



NA-MIC

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Automatic SPHARM Shape Analysis in 3D Slicer

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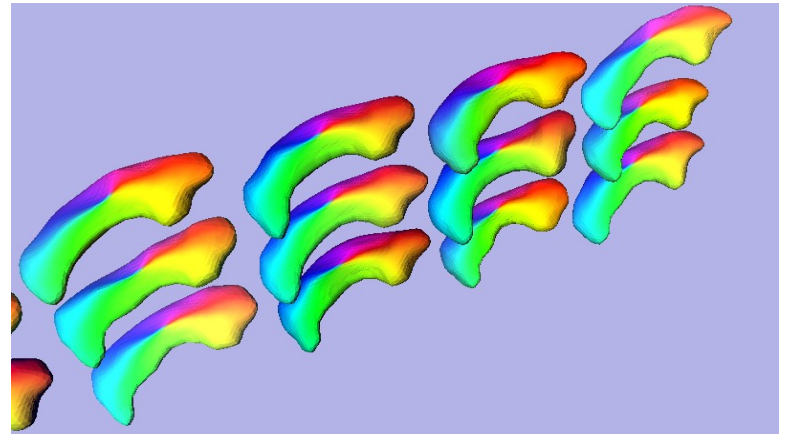
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NA-MIC Tutorial Contest: Summer 2010



Learning Objective

- **Be able to perform shape analysis studies**
- **Learn how to:**
 - ⇒ Load input file.
 - ⇒ Run the **ShapeAnalysisModule**.
 - ⇒ Display output scenes.





Prerequisites

This tutorial assumes that you have already completed the tutorial **Data Loading and Visualization**.

Tutorials for **Slicer3** are available at the following location:

- **Slicer3** tutorials

<http://www.na-mic.org/Wiki/index.php/Slicer3.2:Training>



Material

This tutorial requires the installation of the **Slicer3.6 release**, **BatchMake**, **some external applications** and the tutorial dataset. They are available at the following locations:

⇒ **Slicer3.6** download page:

<http://www.slicer.org/pages/Downloads/>

⇒ **BatchMake** download page (BatchMake 1.0.6):

<http://www.batchmake.org/batchmake/resources/software.html>

⇒ **External applications** download page (spharm-pdm v1.9 Linux32.zip or Linux64.zip):

<http://www.nitrc.org/projects/spharm-pdm>

⇒ **Tutorial dataset** download page (spharm-pdm v1.9 ShapeAnalysis_Data_Example.zip):

<http://www.nitrc.org/projects/spharm-pdm>

Disclaimer: *It is the responsibility of the user of Slicer to comply with both the terms of the license and with the applicable laws, regulations, and rules.*



Platform

This tutorial has been developed and performed on Linux.



Material: External Applications

- Executables are in [spharm-pdm_Linux32or64.zip](#).
- **Download** and **unzip** this file somewhere in your computer.
- A “[spharm-pdm_linux32or64](#)” folder will be created, containing executables needed to perform the shape analysis.
- Executables are: [ShapeAnalysisModule](#), [SegPostProcessCLP](#), [GenParaMeshCLP](#), [ParaToSPHARMMeshCLP](#) and [MeshMath](#).



Materials: Data Example

- **Download** the data located in [*ShapeAnalysis_Data_Example.zip*](#).
- **Unzip** this file somewhere in your computer.
- A “[*ShapeAnalysis_Data_Example/origData*](#)” folder will be created containing two set of binary segmentation of hippocampus.
- **Modify** the CSV file, **replace** the path of the data by your path.
e.g: /.../ShapeAnalysis_Data_Example/origData/groupA_01_hippo.gipl.gz



The first line of the CSV file, needs to be the headers of the columns.



Prerequisites

- Add the **external applications** in your PATH:

⇒ **tssh usage** : `setenv PATH ../../spharm-pdm_linux32or64/${PATH}`

⇒ **bash usage** : `export PATH=../../spharm-pdm_linux32or64/${PATH}`

- Add the **BatchMake Applications** (two different ways):

⇒ Add the folder `BatchMake_Applications` in the same folder as the `ShapeAnalysisModule` executable.

⇒ Set the environment variable **BatchmakeShapeAnalysisModule_Dir**:

* **tssh usage** :

`setenv BatchmakeShapeAnalysisModule_Dir ../../spharm-pdm_linux32or64/BatchMake_Applications`

* **bash usage** :

`export BatchmakeShapeAnalysisModule_Dir=../../spharm-pdm_linux32or64/BatchMake_Applications`



Prerequisites

Add **ShapeAnalysisModule** as Slicer3 external module:

- ⇒ Open Slicer3.
- ⇒ Go to **View** → **Application Settings** → **Module Settings**.
- ⇒ Click on the “**add a preset**” button.
- ⇒ Select the “**spharm-pdm_Linux32or64**” folder and confirm.
- ⇒ Close Slicer3.



Overview

- 1- Input file
- 2- Pipeline description
- 3- Output images and organisation
- 4- Execution within Slicer
- 5- Command line execution



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Input File

The input file:

- Is a **CSV** file (Comma Separated Value).
- Contains all the information concerning the subject.
e.g: Age, Group, MRI...
- Contains the path of all the data.
e.g: /devel/linux/ShapeTools/hippocampi/GroupA_01.gipl.gz

The first line of the CSV file, needs to be the headers of the columns.

The data are:

- A set of binary segmentation of a single brain structure.

```
Case ID,Group Type,Input File,Input File Description
1,0,/devel/linux/ShapeTools/example/hippocampi/origData/groupA_01_hippo.gipl.gz,none
2,1,/devel/linux/ShapeTools/example/hippocampi/origData/groupA_02_hippo.gipl.gz,none
3,0,/devel/linux/ShapeTools/example/hippocampi/origData/groupA_03_hippo.gipl.gz,none
4,1,/devel/linux/ShapeTools/example/hippocampi/origData/groupA_04_hippo.gipl.gz,none
5,0,/devel/linux/ShapeTools/example/hippocampi/origData/groupA_05_hippo.gipl.gz,none
6,0,/devel/linux/ShapeTools/example/hippocampi/origData/groupA_06_hippo.gipl.gz,none
```

Fig: a CSV file.

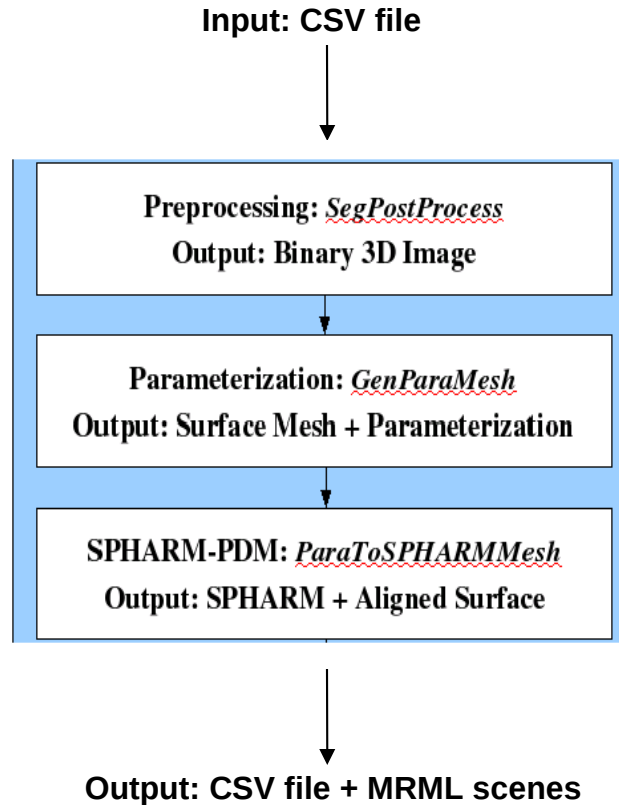


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Pipeline Description





Pipeline Description

- **Post Process Segmentation**

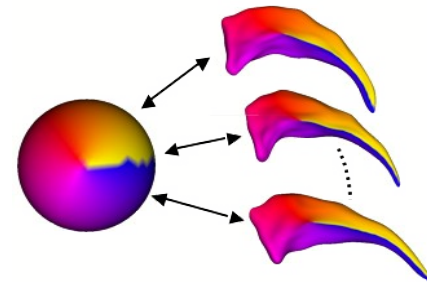
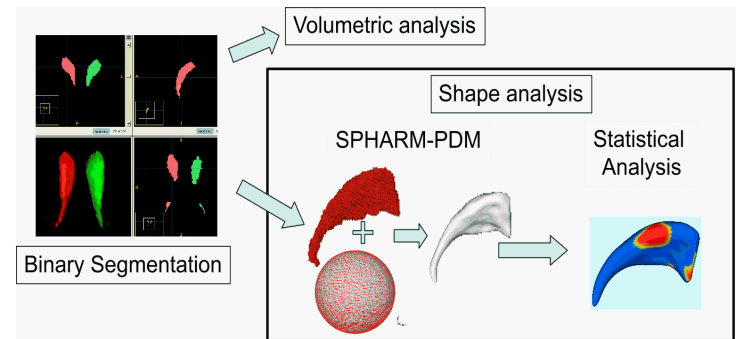
- ⇒ Fills interior holes.
- ⇒ Performs minimal smoothing operation and ensures spherical topology.

- **GenParaMesh**

- ⇒ Processed binary segmentations are converted to raw surfaces meshes.
- A spherical parametrization is computed.

- **ParaToSPHARMMesh**

- ⇒ The SPHARM description with inherent correspondence is then computed from the mesh and its spherical parametrization.
- ⇒ Triangulated surfaces with correspondences are computed next (SPHARM-PDM) via icosahedron of the spherical parametrization



To get more information about the pipeline: <http://www.nitrc.org/projects/spharm-pdm> -> *MediaWiki*



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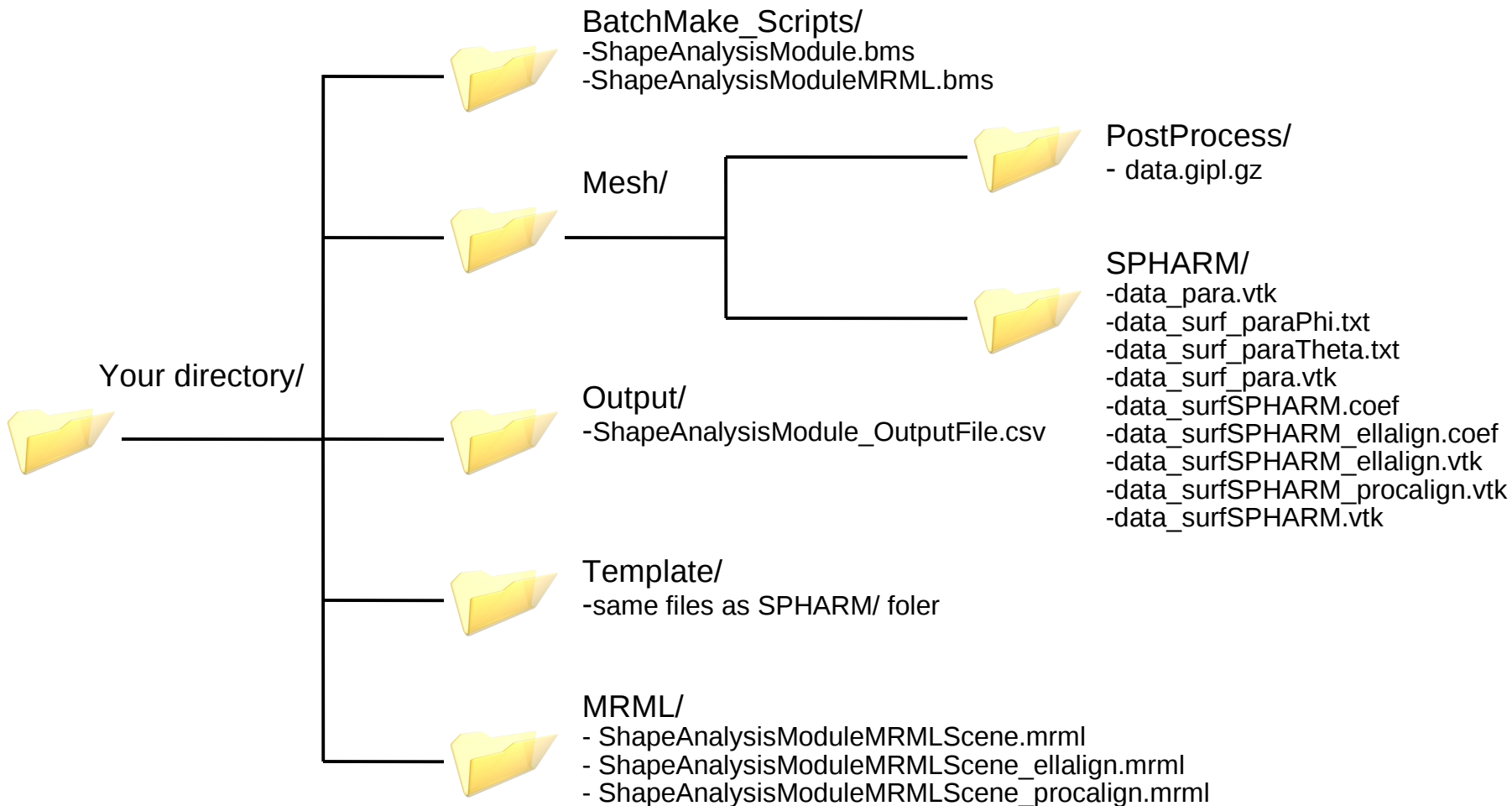


Output files and organisation

- A **CSV** file:
 - ⇒ Contains all the information from the input file.
 - ⇒ Contains the path of the output images.
 - ⇒ Can be use with the UNC statistics module shapeAnalysisMANCOVA.
- Three **MRML scenes**:
 - ⇒ Scene displayed within Slicer3.
 - ⇒ Allow the user to visualize all the data on the same scene.
- Images:
 - ⇒ Binary 3D Images.
 - ⇒ Surfaces meshes.
 - ⇒ Aligned surface meshes.



Output files and organisation





Overview

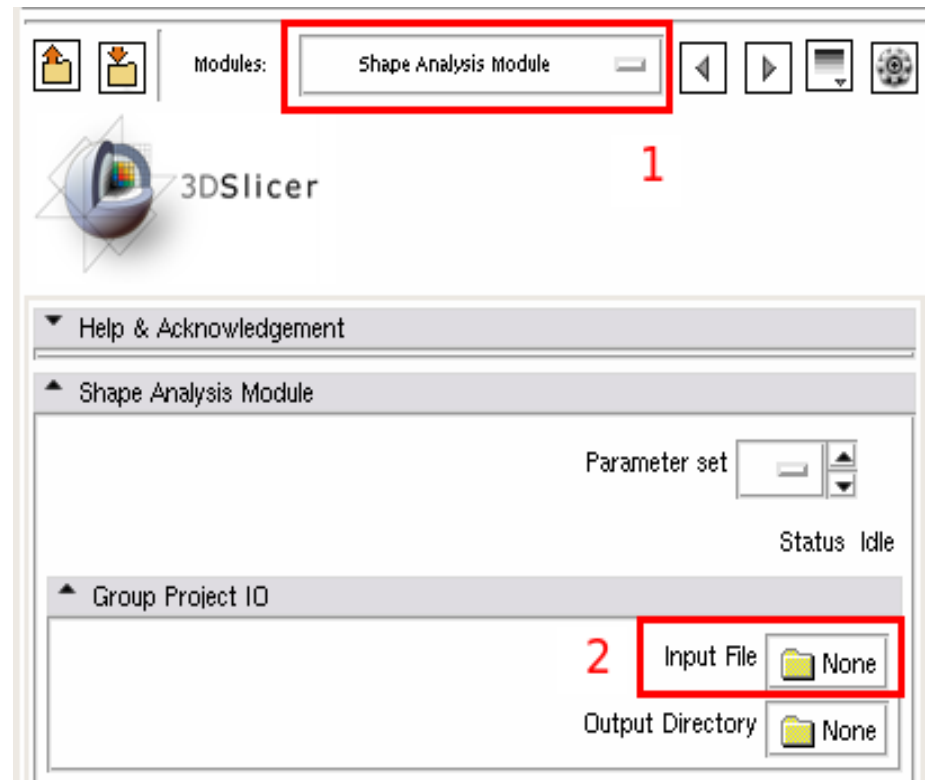
- 1- Input file
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Execution within Slicer

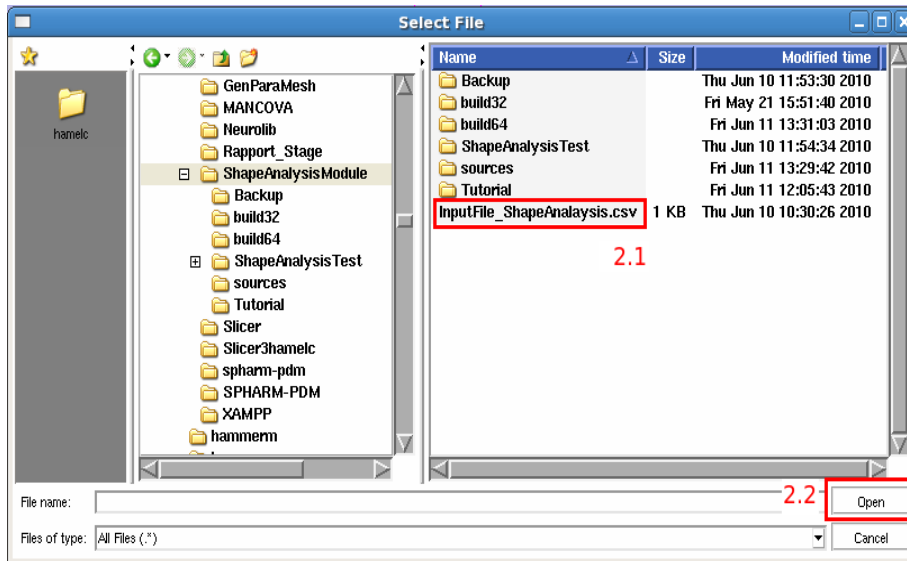
1- Select the “ShapeAnalysisModule” in Modules ->Shape Analysis.

2- Click on Input File





Execution within Slicer



2.1- Select the input file (**CSV file**).

2.2- Click on the **“Open”** button.

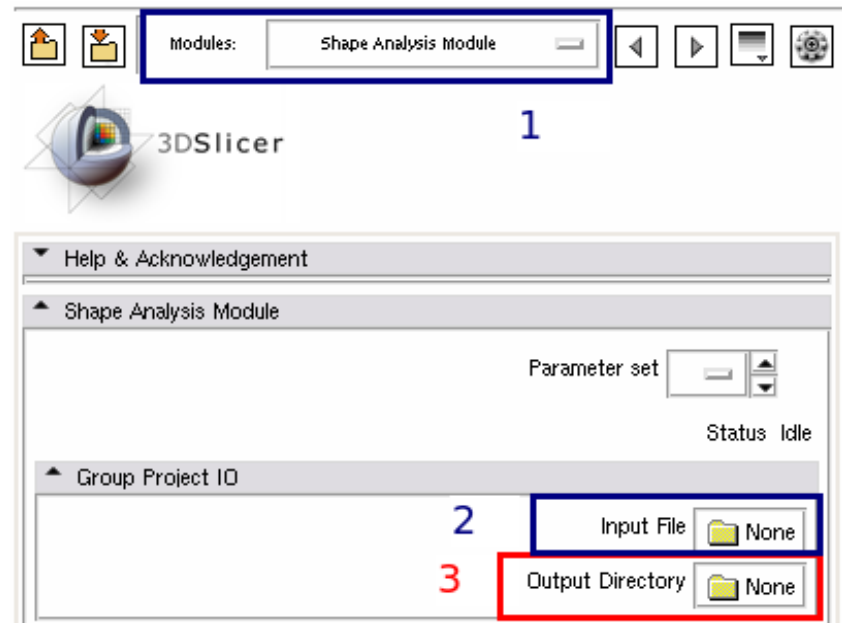


Execution within Slicer

1- Select the “ShapeAnalysisModule” in Modules ->Shape Analysis.

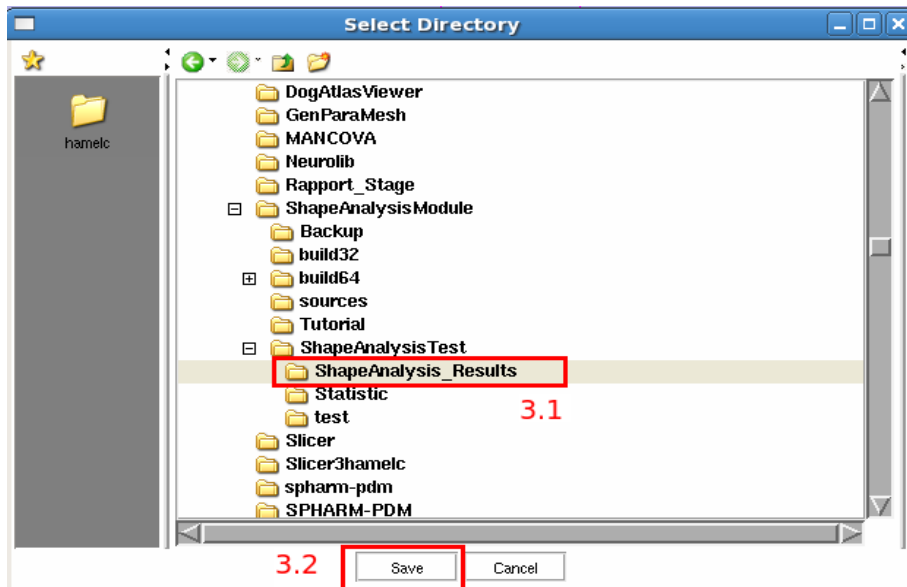
2- Click on Input File.

3- Click on the Output Directory.





Execution within Slicer



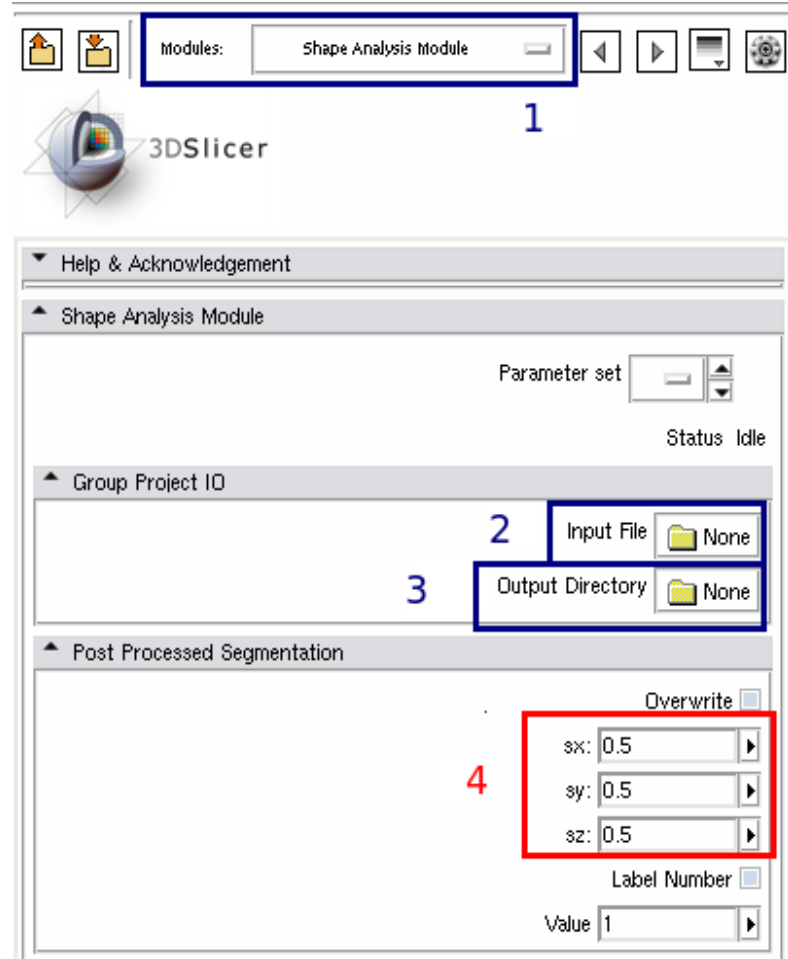
3.1- Select the output directory.

3.2- Click on the “**Save**” button.



Execution within Slicer

- 1- Select the “ShapeAnalysisModule” in Modules ->Shape Analysis.
- 2- Click on Input File.
- 3- Click on Output Directory.
- 4- Set the enforced spacing in x,y and z direction.

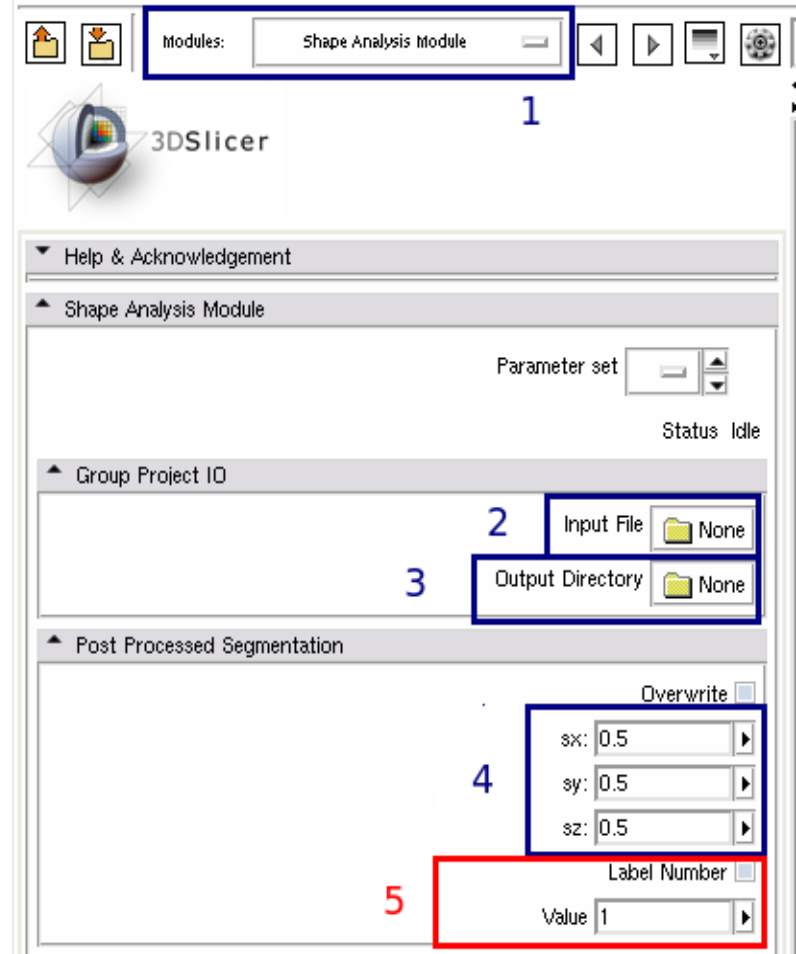




Execution within Slicer

- 1- Select the "ShapeAnalysisModule" in Modules ->Shape Analysis.
- 2- Click on Input File.
- 3- Click on Output Directory.
- 4- Set the enforced spacing in x,y and z direction.

5- (optional) Check the box "Label Number" and set "Value" to first extract this label before processing.

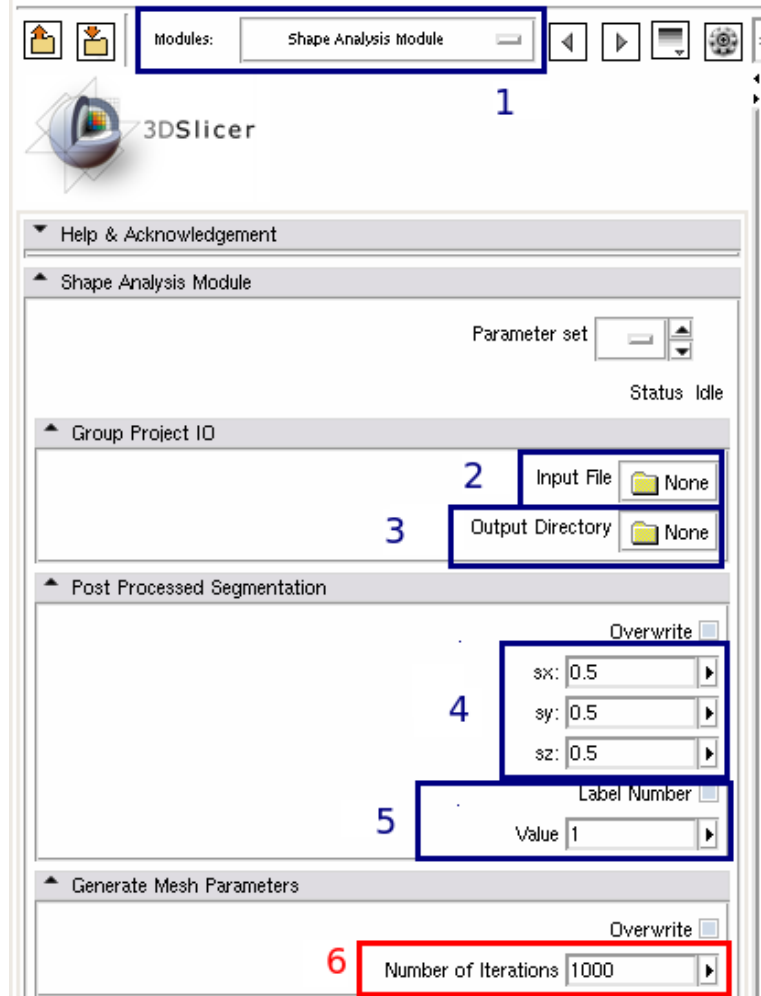




Execution within Slicer

- 1- Select the “ShapeAnalysisModule” in Modules ->Shape Analysis.
- 2- Click on Input File.
- 3- Click on Output Directory.
- 4- Set the enforced spacing in x,y and z direction.
- 5- (optional) Check the box “Label Number” and set “Value” to first extract this label before processing.

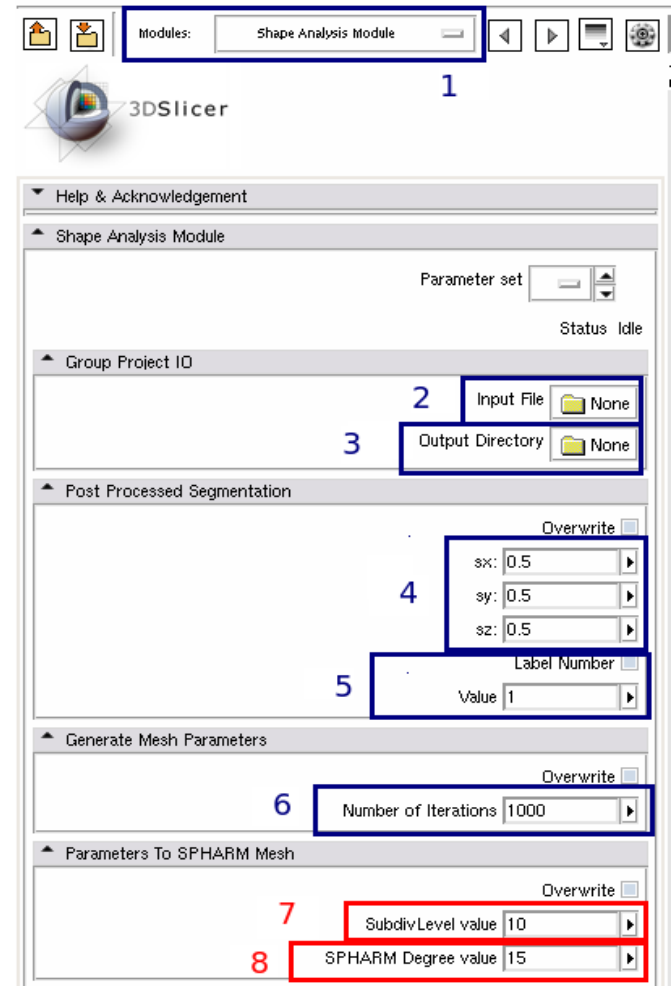
6- Set “Number of Iterations”





Execution within Slicer

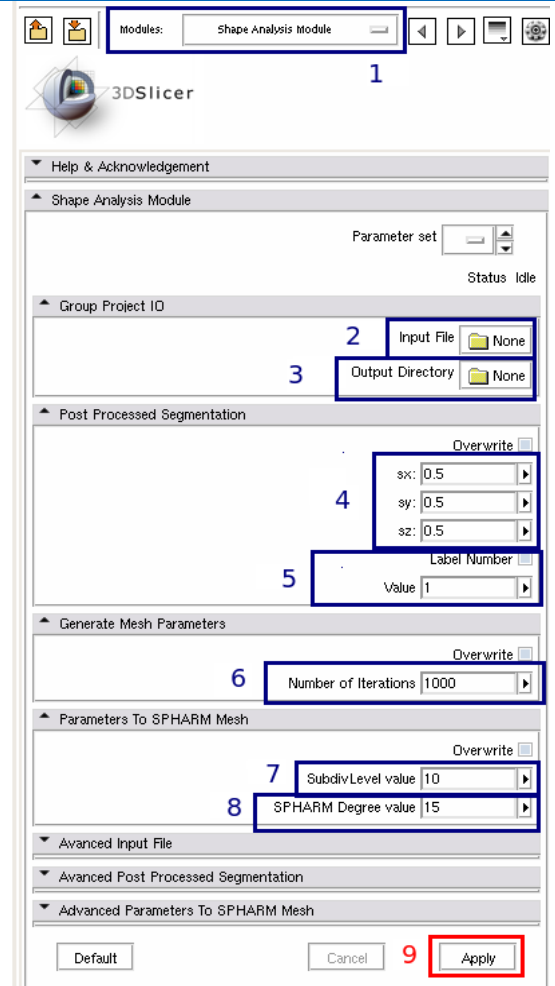
- 1- Select the “ShapeAnalysisModule” in Modules ->Shape Analysis.
- 2- Click on Input File.
- 3- Click on Output Directory.
- 4- Set the enforced spacing in x,y and z direction.
- 5- (optional) Check the box “Label Number” and set “Value” to first extract this label before processing.
- 6- Set “Number of Iterations”.
- 7- Set the subdivision level for the icosahedron subdivision.**
- 8- Set the maximal degree for the SPHARM computation.**





Execution within Slicer

- 1- Select the “ShapeAnalysisModule” in Modules ->Shape Analysis.
- 2- Click on Input File.
- 3- Click on Output Directory.
4. Set the enforced spacing in x,y and z direction before any processing.
- 5- (optionnal) Check the box “Label Number” and set “Value” to first extract this label before processing.
- 6- Set “Number of Iterations”.
- 7- Set the subdivision level for the icosahedron subdivision.
- 8- Set the the maximal degree for the SPHARM computation.
- 9- Click on the “Apply” button to process the data.

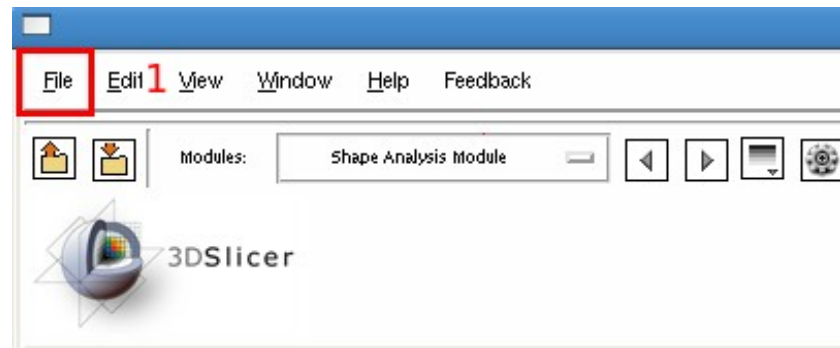




Execution within Slicer

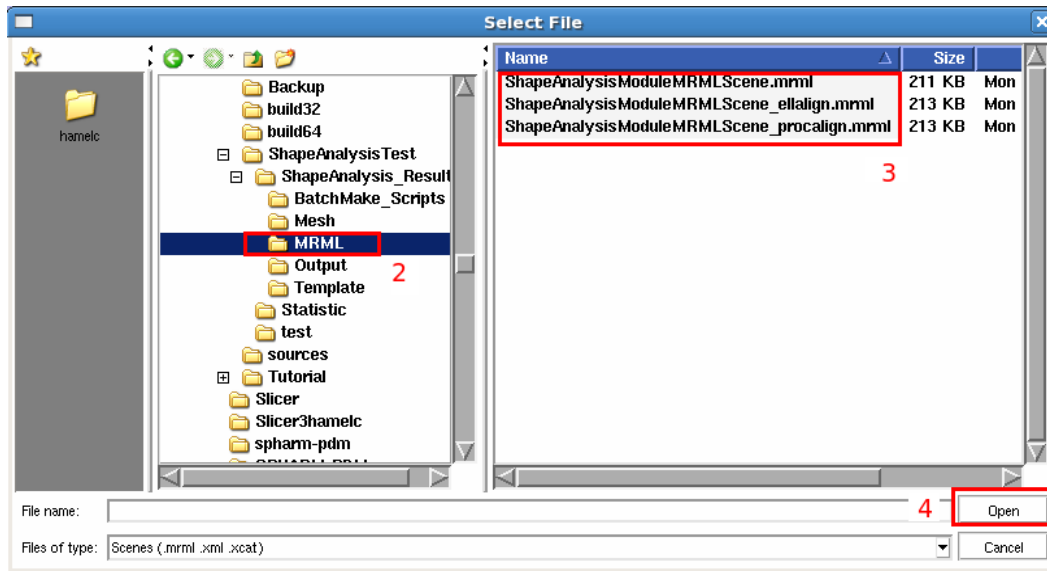
Load the MRML scenes:

1- Click on File -> Load Scene.





Execution within Slicer



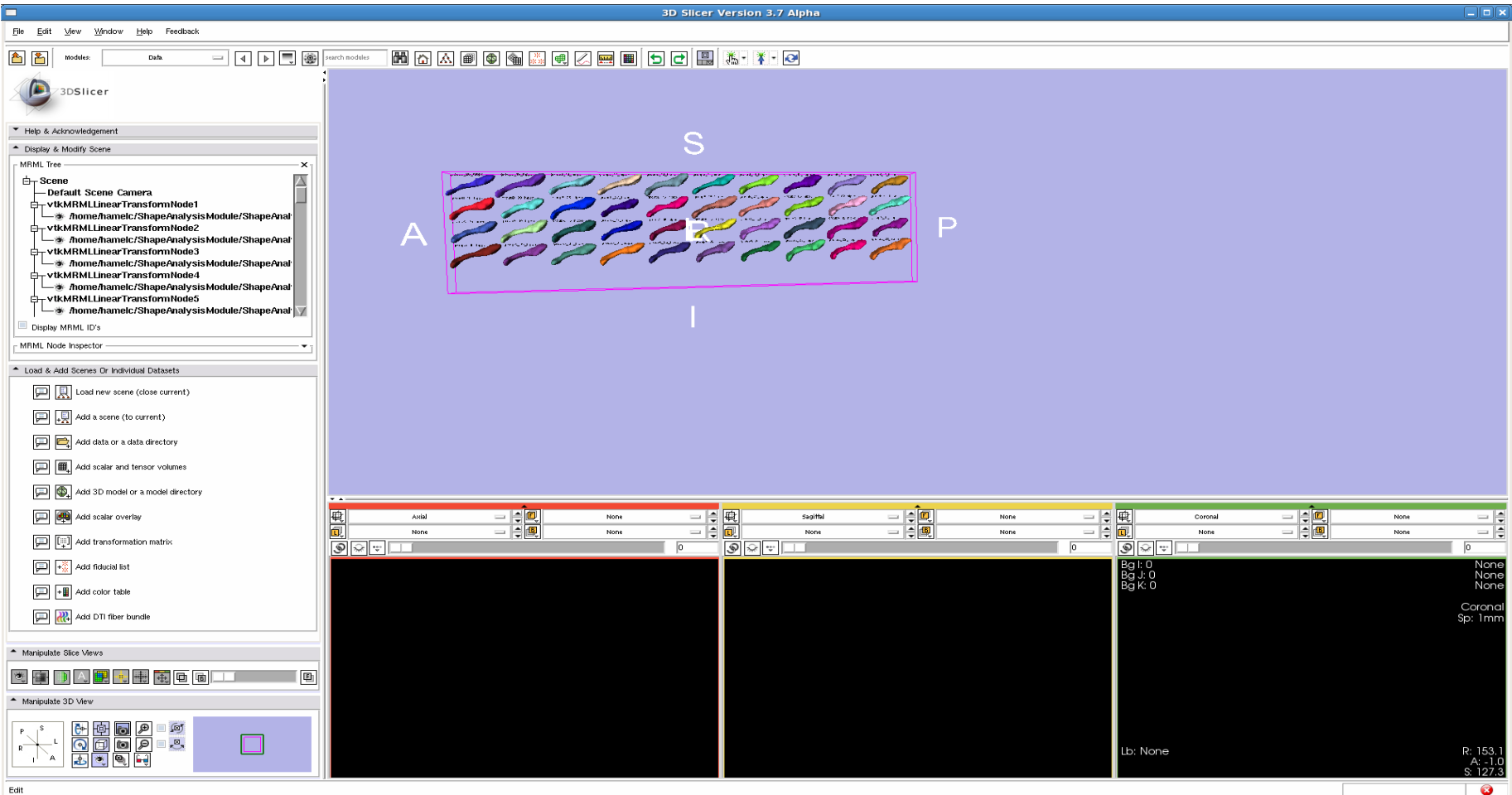
2- Go in
ShapeAnalysis_Results/MRML/

3- Select one of the three MRML
scene

4- Click on the “Open” button

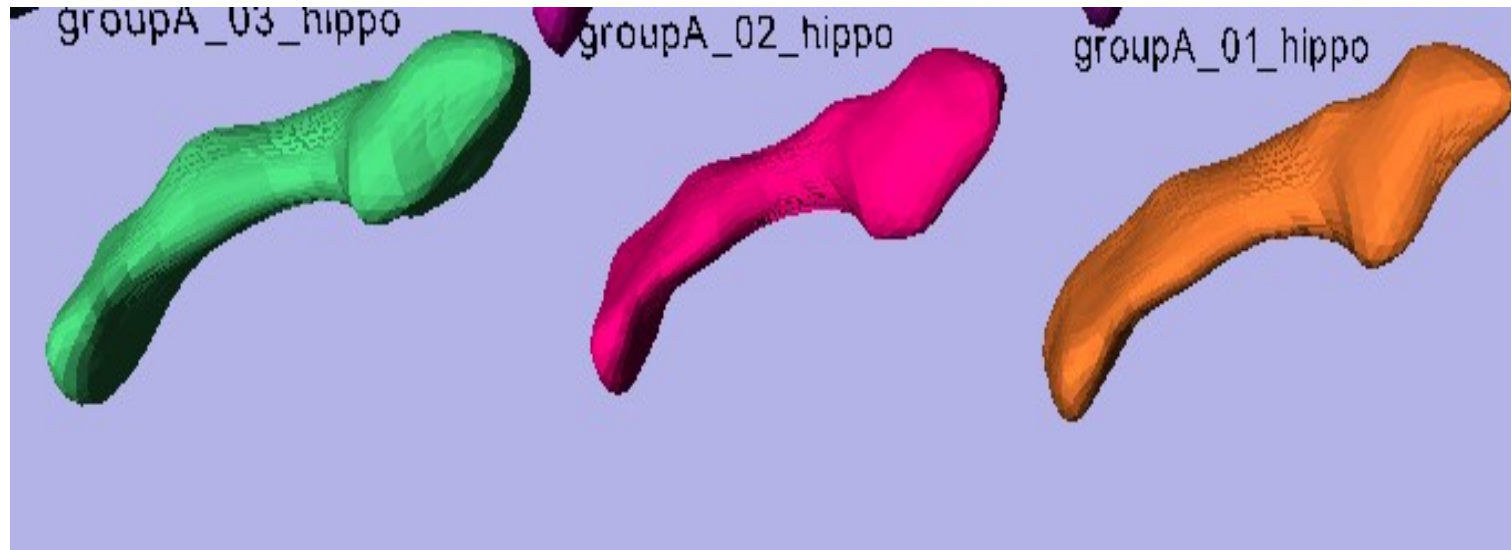


Execution within Slicer





Execution within Slicer



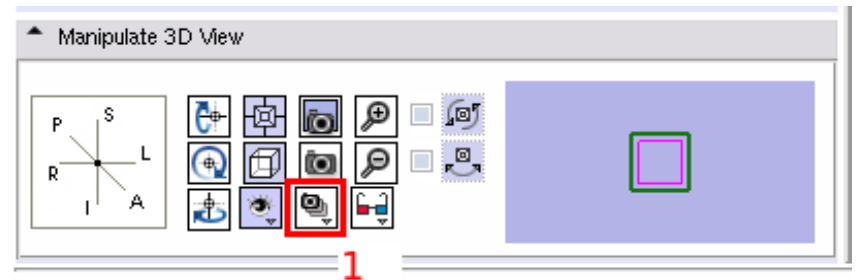
All the data are displayed with their name.



Execution within Slicer

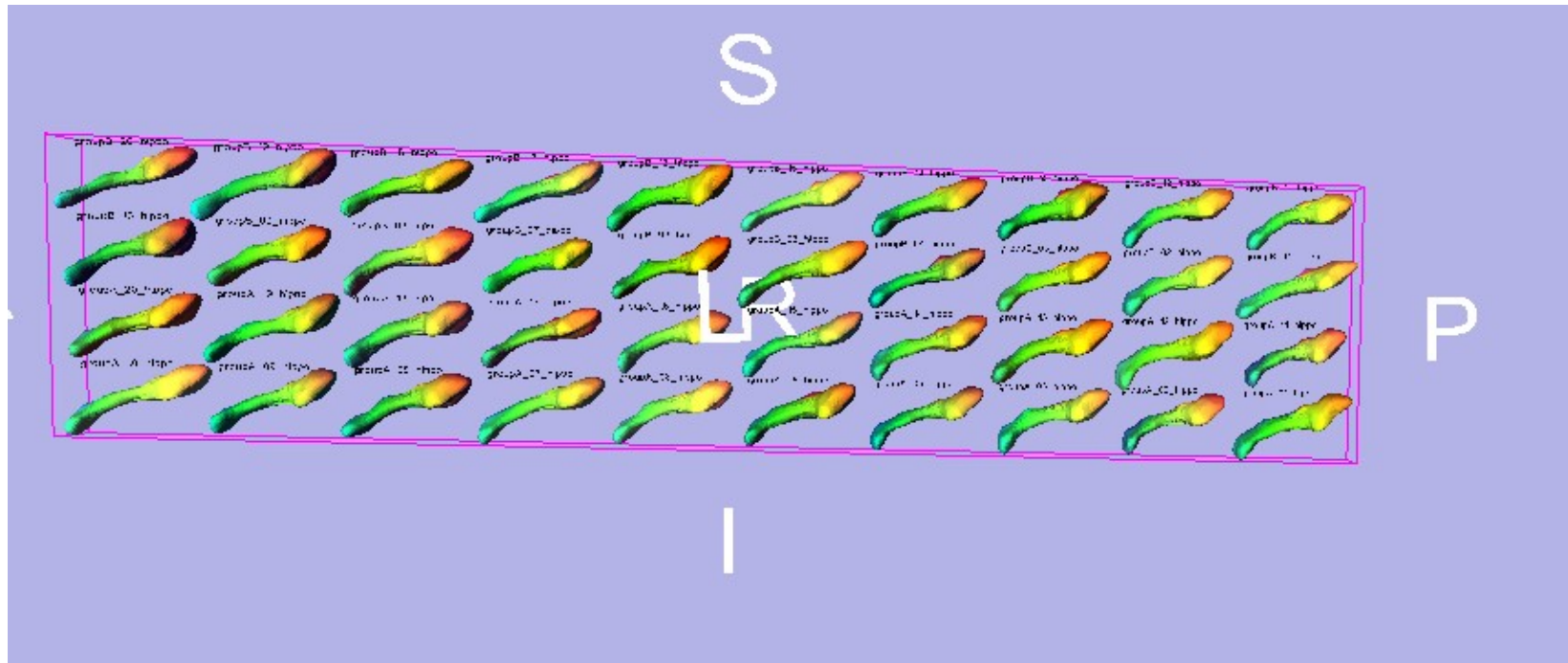
Display the color maps:

1. Click on the "Snapshots" button.
2. Select **Color Map Phi** or **Color Map Theta**.
3. Click on **Restore**.





Execution within Slicer



Quality Control visualization of the SPHARM correspondence using the color map Phi. Same color represent the same Φ parameter value of the spherical parameterization.



Execution within Slicer

You can recompute the modules of the ShapeAnalysisModule pipeline.

- Check one (or more) “**Overwrite**” box.
- Click on the “**Apply**” button to recompute the module.

The screenshot shows the Slicer Shape Analysis Module interface. The 'Post Processed Segmentation' section has an 'Overwrite' checkbox checked. The 'Generate Mesh Parameters' section has an 'Overwrite' checkbox checked. The 'Parameters To SPHARM Mesh' section has an 'Overwrite' checkbox checked. The 'Apply' button is highlighted.



Execution within Slicer

- **Input file:**

⇒ By default the first column containing a volume file (.vtk, .meta etc..) is computed. But if you have multiple files in your CSV file, you can choose the column of the input data file.

⇒ Check the box and enter the column.

- **Post Process Segmentation:**

⇒ You can apply a Gaussian filter.

⇒ Check the box and set the value of the variance.

Advanced Input File

Choose input volume column

Column number of volume input file: 0

Advanced Post Processed Segmentation

Gaussian filtering

Variance of Gauss filter (x): 10

Variance of Gauss filter (y): 10

Variance of Gauss filter (z): 10

Advanced Parameters To SPHARM Mesh

Use Flip/Reg Template

Flip Template (coef file): None

Reg Template (mesh file): None

Use Mean as the Template

ParaOut (template)

No Flip

Flip Along Axis of x

Flip Along Axis of y

Flip Along Axis of z

Flip Along Axis of x and y

Flip Along Axis of y and z

Flip Along Axis of x and z

Flip Along Axis of x and y and z

Default Cancel Apply



Execution within Slicer

Parameters to SPHARM Mesh:

1. You can choose to set the template (by default the template is the first data computed)

⇒ Flip template is used to test all possible flips of the parametrization along the first order ellipsoid axis and select the one whose reconstruction has minimal distance to the flip-template.

⇒ Reg template.

⇒ Mean Template: a mean file is computed and use as a template.

⇒ ParaOut is use to write The spherical icosahedron subdivision, as well as local phi and theta attribute files for the quality control visualization.

2. You can choose to flip of the parametrization along different axis.

Advanced Input File

Choose input volume column

Column number of volume input file

Advanced Post Processed Segmentation

Gaussian filtering

Variance of Gauss filter (x)

Variance of Gauss filter (y)

Variance of Gauss filter (z)

Advanced Parameters To SPHARM Mesh

1

Use Flip/Reg Template

Flip Template (coef file)

Reg Template (mesh file)

Use Mean as the Template

ParaOut (template)

2

No Flip

Flip Along Axis of x

Flip Along Axis of y

Flip Along Axis of z

Flip Along Axis of x and y

Flip Along Axis of y and z

Flip Along Axis of x and z

Flip Along Axis of x and y and z

Default Cancel Apply



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Command line execution

The module can also be use as a command line tool:

```
ShapeAnalysisModule --sx 0.5 --sy 0.5 --sz 0.5 --label 1 --NumberofIterations 1000 --  
SubdivLevelValue 10 --SPHARMDegreeValue 15 --columnVolumeFile 0 --varX 10 --  
varY 10 --varZ 10 --flipTemplate None --regTemplate None --paraOutTemplate --  
noFlip /home/hamelc/ShapeAnalysisModule/InputFile_ShapeAnalaysis.csv /home/ha  
melc/ShapeAnalysisModule/ShapeAnalysisTest/ShapeAnalysis_Results
```



Conclusion

The ShapeAnalysisModule is a 3D Slicer module that allows efficient computation of structural shape analysis via the SPHARM-PDM UNC pipeline including intuitive quality control visualizations.

Thanks to this tutorial you are now able to perform shape analysis on your own dataset.



Acknowledgments



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