Imaging Phenotypes

- Imaging phenotypes describe features of disease that can be detected through medical imaging combined with feature detection, machine learning and statistical analysis, and correlated with other indicators of disease.

Gillies et al. Radiology 2015
Clinical Case: Meningioma

- Meningiomas are slow-growing extra axial brain tumor arising from arachnoidal cells
- Treatment options include observation, surgery and radiation therapy
- Image-based predictors of tumor grades have the potential to enhance clinical decision-making
Overall Goal

This tutorial is an introduction to the basics of image phenotyping for tumor characterization using the 3D Slicer platform.
Imaging Features

Quantitative features derived from imaging data have the potential to provide clinically relevant information for predicting tumor grade and evaluating response treatment.
Tutorial materials

• 3D Slicer release version 4.10.1

• Slicer Radiomics Extension

• Meningioma dataset
3D Slicer installation

- To install and start the 3D Slicer software on your computer, follow the instructions of the Quick Start Guide tutorial available at https://www.slicer.org/wiki/Documentation/4.10/Training

<table>
<thead>
<tr>
<th>Stable Release</th>
<th>Windows</th>
<th>Mac OS X</th>
<th>Linux</th>
</tr>
</thead>
<tbody>
<tr>
<td>version 4.10.1</td>
<td>version 4.10.1</td>
<td>version 4.10.1</td>
<td>version 4.10.1</td>
</tr>
<tr>
<td>revision 27931</td>
<td>revision 27931</td>
<td>revision 27931</td>
<td>revision 27931</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Nightly Build</th>
<th>Windows</th>
<th>Mac OS X</th>
<th>Linux</th>
</tr>
</thead>
<tbody>
<tr>
<td>version 4.11.0</td>
<td>version 4.11.0</td>
<td>version 4.11.0</td>
<td>version 4.11.0</td>
</tr>
<tr>
<td>revision 28040</td>
<td>revision 28040</td>
<td>revision 28040</td>
<td>revision 28040</td>
</tr>
</tbody>
</table>
Disclaimer

• 3D Slicer is a free open source software for medical image computing research distributed under a BDS style license.

• The software is not FDA approved or CE-Marked, and is for research use only.
Workflow Overview

Step 1: Data Loading

Step 2: Tumor Segmentation

Step 3: Tumor Volume Calculation

Step 4: Imaging Features Extraction
Part 1: Data Loading and tumor diameter measurements
Data Loading

Drag and drop the file *Meningioma.nrrd* into the Slicer
Data Loading

Click on OK to load the files in Slicer
Slicer displays the axial, sagittal and coronal images of the meningioma dataset.
Data Loading

Select the Red Slicer Only Layout from the Layout Menu
Data Loading

Select the Ruler tool in the main menu

Find the slice that you want to use to measure the largest diameter.
Position two fiducials using the Ruler tool to measure the largest diameter on an axial image.
Slicer displays the value of the tumor diameter as measured on an axial slice.
Part 2: Tumor Segmentation
Image Segmentation

• Image Segmentation is the process of identifying the contours of structures of interest in imaging data

• Image Segmentation can be performed by manual contouring or by using automated segmentation algorithms
Image Segmentation

• The Segment Editor module of 3D Slicer provides powerful tools for manual and semi-automated segmentation

• The module takes a reference image (Master Volume) as input and produces a segmented image (Segmentation) in output
In this tutorial,
- The Master Volume **Meningioma** is the initial brain MRI dataset
- The Segmentation Volume **Segmentation** is a segmentation object with the same dimensions and origin as the Master Volume
Left Click on **Data** in the Modules menu and select the **Segment Editor** module in the list of Modules.
The **Master Volume** is the Meningioma dataset.
The **Segmentation** volume is the segmentation object created by Slicer with the same dimensions and origin as the Master Volume.
Segment Editor Module

Click on Add to add a segment to the Segmentation and rename it Tumor
Select the **Paint tool** and draw a small mark inside the tumor on 2-3 consecutive slices.
Segment Editor Module

Click on Add to add a new segment and rename it Background
Segment Editor Module

Select the Paint Tool and draw a circle around the tumor.
Segment Editor Module

Select the Four-Up slice layout
Select the Paint Tool and draw a circle around the tumor in the sagittal and coronal slices.
Segment Editor Module

Select the **Grow from seeds** tool

Click on **Initialize**
Segment Editor Module

Slicer shows a preview of the segmentation result
Segment Editor Module

Click on **Apply** to accept the result.
Segment Editor Module

Slicer shows the segmentation result
Segment Editor Module

Click on Show 3D
Segment Editor Module

Slicer shows the segmentation result in 3D
Segment Editor Module

Select the 3D only layout
Select the **Scissors** tool and remove the segmented sections which are not part of the tumor.
Select the **Scissors** tool and remove the segmented sections which are not part of the tumor.
Select the **Scissors** tool and remove the segmented sections which are not part of the tumor.
Part 3: Tumor Volume Calculation
This section shows how to compute the volume of the segmented tumor using the Segment Statistics module.
Tumor Measurements

Select the **Segment Statistics** module in the **Quantification** category.
Tumor Measurements

Select the Segmentation **Segmentation**
Select the Scalar Volume **Meningioma**
Select the **Conventional layout** and click on Apply
Slicer displays the computed tumor volume: 17.053 cm³
Part 4: Quantitative Imaging features computation
PyRadiomics package

- **Pyradiomics** is an open source python package that enables the automated extraction of over 1,500 quantitative features from medical imaging data.

- The package includes tools for image pre-processing and filtering based on SimpleITK

- Pyradiomics command line tools enable batchprocessing

[https://pyradiomics.readthedocs.io](https://pyradiomics.readthedocs.io)


The Slicer Radiomics extension provides a graphical user interface to the pyradiomics library.
The Slicer Radiomics Extension enables interactive imaging features exploration and configuration of extraction parameters.
Left click on the module **Data** to display the list of modules
Select the module **Radiomics** in the category **Informatics**
Radiomics Module Installation

Select the Image Volume **Meningioma**
Select the Input Regions **Segmentation**

Select the feature class First Order and **glcm**

Select **Output Table** ➔ Create New and click on **Apply**
Features Computation

Slicer displays the result of the features computation
Features Computation

<table>
<thead>
<tr>
<th></th>
<th></th>
<th>firstorder</th>
<th>InterquartileRange</th>
<th>20.0</th>
</tr>
</thead>
<tbody>
<tr>
<td>35</td>
<td>original</td>
<td>firstorder</td>
<td>Skewness</td>
<td>1.99316623652</td>
</tr>
<tr>
<td>36</td>
<td>original</td>
<td>firstorder</td>
<td>Uniformity</td>
<td>0.358800750225</td>
</tr>
<tr>
<td>37</td>
<td>original</td>
<td>firstorder</td>
<td>Median</td>
<td>177.0</td>
</tr>
<tr>
<td>38</td>
<td>original</td>
<td>firstorder</td>
<td>Energy</td>
<td>453513881.0</td>
</tr>
<tr>
<td>39</td>
<td>original</td>
<td>firstorder</td>
<td>RobustMeanAbsoluteDeviation</td>
<td>9.02739158026</td>
</tr>
<tr>
<td>40</td>
<td>original</td>
<td>firstorder</td>
<td>MeanAbsoluteDeviation</td>
<td>15.6561086211</td>
</tr>
<tr>
<td>41</td>
<td>original</td>
<td>firstorder</td>
<td>TotalEnergy</td>
<td>558034658.262</td>
</tr>
<tr>
<td>42</td>
<td>original</td>
<td>firstorder</td>
<td>Maximum</td>
<td>370.0</td>
</tr>
<tr>
<td>43</td>
<td>original</td>
<td>firstorder</td>
<td>RootMeanSquared</td>
<td>180.8961587</td>
</tr>
<tr>
<td>44</td>
<td>original</td>
<td>firstorder</td>
<td>90Percentile</td>
<td>202.0</td>
</tr>
<tr>
<td>45</td>
<td>original</td>
<td>firstorder</td>
<td>Minimum</td>
<td>36.0</td>
</tr>
<tr>
<td>46</td>
<td>original</td>
<td>firstorder</td>
<td>Entropy</td>
<td>1.83048891173</td>
</tr>
<tr>
<td>47</td>
<td>original</td>
<td>firstorder</td>
<td>Range</td>
<td>334.0</td>
</tr>
<tr>
<td>48</td>
<td>original</td>
<td>firstorder</td>
<td>Variance</td>
<td>575.802209976</td>
</tr>
<tr>
<td>49</td>
<td>original</td>
<td>firstorder</td>
<td>10Percentile</td>
<td>156.0</td>
</tr>
<tr>
<td>50</td>
<td>original</td>
<td>firstorder</td>
<td>Kurtosis</td>
<td>12.4315749384</td>
</tr>
<tr>
<td>51</td>
<td>original</td>
<td>firstorder</td>
<td>Mean</td>
<td>179.297568367</td>
</tr>
</tbody>
</table>

Slicer displays the values of the 18 features for the **FirstOrder** class.
Conclusion

• This tutorial provides a basic introduction to image phenotyping using the Slicer Radiomics extension.
• The extension enables the computation of feature classes implemented in pyradiomics
• The description of each class is available at https://pyradiomics.readthedocs.io/
Acknowledgments:
Neuroimaging Analysis Center

The mission of the Neuroimage Analysis Center (NAC) (NIH P41 EB015902) is to advance the role of neuroimaging in health care.