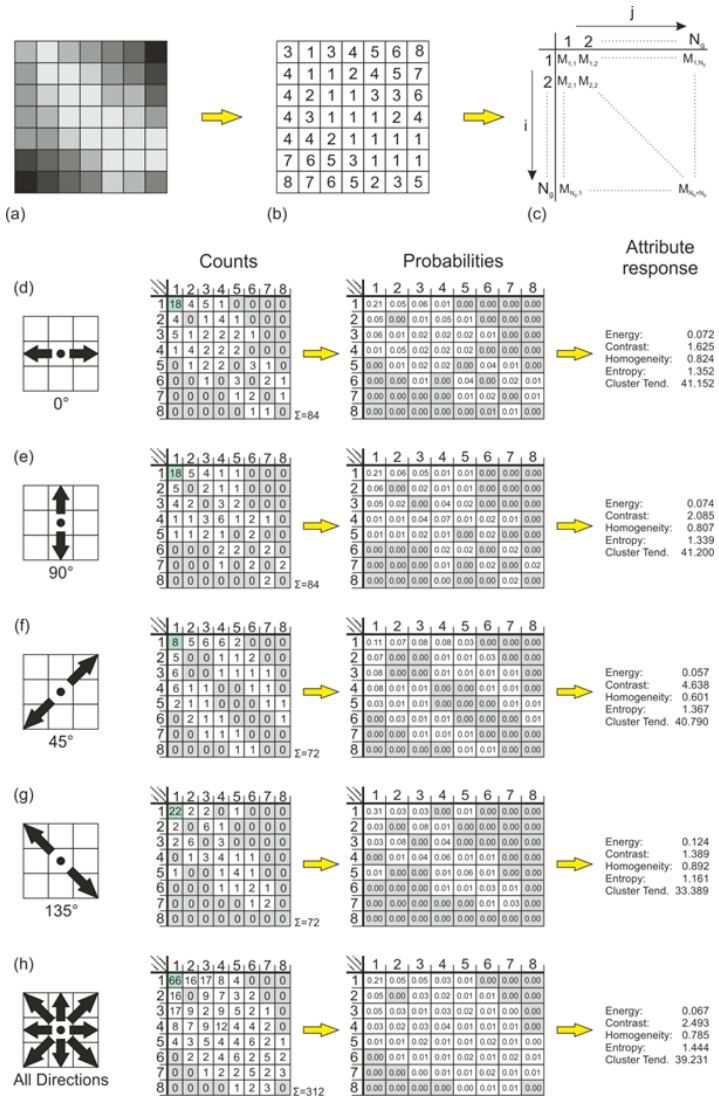


Figure 7: : Different Parameters to calculate GLCM

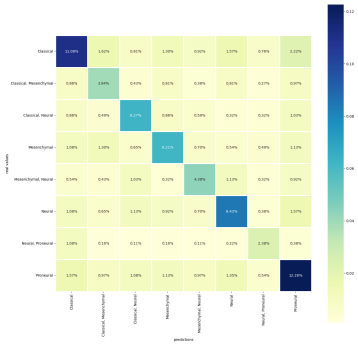
In this stage, we calculate every patients' features, which are with GBM subtype label, into a .csv file to prepare our data analysis.

2.3 Data Analysis

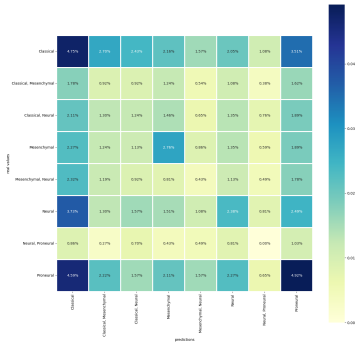
In this step, you can do lots of data analyzing to help doctor to treat GBM, such as predicting tumors' subtypes, predicting some genes' alternation or not, such as IDH or you can use regression to train model to predict specific gene expression number to generate gene expression profile.

Till now, we try to predict tumors' subtypes by using different algorithms such as Decision Tree, Random forest, SVM and Neural Network.

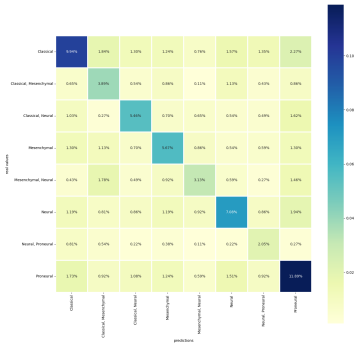
The all results I will attach in the last. There are some conclusions we can get from the result.



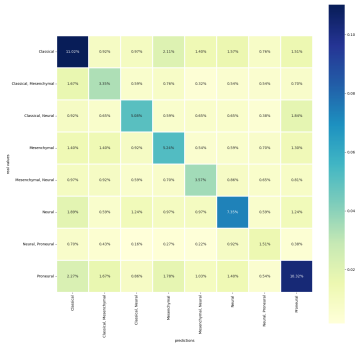
(a) ConfusionMatrix of Decision Tree algorithm, original data



(b) ConfusionMatrix of Decision Tree algorithm, data after PCA



(c) ConfusionMatrix of Decision Tree algorithm, normalize original data

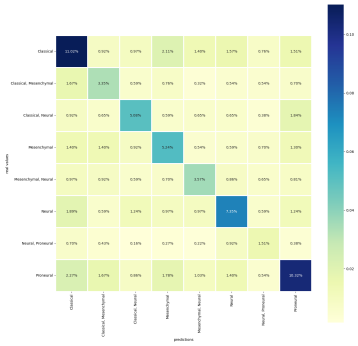


(d) ConfusionMatrix of Decision Tree algorithm, normalize principal components of the data

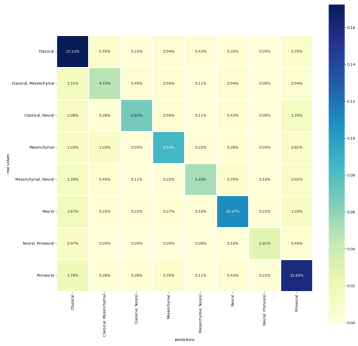
Figure 8: Assessment about PCA and normalize preprocessing before classification

Take decision tree algorithm's results as example, other algorithms are the same. You need to normalize data before you do PCA algorithm to your data. Specifically, normalize and PCA preprocessing are both bad for decision tree and random forest model, but normalize is very important for neural networks.

Compared each algorithms, we find that random forest and the neural networks are the best classifiers for this dataset prediction, the accuracy is about 78%, the highest sensitivity of each subtypes can be about 84%. There are two problems here: data imbalance and model overfit.

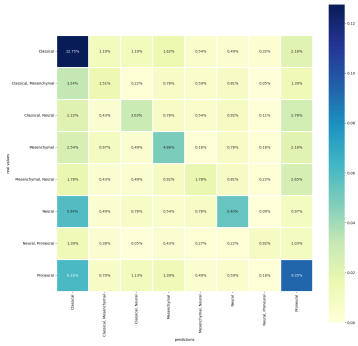


(a) ConfusionMatrix of Decision Tree



(b) ConfusionMatrix of Random Forest

(c) ConfusionMatrix of MLP

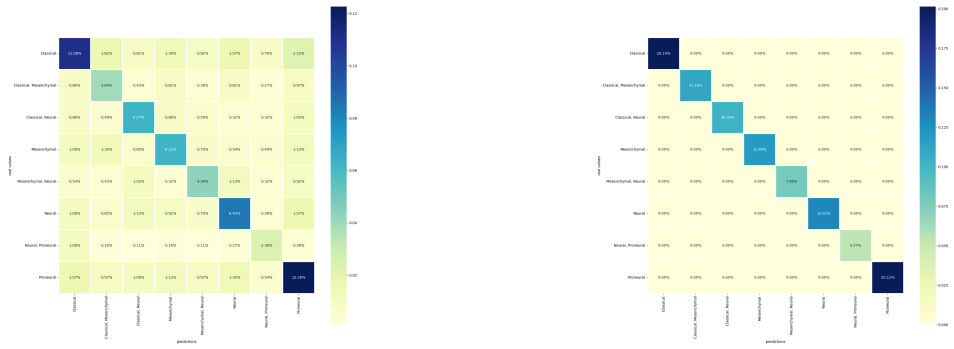


(d) ConfusionMatrix of SVM

Figure 9: Compared different classifiers, data both be normalized and PCA

Data imbalance means that classical and proneural type is the two most subtypes in the dataset, which can lead the classifier model have a force to predict the type to classical and proneural. And the results is also confirmed thisthe classical subtype and proneural subtype have the higher sensitivity, especially, the classical subtype, which occupying the biggest space in the dataset.

Model overfit means that model can work well in the train dataset, but bad in the test dataset, which is the most typical situation in the decision tree algorithm.



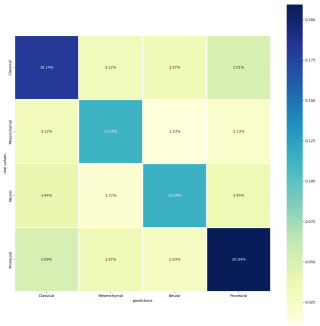
(a) ConfusionMatrix of Decision Tree in test dataset

(b) ConfusionMatrix of Decision Tree in train dataset

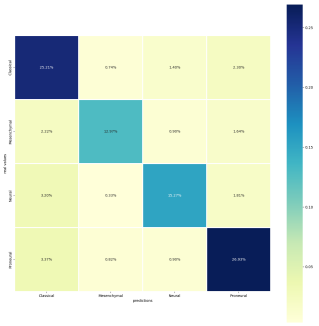
Figure 10: Compared Decision Trees on train dataset and test dataset

We can see that sensitivity in the train dataset can be all 100%, but in test dataset is just about 55%, which means decision tree really have a bad overfit here because decision tree is real sensitive to bad data. Random forest is a advanced algorithm to decision tree by sampling to generate different trees to classify to avoid overfit. In the figure 8, the random forest algorithms improve classifier accuracy from 55% to 78%. But the train dataset accuracy is still 100%. It's definitely still be overfitted, but no matter how much trees we added into random forest, the results can no be optimized, which is weird.

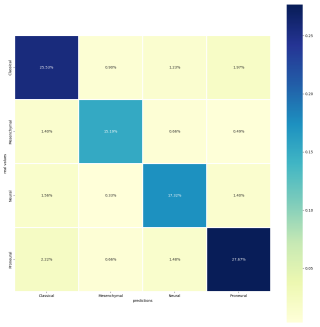
The classification types is still not reasonable here. Because the subtype actually just the subregion of the GBM. A patient can have different subtypes in different subregions of one tumor, so we label the subtype as a combination like (classical, neural) is very unreasonable. So we want to apply classifer just to the patients have one type to see the results.



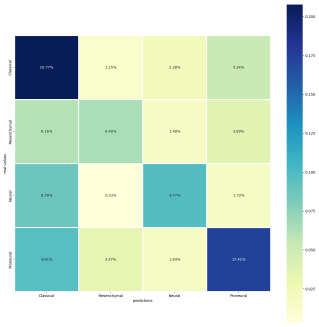
(a) ConfusionMatrix of Decision Tree



(b) ConfusionMatrix of Random Forest



(c) ConfusionMatrix of MLP



(d) ConfusionMatrix of SVM

Figure 11: Compared different classifiers to simplified dataset

After simplified dataset, the accuracy of classification improve from 78% to 88%. But the problem of data imbalance and model overfitting is still existing.

3 Next Plan

There are lots of improvements and different directions of data analysis.sub

3.1 Improvements

For segmentation, considering we use different MRI series as one single input, I don't think it will be a great way to train model, I will use one single MRI series picture to train specific model to detect the specific MRI series image. Meanwhile, we can also stack different MRI series picture in the axis=0 to make it a multi-channel picture to train the model, this can be helpful when we can obtain different MRI series pictures to do the segmentation.

For data imbalance leading to some subtypes' sensitivity are so high to affect whole model's accuracy problem, we can use data augmentation to solve. If we want to get better results, may be we can use GAN to produce data to do data augmentation.

For overfit problem, we need to try some optimizer methods to solve this problem. I think add dropout layer to MLP may solve this problem.

At last, the most interesting improvements for this project is to remake the whole procedures to make a end-to-end networks. Because extract features from ROI by human design will definitely loss information of the radiographic phenotypes, the end-to-end network may be a great improvements.

3.2 Another data analysis we can do

There are still lots of contents we can do for GBM radiogenomics, such as to predict the IDH mutation, to generate gene profile. We will make a more complex data analysis next stage.

4 Appendix

You can find all code here: https://github.com/PinkR1ver/Radiogenemics–on-Ivy-Gap

classification.txt

```
Decision Trees to original Data in TestDataset:
                        precision    recall  f1-score   support

             Classical       0.61      0.55      0.58       375
Classical, Mesenchymal       0.41      0.46      0.44       157
     Classical, Neural       0.54      0.58      0.56       199
           Mesenchymal       0.53      0.51      0.52       224
   Mesenchymal, Neural       0.50      0.48      0.49       168
               Neural        0.59      0.57      0.58       275
     Neural, Proneural       0.44      0.52      0.47        85
             Proneural       0.60      0.62      0.61       368

              accuracy                           0.55      1851
             macro avg       0.53      0.54      0.53      1851
          weighted avg       0.55      0.55      0.55      1851


Decision Trees to original Data in TrainDataset:
                        precision    recall  f1-score   support

             Classical       1.00      1.00      1.00       870
Classical, Mesenchymal       1.00      1.00      1.00       482
     Classical, Neural       1.00      1.00      1.00       445
           Mesenchymal       1.00      1.00      1.00       514
   Mesenchymal, Neural       1.00      1.00      1.00       345
               Neural        1.00      1.00      1.00       562
     Neural, Proneural       1.00      1.00      1.00       232
             Proneural       1.00      1.00      1.00       869

              accuracy                           1.00      4319
             macro avg       1.00      1.00      1.00      4319
          weighted avg       1.00      1.00      1.00      4319


Decision Trees to normalize Data in TestDataset:
                        precision    recall  f1-score   support

             Classical       0.58      0.49      0.53       375
Classical, Mesenchymal       0.35      0.46      0.40       157
     Classical, Neural       0.51      0.51      0.51       199
           Mesenchymal       0.46      0.47      0.47       224
   Mesenchymal, Neural       0.44      0.35      0.39       168
               Neural        0.54      0.48      0.50       275
     Neural, Proneural       0.29      0.45      0.36        85
             Proneural       0.55      0.60      0.57       368

              accuracy                           0.49      1851
             macro avg       0.47      0.47      0.47      1851
          weighted avg       0.50      0.49      0.49      1851


Decision Trees to normalize Data in TrainDataset:
                        precision    recall  f1-score   support
```

Classical	1.00	1.00	1.00	870
Classical, Mesenchymal	1.00	1.00	1.00	482
Classical, Neural	1.00	1.00	1.00	445
Mesenchymal	1.00	1.00	1.00	514
Mesenchymal, Neural	1.00	1.00	1.00	345
Neural	1.00	1.00	1.00	562
Neural, Proneural	1.00	1.00	1.00	232
Proneural	1.00	1.00	1.00	869
accuracy			1.00	4319
macro avg	1.00	1.00	1.00	4319
weighted avg	1.00	1.00	1.00	4319

Decision Trees to PCA Data in TestDataset:

	precision	recall	f1-score	support
Classical	0.21	0.23	0.22	375
Classical, Mesenchymal	0.08	0.11	0.09	157
Classical, Neural	0.12	0.12	0.12	199
Mesenchymal	0.22	0.23	0.22	224
Mesenchymal, Neural	0.06	0.05	0.05	168
Neural	0.19	0.16	0.17	275
Neural, Proneural	0.00	0.00	0.00	85
Proneural	0.26	0.25	0.25	368
accuracy			0.17	1851
macro avg	0.14	0.14	0.14	1851
weighted avg	0.17	0.17	0.17	1851

Decision Trees to PCA Data in TrainDataset:

	precision	recall	f1-score	support
Classical	1.00	1.00	1.00	870
Classical, Mesenchymal	1.00	1.00	1.00	482
Classical, Neural	1.00	1.00	1.00	445
Mesenchymal	1.00	1.00	1.00	514
Mesenchymal, Neural	1.00	1.00	1.00	345
Neural	1.00	1.00	1.00	562
Neural, Proneural	1.00	1.00	1.00	232
Proneural	1.00	1.00	1.00	869
accuracy			1.00	4319
macro avg	1.00	1.00	1.00	4319
weighted avg	1.00	1.00	1.00	4319

Decision Trees to PCA Normalized Data in TestDataset:

	precision	recall	f1-score	support
Classical	0.53	0.54	0.54	375
Classical, Mesenchymal	0.34	0.39	0.36	157
Classical, Neural	0.49	0.47	0.48	199
Mesenchymal	0.42	0.43	0.43	224
Mesenchymal, Neural	0.41	0.39	0.40	168

Neural	0.53	0.49	0.51	275
Neural, Proneural	0.27	0.33	0.29	85
Proneural	0.57	0.52	0.54	368
accuracy			0.47	1851
macro avg	0.44	0.45	0.44	1851
weighted avg	0.48	0.47	0.48	1851

Decision Trees to PCA Normalized Data in TrainDataset:

	precision	recall	f1-score	support
Classical	1.00	1.00	1.00	870
Classical, Mesenchymal	1.00	1.00	1.00	482
Classical, Neural	1.00	1.00	1.00	445
Mesenchymal	1.00	1.00	1.00	514
Mesenchymal, Neural	1.00	1.00	1.00	345
Neural	1.00	1.00	1.00	562
Neural, Proneural	1.00	1.00	1.00	232
Proneural	1.00	1.00	1.00	869
accuracy			1.00	4319
macro avg	1.00	1.00	1.00	4319
weighted avg	1.00	1.00	1.00	4319

Decision Trees to Normalized PCA Data in TestDataset:

	precision	recall	f1-score	support
Classical	0.21	0.22	0.21	375
Classical, Mesenchymal	0.06	0.08	0.07	157
Classical, Neural	0.11	0.11	0.11	199
Mesenchymal	0.13	0.13	0.13	224
Mesenchymal, Neural	0.08	0.07	0.07	168
Neural	0.15	0.12	0.14	275
Neural, Proneural	0.06	0.06	0.06	85
Proneural	0.27	0.29	0.28	368
accuracy			0.16	1851
macro avg	0.13	0.13	0.13	1851
weighted avg	0.16	0.16	0.16	1851

Decision Trees to Normalized PCA Data in TrainDataset:

	precision	recall	f1-score	support
Classical	1.00	1.00	1.00	870
Classical, Mesenchymal	1.00	1.00	1.00	482
Classical, Neural	1.00	1.00	1.00	445
Mesenchymal	1.00	1.00	1.00	514
Mesenchymal, Neural	1.00	1.00	1.00	345
Neural	1.00	1.00	1.00	562
Neural, Proneural	1.00	1.00	1.00	232
Proneural	1.00	1.00	1.00	869
accuracy			1.00	4319

```
            macro avg       1.00      1.00      1.00      4319
         weighted avg       1.00      1.00      1.00      4319


Random Forest to orginal Data in TestDataset:
                        precision    recall  f1-score   support

             Classical       0.71      0.81      0.76       375
Classical, Mesenchymal       0.67      0.65      0.66       157
     Classical, Neural       0.79      0.69      0.74       199
           Mesenchymal       0.80      0.71      0.75       224
   Mesenchymal, Neural       0.80      0.70      0.75       168
               Neural       0.78      0.84      0.81       275
     Neural, Proneural       0.86      0.67      0.75        85
             Proneural       0.77      0.82      0.80       368

              accuracy                           0.76      1851
             macro avg       0.77      0.74      0.75      1851
          weighted avg       0.76      0.76      0.76      1851


Random Forest to original Data in TrainDataset:
                        precision    recall  f1-score   support

             Classical       1.00      1.00      1.00       870
Classical, Mesenchymal       1.00      1.00      1.00       482
     Classical, Neural       1.00      1.00      1.00       445
           Mesenchymal       1.00      1.00      1.00       514
   Mesenchymal, Neural       1.00      1.00      1.00       345
               Neural       1.00      1.00      1.00       562
     Neural, Proneural       1.00      1.00      1.00       232
             Proneural       1.00      1.00      1.00       869

              accuracy                           1.00      4319
             macro avg       1.00      1.00      1.00      4319
          weighted avg       1.00      1.00      1.00      4319


Random Forest to orginal Data in TestDataset, adding tree numbers to 500:
                        precision    recall  f1-score   support

             Classical       0.71      0.81      0.76       375
Classical, Mesenchymal       0.68      0.66      0.67       157
     Classical, Neural       0.79      0.70      0.74       199
           Mesenchymal       0.83      0.75      0.79       224
   Mesenchymal, Neural       0.80      0.70      0.75       168
               Neural       0.77      0.81      0.79       275
     Neural, Proneural       0.88      0.69      0.78        85
             Proneural       0.77      0.82      0.79       368

              accuracy                           0.76      1851
             macro avg       0.78      0.74      0.76      1851
          weighted avg       0.77      0.76      0.76      1851


Random Forest to original Data in TrainDataset, adding tree numbers to 500:
```

	precision	recall	f1-score	support
Classical	1.00	1.00	1.00	870
Classical, Mesenchymal	1.00	1.00	1.00	482
Classical, Neural	1.00	1.00	1.00	445
Mesenchymal	1.00	1.00	1.00	514
Mesenchymal, Neural	1.00	1.00	1.00	345
Neural	1.00	1.00	1.00	562
Neural, Proneural	1.00	1.00	1.00	232
Proneural	1.00	1.00	1.00	869
accuracy			1.00	4319
macro avg	1.00	1.00	1.00	4319
weighted avg	1.00	1.00	1.00	4319

Random Forest to normalized Data in TestDataset, adding tree numbers to 500:

	precision	recall	f1-score	support
Classical	0.69	0.82	0.75	375
Classical, Mesenchymal	0.67	0.64	0.66	157
Classical, Neural	0.83	0.66	0.74	199
Mesenchymal	0.83	0.72	0.77	224
Mesenchymal, Neural	0.82	0.68	0.74	168
Neural	0.78	0.81	0.80	275
Neural, Proneural	0.84	0.66	0.74	85
Proneural	0.76	0.84	0.80	368
accuracy			0.76	1851
macro avg	0.78	0.73	0.75	1851
weighted avg	0.77	0.76	0.76	1851

Random Forest to normalized Data in TrainDataset, adding tree numbers to 500:

	precision	recall	f1-score	support
Classical	1.00	1.00	1.00	870
Classical, Mesenchymal	1.00	1.00	1.00	482
Classical, Neural	1.00	1.00	1.00	445
Mesenchymal	1.00	1.00	1.00	514
Mesenchymal, Neural	1.00	1.00	1.00	345
Neural	1.00	1.00	1.00	562
Neural, Proneural	1.00	1.00	1.00	232
Proneural	1.00	1.00	1.00	869
accuracy			1.00	4319
macro avg	1.00	1.00	1.00	4319
weighted avg	1.00	1.00	1.00	4319

Random Forest to PCA normalized Data in TestDataset, adding tree numbers to 500:

	precision	recall	f1-score	support
Classical	0.65	0.85	0.74	375
Classical, Mesenchymal	0.58	0.55	0.57	157
Classical, Neural	0.82	0.63	0.71	199

Mesenchymal	0.74	0.71	0.72	224
Mesenchymal, Neural	0.82	0.57	0.67	168
Neural	0.79	0.74	0.76	275
Neural, Proneural	0.80	0.61	0.69	85
Proneural	0.73	0.80	0.76	368
accuracy			0.72	1851
macro avg	0.74	0.68	0.70	1851
weighted avg	0.73	0.72	0.72	1851

Random Forest to PCA normalized Data in TrainDataset, adding tree numbers to 500:

	precision	recall	f1-score	support
Classical	1.00	1.00	1.00	870
Classical, Mesenchymal	1.00	1.00	1.00	482
Classical, Neural	1.00	1.00	1.00	445
Mesenchymal	1.00	1.00	1.00	514
Mesenchymal, Neural	1.00	1.00	1.00	345
Neural	1.00	1.00	1.00	562
Neural, Proneural	1.00	1.00	1.00	232
Proneural	1.00	1.00	1.00	869
accuracy			1.00	4319
macro avg	1.00	1.00	1.00	4319
weighted avg	1.00	1.00	1.00	4319

SVM to PCA normalized Data in TestDataset:

	precision	recall	f1-score	support
Classical	0.35	0.63	0.45	375
Classical, Mesenchymal	0.25	0.18	0.21	157
Classical, Neural	0.41	0.28	0.33	199
Mesenchymal	0.43	0.40	0.42	224
Mesenchymal, Neural	0.35	0.20	0.25	168
Neural	0.54	0.36	0.43	275
Neural, Proneural	0.47	0.20	0.28	85
Proneural	0.42	0.47	0.44	368
accuracy			0.40	1851
macro avg	0.40	0.34	0.35	1851
weighted avg	0.41	0.40	0.38	1851

SVM to PCA normalized Data in TrainDataset:

	precision	recall	f1-score	support
Classical	0.40	0.64	0.49	870
Classical, Mesenchymal	0.39	0.26	0.31	482
Classical, Neural	0.49	0.37	0.42	445
Mesenchymal	0.43	0.47	0.45	514
Mesenchymal, Neural	0.41	0.27	0.32	345
Neural	0.55	0.44	0.49	562
Neural, Proneural	0.53	0.22	0.31	232
Proneural	0.44	0.48	0.46	869

accuracy			0.44	4319
macro avg	0.45	0.39	0.41	4319
weighted avg	0.45	0.44	0.43	4319

MLP to Normalized Data in TestDataset:

	precision	recall	f1-score	support
Classical	0.83	0.82	0.83	375
Classical, Mesenchymal	0.69	0.76	0.72	157
Classical, Neural	0.77	0.77	0.77	199
Mesenchymal	0.81	0.84	0.83	224
Mesenchymal, Neural	0.76	0.74	0.75	168
Neural	0.82	0.77	0.79	275
Neural, Proneural	0.75	0.84	0.79	85
Proneural	0.86	0.83	0.84	368
accuracy			0.80	1851
macro avg	0.79	0.80	0.79	1851
weighted avg	0.80	0.80	0.80	1851

MLP to Normalized Data in TrainDataset:

	precision	recall	f1-score	support
Classical	1.00	1.00	1.00	870
Classical, Mesenchymal	1.00	1.00	1.00	482
Classical, Neural	1.00	1.00	1.00	445
Mesenchymal	1.00	1.00	1.00	514
Mesenchymal, Neural	1.00	1.00	1.00	345
Neural	1.00	1.00	1.00	562
Neural, Proneural	1.00	1.00	1.00	232
Proneural	1.00	1.00	1.00	869
accuracy			1.00	4319
macro avg	1.00	1.00	1.00	4319
weighted avg	1.00	1.00	1.00	4319

MLP to PCA Normalized Data in TestDataset:

	precision	recall	f1-score	support
Classical	0.80	0.79	0.79	375
Classical, Mesenchymal	0.64	0.69	0.67	157
Classical, Neural	0.73	0.74	0.74	199
Mesenchymal	0.78	0.77	0.77	224
Mesenchymal, Neural	0.73	0.72	0.73	168
Neural	0.84	0.76	0.80	275
Neural, Proneural	0.64	0.79	0.71	85
Proneural	0.82	0.82	0.82	368
accuracy			0.77	1851
macro avg	0.75	0.76	0.75	1851
weighted avg	0.77	0.77	0.77	1851

MLP to PCA Normalized Data in TrainDataset:

	precision	recall	f1-score	support
Classical	1.00	1.00	1.00	870
Classical, Mesenchymal	1.00	1.00	1.00	482
Classical, Neural	1.00	1.00	1.00	445
Mesenchymal	1.00	1.00	1.00	514
Mesenchymal, Neural	1.00	1.00	1.00	345
Neural	1.00	1.00	1.00	562
Neural, Proneural	1.00	1.00	1.00	232
Proneural	1.00	1.00	1.00	869
accuracy			1.00	4319
macro avg	1.00	1.00	1.00	4319
weighted avg	1.00	1.00	1.00	4319

Decision Trees to original Data in Simplified TestDataset:

	precision	recall	f1-score	support
Classical	0.67	0.65	0.66	361
Mesenchymal	0.62	0.65	0.64	216
Neural	0.63	0.69	0.66	251
Proneural	0.72	0.69	0.71	390
accuracy			0.67	1218
macro avg	0.66	0.67	0.67	1218
weighted avg	0.67	0.67	0.67	1218

Decision Trees to original Data in Simplified TrainDataset:

	precision	recall	f1-score	support
Classical	1.00	1.00	1.00	884
Mesenchymal	1.00	1.00	1.00	522
Neural	1.00	1.00	1.00	586
Proneural	1.00	1.00	1.00	847
accuracy			1.00	2839
macro avg	1.00	1.00	1.00	2839
weighted avg	1.00	1.00	1.00	2839

Decision Trees to normalize Data in Simplified TestDataset:

	precision	recall	f1-score	support
Classical	0.69	0.64	0.66	361
Mesenchymal	0.61	0.72	0.66	216
Neural	0.61	0.59	0.60	251
Proneural	0.68	0.68	0.68	390
accuracy			0.66	1218
macro avg	0.65	0.66	0.65	1218
weighted avg	0.66	0.66	0.65	1218

Decision Trees to normalize Data in Simplified TrainDataset:

	precision	recall	f1-score	support
Classical	1.00	1.00	1.00	884
Mesenchymal	1.00	1.00	1.00	522
Neural	1.00	1.00	1.00	586
Proneural	1.00	1.00	1.00	847
accuracy			1.00	2839
macro avg	1.00	1.00	1.00	2839
weighted avg	1.00	1.00	1.00	2839

Decision Trees to PCA Data in Simplified TestDataset:

	precision	recall	f1-score	support
Classical	0.31	0.33	0.32	361
Mesenchymal	0.22	0.25	0.23	216
Neural	0.22	0.24	0.23	251
Proneural	0.38	0.32	0.35	390
accuracy			0.29	1218
macro avg	0.28	0.28	0.28	1218
weighted avg	0.30	0.29	0.30	1218

Decision Trees to PCA Data in Simplified TrainDataset:

	precision	recall	f1-score	support
Classical	1.00	1.00	1.00	884
Mesenchymal	1.00	1.00	1.00	522
Neural	1.00	1.00	1.00	586
Proneural	1.00	1.00	1.00	847
accuracy			1.00	2839
macro avg	1.00	1.00	1.00	2839
weighted avg	1.00	1.00	1.00	2839

Decision Trees to PCA Normalized Data in Simplified TestDataset:

	precision	recall	f1-score	support
Classical	0.60	0.61	0.61	361
Mesenchymal	0.58	0.63	0.60	216
Neural	0.61	0.56	0.58	251
Proneural	0.66	0.65	0.66	390
accuracy			0.62	1218
macro avg	0.61	0.61	0.61	1218
weighted avg	0.62	0.62	0.62	1218

Decision Trees to PCA Normalized Data in Simplified TrainDataset:

	precision	recall	f1-score	support

Classical	1.00	1.00	1.00	884
Mesenchymal	1.00	1.00	1.00	522
Neural	1.00	1.00	1.00	586
Proneural	1.00	1.00	1.00	847
accuracy			1.00	2839
macro avg	1.00	1.00	1.00	2839
weighted avg	1.00	1.00	1.00	2839

Decision Trees to Normalized PCA Data in Simplified TestDataset:

	precision	recall	f1-score	support
Classical	0.29	0.30	0.30	361
Mesenchymal	0.22	0.22	0.22	216
Neural	0.23	0.25	0.24	251
Proneural	0.38	0.34	0.36	390
accuracy			0.29	1218
macro avg	0.28	0.28	0.28	1218
weighted avg	0.29	0.29	0.29	1218

Decision Trees to Normalized PCA Data in Simplified TrainDataset:

	precision	recall	f1-score	support
Classical	1.00	1.00	1.00	884
Mesenchymal	1.00	1.00	1.00	522
Neural	1.00	1.00	1.00	586
Proneural	1.00	1.00	1.00	847
accuracy			1.00	2839
macro avg	1.00	1.00	1.00	2839
weighted avg	1.00	1.00	1.00	2839

Random Forest to orginal Data in Simplified TestDataset:

	precision	recall	f1-score	support
Classical	0.81	0.85	0.83	361
Mesenchymal	0.87	0.84	0.85	216
Neural	0.85	0.85	0.85	251
Proneural	0.86	0.84	0.85	390
accuracy			0.84	1218
macro avg	0.85	0.84	0.84	1218
weighted avg	0.84	0.84	0.84	1218

Random Forest to original Data in Simplified TrainDataset:

	precision	recall	f1-score	support
Classical	1.00	1.00	1.00	884
Mesenchymal	1.00	1.00	1.00	522
Neural	1.00	1.00	1.00	586
Proneural	1.00	1.00	1.00	847

```
    accuracy                           1.00      2839
   macro avg       1.00      1.00      1.00      2839
weighted avg       1.00      1.00      1.00      2839
```

Random Forest to orginal Data in Simplified TestDataset, adding tree numbers to 500:

```
              precision    recall  f1-score   support

   Classical       0.83      0.85      0.84       361
 Mesenchymal       0.87      0.86      0.86       216
      Neural       0.84      0.84      0.84       251
   Proneural       0.86      0.85      0.86       390

    accuracy                           0.85      1218
   macro avg       0.85      0.85      0.85      1218
weighted avg       0.85      0.85      0.85      1218
```

Random Forest to original Data in Simplified TrainDataset, adding tree numbers to 500:

```
              precision    recall  f1-score   support

   Classical       1.00      1.00      1.00       884
 Mesenchymal       1.00      1.00      1.00       522
      Neural       1.00      1.00      1.00       586
   Proneural       1.00      1.00      1.00       847

    accuracy                           1.00      2839
   macro avg       1.00      1.00      1.00      2839
weighted avg       1.00      1.00      1.00      2839
```

Random Forest to normalized Data in Simplified TestDataset, adding tree numbers to 500:

```
              precision    recall  f1-score   support

   Classical       0.81      0.85      0.83       361
 Mesenchymal       0.89      0.85      0.87       216
      Neural       0.83      0.82      0.83       251
   Proneural       0.85      0.85      0.85       390

    accuracy                           0.84      1218
   macro avg       0.85      0.84      0.85      1218
weighted avg       0.84      0.84      0.84      1218
```

Random Forest to normalized Data in Simplified TrainDataset, adding tree numbers to 500:

```
              precision    recall  f1-score   support

   Classical       1.00      1.00      1.00       884
 Mesenchymal       1.00      1.00      1.00       522
      Neural       1.00      1.00      1.00       586
   Proneural       1.00      1.00      1.00       847

    accuracy                           1.00      2839
   macro avg       1.00      1.00      1.00      2839
weighted avg       1.00      1.00      1.00      2839
```

Random Forest to PCA normalized Data in Simplified TestDataset, adding tree numbers to 500:

	precision	recall	f1-score	support
Classical	0.74	0.85	0.79	361
Mesenchymal	0.87	0.73	0.80	216
Neural	0.83	0.74	0.78	251
Proneural	0.82	0.84	0.83	390
accuracy			0.80	1218
macro avg	0.82	0.79	0.80	1218
weighted avg	0.81	0.80	0.80	1218

Random Forest to PCA normalized Data in Simplified TrainDataset, adding tree numbers to 500:

	precision	recall	f1-score	support
Classical	1.00	1.00	1.00	884
Mesenchymal	1.00	1.00	1.00	522
Neural	1.00	1.00	1.00	586
Proneural	1.00	1.00	1.00	847
accuracy			1.00	2839
macro avg	1.00	1.00	1.00	2839
weighted avg	1.00	1.00	1.00	2839

SVM to PCA normalized Data in Simplified TestDataset:

	precision	recall	f1-score	support
Classical	0.46	0.70	0.55	361
Mesenchymal	0.57	0.36	0.44	216
Neural	0.64	0.47	0.54	251
Proneural	0.62	0.54	0.58	390
accuracy			0.54	1218
macro avg	0.57	0.52	0.53	1218
weighted avg	0.57	0.54	0.54	1218

SVM to PCA normalized Data in Simplified TrainDataset:

	precision	recall	f1-score	support
Classical	0.51	0.69	0.59	884
Mesenchymal	0.53	0.51	0.52	522
Neural	0.61	0.46	0.53	586
Proneural	0.62	0.50	0.55	847
accuracy			0.55	2839
macro avg	0.56	0.54	0.55	2839
weighted avg	0.56	0.55	0.55	2839

MLP to Normalized Data in Simplified TestDataset:

	precision	recall	f1-score	support

```
              precision    recall  f1-score   support

   Classical       0.89      0.83      0.86       361
 Mesenchymal       0.78      0.85      0.81       216
      Neural       0.84      0.80      0.82       251
   Proneural       0.84      0.89      0.87       390

    accuracy                           0.84      1218
   macro avg       0.84      0.84      0.84      1218
weighted avg       0.85      0.84      0.84      1218
```

MLP to Normalized Data in Simplified TrainDataset:

```
              precision    recall  f1-score   support

   Classical       0.99      0.98      0.99       884
 Mesenchymal       0.95      0.98      0.97       522
      Neural       0.99      0.97      0.98       586
   Proneural       0.98      0.99      0.99       847

    accuracy                           0.98      2839
   macro avg       0.98      0.98      0.98      2839
weighted avg       0.98      0.98      0.98      2839
```

MLP to PCA Normalized Data in Simplified TestDataset:

```
              precision    recall  f1-score   support

   Classical       0.83      0.86      0.85       361
 Mesenchymal       0.89      0.86      0.87       216
      Neural       0.84      0.84      0.84       251
   Proneural       0.88      0.86      0.87       390

    accuracy                           0.86      1218
   macro avg       0.86      0.86      0.86      1218
weighted avg       0.86      0.86      0.86      1218
```

MLP to PCA Normalized Data in Simplified TrainDataset:

```
              precision    recall  f1-score   support

   Classical       1.00      1.00      1.00       884
 Mesenchymal       1.00      1.00      1.00       522
      Neural       1.00      1.00      1.00       586
   Proneural       1.00      1.00      1.00       847

    accuracy                           1.00      2839
   macro avg       1.00      1.00      1.00      2839
weighted avg       1.00      1.00      1.00      2839
```