PyRadiomics toolbox in Python

In this notebook, we will load 2 brain datasets with segmentations of brain tumors. The `radiomics` package will be used to extract a set of features, and the "signatures" will be compared.

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

```
In [ ]:  # Radiomics package
         from radiomics import featureextractor

         import six, numpy as np
```

Setting up data

Here we use `SimpleITK` (referenced as `sitk`, see http://www.simpleitk.org/ (http://www.simpleitk.org/) for details) to load two brain images and the corresponding segmentations as label maps.

```
In [ ]:  import os
         import SimpleITK as sitk

         from radiomics import getTestCase

         imagepath_1, labelpath_1 = getTestCase('brain1')
         imagepath_2, labelpath_2 = getTestCase('brain2')

         image_1 = sitk.ReadImage(imagepath_1)
         label_1 = sitk.ReadImage(labelpath_1)
         image_2 = sitk.ReadImage(imagepath_2)
         label_2 = sitk.ReadImage(labelpath_2)
```

Show the images

Using `matplotlib.pyplot` (referenced as `plt`), display the images in grayscale and labels in color.

```
In [ ]:  # Display the images
         %matplotlib inline
         import matplotlib.pyplot as plt

         plt.figure(figsize=(20,20))
         # First image
         plt.subplot(2,2,1)
         plt.imshow(sitk.GetArrayFromImage(image_1)[12,:,:], cmap="gray")
         plt.title("Brain #1")
         plt.subplot(2,2,2)
         plt.imshow(sitk.GetArrayFromImage(label_1)[12,:,:])
         plt.title("Segmentation #1")

         # Second image
         plt.subplot(2,2,3)
         plt.imshow(sitk.GetArrayFromImage(image_2)[8,:,:], cmap="gray")
         plt.title("Brain #2")

         plt.subplot(2,2,4)
         plt.imshow(sitk.GetArrayFromImage(label_2)[8,:,:])
         plt.title("Segmentation #2")

         plt.show()
```

Extract the features

Using the `radiomics` package, first construct an `extractor` object from the parameters set in `Params.yaml`. Then generate features for the two images.

```
In [ ]:  import os
         # Instantiate the extractor
         params = os.path.join(os.getcwd(), '..', 'examples', 'exampleSetting
         s', 'Params.yaml')

         extractor = featureextractor.RadiomicsFeatureExtractor(params)
         result_1 = extractor.execute(image_1, label_1)
         result_2 = extractor.execute(image_2, label_2)
```

Prepare for plotting

Because we'd like to plot the feature vectors, create `numpy` arrays for features starting with `original_` (excluding meta-features).

```
In [ ]:  # Make an array of the values
         feature_1 = np.array([])
         feature_2 = np.array([])

         for key, value in six.iteritems(result_1):
             if key.startswith("original_"):
                 feature_1 = np.append ( feature_1, result_1[key])
                 feature_2 = np.append ( feature_2, result_2[key])
```

Plot

Plot the two feature vectors and the difference. Feature values have a wide range of magnitudes and are plotted on a log scale.

```
In [ ]: plt.figure(figsize=(20,20))
        plt.subplot(3,1,1)
        plt.plot(feature_1)
        plt.yscale('log')
        plt.title ( "Features from brain #1")

        plt.subplot(3,1,2)
        plt.plot(feature_2)
        plt.yscale('log')
        plt.title ( "Features from brain #1")

        plt.subplot(3,1,3)
        plt.plot(feature_1 - feature_2)
        plt.yscale('log')
        plt.title ( "Difference")
        plt.show()
```