

Part1 Assistant Codes

(辅助用的代码，主要是格式转换和重命名)

1.1 把DICOM数据批量转换成nii.gz数据方便nnUNet模型处理

```
In [22]: import os
import pydicom
import SimpleITK as sitk
import nibabel as nib

def convert_dicom_to_nifti(input_folder, output_folder, output_filename):
    # Read DICOM file
    dicom_reader = sitk.ImageSeriesReader()
    dicom_names = dicom_reader.GetGDCMSeriesFileNames(input_folder)
    dicom_reader.SetFileNames(dicom_names)
    dicom_image = dicom_reader.Execute()

    # extract DICOM
    dicom_info = pydicom.read_file(dicom_names[0])

    # change NIfTI format
    nifti_image = sitk.GetImageFromArray(sitk.GetArrayFromImage(dicom_image))
    nifti_image.SetOrigin(dicom_image.GetOrigin())
    nifti_image.SetSpacing(dicom_image.GetSpacing())
    nifti_image.SetDirection(dicom_image.GetDirection())

    # save as nii.gz file
    output_path = os.path.join(output_folder, output_filename)
    sitk.WriteImage(nifti_image, output_path)

    print(f"Conversion completed. NIfTI file saved at: {output_path}")

# father file
input_folder_path = '/Users/shippingguo/Desktop/张裕Dicom/库欣/刘晴_004388908'
entries = os.listdir(input_folder_path) # 获取路径下文件夹和文件名字
# filter the folders
subdirectories = [entry for entry in entries if os.path.isdir(os.path.join(

for i in range(len(subdirectories)):
    output_filename = 'Pituitarytumor' + '_' + str(i) + '_0000' + ".nii.gz"
    input_path = os.path.join(input_folder_path, subdirectories[i])
    # transform
    convert_dicom_to_nifti(input_path, input_folder_path, output_filename)
```

Conversion completed. NIfTI file saved at: /Users/shippingguo/Desktop/张裕Dicom/库欣/刘晴_004388908/Pituitarytumor_0_0000.nii.gz

Conversion completed. NIfTI file saved at: /Users/shippingguo/Desktop/张裕Dicom/库欣/刘晴_004388908/Pituitarytumor_1_0000.nii.gz

WARNING: In /tmp/SimpleITK-build/ITK-prefix/include/ITK-5.3/itkImageSeriesReader.hxx, line 478
ImageSeriesReader (0x1294f14d0): Non uniform sampling or missing slices detected, maximum nonuniformity:53.087

Conversion completed. NIfTI file saved at: /Users/shippingguo/Desktop/张裕Dicom/库欣/刘晴_004388908/Pituitarytumor_2_0000.nii.gz

1.2准备nnUNet所需要的数据

1. 检查标注的文件数量是否一致
2. 修改文件名满足nnUNet的要求
3. 判断标注的ROI是否正确（有的标注的不对）

Reorganize files names

```
In [23]: import nibabel as nib
import numpy as np
from pathlib import Path
import os
import shutil
from difflib import SequenceMatcher
```

```
In [24]: def create_folder_if_not_exists(folder_path):
# Use Path to check the folder exist or not
path = Path(folder_path)

if not path.exists():
# if not exist, creat a new one
path.mkdir(parents=True, exist_ok=True)
print(f"Folder '{folder_path}' created.")
else:
print(f"Folder '{folder_path}' already exists.")
```

```
In [25]: folder1 = "/Users/shippingguo/Library/CloudStorage/OneDrive-NationalUniversity of Singapore/Pituitary-segmentation-and-classification-/Pituitary tumor document/Pituitary_tumor"
folder2 = "/Users/shippingguo/Library/CloudStorage/OneDrive-NationalUniversity of Singapore/Pituitary-segmentation-and-classification-/Pituitary tumor document/Pituitary_tumor_label"

file_Tr = [f for f in os.listdir(folder1) if os.path.isfile(os.path.join(folder1, f))]
file_La = [f for f in os.listdir(folder2) if os.path.isfile(os.path.join(folder2, f))]
file_Tr = sorted(file_Tr)
file_La = sorted(file_La)
N = 0
if len(file_La) == len(file_Tr):
N = len(file_La)
else:
print('The length of training and lables are different')
print(N)
```

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发现手动切割的结果有个别不对，这里筛选一下

```
In [26]: #
def compare_nifti_dimensions(file1_path, file2_path):
# Read.nii.gz file
img1 = nib.load(file1_path)
img2 = nib.load(file2_path)
header1 = img1.header
header2 = img2.header
# The size
shape1 = header1.get_data_shape()
shape2 = header2.get_data_shape()
# read the slice info
spacing1 = header1.get_zooms()
spacing2 = header2.get_zooms()
# check the size
if shape1 != shape2:
return False, "尺寸不同"
# check the distance between slice
if not np.allclose(spacing1, spacing2):
```

```

    return False, "切片间隔不同"
    return True, "两个文件相同"

```

```

In [27]: def check_binary_nifti(file_path):
# read .nii.gz file
img = nib.load(file_path)
# read array file
data = img.get_fdata()
# check the value only contain 0 and 1
is_binary = np.all(np.logical_or(data == 0, data == 1))
return is_binary

```

```

In [28]: Target_path = "/Users/shippingguo/Library/CloudStorage/OneDrive-NationalUnive
imagesTr = os.path.join(Target_path, 'imagesTr_nii.gz')
labelsTr = os.path.join(Target_path, 'labelsTr_nii.gz')
create_folder_if_not_exists(imagesTr)
create_folder_if_not_exists(labelsTr)

similarity_ratio = []
# 这里定义三个list, 分别对应original image name list, 筛选过的image name list和la
PRE_IMAGE_LIST = []
PRE_LABEL_LIST = []
IMAGE_LIST = []
LABEL_LIST = []
IMAGE_LIST_NII = []
LABEL_LIST_NII = []
for i in range(N):
    similarity_ratio.append(SequenceMatcher(None, file_Tr[i], file_La[i]).ra
    if file_Tr[i][-7:] == '.nii.gz' and file_La[i][-7:] == '.nii.gz':
        image = os.path.join(folder1, file_Tr[i])
        mask = os.path.join(folder2, file_La[i])
        result, message = compare_nifti_dimensions(image, mask)
        if result:
            if not check_binary_nifti(mask):
                print('Error 1: ' + file_Tr[i] + "该标注不只包含0和1值" + ' Pitui
            else:
                PRE_IMAGE_LIST.append(file_Tr[i])
                PRE_LABEL_LIST.append(file_La[i])
                if similarity_ratio[i] > 0.8: # 这里模糊匹配一下, 这里不严谨, 有
                    name_Tr = 'Pituitarytumor' + '_' + str(i) + '_0000' + fi
                    IMAGE_LIST.append(name_Tr)
                    IMAGE_LIST_NII.append('Pituitarytumor' + '_' + str(i) +
                    name_La = 'Pituitarytumor' + '_' + str(i) + file_Tr[i][-7:]
                    LABEL_LIST.append(name_La)
                    LABEL_LIST_NII.append('Pituitarytumor' + '_' + str(i) + '.
                    shutil.copy(os.path.join(folder1, file_Tr[i]), os.path.j
                    shutil.copy(os.path.join(folder2, file_La[i]), os.path.j
                else:
                    print('Error 3: ' + "Please check the files " + file_Tr
            else:
                print('Error 2: ' + file_Tr[i] + ' ' + message + ' Pituitarytumor
        else:
            print('Error 0: ' + file_Tr[i][-7:] + ' or ' + file_La[i][-7:] + " fo

```

Folder '/Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniversityofSingapore/Pituitary-segmentation-and-classification-/1_Classifer/imagesTr_nii_gz' already exists.

Folder '/Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniversityofSingapore/Pituitary-segmentation-and-classification-/1_Classifer/labelsTr_nii_gz' already exists.

Error 2: 0gaobo622693SF1.nii.gz 切片间隔不同 Pituitarytumor_23_0000 will be missing

Error 2: 0hanruiping644302PS.nii.gz 尺寸不同 Pituitarytumor_27_0000 will be missing

Error 2: 0hanxu646712SF1.nii.gz 切片间隔不同 Pituitarytumor_28_0000 will be missing

Error 2: 0heliyan660131SF1.nii.gz 切片间隔不同 Pituitarytumor_30_0000 will be missing

Error 2: 0liuzhaoyu447282SF-1.nii.gz 切片间隔不同 Pituitarytumor_44_0000 will be missing

Error 2: 0lixiangju635014SF-1.nii.gz 尺寸不同 Pituitarytumor_46_0000 will be missing

Error 2: 0lixiangju635014SF1.nii.gz 尺寸不同 Pituitarytumor_47_0000 will be missing

Error 2: 0liyue682814T-PIT.nii.gz 切片间隔不同 Pituitarytumor_49_0000 will be missing

Error 2: 0mahaiping675404SF1.nii.gz 尺寸不同 Pituitarytumor_53_0000 will be missing

Error 2: 0malina666082T-PIT.nii.gz 切片间隔不同 Pituitarytumor_55_0000 will be missing

Error 2: 0mengzhanxi668846SF-1.nii.gz 尺寸不同 Pituitarytumor_58_0000 will be missing

Error 2: 0songyijun646056SF-1.nii.gz 切片间隔不同 Pituitarytumor_65_0000 will be missing

Error 0: 1nii.gz or .nii.gz fomate is wrong!

Error 2: 0wangjie660273SF1.nii.gz 尺寸不同 Pituitarytumor_78_0000 will be missing

Error 1: 0wangshuzhen664131SF1.nii.gz该标注不只包含0和1值 Pituitarytumor_80_0000 will be missing

Error 1: 0wangxiaomei658922T-PIT1.nii.gz该标注不只包含0和1值 Pituitarytumor_82_0000 will be missing

Error 2: 0wangzhenhong641359PIT1.nii.gz 尺寸不同 Pituitarytumor_85_0000 will be missing

Error 2: 0wulizhu598705PIT-1.nii.gz 尺寸不同 Pituitarytumor_88_0000 will be missing

Error 2: 0yuanhongye643850PS.nii.gz 切片间隔不同 Pituitarytumor_108_0000 will be missing

Error 2: 0zhangjianmin661591SF1.nii.gz 切片间隔不同 Pituitarytumor_115_0000 will be missing

Error 2: 0zhangjianming661591SF-1.nii.gz 切片间隔不同 Pituitarytumor_116_0000 will be missing

Error 2: liyue.nii.gz 切片间隔不同 Pituitarytumor_144_0000 will be missing

Error 2: malina.nii.gz 切片间隔不同 Pituitarytumor_148_0000 will be missing

Error 0: gnii.gz or .nii.gz fomate is wrong!

Error 2: shuangyuhua.nii.gz 切片间隔不同 Pituitarytumor_150_0000 will be missing

1.3 将原始3D影像和分割得到的Mask叠加在一起方便查看分割后的效果

```
In [29]: import nibabel as nib
import numpy as np

def binarize_mask(mask_data):
    # 将mask数据二值化, 使所有非零值变为1
    return np.where(mask_data > 0, 1, 0)
```

```
def merge_nifti_files(original_file_path, mask_file_path, output_file_path):
    # 读取原始文件和mask文件
    original_image = nib.load(original_file_path)
    mask_image = nib.load(mask_file_path)
    # 获取原始数据和mask数据
    original_data = original_image.get_fdata()
    mask_data = mask_image.get_fdata()
    # 二值化mask数据
    binarized_mask_data = binarize_mask(mask_data)
    # 将二值化后的mask应用于原始数据
    merged_data = original_data - 150 * binarized_mask_data    #将两个文件叠加在
    # 创建一个新的NIFTI文件对象
    merged_image = nib.Nifti1Image(merged_data, original_image.affine)
    # 保存合并后的NIFTI文件
    nib.save(merged_image, output_file_path)

    print(f"Files merged and saved at: {output_file_path}")
```

```
In [30]: # 只对单个文件进行操作, 小程序是对整个文件夹下的文件批量操作
# 指定原始文件和mask文件的路径
original_file_path = '/Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniversityofSingapore/Pituitary-segmentation-and-classification-0_Segmentation/Testing/Combined/Pituitarytumor_0.nii.gz'
mask_file_path = '/Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniversityofSingapore/Pituitary-segmentation-and-classification-0_Segmentation/Testing/Combined/Pituitarytumor_mask_0.nii.gz'

# Point the output folder
output_file_path = '/Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniversityofSingapore/Pituitary-segmentation-and-classification-0_Segmentation/Testing/Combined/Pituitarytumor_0.nii.gz'

# Combine two files
merge_nifti_files(original_file_path, mask_file_path, output_file_path)
```

Files merged and saved at: /Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniversityofSingapore/Pituitary-segmentation-and-classification-0_Segmentation/Testing/Combined/Pituitarytumor_0.nii.gz

Part 2 PyRadiomics feature extraction

特征提取部分

In this notebook, I will use PyRadiomics to extract the features and prepare for training the classifier

For more detailed examples and links to source code, visit <http://radiomics.io>

```
In [31]: # Import the necessary packages
import os # needed navigate the system to get the input data
import radiomics # Radiomics package
from radiomics import featureextractor # This module is used for interactive
import six, numpy as np #
import matplotlib.pyplot as plt # Plot images
import SimpleITK as sitk
```

Input data

Refer to <https://pyradiomics.readthedocs.io/en/latest/customization.html> \ Currently available image types are:

1. Original: No filter applied
2. Wavelet: Wavelet filtering, yields 8 decompositions per level (all possible combinations of applying either a High or a Low pass filter in each of the three

- dimensions. See also **getWaveletImage()**
3. LoG: Laplacian of Gaussian filter, edge enhancement filter. Emphasizes areas of gray level change, where sigma defines how coarse the emphasised texture should be. A low sigma emphasis on fine textures (change over a short distance), where a high sigma value emphasises coarse textures (gray level change over a large distance). See also **getLoGImage()**
 4. Square: Takes the square of the image intensities and linearly scales them back to the original range. Negative values in the original image will be made negative again after application of filter.
 5. SquareRoot: Takes the square root of the absolute image intensities and scales them back to original range. Negative values in the original image will be made negative again after application of filter.
 6. Logarithm: Takes the logarithm of the absolute intensity + 1. Values are scaled to original range and negative original values are made negative again after application of filter.
 7. Exponential: Takes the the exponential, where filtered intensity is $e^{(\text{absolute intensity})}$. Values are scaled to original range and negative original values are made negative again after application of filter.
 8. Gradient: Returns the magnitude of the local gradient. See also **getGradientImage()**
 9. LocalBinaryPattern2D: Computes the Local Binary Pattern in a by-slice operation (2D). See also **getLBP2DImage()**
 10. LocalBinaryPattern3D: Computes the Local Binary Pattern in 3D using spherical harmonics. See also **getLBP3DImage()**

Radiomic Features

Refer to: <https://pyradiomics.readthedocs.io/en/latest/features.html>

1. First Order Statistics (19 features)
2. Shape-based (3D) (16 features)
3. Shape-based (2D) (10 features)
4. Gray Level Co-occurrence Matrix (24 features)
5. Gray Level Run Length Matrix (16 features)
6. Gray Level Size Zone Matrix (16 features)
7. Neighbouring Gray Tone Difference Matrix (5 features)
8. Gray Level Dependence Matrix (14 features)

We need to define the parameters and instantiate the extractor. For this there are three possibilities:

1. Use defaults, don't define custom settings
2. Define parameters in a dictionary, control filters and features after initialisation
3. Use a parameter file

```
In [105... from __future__ import print_function
import six
import os # needed navigate the system to get the input data
import numpy as np
```

```
import radiomics
import pandas as pd
import SimpleITK as sitk
from radiomics import featureextractor # This module is used for interactive
import argparse
import nibabel as nib
import gzip
import shutil
import pandas as pd
import seaborn as sns
```

```
In [33]: def convert_nii_gz_to_nii(input_path, output_path):
        with gzip.open(input_path, 'rb') as f_in:
            with open(output_path, 'wb') as f_out:
                shutil.copyfileobj(f_in, f_out)
```

2.1 Convert .nii.gz files to nii files

```
In [34]: Target_path = "/Users/shippingguo/Library/CloudStorage/OneDrive-NationalUniversity
imagesTr_nii_gz = os.path.join(Target_path, 'imagesTr_nii_gz')
labelsTr_nii_gz = os.path.join(Target_path, 'labelsTr_nii_gz')
images_list = [f for f in os.listdir(imagesTr_nii_gz) if os.path.isfile(os.pa
masks_list = [f for f in os.listdir(labelsTr_nii_gz) if os.path.isfile(os.pa

# images_list = os.listdir(image_dir)
# masks_list = os.listdir(mask_dir)
```

```
In [35]: # Using list comprehension to filter out items not ending with ".nii.gz"
images_list_nii = [file_name for file_name in images_list if file_name.endswith
masks_list_nii = [file_name for file_name in masks_list if file_name.endswith
```

```
In [36]: # Using list comprehension to filter out items not ending with ".nii.gz"
images_list = [file_name for file_name in images_list if file_name.endswith(
masks_list = [file_name for file_name in masks_list if file_name.endswith(
images_list = sorted(images_list, reverse=False)
masks_list = sorted(masks_list, reverse=False)
```

2.2 Create nii files

```
In [37]: imagesTr_nii = os.path.join(Target_path, 'imagesTr_nii')
labelsTr_nii = os.path.join(Target_path, 'labelsTr_nii')
create_folder_if_not_exists(imagesTr_nii)
create_folder_if_not_exists(labelsTr_nii)
```

Folder '/Users/shippingguo/Library/CloudStorage/OneDrive-NationalUniversityofSingapore/Pituitary-segmentation-and-classification-/1_Classifer/imagesTr_nii' already exists.

Folder '/Users/shippingguo/Library/CloudStorage/OneDrive-NationalUniversityofSingapore/Pituitary-segmentation-and-classification-/1_Classifer/labelsTr_nii' already exists.

```
In [38]: # 把nii.gz转换成nii格式:
if len(images_list) > len(images_list_nii): # 原本nii与nii.gz是在同在一个文件夹
    for patient in images_list:
        input_file = os.path.join(imagesTr_nii_gz, patient)
        output_file_name = patient.split('.')[0]+'.nii'
        output_file = os.path.join(imagesTr_nii, output_file_name)
        files_in_directory = os.listdir(imagesTr_nii_gz)

        if output_file_name not in files_in_directory:
```



```

        convert_nii_gz_to_nii(input_file, output_file)

if len(masks_list) > len(masks_list_nii):  # 原本nii与nii.gz是在同在一个文件夹
    for patient in masks_list:
        input_file = os.path.join(labelsTr_nii_gz, patient)
        output_file_name = patient.split('.')[0]+'.nii'
        output_file = os.path.join(labelsTr_nii, output_file_name)
        files_in_directory = os.listdir(labelsTr_nii_gz)
        if output_file_name not in files_in_directory:
            convert_nii_gz_to_nii(input_file, output_file)

```

```

In [39]: images_list = os.listdir(imagesTr_nii)
masks_list = os.listdir(labelsTr_nii)
images_list_nii = [file_name for file_name in images_list if file_name.endswith('.nii')]
masks_list_nii = [file_name for file_name in masks_list if file_name.endswith('.nii')]
images_list = sorted(images_list_nii, reverse=False)
masks_list = sorted(masks_list_nii, reverse=False)

```

2.3 Get nii files currently, next we need do normalization

```

In [40]: import SimpleITK as sitk
from sklearn.preprocessing import StandardScaler

def normalize_nrrd_image(input_path, output_path):
    image = sitk.ReadImage(input_path)
    image_array = sitk.GetArrayFromImage(image)
    flat_image_array = image_array.flatten().reshape(-1, 1)
    scaler = StandardScaler()
    normalized_array = scaler.fit_transform(flat_image_array)
    normalized_image_array = normalized_array.reshape(image_array.shape)
    normalized_image = sitk.GetImageFromArray(normalized_image_array)
    normalized_image.CopyInformation(image)
    # save normalized result
    sitk.WriteImage(normalized_image, output_path)

```

```

In [41]: imagesTr_normalized = os.path.join(Target_path, 'imagesTr_normalized')
labelsTr_normalized = os.path.join(Target_path, 'labelsTr_normalized')
create_folder_if_not_exists(imagesTr_normalized)
create_folder_if_not_exists(labelsTr_normalized)

```

Folder '/Users/shippingguo/Library/CloudStorage/OneDrive-NationalUniversity of Singapore/Pituitary-segmentation-and-classification-/1_Classifer/imagesTr_normalized' already exists.

Folder '/Users/shippingguo/Library/CloudStorage/OneDrive-NationalUniversity of Singapore/Pituitary-segmentation-and-classification-/1_Classifer/labelsTr_normalized' already exists.

```

In [42]: for nii in images_list_nii:
    input_file = os.path.join(imagesTr_nii, nii)
    output_file = os.path.join(imagesTr_normalized, nii)
    normalize_nrrd_image(input_file, output_file)

    for nii in masks_list_nii:
        input_file = os.path.join(labelsTr_nii, nii)
        output_file = os.path.join(labelsTr_normalized, nii)
        normalize_nrrd_image(input_file, output_file)

```

```

In [43]: # Check the normalized file

input_path = '/Users/shippingguo/Library/CloudStorage/OneDrive-NationalUniversity of Singapore/Pituitary-segmentation-and-classification-/1_Classifer/imagesTr_normalized'
# read NRRD image
image = sitk.ReadImage(input_path)

```



```
# Check the file
image_array = sitk.GetArrayFromImage(image)
print((image_array[:, :, :].max()))
```

5.430416933444578

2.4 Refer to the paper "A machine learning model to precisely immunohistochemically classify T pituitary adenoma subtypes with radiomics based on preoperative magnetic resonance imaging" extract the features

Extract radiomics features. 18 first-order statistical features were extracted from the original images, including 14 shape features, 22 gray level cooccurrence matrix (GLCM) features, 16 gray level run length matrix (GLRLM) features, 16 gray level size zone matrix (GLSZM) features, and 14 gray level dependence matrix (GLDM) features. Thus, a total of 100 features were extracted from the original images of each MR sequence.

Additionally, 688 texture features of the same type were extracted from eight wavelet transform images.

Therefore, 788 individual radiomics features were extracted from each MR sequence.

```
In [44]: def catch_features(imagePath, maskPath):
    if imagePath is None or maskPath is None: # Something went wrong, in the
        raise Exception('Error getting testcase!') # Raise exception to prevent
    settings = {}
    settings['binWidth'] = 25 # 5
    settings['sigma'] = [3, 5]
    settings['Interpolator'] = sitk.sitkBSpline
    settings['resampledPixelSpacing'] = [1, 1, 1] # 3,3,3
    settings['voxelArrayShift'] = 1000 # 300
    settings['normalize'] = True
    settings['normalizeScale'] = 100
    extractor = featureextractor.RadiomicsFeatureExtractor(**settings)
    extractor.enableImageTypeByName('Wavelet')
    extractor.enableFeatureClassByName('firstorder')

    feature_cur = []
    feature_name = []
    result = extractor.execute(imagePath, maskPath, label=1)
    for key, value in six.iteritems(result):
        feature_name.append(key)
        feature_cur.append(value)
    name = feature_name[37:]
    name = np.array(name)

    for i in range(len(feature_cur[37:])):
        #if type(feature_cur[i+22]) != type(feature_cur[30]):
        feature_cur[i+37] = float(feature_cur[i+37])
    return feature_cur[37:], name
```

```
In [45]: # Test codes
imagePath = '/Users/shippingguo/Library/CloudStorage/OneDrive-National University of Singapore/Pituitary-segmentation-and-classification-/Pituitary tumor document/Pituitary_tumor.ipynb'
maskPath = '/Users/shippingguo/Library/CloudStorage/OneDrive-National University of Singapore/Pituitary-segmentation-and-classification-/Pituitary tumor document/Pituitary_tumor_mask.ipynb'
feature_name, feature_cur = catch_features(imagePath, maskPath)
feature_N = len(feature_cur)
save_file = np.empty(shape=[1, feature_N])
```

GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to be calculated
 GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to be calculated
 GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to be calculated
 GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to be calculated
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```
In [46]: # PRE_IMAGE_LIST
# PRE_LABEL_LIST
# IMAGE_LIST
# LABEL_LIST

class_list = []
for i in range(len(PRE_IMAGE_LIST)):
    if PRE_IMAGE_LIST[i][0] == '0':
        class_list.append(0)
    else:
        class_list.append(1)
```

```
In [47]: save_file = np.empty(shape=[1, feature_N])
save_file = np.delete(save_file, 0, 0)
```

```
In [48]: FEATURE_N = save_file.shape[1]    # Total number of features before reduce fe
```

```
In [49]: for patient_index in range (len(IMAGE_LIST)):
    imagePath = os.path.join(imagesTr_normalized, IMAGE_LIST_NII[patient_index])
    maskPath = os.path.join(labelsTr_nii, LABEL_LIST_NII[patient_index])
    print(imagePath)
    print(maskPath)

    save_curdata, features_name = catch_features(imagePath, maskPath)
    # print(len(save_curdata))
    save_curdata = np.array(save_curdata)
    save_curdata = save_curdata.reshape([1, feature_N])
    save_file = np.append(save_file, save_curdata, axis=0)
```

/Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniversityofSingapore/Pituitary-segmentation-and-classification-/1_Classifer/imagesTr_normalized/Pituitarytumor_0_0000.nii
 /Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniversityofSingapore/Pituitary-segmentation-and-classification-/1_Classifer/labelsTr_nii/Pituitarytumor_0.nii

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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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GLCM is symmetrical, therefore $\text{Sum Average} = 2 * \text{Joint Average}$, only 1 needs to be calculated
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```
In [51]: features_df = pd.DataFrame(save_file)
features_df.columns = features_name
features_df['Class'] = class_list
features_df = features_df.reset_index(drop=True)

export_dir = '/Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniversity of Singapore/Pituitary-segmentation-and-classification-/Pituitary tumor document/Pituitary_tumor.ipynb'
features_xlsx = os.path.join(export_dir, 'Radiomics-features.xlsx')
writer = pd.ExcelWriter(features_xlsx)
features_df.to_excel(writer)
writer.save()
```

```
/var/folders/53/tlbwbq3n5lz3nsqwqwk1p30w0000gn/T/ipykernel_16576/4245081323.py:10: FutureWarning: save is not part of the public API, usage can give unexpected results and will be removed in a future version
writer.save()
```

```
In [52]: features_df.shape
```

```
Out[52]: (132, 852)
```

一共有852个features, 132个数据, 后面会进一步降维

Part3 Design classifier

分类器设计

```
In [53]: X = features_df.iloc[:, 0:-1].values # we only take the first two features.
Y = features_df['Class']
```

```
In [54]: from mpl_toolkits.mplot3d import Axes3D
from sklearn.decomposition import PCA
# Import matplotlib for graphs, set inline
from matplotlib import pyplot as plt

from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, classification_report
import numpy as np
from sklearn.neural_network import MLPClassifier
```

3.1 不降维分类准确率

```
In [55]: # divide into test dataset and train dataset
X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size=0.2, random_state=42)
# initialize model
model = RandomForestClassifier() # 随机森林
# train
model.fit(X_train, Y_train)
# test
Y_pred = model.predict(X_test)
# check accuracy
accuracy = accuracy_score(Y_test, Y_pred)
classification_report_str = classification_report(Y_test, Y_pred)
# result
print(f"Accuracy: {accuracy}")
print("Classification Report:\n", classification_report_str)
```

Accuracy: 0.8148148148148148

Classification Report:

	precision	recall	f1-score	support
0	0.88	0.92	0.90	24
1	0.00	0.00	0.00	3
accuracy			0.81	27
macro avg	0.44	0.46	0.45	27
weighted avg	0.78	0.81	0.80	27

```
In [56]: model = MLPClassifier() # 机器学习分类器
model.fit(X_train, Y_train)
Y_pred = model.predict(X_test)
accuracy = accuracy_score(Y_test, Y_pred)
classification_report_str = classification_report(Y_test, Y_pred)

# Print the result
print(f"Accuracy: {accuracy}")
print("Classification Report:\n", classification_report_str)
```

Accuracy: 0.8888888888888888

Classification Report:

	precision	recall	f1-score	support
0	0.89	1.00	0.94	24
1	0.00	0.00	0.00	3
accuracy			0.89	27
macro avg	0.44	0.50	0.47	27
weighted avg	0.79	0.89	0.84	27

```

/Users/shipingguo/anaconda3/lib/python3.11/site-packages/sklearn/metrics/_classification.py:1469: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.
    _warn_prf(average, modifier, msg_start, len(result))
/Users/shipingguo/anaconda3/lib/python3.11/site-packages/sklearn/metrics/_classification.py:1469: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.
    _warn_prf(average, modifier, msg_start, len(result))
/Users/shipingguo/anaconda3/lib/python3.11/site-packages/sklearn/metrics/_classification.py:1469: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.
    _warn_prf(average, modifier, msg_start, len(result))

```

Part 4 Decrease dimension 特征降维度

4.1 独立样本t检验

衡量二分类数据中，两个类别下连续型数据均值的差异是否显著，当差异显著时，认为二分类数据对连续型数据有影响，否则没有。

```

In [98]: def t_test(name_x, name_y, df):
        """
        独立样本t检验，二值类别变量与连续型变量间的相关性，原假设是两类别对应的值均值相等，即
        :param name_x: dataframe中一个列名，二值变量
        :param name_y: dataframe中一个列名，连续型变量
        :param df: 数据集dataframe
        :return: p_t: t检验的p值，当p < 0.05时拒绝原假设，即两变量相关
        """

        from scipy.stats import ttest_ind, levene
        namex_list = df[name_x].tolist()
        namey_list = df[name_y].tolist()
        type_one = []; type_two = []
        for i in range(len(namex_list)):
            if namex_list[i] == list(set(df[name_x].tolist()))[0]:
                type_one.append(namey_list[i])
            else:
                type_two.append(namey_list[i])
        # 方差齐性检验 当检验结果为p>0.05所以，可以认为方差是相等的。
        p_s = levene(type_one, type_two)
        # print("方差齐性检验:", p_s, p_s[1])
        if p_s[1] > 0.05: ## 当方差齐
            # 独立样本T检验，默认方差齐性 当p值>0.05，接受原假设，认为两台机床的加工精度无显著差异
            p_t = ttest_ind(type_one, type_two)
        else: ### 当方差不齐
            ### 如果方差不齐性，则equal_var=False
            p_t = ttest_ind(type_one, type_two, equal_var=False)
        return p_t[1]

```

```

In [99]: columns = features_df.columns
        related_features_name = []
        print('Related features:')
        for column in columns[0:-1]:
            t_score = t_test('Class', column, features_df)
            if t_score < 0.1:
                related_features_name.append(column)
                print(column)

```


Related features:
original_firstorder_Minimum
original_glszm_LargeAreaLowGrayLevelEmphasis
wavelet-LHL_glcmm_Correlation
wavelet-LHH_glcmm_ClusterShade
wavelet-LHH_glcmm_Correlation
wavelet-LHH_glcmm_Imc2
wavelet-LHH_glcmm_InverseVariance
wavelet-LHH_glcmm_MCC
wavelet-LHH_gldm_DependenceEntropy
wavelet-LHH_gldm_DependenceNonUniformityNormalized
wavelet-LHH_gldm_DependenceVariance
wavelet-LHH_glszm_LargeAreaHighGrayLevelEmphasis
wavelet-LHH_glszm_SmallAreaLowGrayLevelEmphasis
wavelet-HLH_glcmm_ClusterProminence
wavelet-HLH_gldm_DependenceEntropy
wavelet-HLH_gldm_DependenceNonUniformityNormalized
wavelet-HLH_gldm_DependenceVariance
wavelet-HLH_glszm_ZonePercentage
wavelet-HHL_firstorder_Maximum
wavelet-HHL_firstorder_Median
wavelet-HHL_glcmm_ClusterShade
wavelet-HHL_glszm_GrayLevelNonUniformity
wavelet-HHL_ngtdm_Complexity
wavelet-HHH_gldm_DependenceEntropy
wavelet-HHH_gldm_DependenceNonUniformityNormalized
wavelet-HHH_gldm_DependenceVariance
wavelet-HHH_gldm_SmallDependenceEmphasis
wavelet-HHH_glszm_GrayLevelNonUniformity
wavelet-HHH_glszm_SizeZoneNonUniformityNormalized
wavelet-HHH_glszm_SmallAreaEmphasis
wavelet-HHH_glszm_SmallAreaLowGrayLevelEmphasis
wavelet-HHH_glszm_ZoneEntropy
wavelet-LLL_firstorder_Energy
wavelet-LLL_firstorder_Minimum
wavelet-LLL_firstorder_TotalEnergy

```
In [100... XX = features_df[related_features_name]
XX
```

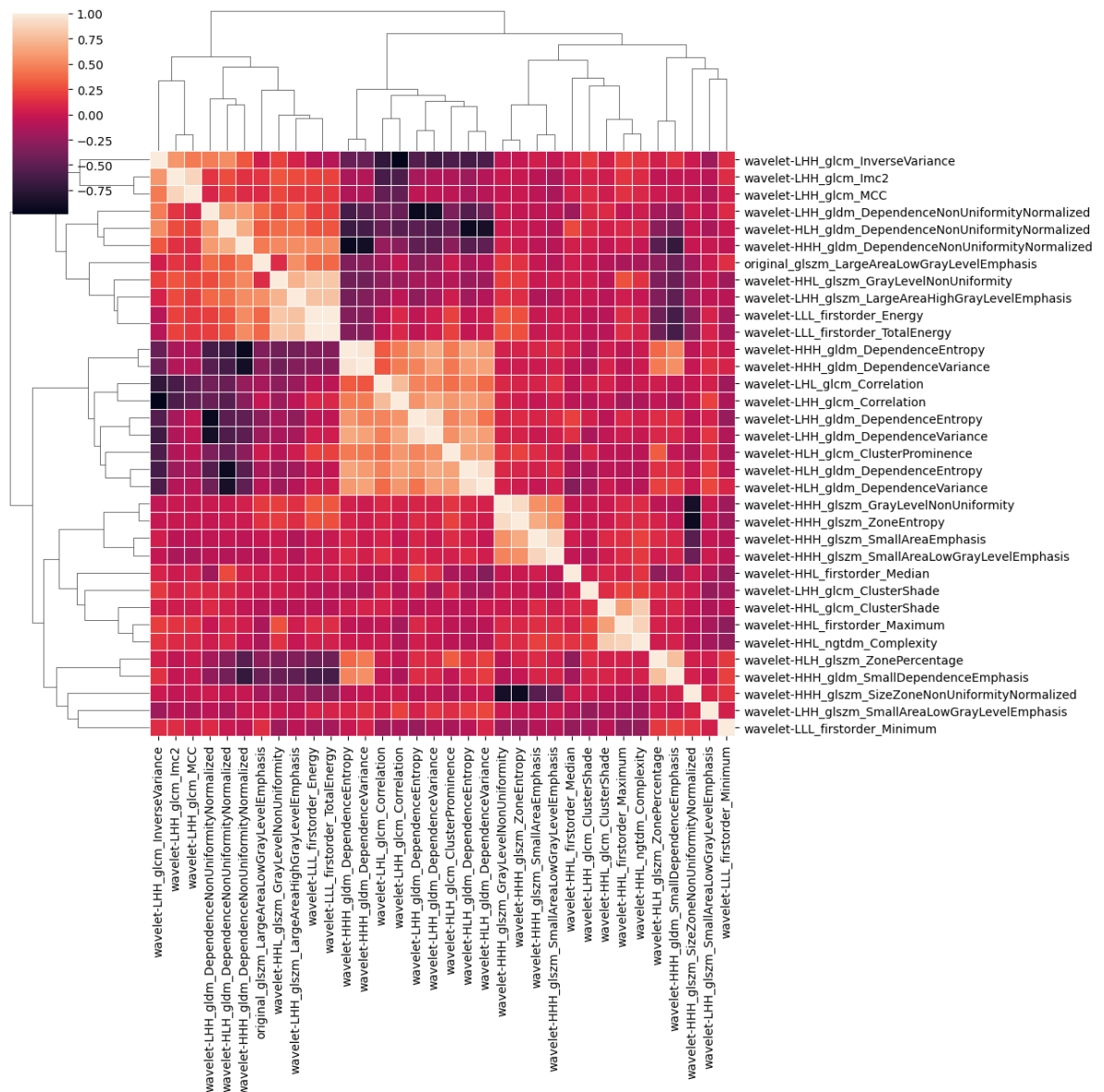
Out[100]:

	original_firstorder_Minimum	original_glszm_LargeAreaLowGrayLevelEmphasis	LHL_glcmm
0	-50.486772	121.465705	
1	-114.678182	3758.947644	
2	-81.730829	621.834416	
3	-62.198004	10.994925	
4	-74.689596	59.094826	
...	
127	-81.223943	9556.232728	
128	-49.049139	30.135605	
129	-76.144664	498.821589	
130	-62.101043	4266.877599	
131	-77.181421	133.794698	

132 rows x 35 columns

Heatmap showing the correlation matrix between 36 different features. The features are listed on both the x-axis and y-axis. The color scale ranges from -0.8 (dark purple) to 0.8 (dark red), with 0.0 being white. The diagonal is black, indicating a correlation of 1.0. The matrix is symmetric, with the lower triangle being a mirror image of the upper triangle. The features are grouped into several categories: original features, wavelet-LHH, wavelet-LHL, wavelet-HHH, wavelet-HLL, and wavelet-LLL. The correlation values are generally low, with some notable positive correlations between certain wavelet features and the original features.

localhost:8888/lab/tree/OneDrive - National University of Singapore/Pituitary-segmentation-and-classification-/Pituitary tumor document/Pituitary_tumor.ip... 80/227



4.2 多重共线性检测

```
In [101... from statsmodels.stats.outliers_influence import variance_inflation_factor
# 当VIF<10, 说明不存在多重共线性; 当10<=VIF<100, 存在较强的多重共线性, 当VIF>=100, 存在
vif = [variance_inflation_factor(XX.values, XX.columns.get_loc(i)) for i in
```

```
/Users/shippingguo/anaconda3/lib/python3.11/site-packages/statsmodels/stats/
outliers_influence.py:198: RuntimeWarning: divide by zero encountered in sc
alar divide
    vif = 1. / (1. - r_squared_i)
```

```
In [106... print('before vif check: ' + str(len(related_features_name)))
features_vif = []
for i in range(len(vif)):
    if vif[i]<10:
        features_vif.append(related_features_name[i])
print('after vif check: ' + str(len(features_vif)))

XXX = features_df[features_vif]
```

```
before vif check: 35
after vif check: 18
```

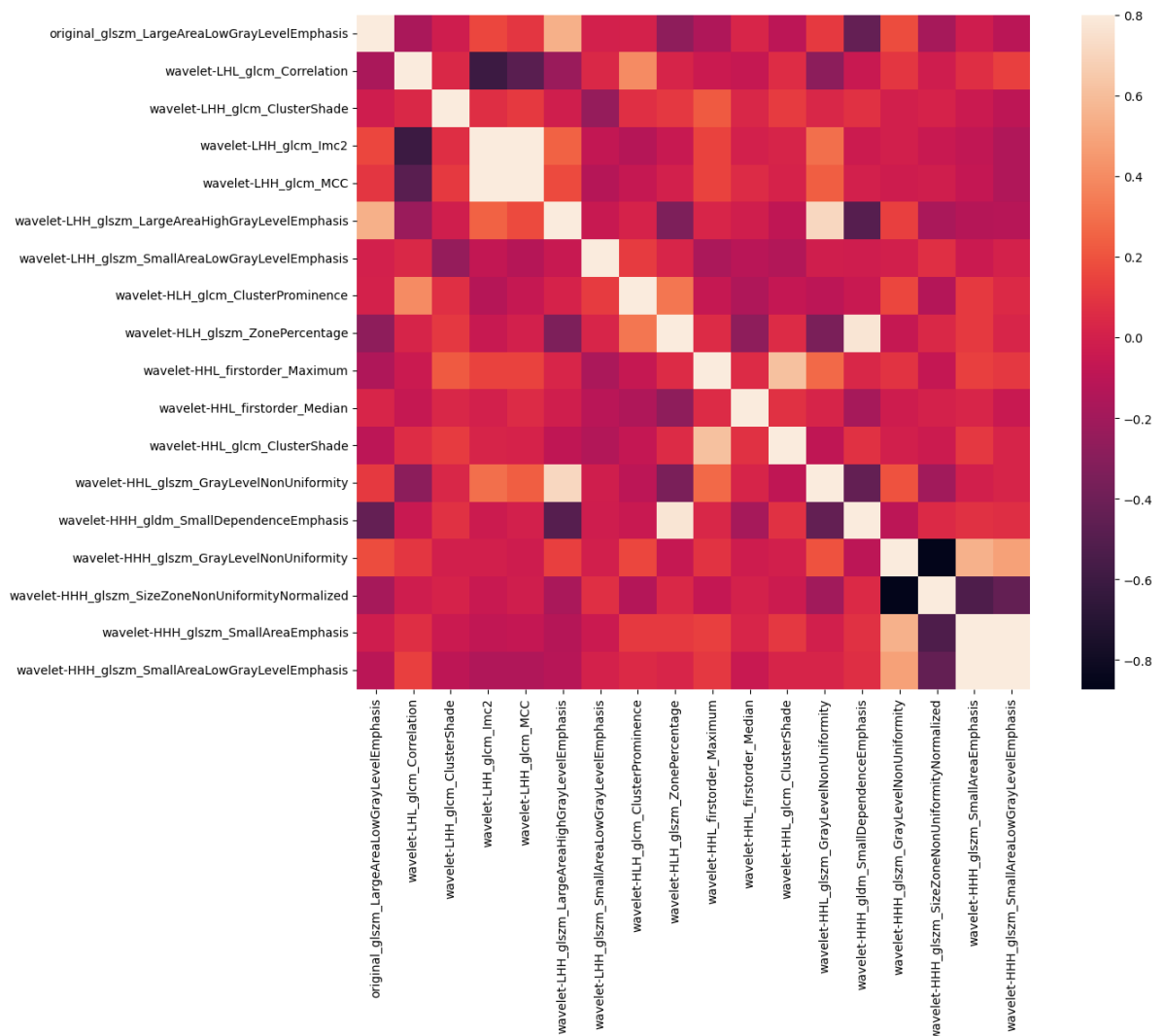
```
In [107... # 最终想要的18个特征
features_vif
```

```
Out[107]: ['original_glszm_LargeAreaLowGrayLevelEmphasis',
'wavelet-LHL_glcml_Correlation',
'wavelet-LHH_glcml_ClusterShade',
'wavelet-LHH_glcml_Imc2',
'wavelet-LHH_glcml_MCC',
'wavelet-LHH_glszm_LargeAreaHighGrayLevelEmphasis',
'wavelet-LHH_glszm_SmallAreaLowGrayLevelEmphasis',
'wavelet-HLH_glcml_ClusterProminence',
'wavelet-HLH_glszm_ZonePercentage',
'wavelet-HHL_firstorder_Maximum',
'wavelet-HHL_firstorder_Median',
'wavelet-HHL_glcml_ClusterShade',
'wavelet-HHL_glszm_GrayLevelNonUniformity',
'wavelet-HHH_gldm_SmallDependenceEmphasis',
'wavelet-HHH_glszm_GrayLevelNonUniformity',
'wavelet-HHH_glszm_SizeZoneNonUniformityNormalized',
'wavelet-HHH_glszm_SmallAreaEmphasis',
'wavelet-HHH_glszm_SmallAreaLowGrayLevelEmphasis']
```

```
In [103... # Construct a pandas dataframe from the samples
d = pd.DataFrame(data=features_df, columns=features_vif)
corr = d.corr()

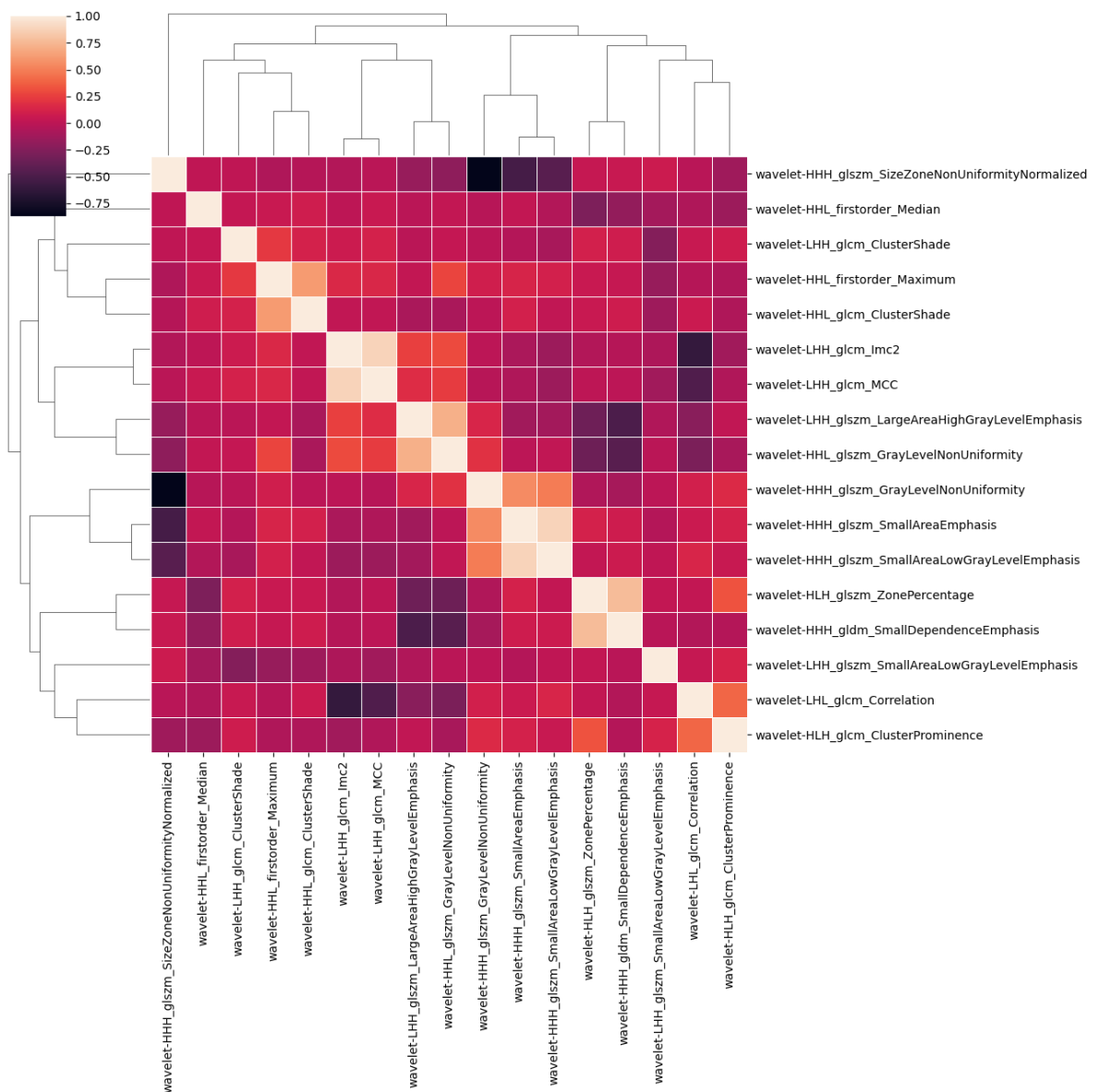
# Set up the matplotlib figure, make it big!
f, ax = plt.subplots(figsize=(15, 10))

# Draw the heatmap using seaborn
sns.heatmap(corr, vmax=.8, square=True)
plt.show()
```



In [104...

```
dd = d.iloc[:,1:50]
pp = sns.clustermap(dd.corr(), linewidths=.5, figsize=(13,13))
_ = plt.setp(pp.ax_heatmap.get_yticklabels(), rotation=0)
plt.show()
```



In [63]: len(features_vif)

Out[63]: 18

In [108...

```
# 将降维后的结果
X_train, X_test, Y_train, Y_test = train_test_split(XX, Y, test_size=0.15,
model = RandomForestClassifier()
model.fit(X_train, Y_train)
Y_pred = model.predict(X_test)
accuracy = accuracy_score(Y_test, Y_pred)
classification_report_str = classification_report(Y_test, Y_pred)
print(f"Accuracy: {accuracy}")
print("Classification Report:\n", classification_report_str)
```

Accuracy: 0.9

Classification Report:

	precision	recall	f1-score	support
0	0.90	1.00	0.95	18
1	0.00	0.00	0.00	2
accuracy			0.90	20
macro avg	0.45	0.50	0.47	20
weighted avg	0.81	0.90	0.85	20

```

/Users/shipingguo/anaconda3/lib/python3.11/site-packages/sklearn/metrics/_c
lassification.py:1469: UndefinedMetricWarning: Precision and F-score are ill-
defined and being set to 0.0 in labels with no predicted samples. Use `zero_
division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
/Users/shipingguo/anaconda3/lib/python3.11/site-packages/sklearn/metrics/_c
lassification.py:1469: UndefinedMetricWarning: Precision and F-score are ill-
defined and being set to 0.0 in labels with no predicted samples. Use `zero_
division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
/Users/shipingguo/anaconda3/lib/python3.11/site-packages/sklearn/metrics/_c
lassification.py:1469: UndefinedMetricWarning: Precision and F-score are ill-
defined and being set to 0.0 in labels with no predicted samples. Use `zero_
division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))

```

4.3 PCA降维

```

In [65]: def pca(data, n_dim):
        """
        pca is 0(D^3)
        :param data: (n_samples, n_features(D))
        :param n_dim: target dimensions
        :return: (n_samples, n_dim)
        """
        data = data - np.mean(data, axis = 0, keepdims = True)
        cov = np.dot(data.T, data)
        eig_values, eig_vector = np.linalg.eig(cov)
        # print(eig_values)
        indexs_ = np.argsort(-eig_values)[:n_dim]
        picked_eig_values = eig_values[indexs_]
        picked_eig_vector = eig_vector[:, indexs_]
        data_ndim = np.dot(data, picked_eig_vector)
        return data_ndim

```

```

In [66]: feature_pca3 = pca(X, 3)
        feature_pca3.shape

```

```

Out[66]: (132, 3)

```

```

In [67]: import random
        random_numbers = [random.randint(0, 131) for _ in range(len(Y))]
        fig = plt.figure()
        ax = fig.add_subplot(111, projection='3d')

        ax.scatter(feature_pca3[:, 0], feature_pca3[:, 1], feature_pca3[:, 2], c='r')
        ax.scatter(np.array(feature_pca3[random_numbers, 0])[np.array(Y[random_numbers, 0])],
                    np.array(feature_pca3[random_numbers, 1])[np.array(Y[random_numbers, 1])],
                    np.array(feature_pca3[random_numbers, 2])[np.array(Y[random_numbers, 2])],
                    c='b', marker='s', label='Group 1')

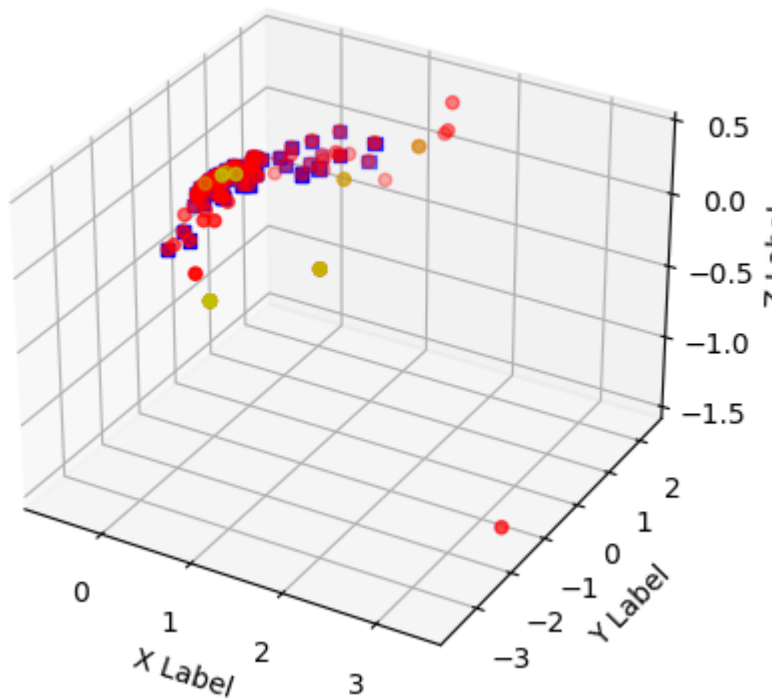
```

```
# Scatter plot for the second group (color_column == 1)
ax.scatter(np.array(feature_pca3[random_numbers, 0])[np.array(Y[random_numbers, 0])],
           np.array(feature_pca3[random_numbers, 1])[np.array(Y[random_numbers, 1])],
           np.array(feature_pca3[random_numbers, 2])[np.array(Y[random_numbers, 2])],
           c='y', marker='o', label='Group 2')

# Set labels for the axes
ax.set_xlabel('X Label')
ax.set_ylabel('Y Label')
ax.set_zlabel('Z Label')

# Show the plot
plt.show()
```

```
/Users/shipingguo/anaconda3/lib/python3.11/site-packages/matplotlib/collect
ions.py:192: ComplexWarning: Casting complex values to real discards the im
aginary part
    offsets = np.asanyarray(offsets, float)
/Users/shipingguo/anaconda3/lib/python3.11/site-packages/matplotlib/cbook/_
_init__.py:1335: ComplexWarning: Casting complex values to real discards th
e imaginary part
    return np.asarray(x, float)
/Users/shipingguo/anaconda3/lib/python3.11/site-packages/matplotlib/collect
ions.py:192: ComplexWarning: Casting complex values to real discards the im
aginary part
    offsets = np.asanyarray(offsets, float)
/Users/shipingguo/anaconda3/lib/python3.11/site-packages/matplotlib/cbook/_
_init__.py:1335: ComplexWarning: Casting complex values to real discards th
e imaginary part
    return np.asarray(x, float)
/Users/shipingguo/anaconda3/lib/python3.11/site-packages/matplotlib/collect
ions.py:192: ComplexWarning: Casting complex values to real discards the im
aginary part
    offsets = np.asanyarray(offsets, float)
/Users/shipingguo/anaconda3/lib/python3.11/site-packages/matplotlib/cbook/_
_init__.py:1335: ComplexWarning: Casting complex values to real discards th
e imaginary part
    return np.asarray(x, float)
/Users/shipingguo/anaconda3/lib/python3.11/site-packages/matplotlib/collect
ions.py:551: ComplexWarning: Casting complex values to real discards the im
aginary part
    (np.asanyarray(self.convert_xunits(offsets[:, 0]), float),
/Users/shipingguo/anaconda3/lib/python3.11/site-packages/matplotlib/collect
ions.py:552: ComplexWarning: Casting complex values to real discards the im
aginary part
    np.asanyarray(self.convert_yunits(offsets[:, 1]), float)))
/Users/shipingguo/anaconda3/lib/python3.11/site-packages/matplotlib/colors.
py:389: ComplexWarning: Casting complex values to real discards the imagina
ry part
    c = tuple(map(float, c))
```

4.4 查看一下在现有的数据上哪种分类表现的比较好

```
In [68]: from sklearn.ensemble import GradientBoostingClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.svm import SVC
from sklearn.neural_network import MLPClassifier
```

```
In [69]: model_score = np.zeros([30, 5])

for i in range(30):
    X_train, X_test, Y_train, Y_test = train_test_split(XXX, Y, test_size=0.2, random_state=i)
    # 随机森林模型
    model1 = RandomForestClassifier()
    model1.fit(X_train, Y_train)
    Y_pred1 = model1.predict(X_test)
    model_score[i, 0] = accuracy_score(Y_test, Y_pred1)

    model2 = GradientBoostingClassifier()
    model2.fit(X_train, Y_train)
    Y_pred2 = model2.predict(X_test)
    model_score[i, 1] = accuracy_score(Y_test, Y_pred2)

    model4 = DecisionTreeClassifier()
    model4.fit(X_train, Y_train)
    Y_pred4 = model4.predict(X_test)
    model_score[i, 2] = accuracy_score(Y_test, Y_pred4)

    model5 = SVC()
    model5.fit(X_train, Y_train)
    Y_pred5 = model5.predict(X_test)
    model_score[i, 3] = accuracy_score(Y_test, Y_pred5)

    model6 = MLPClassifier()
    model6.fit(X_train, Y_train)
    Y_pred6 = model6.predict(X_test)
    model_score[i, 4] = accuracy_score(Y_test, Y_pred6)
```

```
In [70]: print("Random forest: " + str(sum(model_score[:, 0])/30) )
print("Gradient Boosting: " + str(sum(model_score[:, 1])/30) )
print("Decision Tree: " + str(sum(model_score[:, 2])/30) )
print("SVC: " + str(sum(model_score[:, 3])/30) )
print("MLP: " + str(sum(model_score[:, 4])/30) )
```

```
Random forest: 0.9135802469135806
Gradient Boosting: 0.7654320987654322
Decision Tree: 0.7111111111111111
SVC: 0.8518518518518514
MLP: 0.6555555555555556
```

随机森林的效果比较好

下面以随机森林和支持向量机来判断哪一个降维的效果比较好

```
In [71]: accuracy_list = []
for i in range(2, 150, 2):
    feature_pca = pca(X, i)
    temp_accuracy = 0
    for j in range(10):
        X_train, X_test, Y_train, Y_test = train_test_split(np.real(feature_pca), Y, test_size=0.2, random_state=j)
        # 初始化随机森林模型
        model1 = RandomForestClassifier()
        model1.fit(X_train, Y_train)
        Y_pred = model1.predict(X_test)
        accuracy1 = accuracy_score(Y_test, Y_pred)
        # SVC
        model2 = SVC()
        model2.fit(X_train, Y_train)
        Y_pred = model2.predict(X_test)
        accuracy2 = accuracy_score(Y_test, Y_pred)
        accuracy = (accuracy1 + accuracy2)/2
```

```
temp_accuracy = temp_accuracy + accuracy
accuracy_list.append(temp_accuracy)
```

```
In [72]: # 找一下PCA降维哪个维度比较合适
for i in range(len(accuracy_list)):
    if accuracy_list[i]/10 > 0.85:
        print("Dimentions:" + str(2+5*i))
```

Dimensions:17
Dimensions:62
Dimensions:77
Dimensions:82
Dimensions:87
Dimensions:97
Dimensions:102
Dimensions:107
Dimensions:112
Dimensions:117
Dimensions:122
Dimensions:127
Dimensions:132
Dimensions:137
Dimensions:142
Dimensions:147
Dimensions:152
Dimensions:157
Dimensions:162
Dimensions:167
Dimensions:172
Dimensions:177
Dimensions:182
Dimensions:187
Dimensions:192
Dimensions:197
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Dimensions:242
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Dimensions:252
Dimensions:257
Dimensions:262
Dimensions:267
Dimensions:272
Dimensions:277
Dimensions:282
Dimensions:287
Dimensions:292
Dimensions:297
Dimensions:302
Dimensions:307
Dimensions:312
Dimensions:317
Dimensions:322
Dimensions:327
Dimensions:332
Dimensions:337
Dimensions:342
Dimensions:347
Dimensions:352
Dimensions:357
Dimensions:362
Dimensions:367

在维度比较低的时候准确率比较高

4.5 对比一下t检验和PCA降维

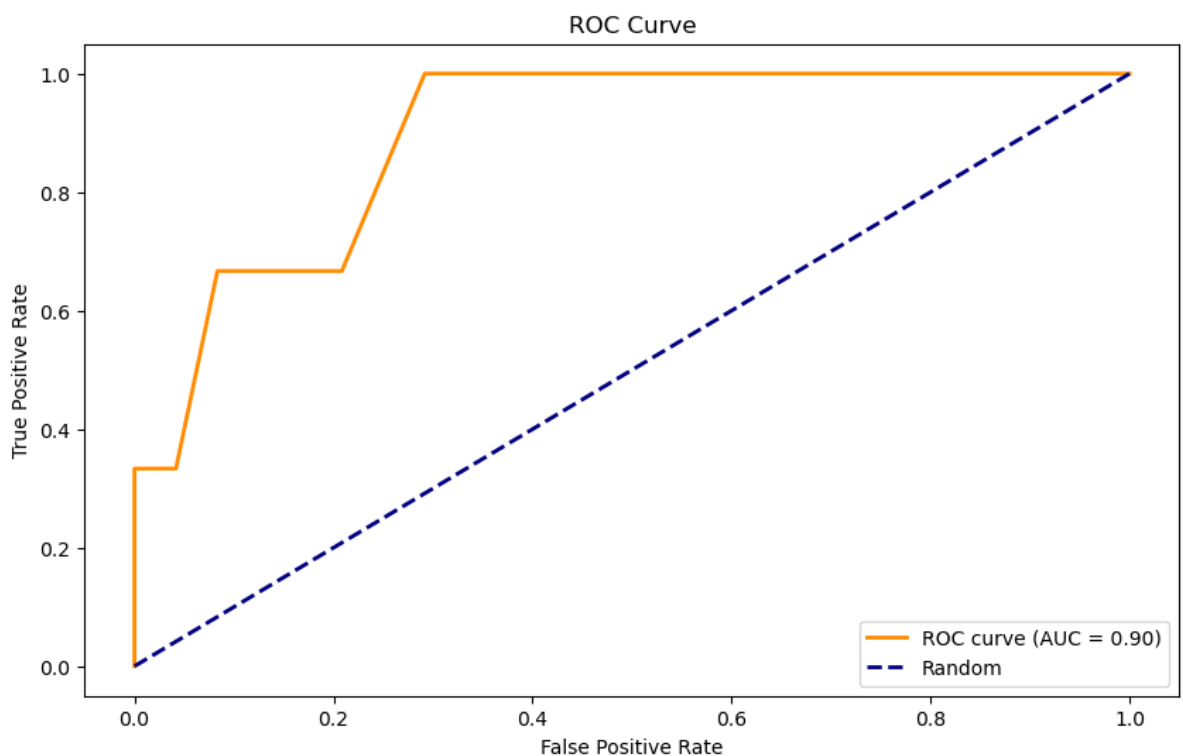
```
In [73]: t_model_score = []
#feature_pca = highdim_pca(X, 300)
# 测30次看平均准确率
for i in range(30):
    X_train, X_test, Y_train, Y_test = train_test_split(XXX, Y, test_size=0.2)
    # 随机森林模型
    model1 = RandomForestClassifier()
    model1.fit(X_train, Y_train)
    Y_pred1 = model1.predict(X_test)
    t_model_score.append(accuracy_score(Y_test, Y_pred1))
```

```
In [74]: sum(t_model_score)/30
```

```
Out[74]: 0.9135802469135808
```

```
In [75]: from sklearn.metrics import roc_curve, auc

# Get predicted probabilities for the positive class
y_pred_proba = model1.predict_proba(X_test)[: , 1]
# Calculate the ROC curve
fpr, tpr, thresholds = roc_curve(Y_test, y_pred_proba)
# Calculate the Area Under the Curve (AUC)
roc_auc = auc(fpr, tpr)
# Plot the ROC curve
plt.figure(figsize=(10, 6))
plt.plot(fpr, tpr, color='darkorange', lw=2, label=f'ROC curve (AUC = {roc_auc})')
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--', label='Random')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve')
plt.legend(loc='lower right')
plt.show()
```



PCA降维的结果并不怎么理想

Part 5. 探索一下提取更多特征看效果是否有提升

```
In [76]: def catch_features(imagePath, maskPath):
    if imagePath is None or maskPath is None: # Something went wrong, in the
        raise Exception('Error getting testcase!') # Raise exception to prevent
    settings = {}
    settings['binWidth'] = 25 # 5
    settings['sigma'] = [3, 5]
    settings['Interpolator'] = sitk.sitkBSpline
    settings['resampledPixelSpacing'] = [1, 1, 1] # 3,3,3
    settings['voxelArrayShift'] = 1000 # 300
    settings['normalize'] = True
    settings['normalizeScale'] = 100
    extractor = featureextractor.RadiomicsFeatureExtractor(**settings)

    extractor.enableImageTypeByName('LoG')
    extractor.enableImageTypeByName('Wavelet')
    extractor.enableAllImageTypes()
    extractor.enableAllFeatures()
    extractor.enableFeatureClassByName('firstorder')

    feature_cur = []
    feature_name = []
    result = extractor.execute(imagePath, maskPath, label=1)
    for key, value in six.iteritems(result):
        feature_name.append(key)
        feature_cur.append(value)

    name = feature_name[37:]
    name = np.array(name)
    for i in range(len(feature_cur[37:])):
        #if type(feature_cur[i+22]) != type(feature_cur[30]):
        feature_cur[i+37] = float(feature_cur[i+37])
    return feature_cur[37:], name
```

```
In [77]: # Test codes
imagePath = '/Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniversity of Singapore/Pituitary-segmentation-and-classification/Pituitary tumor document/Pituitary_tumor.ip...
maskPath = '/Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniversity of Singapore/Pituitary-segmentation-and-classification/Pituitary tumor document/Pituitary_tumor.ip...
feature_name, feature_cur = catch_features(imagePath, maskPath)
```

```

parameter force2D must be set to True to enable shape2D extraction
GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 need
s to be calculated
GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 need
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GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 need
s to be calculated
GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 need
s to be calculated
Calculating Local Binary Pattern in 2D, but extracting features in 3D. Use
with caution!
/Users/shipingguo/anaconda3/lib/python3.11/site-packages/skimage/feature/te
xture.py:353: UserWarning: Applying `local_binary_pattern` to floating-poin
t images may give unexpected results when small numerical differences betwe
en adjacent pixels are present. It is recommended to use this function with
images of integer dtype.
  warnings.warn(
GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 need
s to be calculated
Could not load required package "scipy" or "trimesh", cannot implement filt
er LBP 3D
GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 need
s to be calculated
GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 need
s to be calculated
GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 need
s to be calculated
GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 need
s to be calculated

```

```
In [78]: feature_N2 = len(feature_name)
```

```
In [79]: save_file2 = np.empty(shape=[1, feature_N2])
```

```
In [80]: save_file2 = np.delete(save_file2, 0, 0)
```

```
In [81]: save_file2
```

```
Out[81]: array([], shape=(0, 1595), dtype=float64)
```

1595个特征，然后用同样的方式分类查看准确率

```
In [82]: for patient_index in range (len(IMAGE_LIST)):
          # print("Images:" + images_list[patient_index])
          # print("Masks:" + masks_list[patient_index])
```



```

imagePath = os.path.join(imagesTr_normalized, IMAGE_LIST_NII[patient_index])
maskPath = os.path.join(labelsTr_nii, LABEL_LIST_NII[patient_index])
print(imagePath)
print(maskPath)

save_curdata, features_name = catch_features(imagePath, maskPath)
# print(len(save_curdata))
save_curdata = np.array(save_curdata)
save_curdata = save_curdata.reshape([1, feature_N2])
# id.append(PRE_IMAGE_LIST[patient_index].split('.')[0]) # Don't
# print(save_curdata)
# print(images_list[patient_index])
# np.concatenate((images_list[patient_index], save_curdata), axis=1)
save_file2 = np.append(save_file2, save_curdata, axis=0)
# print(save_file.shape)

```

/Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniversityofSingapore/Pituitary-segmentation-and-classification-/1_Classifer/imagesTr_normalized/Pituitarytumor_0_0000.nii

/Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniversityofSingapore/Pituitary-segmentation-and-classification-/1_Classifer/labelsTr_nii/Pituitarytumor_0.nii

parameter force2D must be set to True to enable shape2D extraction
 GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to be calculated
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 GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to be calculated
 GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to be calculated
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 GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to be calculated
 GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to be calculated
 Calculating Local Binary Pattern in 2D, but extracting features in 3D. Use with caution!
 GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to be calculated
 Could not load required package "scipy" or "trimesh", cannot implement filter LBP 3D
 GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to be calculated
 GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to be calculated
 GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to be calculated

/Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniversityofSingapore/Pituitary-segmentation-and-classification-/1_Classifer/imagesTr_normaliz
ed/Pituitarytumor_1_0000.nii

/Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniversityofSingapore/Pituitary-segmentation-and-classification-/1_Classifer/labelsTr_nii/Pitu
itarytumor_1.nii

parameter force2D must be set to True to enable shape2D extraction
GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 need
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parameter force2D must be set to True to enable shape2D extraction
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parameter force2D must be set to True to enable shape2D extraction
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```
In [83]: # save_file = np.delete(save_file, 0, 0)
# save_file = save_file.transpose()
# print(save_file.shape)
# id_num = len(id)
# id = np.array(id)
features_df2 = pd.DataFrame(save_file2)
# name_df.index = id
features_df2.columns = features_name
features_df2['Class'] = class_list
features_df2 = features_df2.reset_index(drop=True)

export_dir = '/Users/shipingguo/Library/CloudStorage/OneDrive-NationalUniver
# parent_directory = os.path.dirname(export_dir)
features_xlsx = os.path.join(export_dir, 'Radiomics-features2.xlsx')
writer = pd.ExcelWriter(features_xlsx)
features_df2.to_excel(writer)
writer.save()
```

```
/var/folders/53/tlbwbq3n5lz3nsqwqwk1p30w0000gn/T/ipykernel_16576/347745362
4.py:17: FutureWarning: save is not part of the public API, usage can give
unexpected results and will be removed in a future version
writer.save()
```

```
In [84]: X_2 = features_df2.iloc[:, 0:-1].values # we only take the first two featur
Y_2 = features_df2['Class']
columns = features_df2.columns
related_features_name = []
print('Related features:')
for column in columns[0:-1]:
    t_score = t_test('Class', column, features_df2)
    if t_score<0.1:
        related_features_name.append(column)
        print(column)
```


Related features:

original_firstorder_Minimum
original_glszm_LargeAreaLowGrayLevelEmphasis
log-sigma-3-mm-3D_glr1m_ShortRunLowGrayLevelEmphasis
log-sigma-5-mm-3D_gldm_DependenceNonUniformityNormalized
wavelet-LHL_glc1m_Correlation
wavelet-LHH_glc1m_ClusterShade
wavelet-LHH_glc1m_Correlation
wavelet-LHH_glc1m_Imc2
wavelet-LHH_glc1m_InverseVariance
wavelet-LHH_glc1m_MCC
wavelet-LHH_gldm_DependenceEntropy
wavelet-LHH_gldm_DependenceNonUniformityNormalized
wavelet-LHH_gldm_DependenceVariance
wavelet-LHH_glszm_LargeAreaHighGrayLevelEmphasis
wavelet-LHH_glszm_SmallAreaLowGrayLevelEmphasis
wavelet-HLH_glc1m_ClusterProminence
wavelet-HLH_gldm_DependenceEntropy
wavelet-HLH_gldm_DependenceNonUniformityNormalized
wavelet-HLH_gldm_DependenceVariance
wavelet-HLH_glszm_ZonePercentage
wavelet-HHL_firstorder_Maximum
wavelet-HHL_firstorder_Median
wavelet-HHL_glc1m_ClusterShade
wavelet-HHL_glszm_GrayLevelNonUniformity
wavelet-HHL_ngtdm_Complexity
wavelet-HHH_gldm_DependenceEntropy
wavelet-HHH_gldm_DependenceNonUniformityNormalized
wavelet-HHH_gldm_DependenceVariance
wavelet-HHH_gldm_SmallDependenceEmphasis
wavelet-HHH_glszm_GrayLevelNonUniformity
wavelet-HHH_glszm_SizeZoneNonUniformityNormalized
wavelet-HHH_glszm_SmallAreaEmphasis
wavelet-HHH_glszm_SmallAreaLowGrayLevelEmphasis
wavelet-HHH_glszm_ZoneEntropy
wavelet-LLL_firstorder_Energy
wavelet-LLL_firstorder_Minimum
wavelet-LLL_firstorder_TotalEnergy
exponential_glr1m_RunEntropy
exponential_glszm_ZoneVariance
gradient_glc1m_Imc1
gradient_glszm_LargeAreaEmphasis
gradient_glszm_LargeAreaLowGrayLevelEmphasis
gradient_glszm_SmallAreaLowGrayLevelEmphasis
gradient_glszm_ZoneVariance
lbp-2D_firstorder_90Percentile
lbp-2D_firstorder_Entropy
lbp-2D_firstorder_RobustMeanAbsoluteDeviation
lbp-2D_glc1m_DifferenceEntropy
lbp-2D_glc1m_JointEntropy
lbp-2D_glc1m_SumEntropy
lbp-2D_gldm_SmallDependenceEmphasis
lbp-2D_gldm_SmallDependenceHighGrayLevelEmphasis
lbp-2D_gldm_SmallDependenceLowGrayLevelEmphasis
lbp-2D_glr1m_ShortRunEmphasis
lbp-2D_glr1m_ShortRunHighGrayLevelEmphasis
lbp-2D_glr1m_ShortRunLowGrayLevelEmphasis
logarithm_glc1m_InverseVariance
square_glr1m_RunEntropy
square_glszm_SmallAreaLowGrayLevelEmphasis
squareroot_glc1m_InverseVariance

```

/var/folders/53/tlbwbq3n5lz3nsqwqwk1p30w0000gn/T/ipykernel_16576/967509918.
py:23: RuntimeWarning: Precision loss occurred in moment calculation due to
catastrophic cancellation. This occurs when the data are nearly identical.
Results may be unreliable.
    p_t = ttest_ind(type_one, type_two)
/Users/shipingguo/anaconda3/lib/python3.11/site-packages/scipy/stats/_morest
ats.py:2710: RuntimeWarning: invalid value encountered in scalar divide
    W = numer / denom
/var/folders/53/tlbwbq3n5lz3nsqwqwk1p30w0000gn/T/ipykernel_16576/967509918.
py:26: RuntimeWarning: Precision loss occurred in moment calculation due to
catastrophic cancellation. This occurs when the data are nearly identical.
Results may be unreliable.
    p_t = ttest_ind(type_one, type_two, equal_var=False)

```

```
In [85]: len(related_features_name)
```

```
Out[85]: 60
```

```
In [86]: XX_2 = features_df2[related_features_name]
vif = [variance_inflation_factor(XX_2.values, XX_2.columns.get_loc(i)) for i in range(XX_2.shape[1])]

/Users/shipingguo/anaconda3/lib/python3.11/site-packages/statsmodels/stats/outliers_influence.py:198: RuntimeWarning: divide by zero encountered in scalar divide
    vif = 1. / (1. - r_squared_i)
```

```
In [87]: print(len(related_features_name))
features_vif = []
for i in range(len(vif)):
    if vif[i]<10:
        features_vif.append(related_features_name[i])
print(len(features_vif))

XXX_2 = features_df2[features_vif]

60
24
```

```
In [88]: t_model_score = []
#feature_pca = highdim_pca(X, 300)

for i in range(30):
    X_train, X_test, Y_train, Y_test = train_test_split(XXX_2, Y_2, test_size=0.2, random_state=i)
    # 随机森林模型
    model1 = RandomForestClassifier()
    model1.fit(X_train, Y_train)
    Y_pred1 = model1.predict(X_test)
    t_model_score.append(accuracy_score(Y_test, Y_pred1))
```

```
In [89]: sum(t_model_score)/30
```

```
Out[89]: 0.8703703703703703
```

效果并不理想，所以保持原来的特征与降维方式