



NA-MIC

National Alliance for Medical Image Computing

<http://www.na-mic.org>

Shape analysis using spherical harmonics

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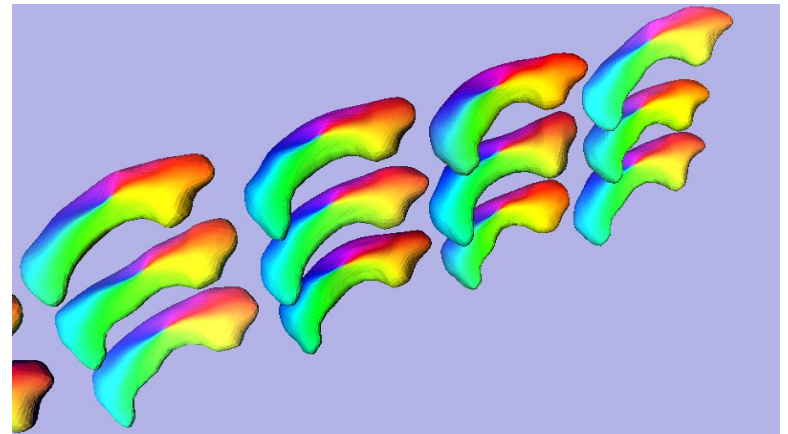
NA-MIC Tutorial Contest: Summer 2011



Learning Objective

This tutorial shows how to perform shape analysis studies using :

- ShapeAnalysisModule
- ParticulesModule.





Pre-requisite

This tutorial assumes that you have already completed the Slicer3Visualization Tutorial (by Sonia Pujol)

The tutorial is available at:

<http://www.slicer.org/slicerWiki/index.php/Slicer3.6:Training>



Material

This tutorial requires the installation of the **Slicer3.6** release, **BatchMake**, some **Slicer extensions** and the **tutorial dataset**.

They are available at the following locations:

→ **Slicer3.6** download page

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

→ **Extension** *we are still working on adding the tools the the Slicer extension : it will be available under the name : spharm-pdm*

If you do not find it :

→ **External application** the last release on the download page :
http://www.nitrc.org/frs/?group_id=308

→ **Tutorial dataset:**ShapeAnalysis_TutorialData

http://www.nitrc.org/docman/index.php?group_id=308&selected_doc_group_id=760&language_id=1#folder



Platforms

This tutorial has been developed and performed on Linux64.

http://wiki.na-mic.org/Wiki/index.php/Training:Summer_2011_Contest_Table



Prerequisites

Add the **BatchMake Applications** :

Set the environment variable `BatchmakeShapeAnalysisModule_Dir`

→ *tcs*h usage :

```
setenv BatchmakeShapeAnalysisModule_Dir /your absolute path/spharm-pdm_Linux32or64/BatchMake_Applications
```

→ *bash* usage :

```
export BatchmakeShapeAnalysisModule_Dir=/your absolute path/spharm-pdm_Linux32or64/BatchMake_Applications
```

Add the **external applications** : (command line usage)

→ *tcs*h usage :

```
setenv PATH /your absolute path/spharm-pdm_Linux32or64:${PATH}
```

→ *bash* usage :

```
export PATH=/your absolute path/spharm-pdm_Linux32or64:${PATH}
```



Prerequisites

To add the extension ShapeAnalysisModule:

→ Use the View → Extension Manager menu option
→ Next

Find and install **SPHARM-PDM** extension.

*NB : we are still working on this extension, if you do not find it, please, download the executables here: http://www.nitrc.org/frs/?group_id=308
(The last release)*



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
- 6- Conclusion



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Input File

- A CSV file : **C**omma **S**eparated **V**alue
- Contains all the subjects information : age, group, MRI...
- Contains the path to the data, which are binary segmentation of a single brain structure

```
Gender,InputFile1,Input File Description
0,/devel/linux/ShapeTools/example/hippocampi/origData/groupA_01_hippo.gipl.gz,none
0,/devel/linux/ShapeTools/example/hippocampi/origData/groupA_02_hippo.gipl.gz,none
1,/devel/linux/ShapeTools/example/hippocampi/origData/groupB_01_hippo.gipl.gz,none
1,/devel/linux/ShapeTools/example/hippocampi/origData/groupB_02_hippo.gipl.gz,none
```

Fig: a CSV file.



Input File -with the dataset-

The data set for this tutorial:

- Download and unzip : ShapeAnalysis_Data_Example.zip
- All the hippocampus needed are in the folder “origData”
- Modify the -4data- CSV file : replace the path of the data by yours.

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

We will use the CSV with only 4 of the 40 hippocampus available, in order to increase the speed of the running



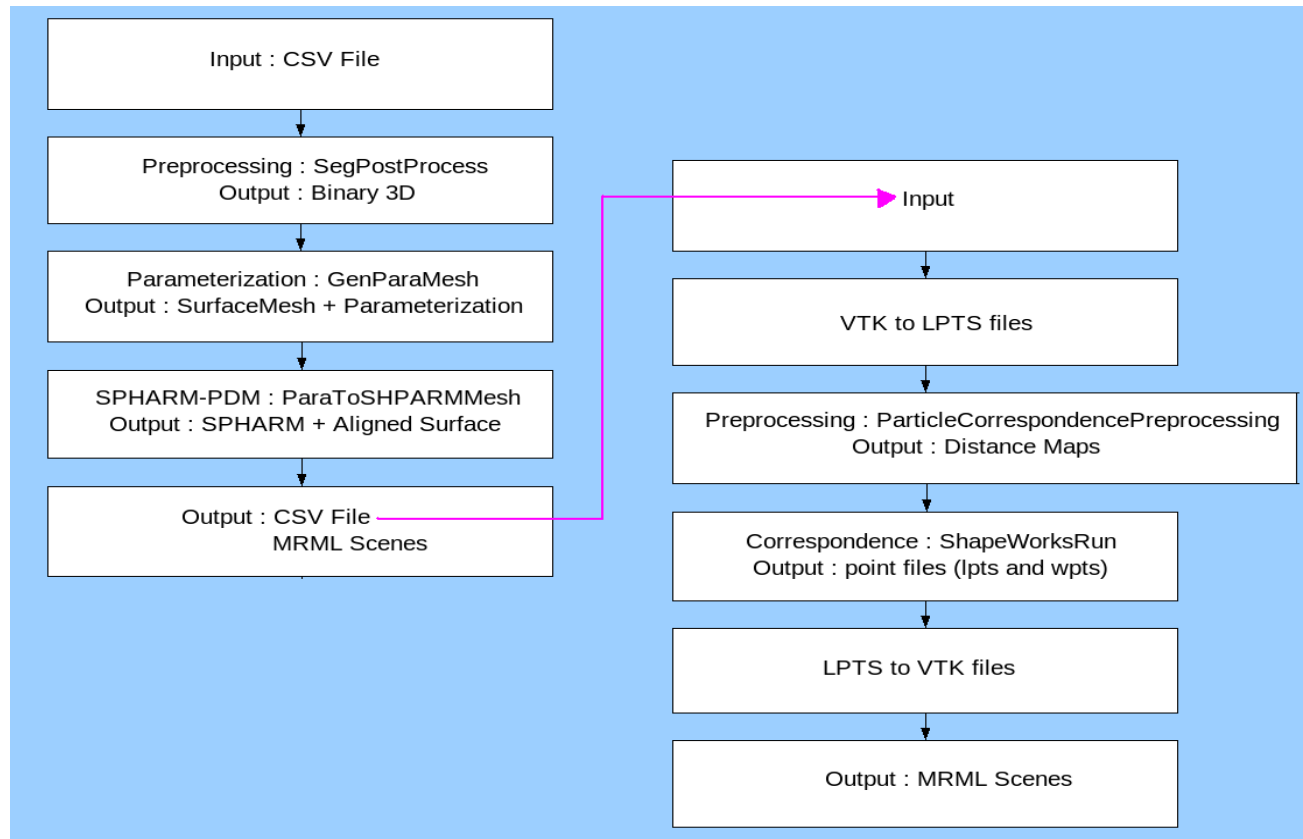
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Pipeline Description

ShapeAnalysisModule



ParticleModule



Pipeline Description -ShapeAnalysisModule-

→ SegPostProcess

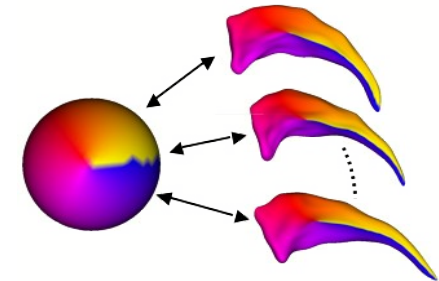
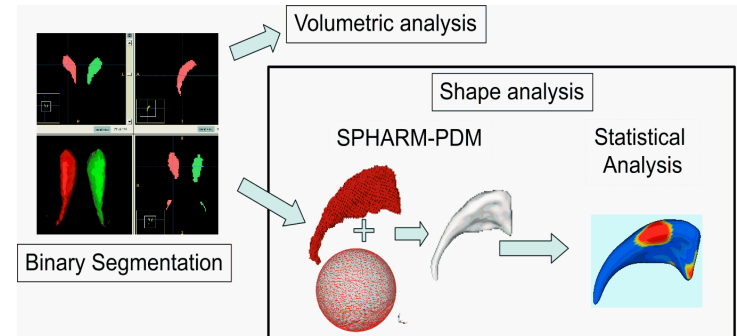
- Fills interior holes.
- Performs minimal smoothing operation and ensures spherical topology.

→ 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.





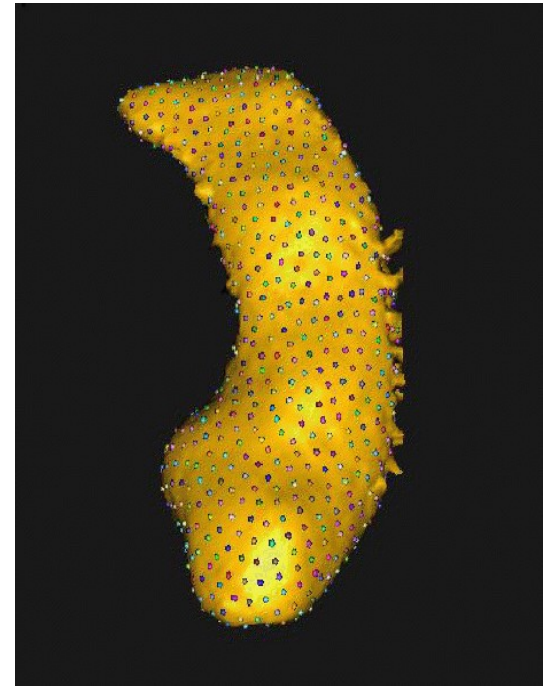
Pipeline Description -ParticleModule-

→ PreProcessing

- Remove the high-frequency artefacts

→ ShapeWorks

- Optimization of the positions of the correspondences





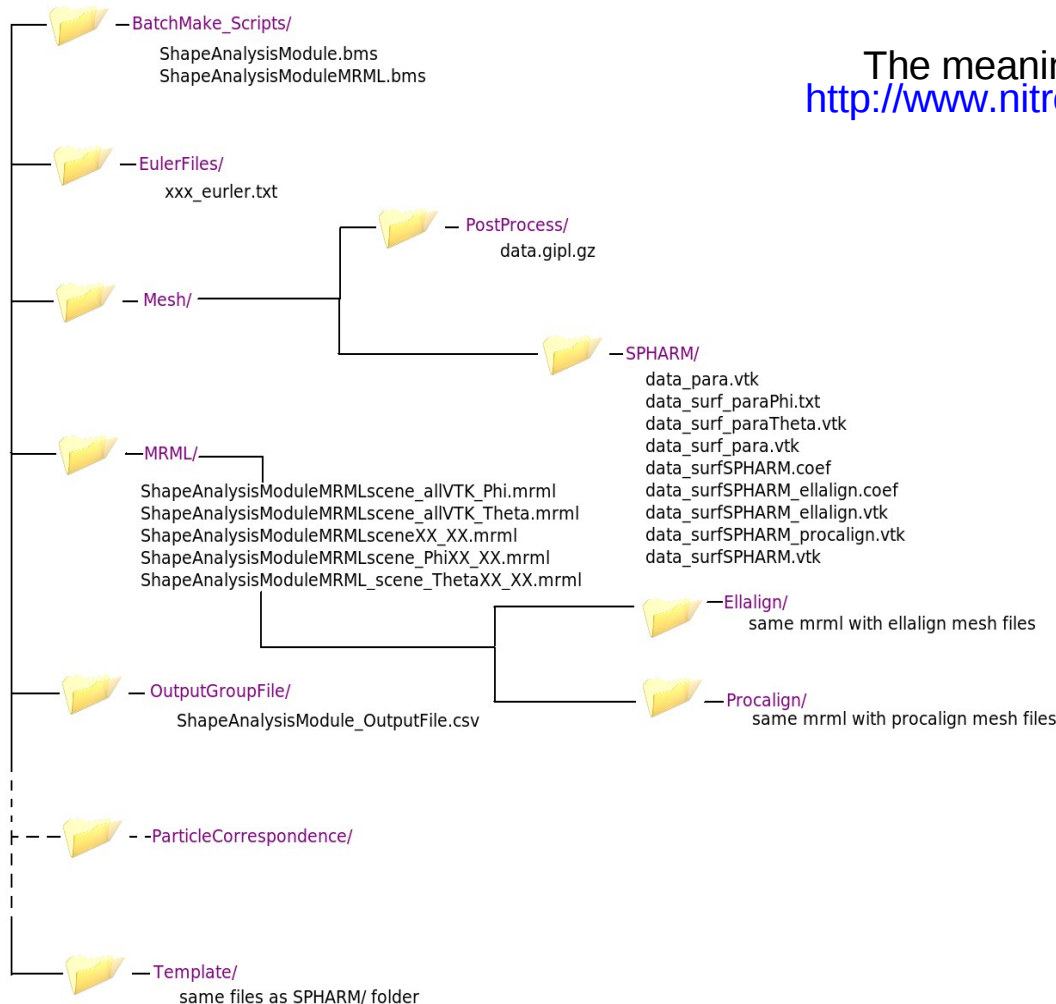
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Output files and organisation: -ShapeAnalysisModule -

The meanings of all those outputs are explained :
http://www.nitrc.org/plugins/mwiki/index.php/spharm-pdm:Pipeline_Doc_V1.9#Template





Output files and organisation: -ParticleModule -

-  — Corresponding Meshes
(5) Lpts - Corresponding_Particles - to VTK
 - * your_data_corr.vtkwithin ShapeAnalysisModule :
 - * customLUT_Color_Map_Phi and Theta.txt
 - * distances_scaled.txt
-  — Corresponding_Meshes_scale
(5) Lpts - Corresponding_Particles - to VTK
 - * your_data_corr_scale.vtk
-  — Corresponding_Particles
(4) Outputs of ShapeWorksRun
 - * Correspondence.params
 - * your_data.lpts
 - * your_data.wpts
 - * ShapeWorksView.params
-  — Initialization Particles
(2) VTK to LPTS
 - * your_data_scale.lpts
-  — InputMeshes_scale
(1) VTK with the enforced spacing
 - * your_data_scale.vtk
-  — MRML
(6) Using the Corresponding_Meshes
 - * ParticleModuleMRMLscene.mrmlwithin ShapeAnalysisModule:
 - * ParticleModuleMRMLscene_ColorMap_X_X.mrml
 - * ParticleModuleMRMLscene_ColorMap_allVTK.mrml
-  — PreProcessing
(3) using VTKFiles_withScaleFactor
 - * CorrespondencePreProcessing.params
 - * subject_XXX_DistanceMap.mha



Overview

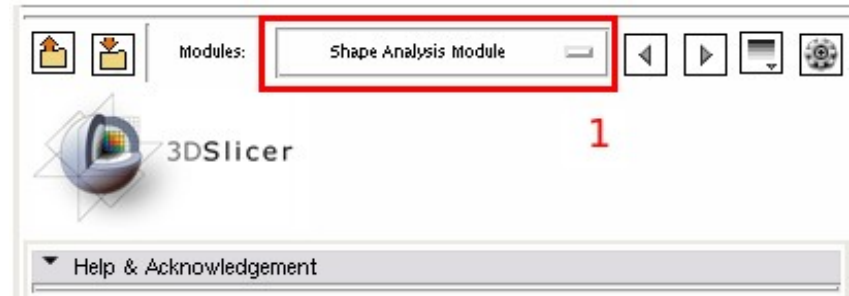
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Execution within Slicer : Start the ShapeAnalysisModule

When 3D Slicer is started it shows the Welcome window on the left.

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





Execution within Slicer : Input and Output directory

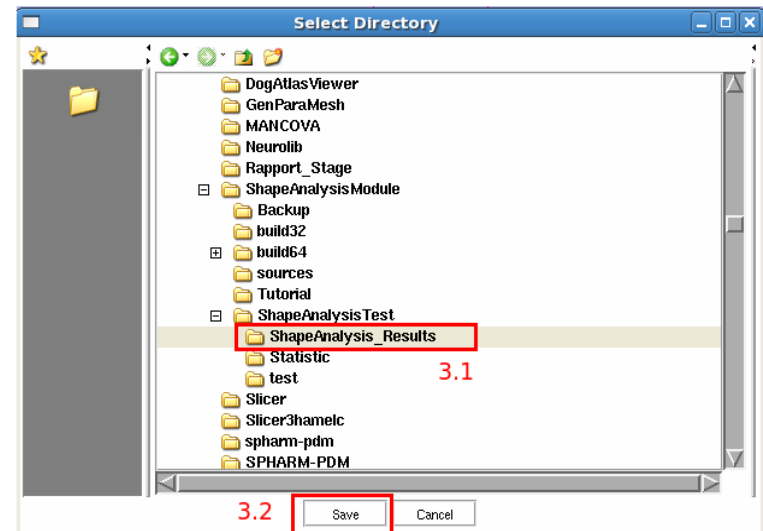
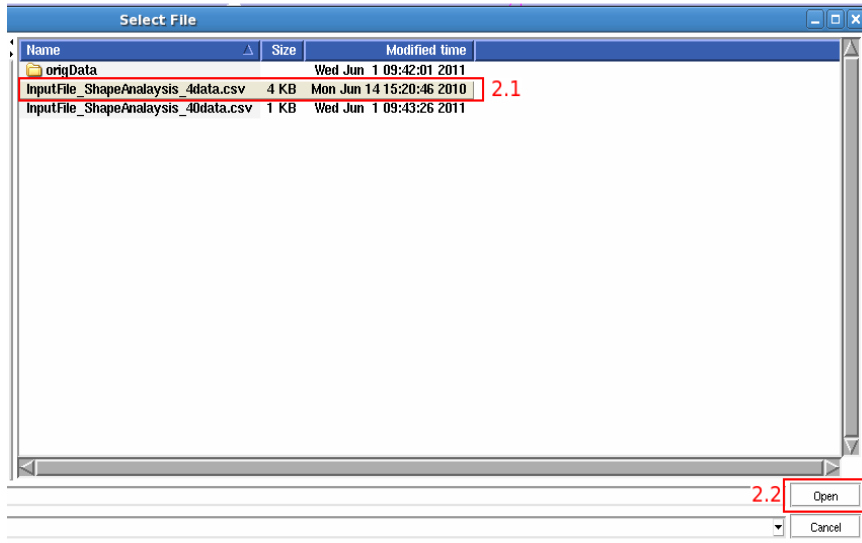
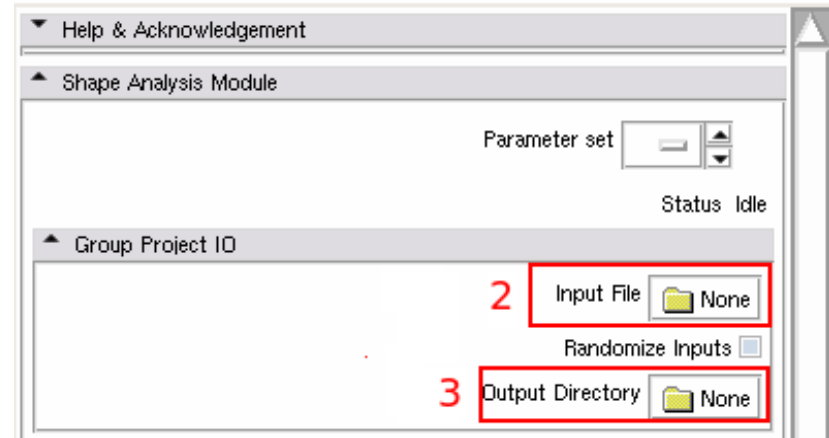
1- Select the “ShapeAnalysisModule” in Modules ->Shape Analysis.

2- Click on “Input File”

Select the input file (CVS) (2.1) and then click on the “Open” button (2.2)

3- Click on “Output Directory”

Select the output directory (3.1) and then click on the “Save” button(3.2)





Execution within Slicer : *SegPostProcess* Parameters

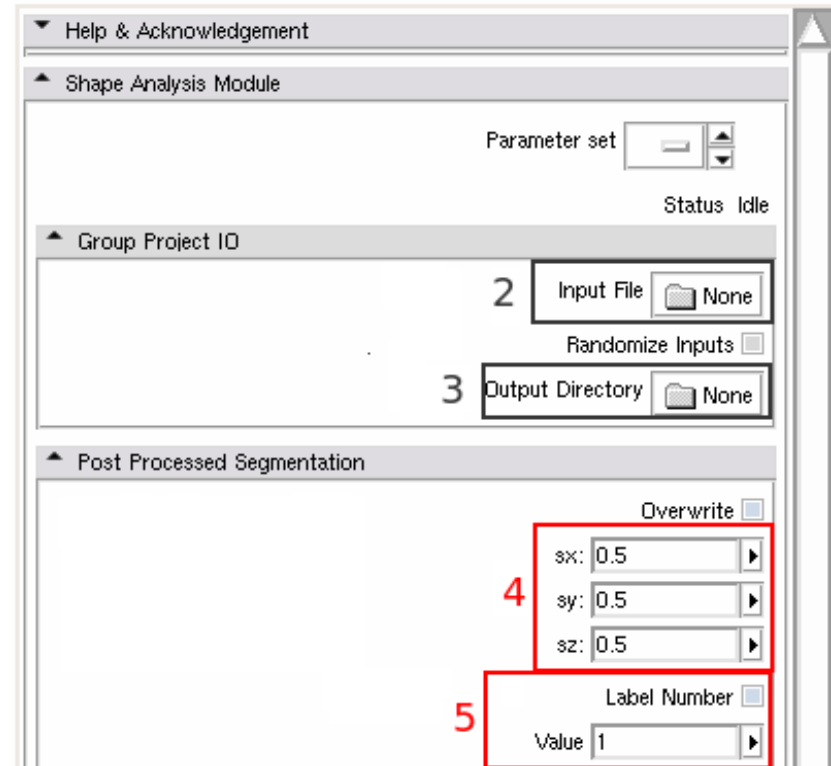
1- Select the “*ShapeAnalysisModule*” in *Modules* ->*Shape Analysis*.

2- Click on “*Input File*”

3- Click on “*Output Directory*”

4- Set the enforced spacing in x,y and z direction.

5- (optionnal) Check the box “**Label Number**” and set “**Value**” to first extract this label before processing.





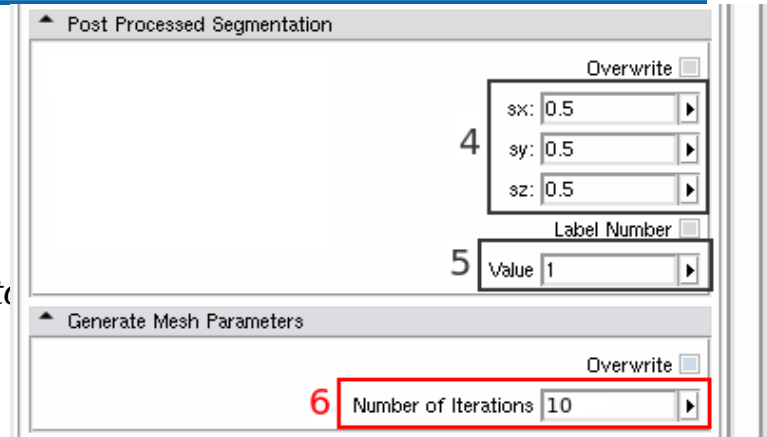
Execution within Slicer : *GenParaMesh* Parameters

- 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” to 10.

The number of iterations is greatly reduced (1000 to 10),
to increase the speed of the running.

Outside this tutorial, you should use the default value
(1000) or even more.

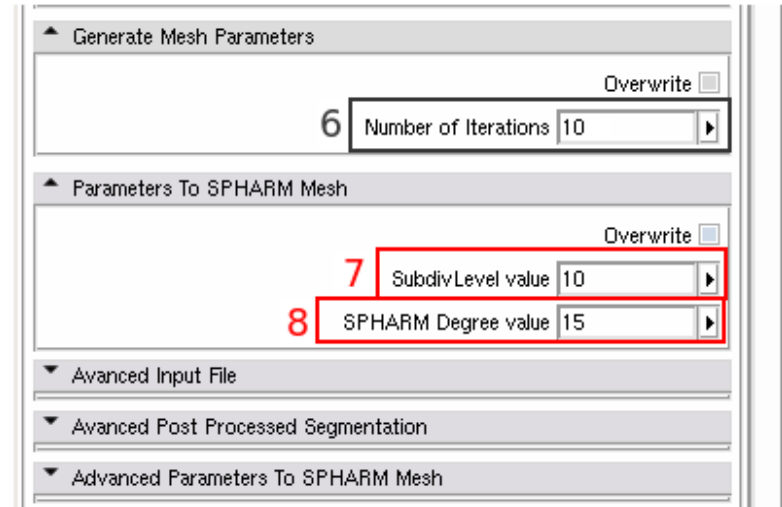




Execution within Slicer :

ParaToSPHARMMesh Parameters

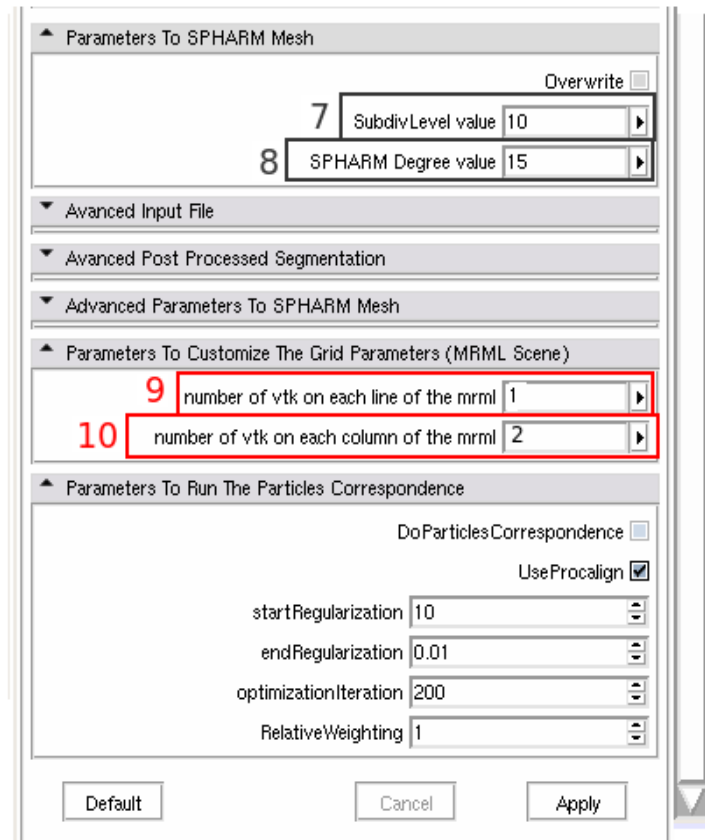
- 1- Select the “ShapeAnalysisModule” in Modules ->Shape Analysis.
- 2-Click on “Input File”
- 3- Click on “Output Directory”
- 4- Set the enforced spacing in x,y and z direction.
- 5- (optional) Check the box “Label Number” and set “Value” to first extract this label before processing.
- 6- Set “Number of Iterations” to 10
- 7- Set the subdivision level for the icosahedron subdivision**
- 8- Set the maximal degree for the SPHARM computation**





Execution within Slicer : MRML Scene Parameters

- 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
- 9- 10- Set the number of shapes you want horizontally (1) and vertically (2) in each MRML scene**



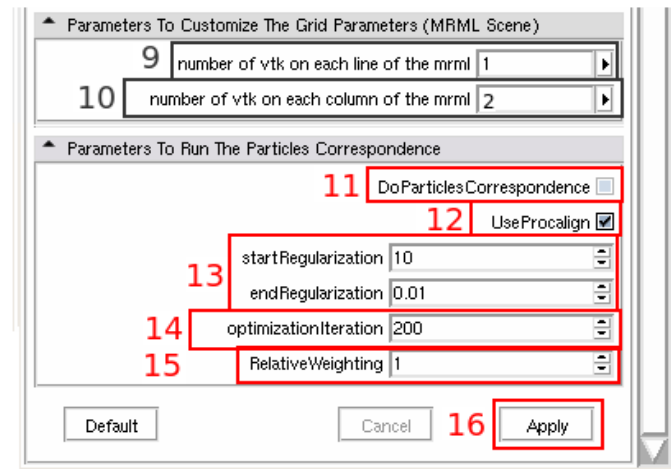


Execution within Slicer : *ParticleModule* Parameters

- 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
- 9- 10- Set the number of shapes you want horizontally (9) and vertically (10) in each MRML scene

To run a **Particle study** at the end of the pipeline :

- 11- Check the Box “DoParticleCorrespondence”**
- 12- If you want to use the meshes in their original space, uncheck the box. Otherwise the meshes in procalign space will be used.**



13- Starting and ending regularization for the entropy-based correspondence optimization

14- Number of iterations for the entropy-based correspondence

15- This is the value α between the 2 energies

16- Click on the “Apply” button to process the data



Execution within Slicer : Load a MRML Scene

1- Click on File -> Load Scene

2- Go in your _Output_Directory/MRML

3- Select one MRML scene

4- Click on the “Open” button

The screenshot shows the Slicer software interface. The 'File' menu is open, and the 'Load Scene' option is highlighted. The 'Select File' dialog box is open, showing a file tree on the left and a list of files on the right. The 'MRML' folder is selected in the file tree, and the file 'ShapeAnalysisModuleMRMLscene_allVTK_Theta.mrml' is selected in the list. The 'Open' button is highlighted in the bottom right corner of the dialog box.

Name	Size	Modified time
Ellalign		Tue May 31 15:40:29 2011
Procalign		Tue May 31 15:40:31 2011
TransformFiles		Tue May 31 16:13:13 2011
ShapeAnalysisModuleMRMLscene0_1.mrml	27 KB	Tue May 31 16:13:16 2011
ShapeAnalysisModuleMRMLscene2_3.mrml	27 KB	Tue May 31 16:13:24 2011
ShapeAnalysisModuleMRMLscene_allVTK_Phi.mrml	11 KB	Tue May 31 16:13:06 2011
ShapeAnalysisModuleMRMLscene_allVTK_Theta.mrml	11 KB	Tue May 31 16:13:07 2011
ShapeAnalysisModuleMRMLscene_Phi0_1.mrml	8 KB	Tue May 31 16:13:13 2011
ShapeAnalysisModuleMRMLscene_Phi2_3.mrml	8 KB	Tue May 31 16:13:22 2011
ShapeAnalysisModuleMRMLscene_Theta0_1.mrml	8 KB	Tue May 31 16:13:14 2011
ShapeAnalysisModuleMRMLscene_Theta2_3.mrml	8 KB	Tue May 31 16:13:23 2011



Execution within Slicer :

Load a MRML Scene : Which MRML?

There are several kind of MRML scene
You can visualize the shapes with a Phi or a Theta
ColorMap

→ with all the data

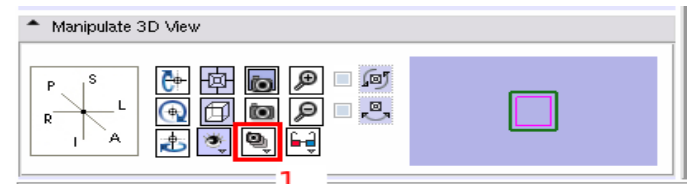
→ with only A*B shapes : the grid
parameters chosen

In the first MRML scenes, you can find
the template with a random color and
then with the snapshots, you can the
shapes A to B with a Phi *colormap* or a
Theta

▶	Ellalign	-- folder
▶	Procalign	-- folder
▶	TransformFiles	-- folder
	ParticleModuleMRMLscene.mrml	44.5 KB plain t
	ShapeAnalysisModuleMRMLscene0_1.mrml	26.5 KB plain t
	ShapeAnalysisModuleMRMLscene2_3.mrml	26.5 KB plain t
	ShapeAnalysisModuleMRMLscene_allVTK_Phi.mrml	10.9 KB plain t
	ShapeAnalysisModuleMRMLscene_allVTK_Theta.mrml	10.9 KB plain t
	ShapeAnalysisModuleMRMLscene_Phi0_1.mrml	7.0 KB plain t
	ShapeAnalysisModuleMRMLscene_Phi2_3.mrml	7.0 KB plain t
	ShapeAnalysisModuleMRMLscene_Theta0_1.mrml	7.1 KB plain t
	ShapeAnalysisModuleMRMLscene_Theta2_3.mrml	7.1 KB plain t

Display the *colormaps*:

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





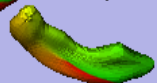
Execution within Slicer :

MRML Scene

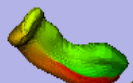
- groupB_02_hippo_pp_surfSPHARM



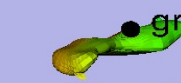
- groupB_01_hippo_pp_surfSPHARM



- groupA_02_hippo_pp_surfSPHARM



- groupA_01_hippo_pp_surfSPHARM



- groupB_02_hippo_pp_surfSPHARM



- groupB_01_hippo_pp_surfSPHARM



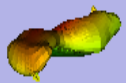
TEMPLATE
(no template for procalign)

Quality Control visualization of the SPHARM correspondence using the Phi colormap (above) or the Theta colormap (below). Same colour represent the same Phi/Theta parameter value of the spherical parameterization.

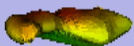
On the left, MRML scenes with all the data.

On the right, MRML scenes with only X data and the template

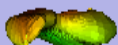
- groupB_02_hippo_pp_surfSPHARM



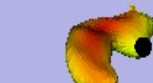
- groupB_01_hippo_pp_surfSPHARM



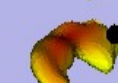
- groupA_02_hippo_pp_surfSPHARM



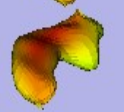
- groupA_01_hippo_pp_surfSPHARM



- groupB_02_hippo_pp_surfSPHARM



- groupB_01_hippo_pp_surfSPHARM





Execution within Slicer : Recompute

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 displays three panels from the Slicer software interface, each with an 'Overwrite' checkbox highlighted in a red box:

- Post Processed Segmentation**: Contains sliders for 'sx: 0.5', 'sy: 0.5', and 'sz: 0.5', a 'Label Number' checkbox, and a 'Value' dropdown set to '1'.
- Generate Mesh Parameters**: Contains a 'Number of Iterations' dropdown set to '1000'.
- Parameters To SPHARM Mesh**: Contains a 'SubdivLevel value' dropdown set to '10' and a 'SPHARM Degree value' dropdown set to '15'.



Execution within Slicer : Advanced Parameters

Input file:

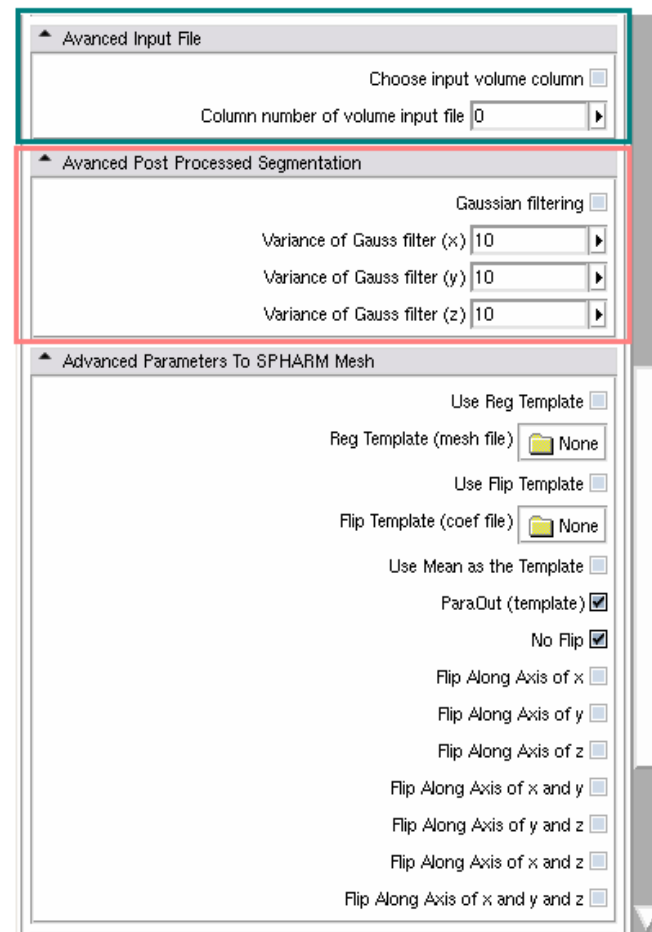
→ By default the first column containing a volume file (.vtk, .meta etc..) is computed. But if you have multiple files in your CSV file, you can choose the column of the input data file

→ 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





Execution within Slicer : Advanced Parameters -2-

SPHARM Mesh :

Choose the template: (by default the template is the first data computed)

- Reg template is used to set the procrustes alignment
- 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
- 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

Choose the Flip:

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

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 Reg Template

Reg Template (mesh file) None

Use Flip Template

Flip Template (coef 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

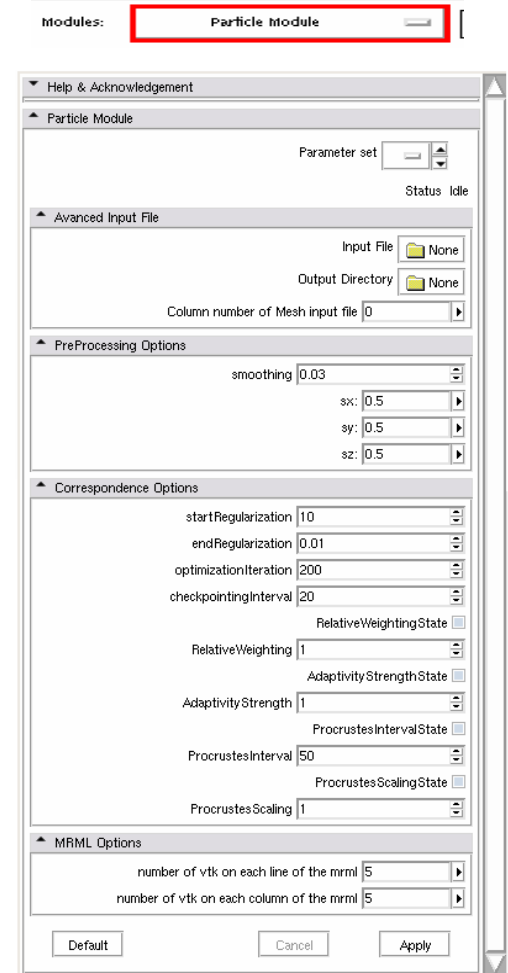
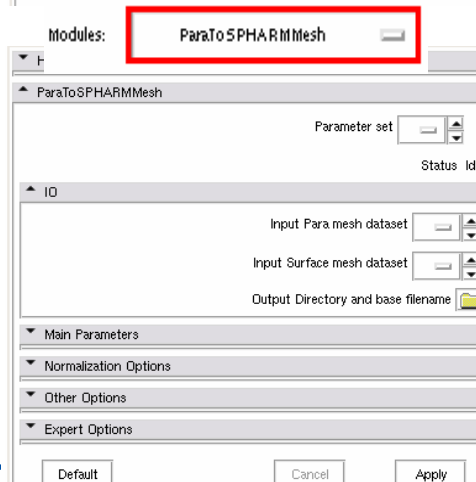
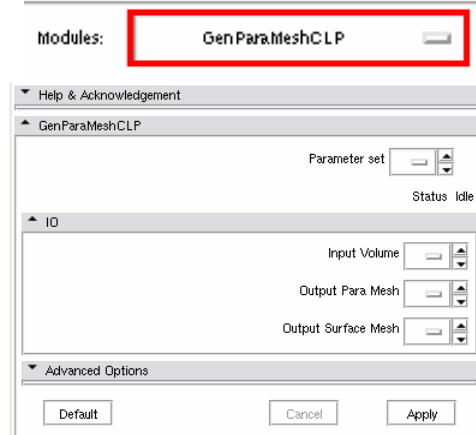
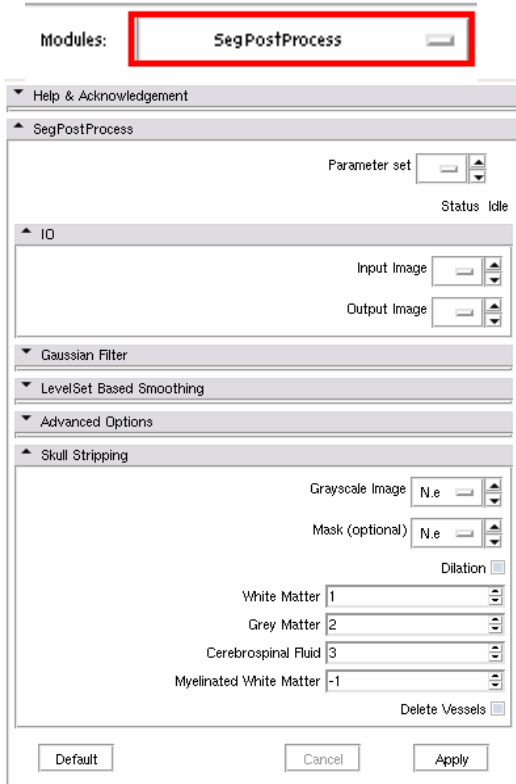
Flip Along Axis of x and z

Flip Along Axis of x and y and z



Execution within Slicer : Step by step

In Module > ShapeAnalysis:
You can find all the modules used in the pipeline.





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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 10 --  
SubdivLevelValue 10 --SPHARMDegreeValue 15 --columnVolumeFile 0 --varX 10 --  
varY 10 --varZ 10 --regTemplate None --flipTemplate None --paraOutTemplate --  
noFlip --HorizontalGridPara 1 --VerticalGridPara 2 --DoParticlesCorrespondence --  
UseProcalign /your_path_to_the_csv_file/InputFile ShapeAnalaysis.csv /your_path  
to_your_outputdirectory/ShapeAnalysis_Data_Example_FILES
```



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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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Neuro Image Research Analysis Laboratories