

BMI260_Problem_Set_2_XZhan

April 20, 2024

1 BIOMEDIN 260/RAD260: Problem Set 2 - Mammography Binary Classification

1.1 Spring 2024

1.2 Group Members

Person 1:

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Welcome to Problem Set 2!

1.3 Problem 1: Geometric Features (20 points)

As you may recall from class, the geometric features of a tumor can sometimes reveal significant information about whether it is benign or malignant. [Radiologists frequently assess the geometry of lesions in mammograms when attempting to diagnose breast cancer.](#)

In this exercise, we will attempt to explore some quantitative methods of differentiating between certain lesion shapes.

Download the two mammograms from Canvas. `LEFT_CC_BENIGN.tif` depicts a cranial-caudal view (looking down on the breast from the patient's perspective) of the left breast. There is a benign lesion present in the mammogram. Can you locate it?

If you are having difficulty locating the lesion, try seeing if you can spot it in the mask `LEFT_CC_BENIGN_MASK.tif`, which consists of a rough segmentation of the lesion. `RIGHT_CC_MALIGNANT.tif` and `RIGHT_CC_MALIGNANT_MASK.tif` are the mammogram and corresponding lesion segmentation of a different patient, but this mammogram depicts a breast with a **malignant** tumor.

a. Start by loading these two mammograms and their corresponding masks as image matrices. Plot them on a single figure (using a 2-by-2 grid of subplots). You should use reasonable `x` and `y` limits in your figures to get a reasonable depiction of your lesion segmentations.

Qualitatively describe the shape differences between the two lesions. What types of shapes and margins are indicative of malignant tumors?

```
[1]: # If using Google Colab:
import os
from google.colab import drive
```

```
drive.mount('/content/drive/')  
# TODO: Import data from Google Drive
```

Mounted at /content/drive/

```
[2]: #lets install SimpleITK first  
import sys  
!{sys.executable} -m pip install SimpleITK
```

Collecting SimpleITK

Downloading

SimpleITK-2.3.1-cp310-cp310-manylinux_2_17_x86_64.manylinux2014_x86_64.whl (52.7 MB)

52.7/52.7 MB

11.2 MB/s eta 0:00:00

Installing collected packages: SimpleITK

Successfully installed SimpleITK-2.3.1

```
[3]: cd "/content/drive/MyDrive/Stanford ACA/BIOMEDIN 260/PSet 2"
```

/content/drive/MyDrive/Stanford ACA/BIOMEDIN 260/PSet 2

```
[4]: import matplotlib.pyplot as plt  
from skimage.filters import threshold_otsu  
import SimpleITK as sitk  
%matplotlib inline  
  
## Load mammograms showing benign and malignant tumors.  
  
img_benign = sitk.ReadImage('LEFT_CC_BENIGN.tif')  
mask_benign = sitk.ReadImage('LEFT_CC_BENIGN_MASK.tif')  
  
img_malignant = sitk.ReadImage('RIGHT_CC_MALIGNANT.tif')  
mask_malignant = sitk.ReadImage('RIGHT_CC_MALIGNANT_MASK.tif')  
  
# converting sitk images to np arrays  
img_benign_np = sitk.GetArrayFromImage(img_benign)  
mask_benign_np = sitk.GetArrayFromImage(mask_benign)  
  
img_malignant_np = sitk.GetArrayFromImage(img_malignant)  
mask_malignant_np = sitk.GetArrayFromImage(mask_malignant)  
  
## TODO: Plotting code here  
  
### WRITE CODE IN HERE. You can have up to 2 cells for this question, but only 1  
→ one is required #####  
  
# Create a 2x2 subplot
```

```
fig, ax = plt.subplots(2, 2, figsize=(10, 10))
```

```
# Plotting the images and masks
```

```
ax[0, 0].imshow(img_benign_np, cmap='gray')
```

```
ax[0, 0].set_title('Benign Mammogram')
```

```
ax[0, 0].set_xlim([1000,2000])
```

```
ax[0, 0].set_ylim([2000,3000])
```

```
ax[0, 1].imshow(mask_benign_np, cmap='gray')
```

```
ax[0, 1].set_title('Mask for Benign')
```

```
ax[0, 1].set_xlim([1000,2000])
```

```
ax[0, 1].set_ylim([2000,3000])
```

```
ax[1, 0].imshow(img_malignant_np, cmap='gray')
```

```
ax[1, 0].set_title('Malignant Mammogram')
```

```
ax[1, 0].set_xlim([1000,2000])
```

```
ax[1, 0].set_ylim([3000,4000])
```

```
ax[1, 1].imshow(mask_malignant_np, cmap='gray')
```

```
ax[1, 1].set_title('Mask for Malignant')
```

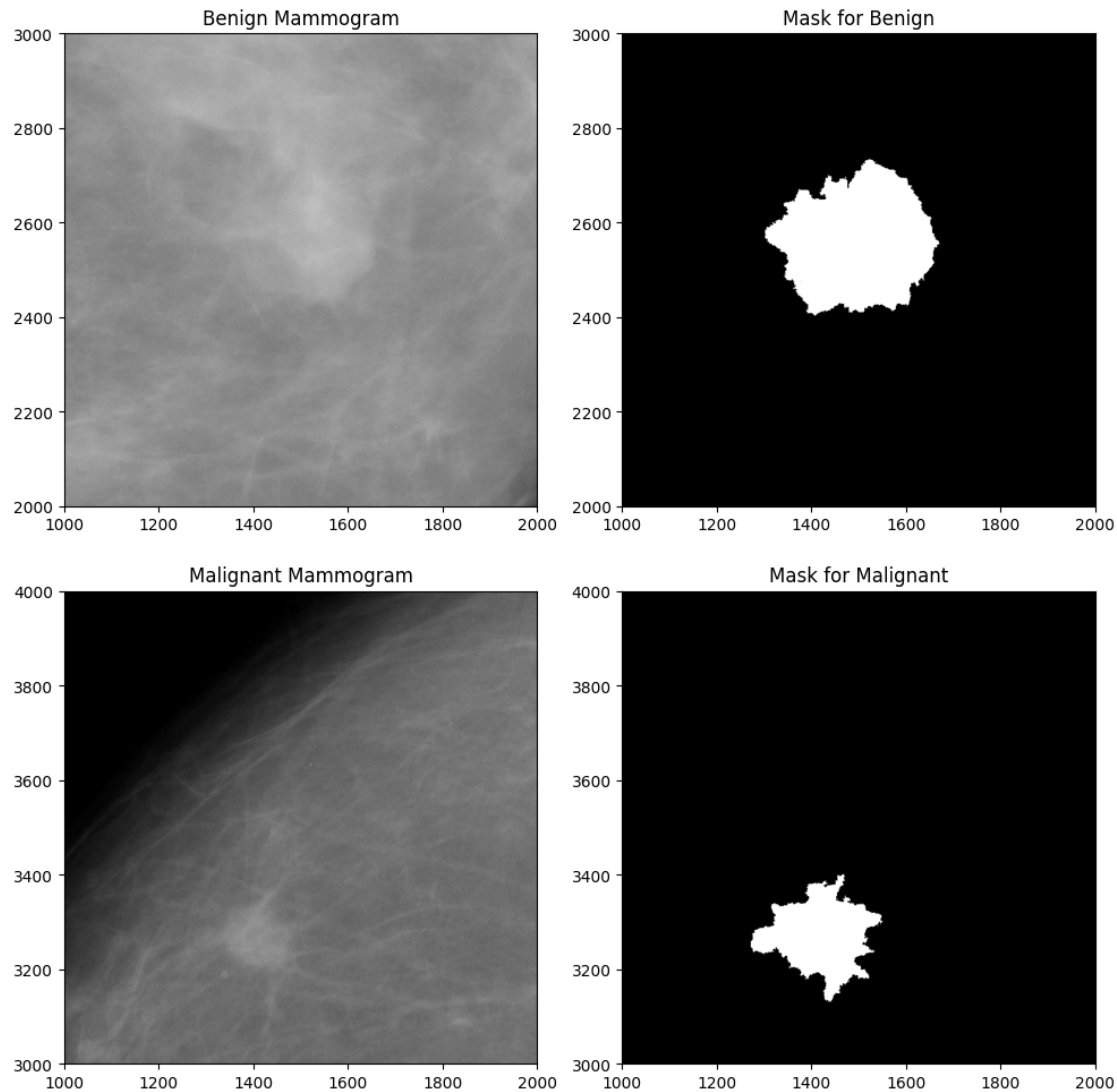
```
ax[1, 1].set_xlim([1000,2000])
```

```
ax[1, 1].set_ylim([3000,4000])
```

```
plt.tight_layout()
```

```
plt.show()
```

```
#####
```



Answer: The more spiky shape is indicative of the malignant tumors

b. Next, try computing some basic geometric features of the two lesions. Which features are the most significant for differentiating between them? Is this what you expected? The `regionprops()` function in the `skimage` library will automatically compute several geometric features for you, but you might choose to code up some of your own. If you don't trust the provided segmentations, feel free to create your segmentation method or modify the provided ones to get a better estimate of the lesion shapes! Finally, it could be interesting to apply some edge-detection filters to the mammograms to better emphasize the margins.

You can also test your approach on other mammograms from a [larger dataset \(~20 GB\)](#) (Stanford Google account required for access). You will need these mammograms for the next part of the problem set, so there's no harm in loading in or downloading the images now!

There is no single correct answer for this exercise, and you should definitely try several

different approaches and explore, and be sure to explain your interpretation of your findings!

Answer: According to the results, it seems that solidity is a good feature to discriminate benign tumors from malignant tumors.

```
[5]: from skimage.measure import regionprops

    ### WRITE CODE IN HERE. You can have up to 2 cells for this question, but only
    →one is required #####
    from skimage.measure import label, regionprops_table

    label_benign = label(mask_benign_np)
    label_malignant = label(mask_malignant_np)

    regions_benign = regionprops(label_benign)
    regions_malignant = regionprops(label_malignant)

    def print_region_properties(regions, tumor_type, min_area=100):
        print(f"Properties for {tumor_type} tumors:")
        for i, region in enumerate(regions):
            if region.area > min_area: # Filter out very small regions
                print(f"  Tumor {i+1}:")
                print(f"    Area: {region.area}")
                print(f"    Perimeter: {region.perimeter}")
                print(f"    Eccentricity: {region.eccentricity}")
                print(f"    Solidity: {region.solidity}")

    print_region_properties(regions_benign, "Benign")
    print_region_properties(regions_malignant, "Malignant")
    #####
```

Properties for Benign tumors:

Tumor 1:

Area: 79148

Perimeter: 1696.481456229631

Eccentricity: 0.4772014180075201

Solidity: 0.8917783060854281

Properties for Malignant tumors:

Tumor 2:

Area: 35507

Perimeter: 1499.2844507162113

Eccentricity: 0.4845676212963806

Solidity: 0.7188233865090291

1.4 Problem 2: Radiomic Classifier (80 points)

Start by loading in / downloading the large mammogram set from [here](#) (~20 GB) (Stanford Google account required for access).

Computing features can be complicated very quickly, and specialized radiomics packages exist to help the process (e.g., [pyradiomics](#)). Such packages are often well tested and are used by many in research studies and described in papers.

For the next exercise, you will use the package `pyradiomics` and perform a binary classification task, to distinguish between two categories, benign and malignant breast nodules (labels provided in [labels_small.csv](#)). Here, we are interested in implementing and testing the different steps required to implement a machine learning classifier and the experimental design for how to train a classifier using medical images.

Training classifiers using medical data can be tricky, so in this exercise, the experimental design (how you compute the features, what classifier and evaluation strategies), are more important than the final accuracy. **You are not going to be graded on the accuracy of your model, but on how you got to your answers.**

1.4.1 a) Extract Features (20 points)

Install [pyradiomics](#), and go over the online documentation to identify what features can be extracted and how one can adjust their parameters within `pyradiomics`.

Extract the following three types of features: * morphologic shape2D features * first order statistics * haralick features (derived from Gray Level Co-occurrence Matrices)

By default, the feature extractor in `pyradiomics` will extract a lot more features, so follow the documents to figure out how to extract only a subset of features.

Side note: `Pyradiomics` requires a well know package for medical images, i.e., [SimpleITK](#). While you can read your data using other packages, its a lot easier to just use `SimpleITK` for both reading and pushing images into `pyradiomics`.

Follow the next steps to answer this question:

- (i) Use `SimpleITK` (`sitk`) to read one image and the corresponding mask from the dataset. Check if the size, origin, spacing, and direction of the image and the corresponding mask are same using `sitk` functions. Use `sitk.SetOrigin()`, `sitk.SetSpacing()` etc. functions to align the origin, spacing, and direction of the mask to the image, if they are not aligned. Why is this alignment important?
- (ii) Use a parameter file to specify parameters for feature extraction and extract radiomics features using this parameter file. See an example parameter file for 2D images here: https://github.com/AIM-Harvard/pyradiomics/blob/master/examples/exampleSettings/MR_2D_extraction.yaml. Modify this parameter file to (1) use original images without any filtering, and (2) extract morphologic features, first order statistics, and Haralick features only, (3) remove the `resampledPixelSpacing` parameter, (4) set `binwidth` to 40. You can leave the other parameter settings in this file intact.
- (iii) Play with the parameter setting 'binwidth' and extract features with 3 widely different binwidth values. Does varying binwidth affect extracted features? Why?

Note: You only need to extract features for *1000 randomly sampled images*.

Answer: i) Alignment makes the masks meaningful segmentation of the tumor. Otherwise, the segmentation doesn't have a value if not overlapping with the raw images.

ii) imageType: Original: {}

featureClass: shape2D:{} firstorder:{} glcm:{}
setting: normalize: true normalizeScale: 100

padDistance: 10 preCrop: true

force2D: true force2Ddimension: 0

binWidth: 40

voxelArrayShift: 300

label: 1

iii) Yes because bin width is a parameter used in the discretization process of image intensities. It defines the size of the intervals that the range of image intensities is divided into before calculating texture and other statistical features. Too coarse the bins are will lead to loss of information while too fine the bins are will lead to noise in the fine details of the relative changes in the pixel intensities.

```
[5]: #lets install pyradiomics first
import sys
!{sys.executable} -m pip install pyradiomics
```

Collecting pyradiomics

Downloading pyradiomics-3.1.0.tar.gz (34.5 MB)

34.5/34.5 MB

9.6 MB/s eta 0:00:00

Installing build dependencies ... done

Getting requirements to build wheel ... done

Installing backend dependencies ... done

Preparing metadata (pyproject.toml) ... done

Discarding

→ [https://files.pythonhosted.org/packages/03/c1/20fc2c50ab1e3304da36d866042a1905a2b05a1431ece3](https://files.pythonhosted.org/packages/03/c1/20fc2c50ab1e3304da36d866042a1905a2b05a1431ece35448ab6b4578f2/pyradiomics-3.1.0.tar.gz)

→ Requested pyradiomics from https

://files.pythonhosted.org/packages/03/c1/20fc2c50ab1e3304da36d866042a1905a2b05a1

431ece35448ab6b4578f2/pyradiomics-3.1.0.tar.gz has inconsistent version:

expected '3.1.0', but metadata has '3.0.1a1'

Downloading pyradiomics-3.0.1.tar.gz (34.5 MB)

34.5/34.5 MB

39.4 MB/s eta 0:00:00

Preparing metadata (setup.py) ... done

Requirement already satisfied: numpy>=1.9.2 in /usr/local/lib/python3.10/dist-packages (from pyradiomics) (1.25.2)

Requirement already satisfied: SimpleITK>=0.9.1 in

/usr/local/lib/python3.10/dist-packages (from pyradiomics) (2.3.1)

```

Requirement already satisfied: PyWavelets>=0.4.0 in
/usr/local/lib/python3.10/dist-packages (from pyradiomics) (1.6.0)
Collecting pykwality>=1.6.0 (from pyradiomics)
  Downloading pykwality-1.8.0-py2.py3-none-any.whl (24 kB)
Requirement already satisfied: six>=1.10.0 in /usr/local/lib/python3.10/dist-
packages (from pyradiomics) (1.16.0)
Collecting docopt>=0.6.2 (from pykwality>=1.6.0->pyradiomics)
  Downloading docopt-0.6.2.tar.gz (25 kB)
  Preparing metadata (setup.py) ... done
Requirement already satisfied: python-dateutil>=2.8.0 in
/usr/local/lib/python3.10/dist-packages (from pykwality>=1.6.0->pyradiomics)
(2.8.2)
Collecting ruamel.yaml>=0.16.0 (from pykwality>=1.6.0->pyradiomics)
  Downloading ruamel.yaml-0.18.6-py3-none-any.whl (117 kB)
    117.8/117.8

kB 12.1 MB/s eta 0:00:00
Collecting ruamel.yaml.clib>=0.2.7 (from
ruamel.yaml>=0.16.0->pykwality>=1.6.0->pyradiomics)
  Downloading ruamel.yaml.clib-0.2.8-cp310-cp310-manylinux_2_17_x86_64.manylinux
2014_x86_64.manylinux_2_24_x86_64.whl (526 kB)
    526.7/526.7

kB 32.4 MB/s eta 0:00:00
Building wheels for collected packages: pyradiomics, docopt
  Building wheel for pyradiomics (setup.py) ... done
  Created wheel for pyradiomics:
filename=pyradiomics-3.0.1-cp310-cp310-linux_x86_64.whl size=169935
sha256=c15306265cd1be40a2361c78b58d14fef943248da6799d6cd2e62615f650629e
  Stored in directory: /root/.cache/pip/wheels/91/c5/13/c5fd4c5ad3edf4062bb3855b
d66fad25871c9c6dc0b3fda544
  Building wheel for docopt (setup.py) ... done
  Created wheel for docopt: filename=docopt-0.6.2-py2.py3-none-any.whl
size=13706
sha256=4ce094cc3157e26e15193af9b103052be4a0f712632a6625838964a505b20fd4
  Stored in directory: /root/.cache/pip/wheels/fc/ab/d4/5da2067ac95b36618c629a5f
93f809425700506f72c9732fac
Successfully built pyradiomics docopt
Installing collected packages: docopt, ruamel.yaml.clib, ruamel.yaml, pykwality,
pyradiomics
Successfully installed docopt-0.6.2 pykwality-1.8.0 pyradiomics-3.0.1
ruamel.yaml-0.18.6 ruamel.yaml.clib-0.2.8

```

```
[7]: ### WRITE CODE IN HERE.#####
```

```

#importing relevant libraries
import SimpleITK as sitk

```

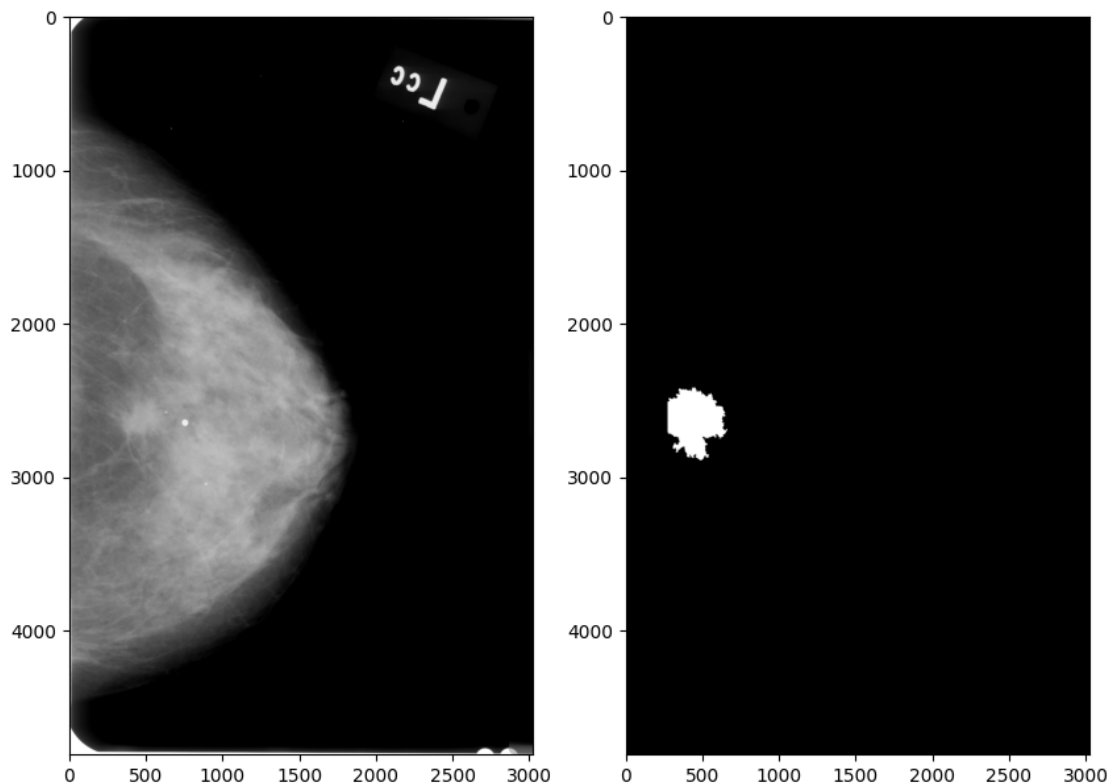


```
##### ----- reading the first image and the correpsonding mask
img = sitk.ReadImage('/content/drive/MyDrive/Stanford ACA/BIOMEDIN 260/PSet 2/
↳images/images/P_00001_LEFT_CC.tif')
mask = sitk.ReadImage('/content/drive/MyDrive/Stanford ACA/BIOMEDIN 260/PSet 2/
↳masks/masks/P_00001_LEFT_CC.tif')

img_np = sitk.GetArrayFromImage(img)
mask_np = sitk.GetArrayFromImage(mask)

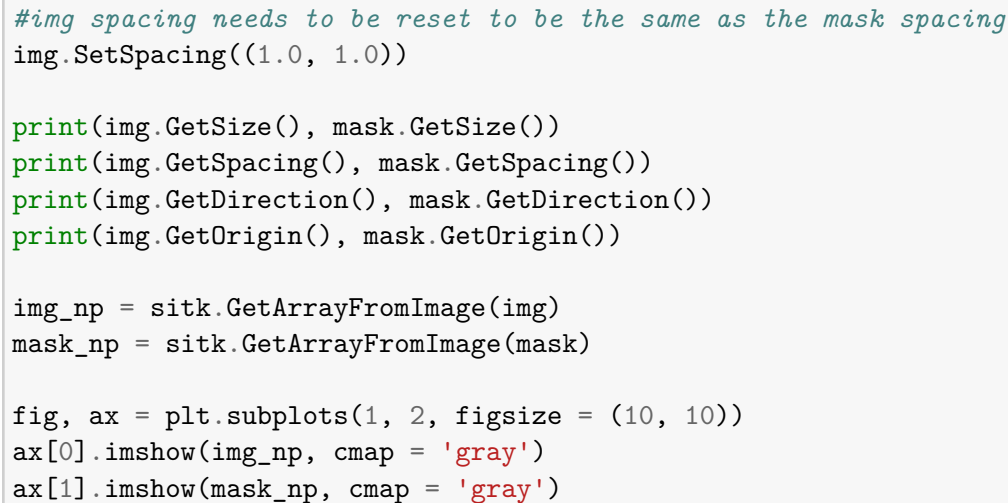
fig, ax = plt.subplots(1, 2, figsize = (10, 10))
ax[0].imshow(img_np, cmap = 'gray')
ax[1].imshow(mask_np, cmap = 'gray')
#####
```

[7]: <matplotlib.image.AxesImage at 0x7d2ea51e6c50>



```
[8]: print(img.GetSize(), mask.GetSize())
print(img.GetSpacing(), mask.GetSpacing())
print(img.GetDirection(), mask.GetDirection())
print(img.GetOrigin(), mask.GetOrigin())
```

```


#img spacing needs to be reset to be the same as the mask spacing
img.SetSpacing((1.0, 1.0))

print(img.GetSize(), mask.GetSize())
print(img.GetSpacing(), mask.GetSpacing())
print(img.GetDirection(), mask.GetDirection())
print(img.GetOrigin(), mask.GetOrigin())

img_np = sitk.GetArrayFromImage(img)
mask_np = sitk.GetArrayFromImage(mask)

fig, ax = plt.subplots(1, 2, figsize = (10, 10))
ax[0].imshow(img_np, cmap = 'gray')
ax[1].imshow(mask_np, cmap = 'gray')

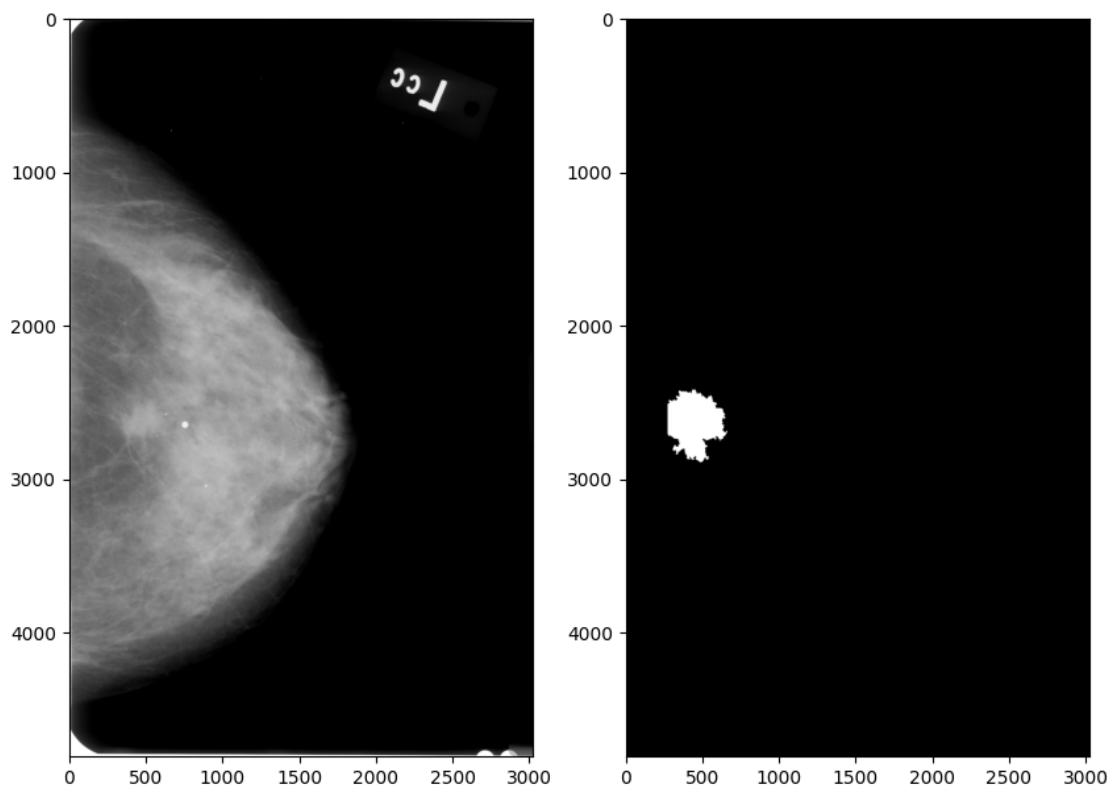
```

```

(3024, 4808) (3024, 4808)
(0.35277777777777775, 0.35277777777777775) (1.0, 1.0)
(1.0, 0.0, 0.0, 1.0) (1.0, 0.0, 0.0, 1.0)
(0.0, 0.0) (0.0, 0.0)
(3024, 4808) (3024, 4808)
(1.0, 1.0) (1.0, 1.0)
(1.0, 0.0, 0.0, 1.0) (1.0, 0.0, 0.0, 1.0)
(0.0, 0.0) (0.0, 0.0)

```

[8]: <matplotlib.image.AxesImage at 0x7d2e42cd6c20>



```
[9]: from radiomics import featureextractor

extractor1 = featureextractor.RadiomicsFeatureExtractor('/content/drive/MyDrive/
↳Stanford ACA/BIOMEDIN 260/PSet 2/modified_Bin40.yaml')
extractor2 = featureextractor.RadiomicsFeatureExtractor('/content/drive/MyDrive/
↳Stanford ACA/BIOMEDIN 260/PSet 2/modified_Bin4.yaml')
extractor3 = featureextractor.RadiomicsFeatureExtractor('/content/drive/MyDrive/
↳Stanford ACA/BIOMEDIN 260/PSet 2/modified_Bin400.yaml')

feature1 = extractor1.execute(img, mask, label = 255)
feature2 = extractor2.execute(img, mask, label = 255)
feature3 = extractor3.execute(img, mask, label = 255)
```

```
INFO:radiomics.featureextractor:Loading parameter file
/content/drive/MyDrive/Stanford ACA/BIOMEDIN 260/PSet 2/modified_Bin40.yaml
INFO:radiomics.featureextractor:Loading parameter file
/content/drive/MyDrive/Stanford ACA/BIOMEDIN 260/PSet 2/modified_Bin4.yaml
INFO:radiomics.featureextractor:Loading parameter file
/content/drive/MyDrive/Stanford ACA/BIOMEDIN 260/PSet 2/modified_Bin400.yaml
INFO:radiomics.featureextractor:Calculating features with label: 255
INFO:radiomics.featureextractor:Loading image and mask
INFO:radiomics.featureextractor:Computing shape2D
INFO:radiomics.featureextractor:Adding image type "Original" with custom
settings: {}
INFO:radiomics.featureextractor:Calculating features for original image
INFO:radiomics.featureextractor:Computing firstorder
INFO:radiomics.featureextractor:Computing glcm
GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to
be calculated
WARNING:radiomics.glcm:GLCM is symmetrical, therefore Sum Average = 2 * Joint
Average, only 1 needs to be calculated
INFO:radiomics.featureextractor:Calculating features with label: 255
INFO:radiomics.featureextractor:Loading image and mask
INFO:radiomics.featureextractor:Computing shape2D
INFO:radiomics.featureextractor:Adding image type "Original" with custom
settings: {}
INFO:radiomics.featureextractor:Calculating features for original image
INFO:radiomics.featureextractor:Computing firstorder
INFO:radiomics.featureextractor:Computing glcm
GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to
be calculated
WARNING:radiomics.glcm:GLCM is symmetrical, therefore Sum Average = 2 * Joint
Average, only 1 needs to be calculated
INFO:radiomics.featureextractor:Calculating features with label: 255
INFO:radiomics.featureextractor:Loading image and mask
```

```
INFO:radiomics.featureextractor:Computing shape2D
INFO:radiomics.featureextractor:Adding image type "Original" with custom
settings: {}
INFO:radiomics.featureextractor:Calculating features for original image
INFO:radiomics.featureextractor:Computing firstorder
INFO:radiomics.featureextractor:Computing glcm
GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to
be calculated
WARNING:radiomics.glcm:GLCM is symmetrical, therefore Sum Average = 2 * Joint
Average, only 1 needs to be calculated
```

```
[10]: keys = list(feature1.keys())
numeric_keys = keys[keys.index('original_shape2D_Elongation'):] # Remove the
↳PyRadiomics and Image information, since "original_shape2D_Elongation" is
↳the first real feature"
#Evaluate the influence of varying bins
for key in numeric_keys:
    print(key, '\t', feature1[key], '\t', feature2[key], '\t', feature3[key])
```

```
original_shape2D_Elongation      0.8444555376960288      0.8444555376960288
0.8444555376960288
original_shape2D_MajorAxisLength      438.5273784954608
438.5273784954608      438.5273784954608
original_shape2D_MaximumDiameter      490.40799340956914
490.40799340956914      490.40799340956914
original_shape2D_MeshSurface      120549.5      120549.5      120549.5
original_shape2D_MinorAxisLength      370.31687320181425
370.31687320181425      370.31687320181425
original_shape2D_Perimeter      3131.2429996246465      3131.2429996246465
3131.2429996246465
original_shape2D_PerimeterSurfaceRatio      0.02597474895893095
0.02597474895893095      0.02597474895893095
original_shape2D_PixelSurface      120561.0      120561.0      120561.0
original_shape2D_Sphericity      0.3930708758396848      0.3930708758396848
0.3930708758396848
original_firstorder_10Percentile      113.66769521217881
113.66769521217881      113.66769521217881
original_firstorder_90Percentile      195.2285988231382
195.2285988231382      195.2285988231382
original_firstorder_Energy      25115065221.36046      25115065221.36046
25115065221.36046
original_firstorder_Entropy      1.683019872318755      4.845505154808474
-3.203426503814917e-16
original_firstorder_InterquartileRange      53.11868159347395
53.11868159347395      53.11868159347395
original_firstorder_Kurtosis      1.9377489568062716      1.9377489568062716
1.9377489568062716
original_firstorder_Maximum      245.6530763934273      245.6530763934273
```

245.6530763934273
 original_firstorder_MeanAbsoluteDeviation 26.818884551211845
 26.818884551211845 26.818884551211845
 original_firstorder_Mean 155.3719983415878 155.3719983415878
 155.3719983415878
 original_firstorder_Median 155.18905312403436 155.18905312403436
 155.18905312403436
 original_firstorder_Minimum 71.47278629452707 71.47278629452707
 71.47278629452707
 original_firstorder_Range 174.18029009890023 174.18029009890023
 174.18029009890023
 original_firstorder_RobustMeanAbsoluteDeviation 21.389863990852252
 21.389863990852252 21.389863990852252
 original_firstorder_RootMeanSquared 456.4190202243421
 456.4190202243421 456.4190202243421
 original_firstorder_Skewness -0.1346149814527423 -0.1346149814527423
 -0.1346149814527423
 original_firstorder_TotalEnergy 25115065221.36046
 25115065221.36046 25115065221.36046
 original_firstorder_Uniformity 0.3480611015382606 0.03737932930847277
 1.0
 original_firstorder_Variance 954.6651489373318 954.6651489373318
 954.6651489373318
 original_glcm_Autocorrelation 11.919311682664972 560.3611073948962
 1.0
 original_glcm_ClusterProminence 13.758217736963676
 108051.89644545689 0.0
 original_glcm_ClusterShade -0.7071014082509358 -502.44144918632765
 0.0
 original_glcm_ClusterTendency 2.4074878411487717 236.5972460002837
 0.0
 original_glcm_Contrast 0.08336399210675942 1.2513461988695274 0.0
 original_glcm_Correlation 0.933063869160131 0.9894777918397618
 1.0
 original_glcm_DifferenceAverage 0.08336399210675942
 0.8250443158634069 0.0
 original_glcm_DifferenceEntropy 0.4139229033586663
 1.5679499535571393 -3.203426503814917e-16
 original_glcm_DifferenceVariance 0.07641443692678358
 0.5706480757310105 0.0
 original_glcm_Id 0.9583180039466203 0.6515093335597366 1.0
 original_glcm_Idm 0.9583180039466203 0.6296316745618523 1.0
 original_glcm_Idmn 0.9977469191322497 0.9993833029286645 1.0
 original_glcm_Idn 0.9880908582704628 0.9822596122540626 1.0
 original_glcm_Imc1 -0.728105321784139 -0.5475867714603969 0.0
 original_glcm_Imc2 0.9557465392631785 0.9975074825813931 0.0
 original_glcm_InverseVariance 0.08336399210675942 0.5150009730415909
 0.0

original_glcm_JointAverage	3.367236362420148	22.39474564366701
1.0		
original_glcm_JointEnergy	0.3025842745601664	0.009668848258080988
1.0		
original_glcm_JointEntropy	2.1373209498618118	7.032228939398056
-3.203426503814917e-16		
original_glcm_MCC	0.952661702709051	0.9913339825341221
1		
original_glcm_MaximumProbability	0.39043111809759523	
0.021948894611859927	1.0	
original_glcm_SumAverage	6.734472724840295	44.78949128733402
2.0		
original_glcm_SumEntropy	2.053956957755054	5.829674594280379
-3.203426503814917e-16		
original_glcm_SumSquares	0.6227129583138826	59.46214804978829
0.0		

```
[13]: import os
import random

image_dir = '/content/drive/MyDrive/Stanford ACA/BIOMEDIN 260/PSet 2/images/
↳images'
mask_dir = '/content/drive/MyDrive/Stanford ACA/BIOMEDIN 260/PSet 2/masks/masks'

image_lst = os.listdir(image_dir)
mask_lst = os.listdir(mask_dir)

random.seed(9001)
sampled_image_filename = random.sample(image_lst, 1000)
```

```
[14]: import pandas as pd
import os.path as osp
final_extractor = extractor1 = featureextractor.RadiomicsFeatureExtractor('/
↳content/drive/MyDrive/Stanford ACA/BIOMEDIN 260/PSet 2/modified_Bin40.yaml')

result_dict = {}
for image_filename in sampled_image_filename:
    # Read images
    image_path = osp.join(image_dir, image_filename)
    mask_path = osp.join(mask_dir, image_filename)
    img = sitk.ReadImage(image_path)
    mask = sitk.ReadImage(mask_path)

    # Perform alignment
    if img.GetSpacing() != mask.GetSpacing():
        img.SetSpacing(mask.GetSpacing())
    if img.GetOrigin() != mask.GetOrigin():
        img.SetOrigin(mask.GetOrigin())
```

```

if img.GetDirection != mask.GetDirection():
    img.SetDirection(mask.GetDirection())

# extract features
feature = final_extractor.execute(img, mask, label = 255)
keys = list(feature.keys())
numeric_keys = keys[keys.index('original_shape2D_Elongation'):] # Remove
→the PyRadiomics and Image information, since "original_shape2D_Elongation"
→is the first real feature"

if len(result_dict.keys()) == 0: # The first image, initialize the
→result_dictionary
    result_dict = {key: [] for key in numeric_keys}
    result_dict['Index'] = [] # Add an index column

# Append the extracted features for a new image to the result dictionary
for key, value in feature.items():
    if key in result_dict.keys():
        result_dict[key].append(value)
    result_dict['Index'].append(image_filename.split('.')[0])

df = pd.DataFrame(result_dict)
df.to_csv('Radiomics_features.csv')

```

Streaming output truncated to the last 5000 lines.

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```
[ ]: df.to_csv('Radiomics_features.csv')
```

```
[11]: import pandas as pd
df = pd.read_csv('Radiomics_features.csv')
```

1.4.2 b) Train a classifier (30 points)

Using the features extracted in step (a) above with a binwidth of 40, train two classifiers, a random forest and a support vector machine classifier to distinguish between benign and malignant nodules. Split the data in training and testing sets with a ratio 80/20 %.

Use traditional metrics to evaluate your two classifiers in the test set, e.g., Accuracy, F1 score. Show the code for the training and evaluation.

Select the following parameters of the classifiers for optimal performance: number of trees and maximum depth of the random forest classifier, kernel functions for the support vector machine classifiers. Comment on why and how you chose specific values for these parameters for your classifier.

Hint: The `scikit-learn` python package might be useful. * `scikit-learn` [installation](#) * `scikit-learn` [random forest classifier](#) * `scikit-learn` [support vector machine](#)

Answer: YOUR WRITTEN ANSWER TO QUESTION 2b HERE

```
[14]: ### WRITE CODE IN HERE.#####
from sklearn.model_selection import train_test_split, GridSearchCV
labels = pd.read_csv('./labels_small.csv')
labels = labels.rename(columns={"name": "Index"})
```

```
df_y = df.merge(labels, on='Index', how = 'inner') # It should be mentioned,
↳ only 943 overlapped samples are there

df_y.set_index('Index', inplace=True)
df = df_y.drop(['Unnamed: 0'], axis = 1)

X_train, X_test, y_train, y_test = train_test_split(df.iloc[:, :-1], df.iloc[:,
↳, -1], test_size=0.2)
#####
```

```
[15]: df_y
```

```
[15]:
```

	Unnamed: 0	original_shape2D_Elongation \
Index		
P_00651_RIGHT_CC	0	0.859609
P_01168_LEFT_CC	1	0.600814
P_01079_RIGHT_MLO	2	0.744454
P_00708_RIGHT_MLO	3	0.830408
P_00135_LEFT_MLO	4	0.640427
...
P_00603_RIGHT_MLO	995	0.691075
P_01013_RIGHT_MLO	996	0.815600
P_00962_RIGHT_MLO	997	0.857538
P_00519_RIGHT_MLO	998	0.834471
P_01130_RIGHT_CC	999	0.839903

	original_shape2D_MajorAxisLength \
Index	
P_00651_RIGHT_CC	395.948952
P_01168_LEFT_CC	325.505564
P_01079_RIGHT_MLO	283.577838
P_00708_RIGHT_MLO	197.179421
P_00135_LEFT_MLO	257.257089
...	...
P_00603_RIGHT_MLO	205.101107
P_01013_RIGHT_MLO	295.769891
P_00962_RIGHT_MLO	260.535928
P_00519_RIGHT_MLO	255.573253
P_01130_RIGHT_CC	382.281842

	original_shape2D_MaximumDiameter \
Index	
P_00651_RIGHT_CC	432.584096
P_01168_LEFT_CC	323.569158
P_01079_RIGHT_MLO	297.578561
P_00708_RIGHT_MLO	230.586209

P_00135_LEFT_MLO	285.630881
...	...
P_00603_RIGHT_MLO	240.852652
P_01013_RIGHT_MLO	297.833846
P_00962_RIGHT_MLO	291.207830
P_00519_RIGHT_MLO	268.486499
P_01130_RIGHT_CC	403.193502

Index	original_shape2D_MeshSurface \
P_00651_RIGHT_CC	102356.5
P_01168_LEFT_CC	47416.0
P_01079_RIGHT_MLO	45781.0
P_00708_RIGHT_MLO	23214.0
P_00135_LEFT_MLO	31108.5
...	...
P_00603_RIGHT_MLO	21468.0
P_01013_RIGHT_MLO	54933.5
P_00962_RIGHT_MLO	41911.5
P_00519_RIGHT_MLO	42094.0
P_01130_RIGHT_CC	93025.5

Index	original_shape2D_MinorAxisLength \
P_00651_RIGHT_CC	340.361208
P_01168_LEFT_CC	195.568385
P_01079_RIGHT_MLO	211.110544
P_00708_RIGHT_MLO	163.739380
P_00135_LEFT_MLO	164.754465
...	...
P_00603_RIGHT_MLO	141.740284
P_01013_RIGHT_MLO	241.229873
P_00962_RIGHT_MLO	223.419583
P_00519_RIGHT_MLO	213.268514
P_01130_RIGHT_CC	321.079692

Index	original_shape2D_Perimeter \
P_00651_RIGHT_CC	2306.608440
P_01168_LEFT_CC	1522.729148
P_01079_RIGHT_MLO	1232.219480
P_00708_RIGHT_MLO	1286.739249
P_00135_LEFT_MLO	1392.444876
...	...
P_00603_RIGHT_MLO	1040.070201
P_01013_RIGHT_MLO	1482.736290
P_00962_RIGHT_MLO	1760.025612

P_00519_RIGHT_MLO	1375.876334
P_01130_RIGHT_CC	2129.329219

Index	original_shape2D_PerimeterSurfaceRatio \
P_00651_RIGHT_CC	0.022535
P_01168_LEFT_CC	0.032114
P_01079_RIGHT_MLO	0.026916
P_00708_RIGHT_MLO	0.055429
P_00135_LEFT_MLO	0.044761
...	...
P_00603_RIGHT_MLO	0.048447
P_01013_RIGHT_MLO	0.026991
P_00962_RIGHT_MLO	0.041994
P_00519_RIGHT_MLO	0.032686
P_01130_RIGHT_CC	0.022890

Index	original_shape2D_PixelSurface	original_shape2D_Sphericity \
P_00651_RIGHT_CC	102369.0	0.491687
P_01168_LEFT_CC	47418.0	0.506926
P_01079_RIGHT_MLO	45785.0	0.615545
P_00708_RIGHT_MLO	23217.0	0.419749
P_00135_LEFT_MLO	31114.0	0.449021
...
P_00603_RIGHT_MLO	21473.0	0.499388
P_01013_RIGHT_MLO	54933.0	0.560350
P_00962_RIGHT_MLO	41915.0	0.412337
P_00519_RIGHT_MLO	42104.0	0.528610
P_01130_RIGHT_CC	93035.0	0.507765

Index	... original_glcmm_InverseVariance \
P_00651_RIGHT_CC	0.022690
P_01168_LEFT_CC	0.015748
P_01079_RIGHT_MLO	0.072307
P_00708_RIGHT_MLO	0.080107
P_00135_LEFT_MLO	0.027628
...	...
P_00603_RIGHT_MLO	0.008696
P_01013_RIGHT_MLO	0.020802
P_00962_RIGHT_MLO	0.049142
P_00519_RIGHT_MLO	0.053209
P_01130_RIGHT_CC	0.087396

Index	original_glcmm_JointAverage	original_glcmm_JointEnergy \
-------	-----------------------------	------------------------------

P_00651_RIGHT_CC	2.541696	0.465914
P_01168_LEFT_CC	1.970058	0.923261
P_01079_RIGHT_MLO	2.588147	0.448546
P_00708_RIGHT_MLO	2.795703	0.542835
P_00135_LEFT_MLO	1.953866	0.885123
...
P_00603_RIGHT_MLO	1.018526	0.955015
P_01013_RIGHT_MLO	1.966777	0.895126
P_00962_RIGHT_MLO	2.064194	0.535063
P_00519_RIGHT_MLO	2.814010	0.542879
P_01130_RIGHT_CC	4.275423	0.304567

Index	original_glcmm_JointEntropy	original_glcmm_MCC \
P_00651_RIGHT_CC	1.402514	0.972858
P_01168_LEFT_CC	0.301346	0.746714
P_01079_RIGHT_MLO	1.353349	0.851418
P_00708_RIGHT_MLO	1.362758	0.825406
P_00135_LEFT_MLO	0.414552	0.686083
...
P_00603_RIGHT_MLO	0.187895	0.760876
P_01013_RIGHT_MLO	0.408705	0.773456
P_00962_RIGHT_MLO	1.475192	0.976953
P_00519_RIGHT_MLO	1.314307	0.886995
P_01130_RIGHT_CC	2.189880	0.953717

Index	original_glcmm_MaximumProbability	original_glcmm_SumAverage \
P_00651_RIGHT_CC	0.617530	5.083392
P_01168_LEFT_CC	0.960524	3.940116
P_01079_RIGHT_MLO	0.552346	5.176294
P_00708_RIGHT_MLO	0.709662	5.591407
P_00135_LEFT_MLO	0.940051	3.907731
...
P_00603_RIGHT_MLO	0.977127	2.037051
P_01013_RIGHT_MLO	0.945543	3.933554
P_00962_RIGHT_MLO	0.713457	4.128388
P_00519_RIGHT_MLO	0.705913	5.628020
P_01130_RIGHT_CC	0.452098	8.550846

Index	original_glcmm_SumEntropy	original_glcmm_SumSquares	label
P_00651_RIGHT_CC	1.379824	0.416089	0
P_01168_LEFT_CC	0.285598	0.030705	1
P_01079_RIGHT_MLO	1.281042	0.242605	1
P_00708_RIGHT_MLO	1.282652	0.216869	0
P_00135_LEFT_MLO	0.386924	0.044006	0

...
P_00603_RIGHT_MLO	0.179199	0.018182	0
P_01013_RIGHT_MLO	0.387903	0.042952	0
P_00962_RIGHT_MLO	1.426050	0.396290	1
P_00519_RIGHT_MLO	1.261098	0.233322	1
P_01130_RIGHT_CC	2.102484	0.764782	1

[943 rows x 53 columns]

```
[16]: from sklearn.preprocessing import StandardScaler
from sklearn.metrics import roc_curve, precision_recall_curve, auc,
      ↪ roc_auc_score, accuracy_score, precision_recall_curve, auc, f1_score
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC, LinearSVC

def modelEval(y_true, y_preds, predict_probs):
    auroc = (roc_auc_score(y_true, predict_probs))
    accuracy = (accuracy_score(y_true, y_preds))
    f1 = f1_score(y_true, y_preds)
    precision, recall, threshold = precision_recall_curve(y_true, predict_probs)
    auprc = auc(recall, precision)
    return {"auroc": auroc, "accuracy": accuracy, "auprc": auprc, "f1_score":
    ↪ f1}

def getPredicts(clf, X):
    predict_probs = clf.predict_proba(X)[: , 1]
    predicts = clf.predict(X)
    return predicts, predict_probs
scaler = StandardScaler()
X_train_std = scaler.fit_transform(X_train)
X_test_std = scaler.transform(X_test)
```

```
[18]: param_grid = {'n_estimators': [50,100,200,300,500],
                    'max_depth': [2,5, 8, 10, 12, 15]}
rf = RandomForestClassifier()
gridsearch = GridSearchCV(rf,
                          param_grid=param_grid,
                          scoring = 'accuracy',
                          cv=5)
gridsearch.fit(X_train_std, y_train)

best_rf = gridsearch.best_estimator_
print('Hyperparameter Tuned', ':', gridsearch.best_params_)

best_rf.fit(X_train_std, y_train)

preds, pred_probs = getPredicts(best_rf, X_test_std)
```

```
result_dict_rf = modelEval(y_test, preds, pred_probs)

print(result_dict_rf)
```

Hyperparameter Tuned : {'max_depth': 8, 'n_estimators': 50}
{'auroc': 0.47885883155262554, 'accuracy': 0.49206349206349204, 'auprc':
0.4383199497438851, 'f1_score': 0.3924050632911392}

Answer: After tuning the hyperparameter via a five-fold cross validation on the training data with accuracy being the optimization goal, it turned out the best hyperparameter set is: {'max_depth': 8, 'n_estimators': 50}

```
[19]: # support vector machine model
param_grid = {'C': [0.1, 1, 10],
              'kernel': ['linear', 'rbf']}
svm = SVC(probability=True)
gridsearch = GridSearchCV(svm,
                           param_grid=param_grid,
                           scoring = 'accuracy',
                           cv=5)
gridsearch.fit(X_train_std, y_train)

best_svm = gridsearch.best_estimator_
print('Hyperparameter Tuned', ': ', gridsearch.best_params_)

best_svm.fit(X_train_std, y_train)

preds, pred_probs = getPredicts(best_svm, X_test_std)
result_dict_svm = modelEval(y_test, preds, pred_probs)

print(result_dict_svm)
```

Hyperparameter Tuned : {'C': 1, 'kernel': 'rbf'}
{'auroc': 0.5466583314389634, 'accuracy': 0.5661375661375662, 'auprc':
0.4754172019521953, 'f1_score': 0.4305555555555556}

Answer: After tuning the hyperparameter via a five-fold cross validation on the training data with accuracy being the optimization goal, it turned out that the best hyperparameter set is: {'C': 1, 'kernel': 'rbf'}

1.4.3 c) Deep Dive into the Random Forest Classifiers (10 points)

c. The random forest classifier can output the importance of the features. Please select the most important 10 features - hint: you could use [scikit-learn feature selection](#), and read about [forest feature importance](#). Retrain the classifier with the top best features. What happens to the performance?

Hint: You may want to check out [scikit-learn random forest classifier documentation](#)

Answer: YOUR WRITTEN ANSWER TO QUESTION 2c HERE

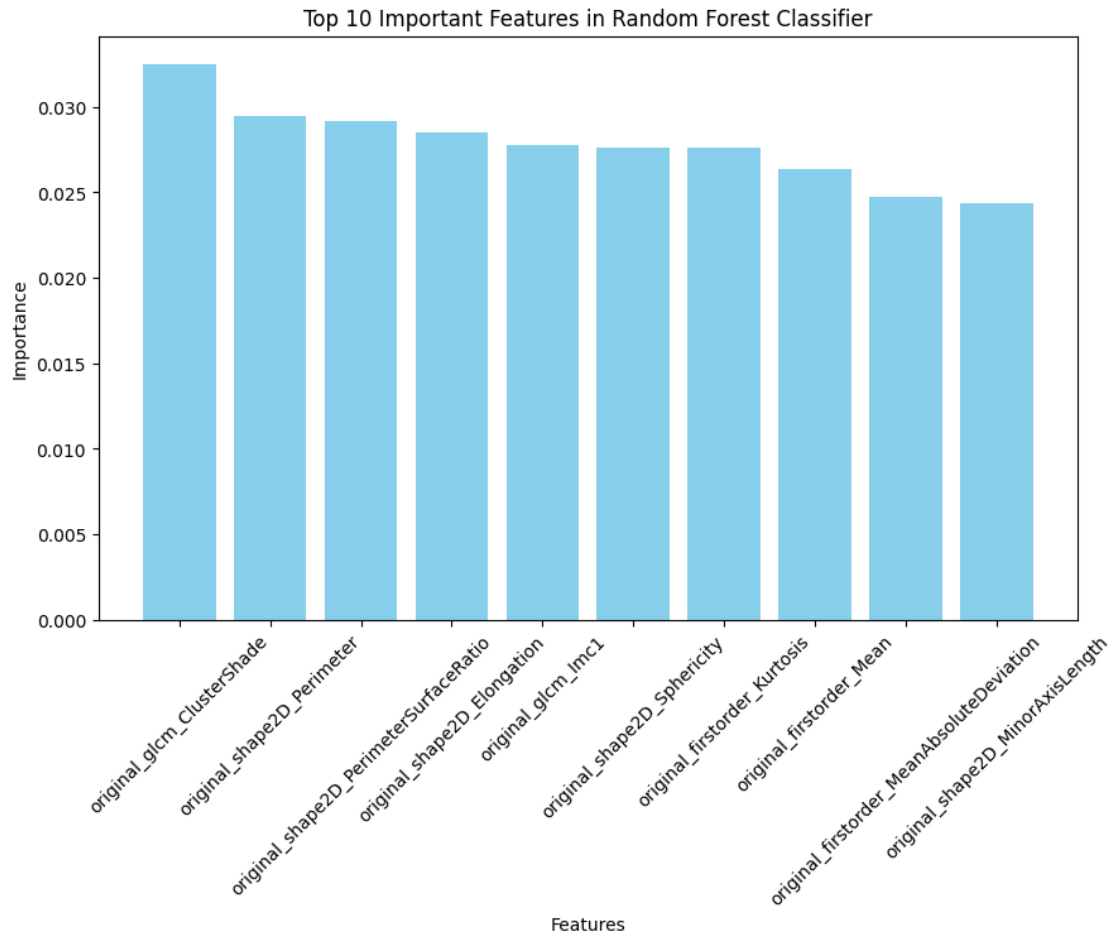

```
[21]: ### WRITE CODE IN HERE.#####
import numpy as np
feature_names = np.array(X_train.columns)

feature_importance = np.sort(best_rf.feature_importances_)[::-1]
feature_importance_idx = np.argsort(best_rf.feature_importances_)[::-1]

# Top 10 feature importances and corresponding indices
feature_importance_top10 = feature_importance[0:10]
feature_importance_idx_top10 = feature_importance_idx[0:10]

# Map indices to names
feature_names_top10 = feature_names[feature_importance_idx_top10]

# Creating the plot
plt.figure(figsize=(10, 6))
plt.bar(feature_names_top10, feature_importance_top10, color='skyblue')
plt.xlabel('Features')
plt.ylabel('Importance')
plt.title('Top 10 Important Features in Random Forest Classifier')
plt.xticks(rotation=45)
plt.show()
#####
```



```
[25]: # subset the top 10 features
X_train_top10 = X_train_std[:, feature_importance_idx_top10]
X_test_top10 = X_test_std[:, feature_importance_idx_top10]

param_grid2 = {'n_estimators': [50,100,200,300,500],
               'max_depth': [2,5, 8, 10, 12, 15]}

rf2 = RandomForestClassifier()
gridsearch2 = GridSearchCV(rf2,
                           param_grid=param_grid2,
                           scoring = 'accuracy',
                           cv=5)
gridsearch2.fit(X_train_top10, y_train)

best_rf2 = gridsearch2.best_estimator_
print('Hyperparameter Tuned', ':', gridsearch2.best_params_)
```

```
best_rf2.fit(X_train_top10, y_train)

preds, pred_probs = getPredicts(best_rf2, X_test_top10)
result_dict_rf2 = modelEval(y_test, preds, pred_probs)

print(result_dict_rf2)
```

```
Hyperparameter Tuned : {'max_depth': 8, 'n_estimators': 100}
{'auroc': 0.5385314844282791, 'accuracy': 0.544973544973545, 'auprc':
0.45376819507551414, 'f1_score': 0.41891891891891886}
```

Answer: The top 10 features lead to a slight increase in both the accuracy and the f1 score. The feature selection process may have improved the model's overfitting issue.

1.4.4 d) Deep dive into the SVM classifier (10 points)

Now train a support vector machine using the top 10 features selected by random forest importance. How does the support vector machine classifier perform?

Answer: YOUR WRITTEN ANSWER TO QUESTION 2d HERE

```
[26]: ### WRITE CODE IN HERE.#####
# support vector machine model
param_grid2 = {'C': [0.1, 1, 10],
               'kernel': ['linear', 'rbf']}
svm2 = SVC(probability=True)
gridsearch2 = GridSearchCV(svm2,
                           param_grid=param_grid2,
                           scoring = 'accuracy',
                           cv=5)
gridsearch2.fit(X_train_top10, y_train)

best_svm2 = gridsearch2.best_estimator_
print('Hyperparameter Tuned', ':', gridsearch2.best_params_)

best_svm2.fit(X_train_top10, y_train)

preds, pred_probs = getPredicts(best_svm2, X_test_top10)
result_dict_svm2 = modelEval(y_test, preds, pred_probs)

print(result_dict_svm2)
#####
```

```
Hyperparameter Tuned : {'C': 1, 'kernel': 'rbf'}
{'auroc': 0.5552398272334621, 'accuracy': 0.5661375661375662, 'auprc':
0.4850977143591553, 'f1_score': 0.4459459459459459}
```

Answer: There is also a slight increase in the classification f1 score.

1.4.5 e) Apply the trained classifiers to images from a different set (10 points)

Using the two images provided in Problem 1, please evaluate all the classifiers trained up to this point. Are they able to discriminate between the two types of nodules - how can you tell yes or no? Are your results in line with what you expected based on the the results of your models in the earlier parts?

Answer: YOUR WRITTEN ANSWER TO QUESTION 2e HERE

```
[35]: ### WRITE CODE IN HERE.#####
from radiomics import featureextractor
img_benign = sitk.ReadImage('LEFT_CC_BENIGN.tif')
mask_benign = sitk.ReadImage('LEFT_CC_BENIGN_MASK.tif')

img_malignant = sitk.ReadImage('RIGHT_CC_MALIGNANT.tif')
mask_malignant = sitk.ReadImage('RIGHT_CC_MALIGNANT_MASK.tif')

img_mask_list = [(img_malignant, mask_malignant), (img_benign, mask_benign)]

final_extractor = extractor1 = featureextractor.RadiomicsFeatureExtractor('/
→content/drive/MyDrive/Stanford ACA/BIOMEDIN 260/PSet 2/modified_Bin40.yaml')

result_dict = {}
for idx, image_mask in enumerate(img_mask_list):
    # Read images
    img = image_mask[0]
    mask = image_mask[1]

    # Perform alignment
    if img.GetSpacing() != mask.GetSpacing():
        img.SetSpacing(mask.GetSpacing())
    if img.GetOrigin() != mask.GetOrigin():
        img.SetOrigin(mask.GetOrigin())
    if img.GetDirection() != mask.GetDirection():
        img.SetDirection(mask.GetDirection())

    # extract features
    feature = final_extractor.execute(img, mask, label = 255)
    keys = list(feature.keys())
    numeric_keys = keys[keys.index('original_shape2D_Elongation'):] # Remove
    →the PyRadiomics and Image information, since "original_shape2D_Elongation"
    →is the first real feature"

    if len(result_dict.keys()) == 0: # The first image, initialize the
    →result_dictionary
        result_dict = {key: [] for key in numeric_keys}
        result_dict['Index'] = [] # Add an index column
```

```

# Append the extracted features for a new image to the result dictionary
for key, value in feature.items():
    if key in result_dict.keys():
        result_dict[key].append(value)
    result_dict['Index'].append(idx)

```

```
df_test = pd.DataFrame(result_dict)
```

```
#####
```

```

INFO:radiomics.featureextractor:Loading parameter file
/content/drive/MyDrive/Stanford ACA/BIOMEDIN 260/PSet 2/modified_Bin40.yaml
INFO:radiomics.featureextractor:Calculating features with label: 255
INFO:radiomics.featureextractor:Loading image and mask
INFO:radiomics.featureextractor:Computing shape2D
INFO:radiomics.featureextractor:Adding image type "Original" with custom
settings: {}
INFO:radiomics.featureextractor:Calculating features for original image
INFO:radiomics.featureextractor:Computing firstorder
INFO:radiomics.featureextractor:Computing glcm
GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to
be calculated
WARNING:radiomics.glcm:GLCM is symmetrical, therefore Sum Average = 2 * Joint
Average, only 1 needs to be calculated
INFO:radiomics.featureextractor:Calculating features with label: 255
INFO:radiomics.featureextractor:Loading image and mask
INFO:radiomics.featureextractor:Computing shape2D
INFO:radiomics.featureextractor:Adding image type "Original" with custom
settings: {}
INFO:radiomics.featureextractor:Calculating features for original image
INFO:radiomics.featureextractor:Computing firstorder
INFO:radiomics.featureextractor:Computing glcm
GLCM is symmetrical, therefore Sum Average = 2 * Joint Average, only 1 needs to
be calculated
WARNING:radiomics.glcm:GLCM is symmetrical, therefore Sum Average = 2 * Joint
Average, only 1 needs to be calculated

```

```
[36]: df_test = df_test.set_index('Index')
```

```

df_test_std = scaler.transform(df_test)
y_test = [0,1]

```

```

[38]: # Use Random Forest Classifier with all features
preds, pred_probs = getPredicts(best_rf, df_test_std)
print(preds)

```

```
[1 0]
```

```
[39]: # Use SVM Classifier with all features
preds, pred_probs = getPredicts(best_svm, df_test_std)
print(preds)
```

```
[0 0]
```

```
[43]: # Use Random Forest Classifier with selected features
preds, pred_probs = getPredicts(best_rf2, df_test_std[:,
↪feature_importance_idx_top10])
print(preds)
```

```
[1 1]
```

```
[44]: # Use SVM Classifier with selected features
preds, pred_probs = getPredicts(best_svm2, df_test_std[:,
↪feature_importance_idx_top10])
print(preds)
```

```
[0 1]
```

Answer: It can be seen that only the SVM with feature selection are able to accurately classify the malignant tumor and benign tumor.

```
[ ]:
```