Shape analysis using spherical harmonics

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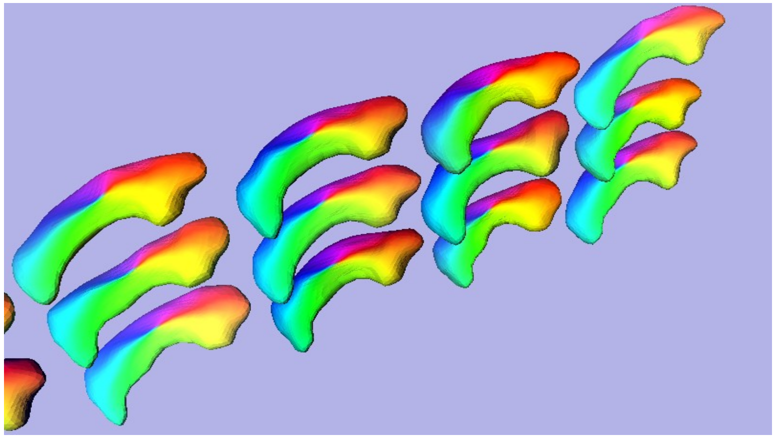
NA-MIC Tutorial Contest: Summer 2011

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 environnement variable BatchmakeShapeAnalysisModule_Dir

➜ tcsh 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)

➜ *tcsh 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 fin it, please, download the executables here: http://www.nitrc.org/frs/?group_id=308

(The last release)

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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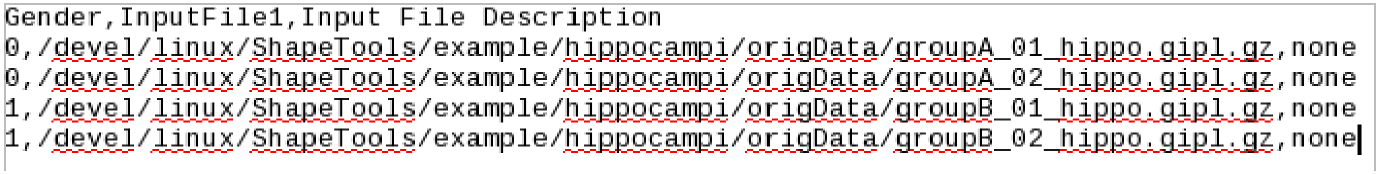
Input File

➜ 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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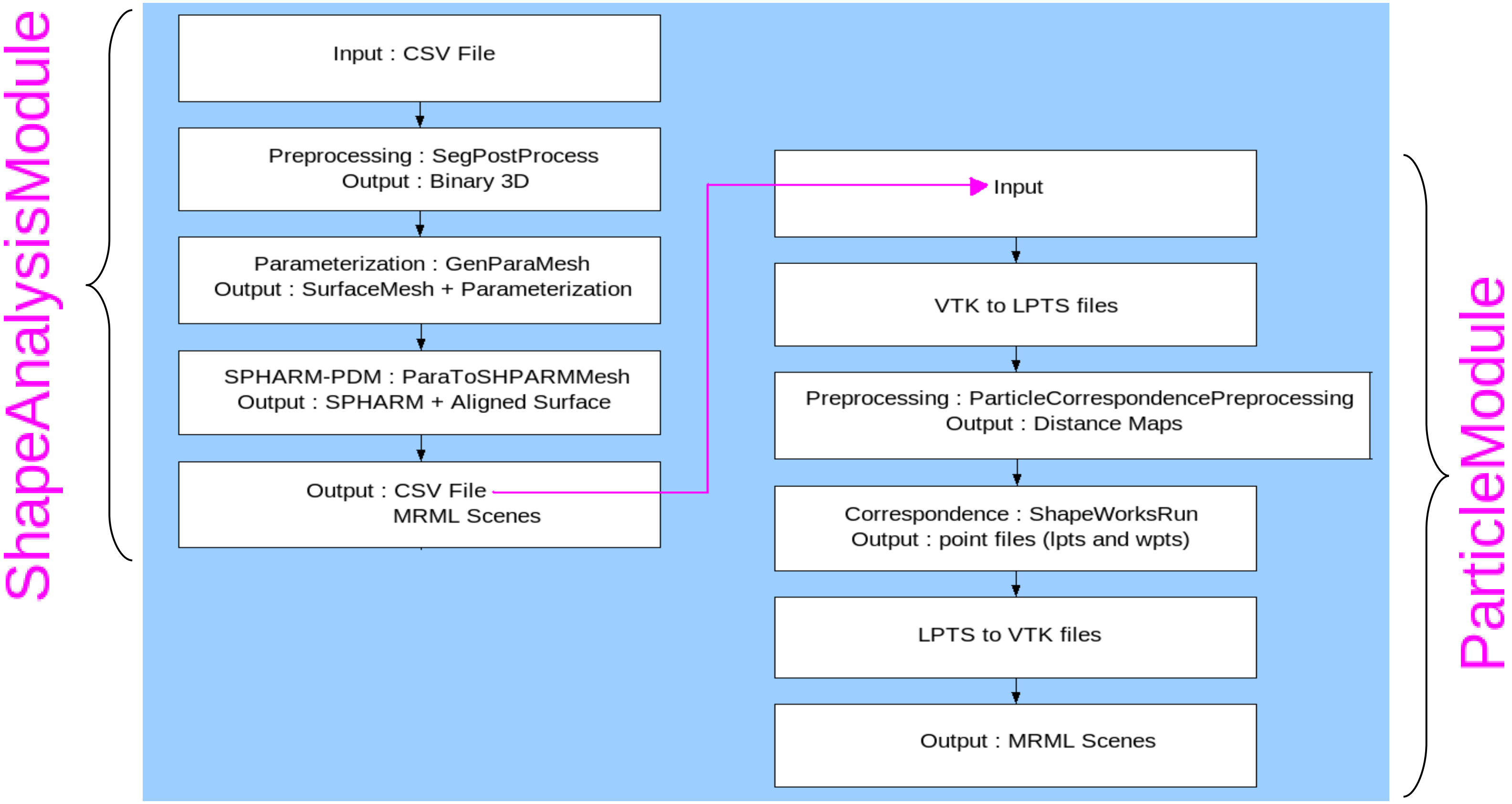
Pipeline Description



ShapeAnalysisModule

Input : CSV File

Preprocessing : SegPostProcess
Output : Binary 3D

Parameterization : GenParaMesh
Output : SurfaceMesh + Parameterization

SPHARM-PDM : ParaToSHPARMMesh
Output : SPHARM + Aligned Surface

Output : CSV File
MRML Scenes

ParticleModule

Input

VTK to LPTS files

Preprocessing : ParticleCorrespondencePreprocessing
Output : Distance Maps

Correspondence : ShapeWorksRun
Output : point files (lpts and wpts)

LPTS to VTK files

Output : MRML Scenes

Pipeline Description -ShapeAnalysisModule-

➜ SegPostProcess

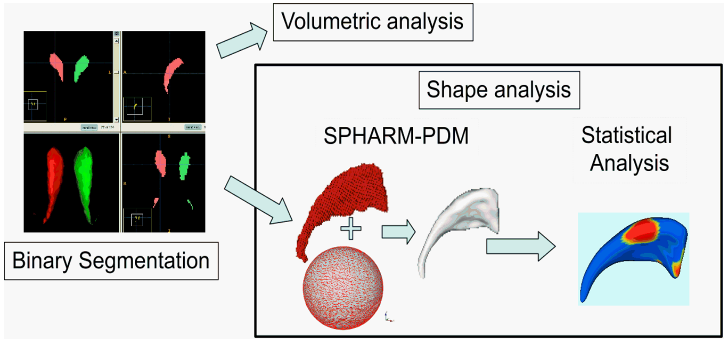
- Fills interior holes.
- Performs minimal smoothing operation and ensures spherical topology.

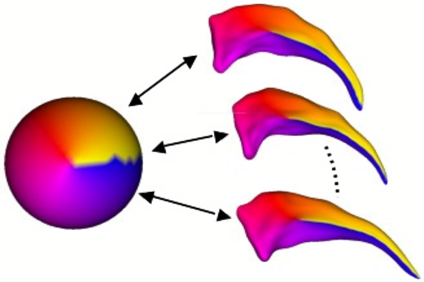
➜ GenParaMesh

- 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.

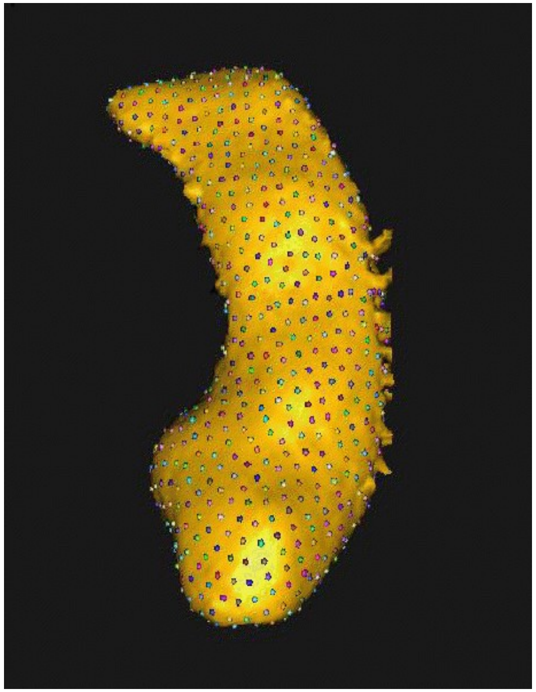




Pipeline Description
-ParticleModule-

- **PreProcessing**
  - Remove the hight-frequency artefacts

- **ShapeWorks**
  - Alignment with respect of the centers of mass and the orientation of the first principal eigenvectors
  - Smoothing of the surfaces
  - Optimization of the positions of the correspondences



Overview

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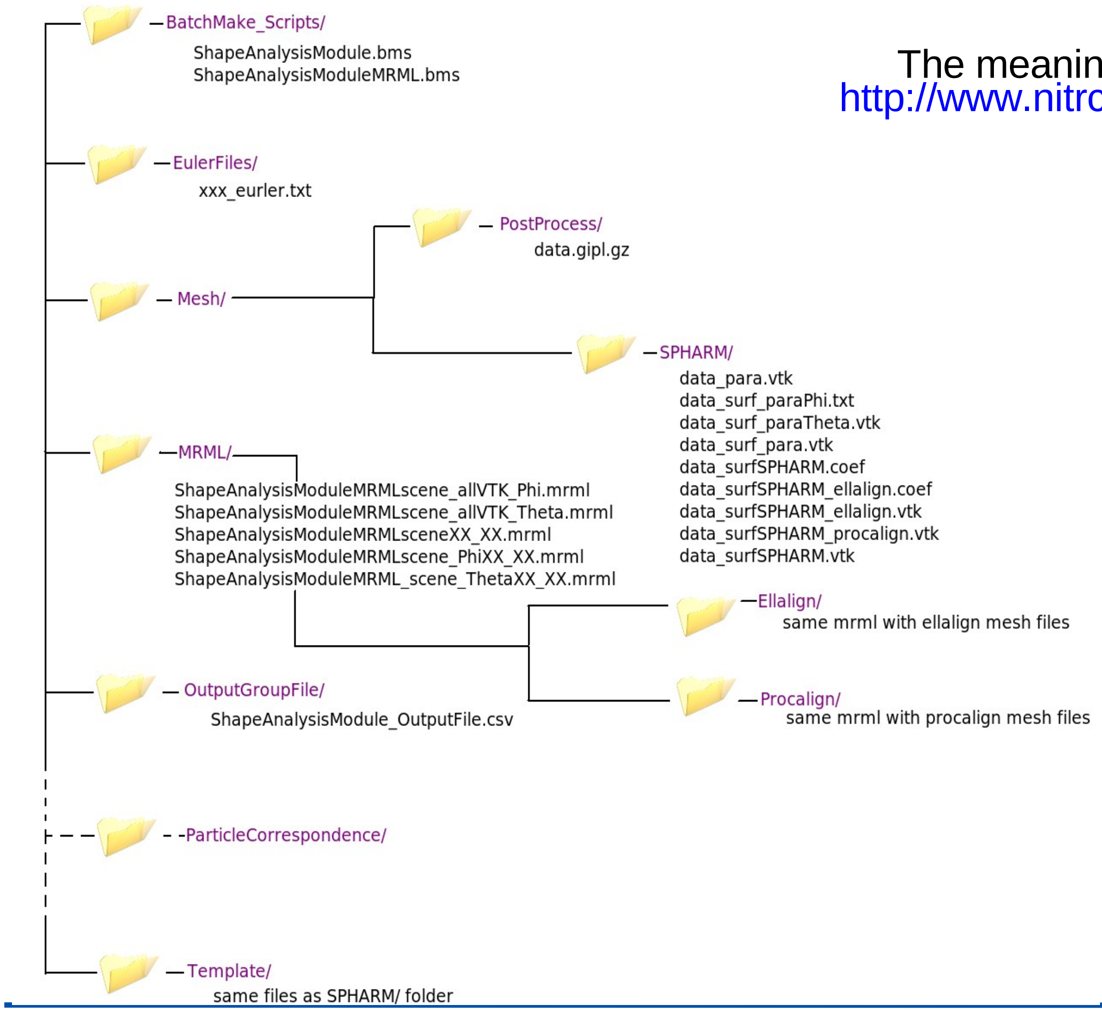
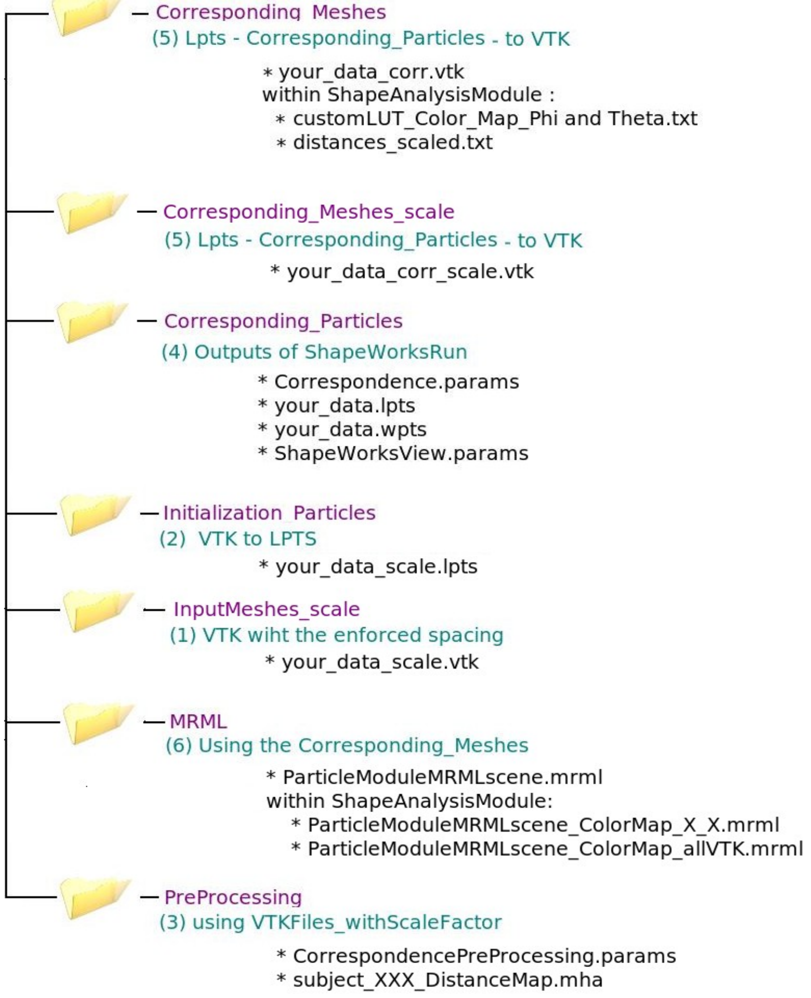
Output files and organisation: -ShapeAnalysisModule -

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



- BatchMake_Scripts/
  - ShapeAnalysisModule.bms
  - ShapeAnalysisModuleMRML.bms
- EulerFiles/
  - xxx_eurler.txt
- Mesh/
  - PostProcess/
    - data.gipl.gz
  - SPHARM/
    - data_para.vtk
    - data_surf_paraPhi.txt
    - data_surf_paraTheta.vtk
    - data_surf_para.vtk
    - data_surfSPHARM.coef
    - data_surfSPHARM_ellalign.coef
    - data_surfSPHARM_ellalign.vtk
    - data_surfSPHARM_procalign.vtk
    - data_surfSPHARM.vtk
- MRML/
  - ShapeAnalysisModuleMRMLscene_allVTK_Phi.mrml
  - ShapeAnalysisModuleMRMLscene_allVTK_Theta.mrml
  - ShapeAnalysisModuleMRMLsceneXX_XX.mrml
  - ShapeAnalysisModuleMRMLscene_PhiXX_XX.mrml
  - ShapeAnalysisModuleMRML_scene_ThetaXX_XX.mrml
  - Ellalign/
    - same mrml with ellalign mesh files
  - Procalign/
    - same mrml with procalign mesh files
- OutputGroupFile/
  - ShapeAnalysisModule_OutputFile.csv
- ParticleCorrespondence/
- Template/
  - same files as SPHARM/ folder

Output files and organisation: -ParticleModule -



— Corresponding Meshes

(5) Lpts - Corresponding_Particles - to VTK

* your_data_corr.vtk
within 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 wiht the enforced spacing

* your_data_scale.vtk

— MRML

(6) Using the Corresponding_Meshes

* ParticleModuleMRMLscene.mrml
within ShapeAnalysisModule:
  * ParticleModuleMRMLscene_ColorMap_X_X.mrml
  * ParticleModuleMRMLscene_ColorMap_allVTK.mrml

— PreProcessing

(3) using VTKFiles_withScaleFactor

* CorrespondencePreProcessing.params
* subject_XXX_DistanceMap.mha

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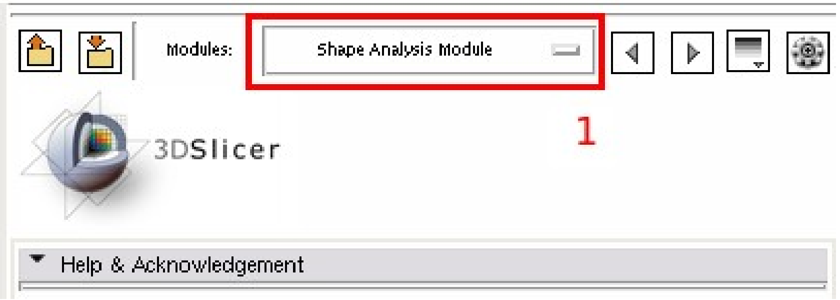
Execution within Slicer :
Start the ShapeAnalysisModule

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

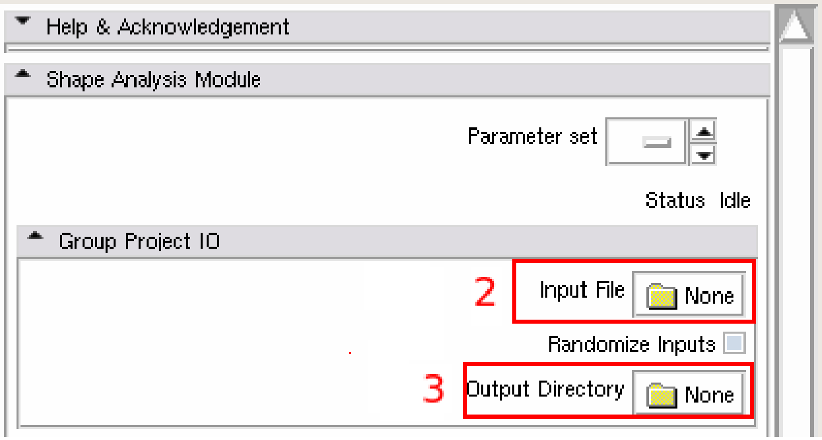
1- Select the "ShapeAnalysisModule" in Modules ->Shape Analysis.

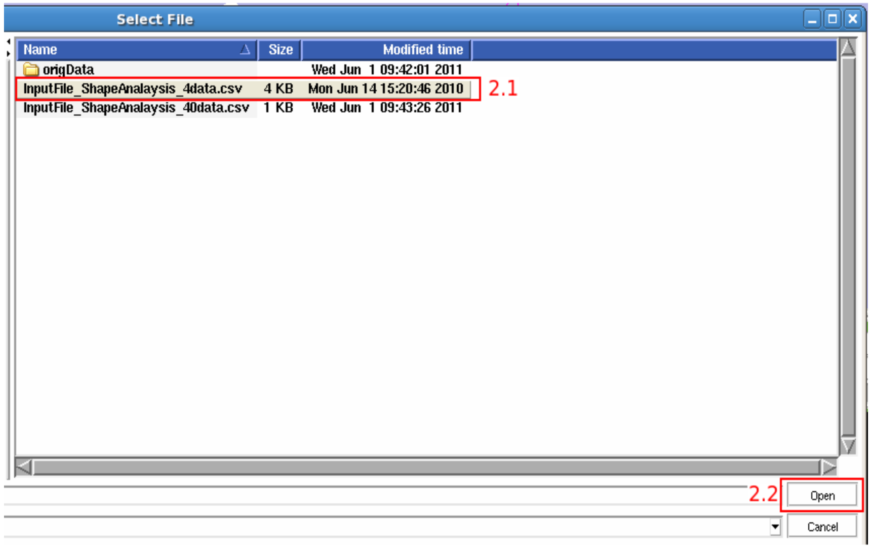
2-Click on "Input File"

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

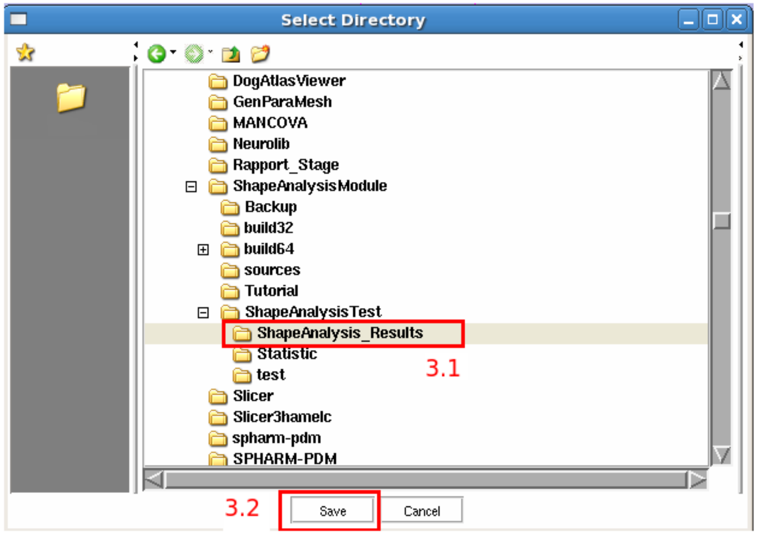
3- Click on "Output Directory"

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





Name	Size	Modified time
origData		Wed Jun 1 09:42:01 2011
InputFile_ShapeAnalaysis_4data.csv	4 KB	Mon Jun 14 15:20:46 2010
InputFile_ShapeAnalaysis_40data.csv	1 KB	Wed Jun 1 09:43:26 2011



Execution within Slicer : *SegPostProcess* Parameters

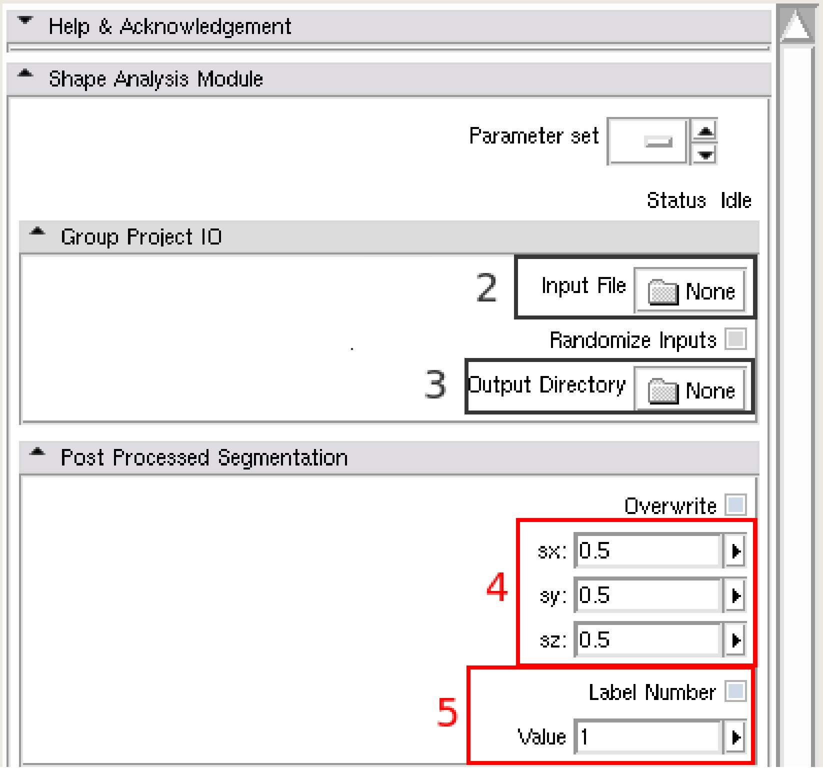
1- Select the "ShapeAnalysisModule" in Modules ->Shape Analysis.

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”

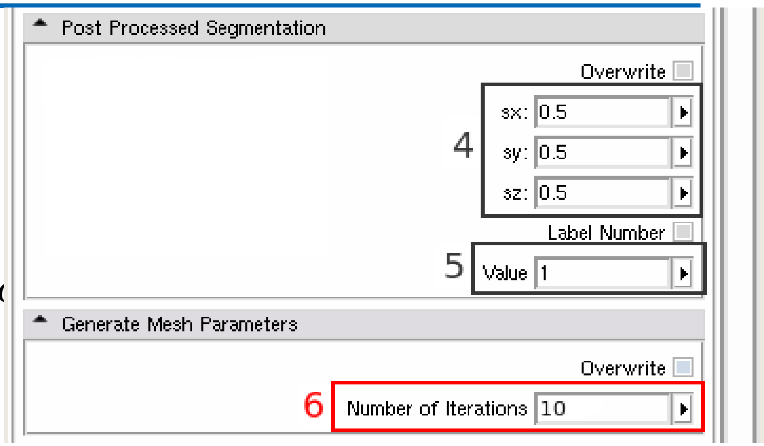
4- Set the enforced spacing in x,y and z direction.

5- (optional) Check the box “Label Number” and set “Value” t 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.



Post Processed Segmentation

Overwrite ☐

4

sx: 0.5

sy: 0.5

sz: 0.5

Label Number ☐

5

Value 1

Generate Mesh Parameters

Overwrite ☐

6

Number of Iterations 10

Execution within Slicer : *ParaToSPHARMMesh* Parameters

1- Select the "ShapeAnalysisModule" in Modules ->Shape Analysis.

2-Click on "Input File"

3- Click on "Output Directory"

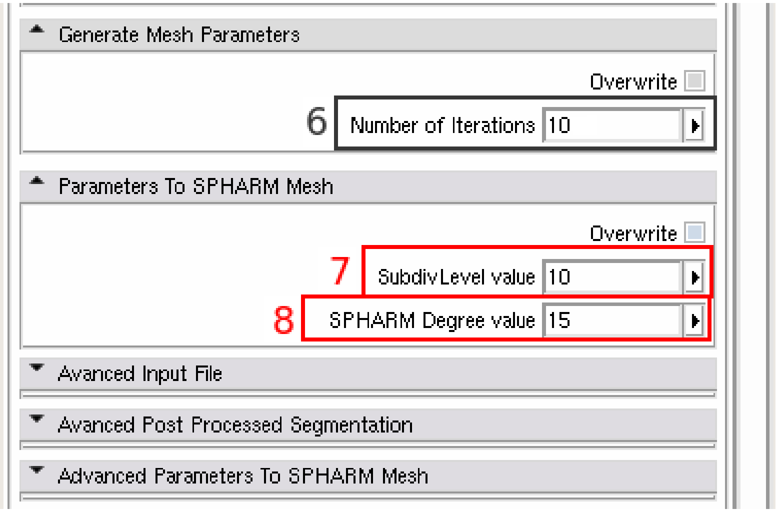
4- Set the enforced spacing in x,y and z direction.

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



Generate Mesh Parameters

Overwrite ☐

6 Number of Iterations 10

Parameters To SPHARM Mesh

Overwrite ☐

7 SubdivLevel value 10

8 SPHARM Degree value 15

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.

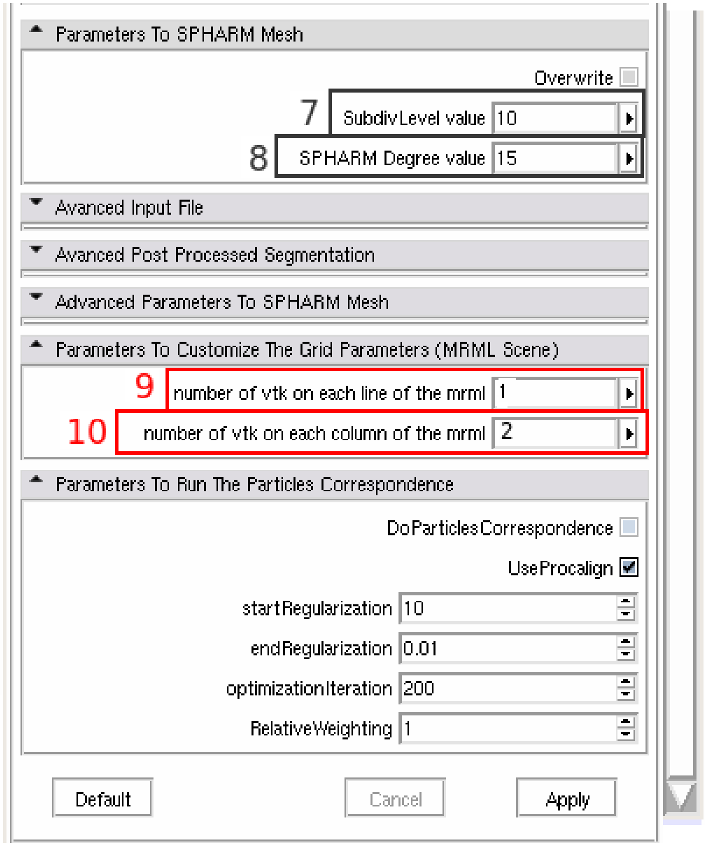
5- (optional) Check the box "Label Number" and set "Value" to first extract this label before processing.

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



Parameters To SPHARM Mesh

Overwrite ☐

7 SubdivLevel value 10

8 SPHARM Degree value 15

Avanced Input File

Avanced Post Processed Segmentation

Advanced Parameters To SPHARM Mesh

Parameters To Customize The Grid Parameters (MRML Scene)

9 number of vtk on each line of the mrml 1

10 number of vtk on each column of the mrml 2

Parameters To Run The Particles Correspondence

DoParticlesCorrespondence ☐

UseProcalign ☑

startRegularization 10

endRegularization 0.01

optimizationIteration 200

RelativeWeighting 1

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

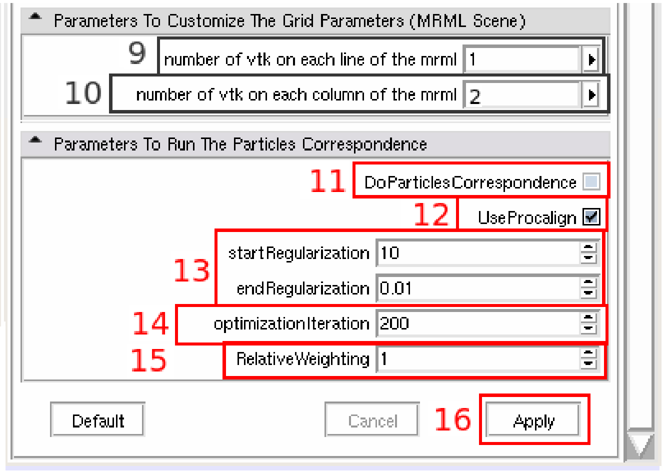
8- Set the maximal degree for the SPHARM computation

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

To run a <u>Particle study</u> 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.



Parameters To Customize The Grid Parameters (MRML Scene)

number of vtk on each line of the mrml: 1

number of vtk on each column of the mrml: 2

Parameters To Run The Particles Correspondence

DoParticlesCorrespondence ☐

UseProcalign ☑

startRegularization: 10

endRegularization: 0.01

optimizationIteration: 200

RelativeWeighting: 1

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

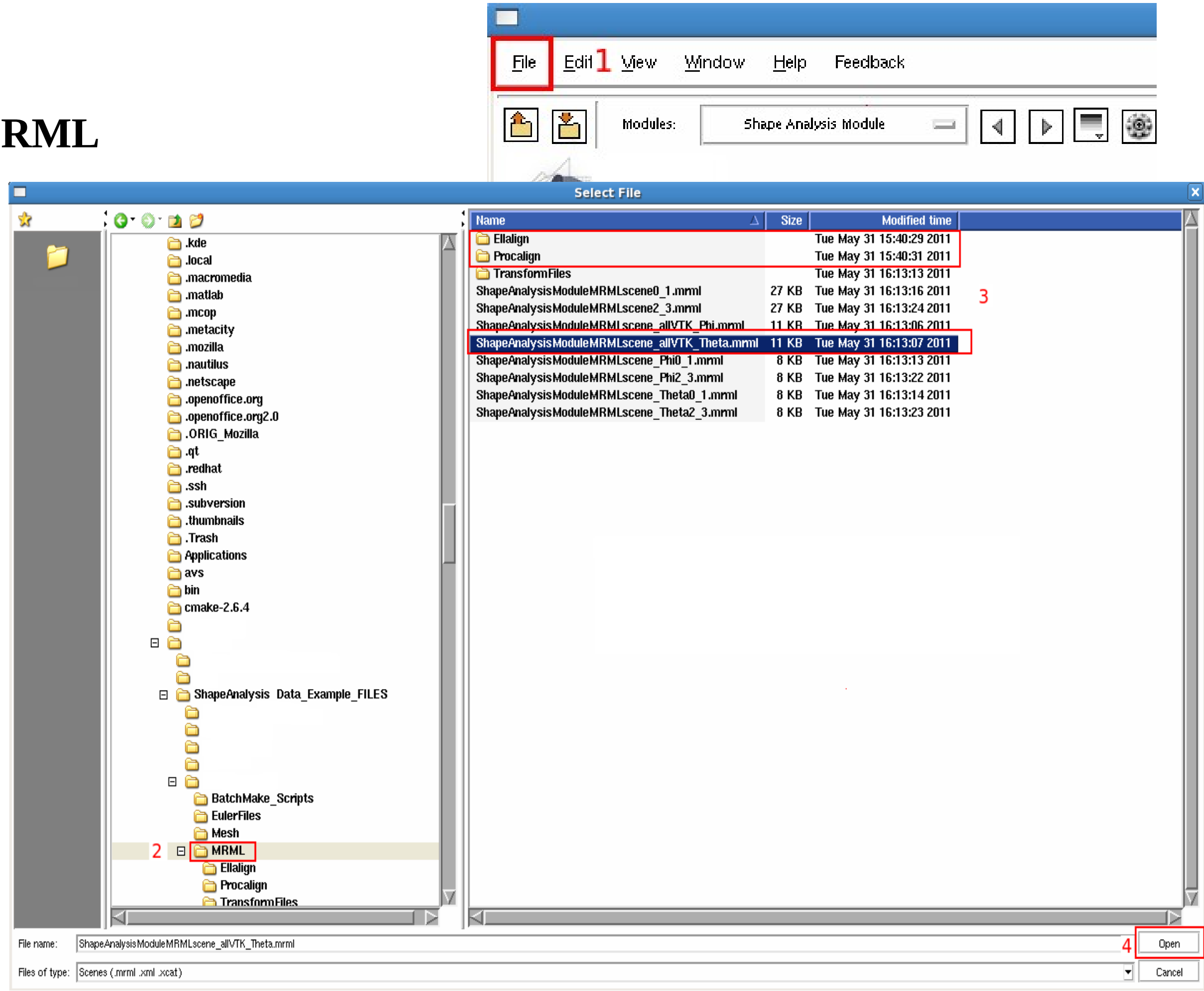
Execution within Slicer :
Load a MRML Scene

1- Click on File -> Load Scene

2- Go in your_Output_Directory/MRML

3- Select one MRML scene

4- Click on the “Open” button



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

File name: ShapeAnalysisModuleMRMLscene_allVTK_Theta.mrml

Files of type: Scenes (.mrml .xml .xcat)

Execution within Slicer :

Load a MRML Scene : Which MRML?

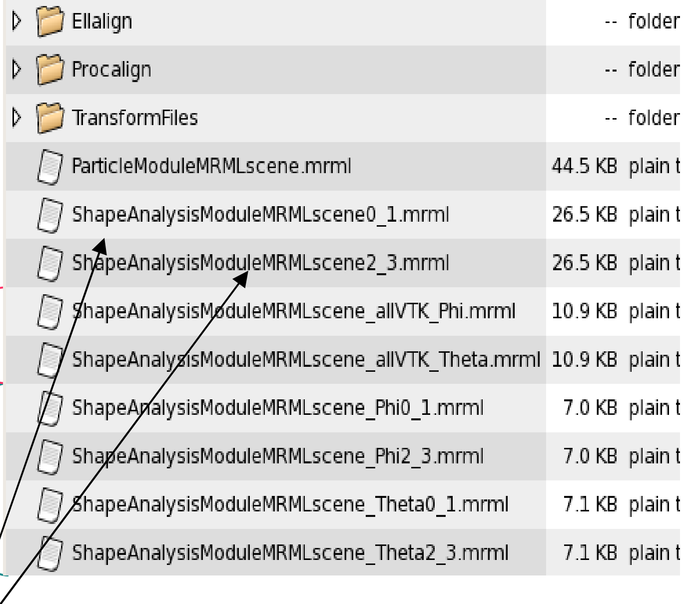
There are several kind of MRML scene

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

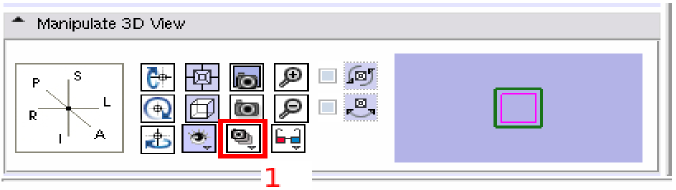
In the first MRML scenes, you can find the template with a random color and then with the snapshots, you can the shapes A to B with a Phi *colormap* or a Theta



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

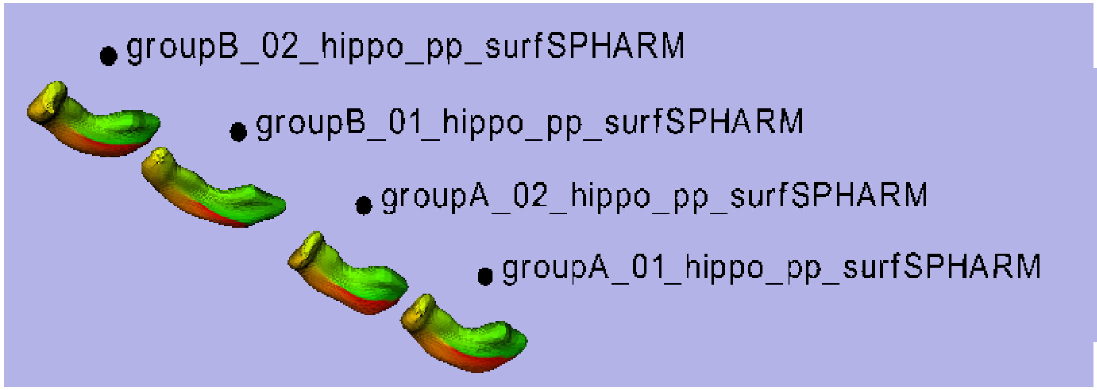
Display the *colormaps:*

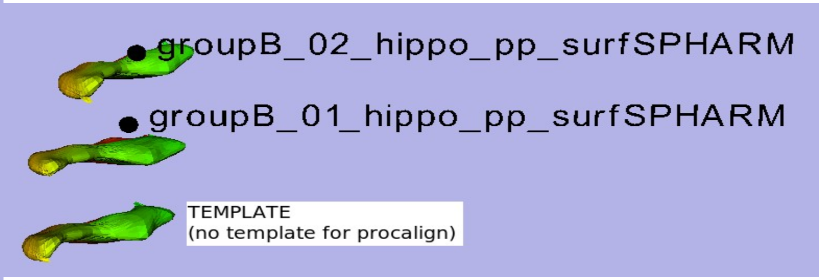
1. Click on the "Snapshots" button.
2. Select **Color Map Phi** or **Color Map Theta.**
3. Click on **Restore.**



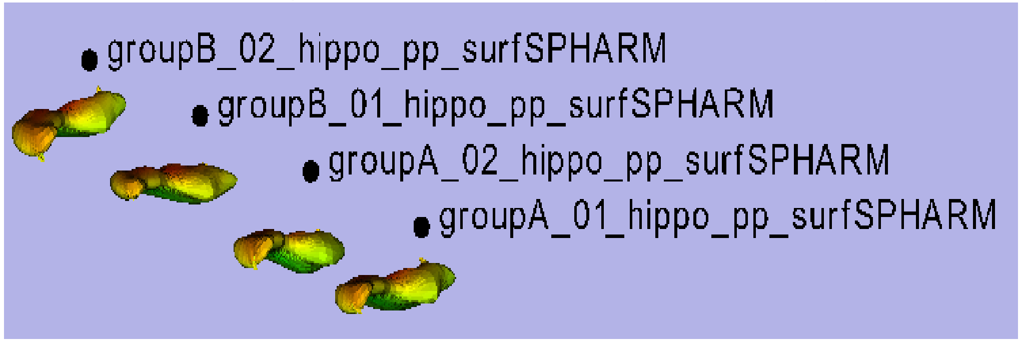
Execution within Slicer :

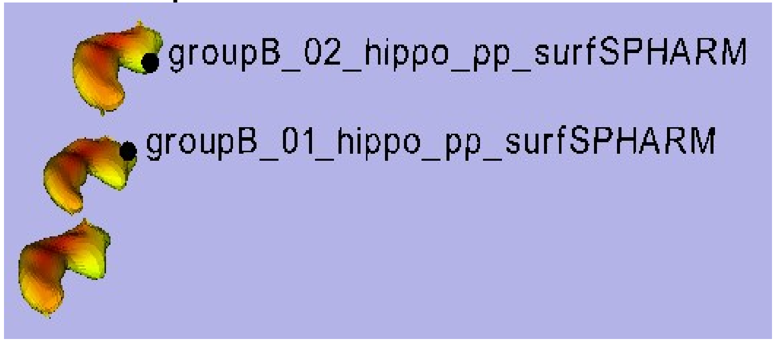
MRML Scene





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



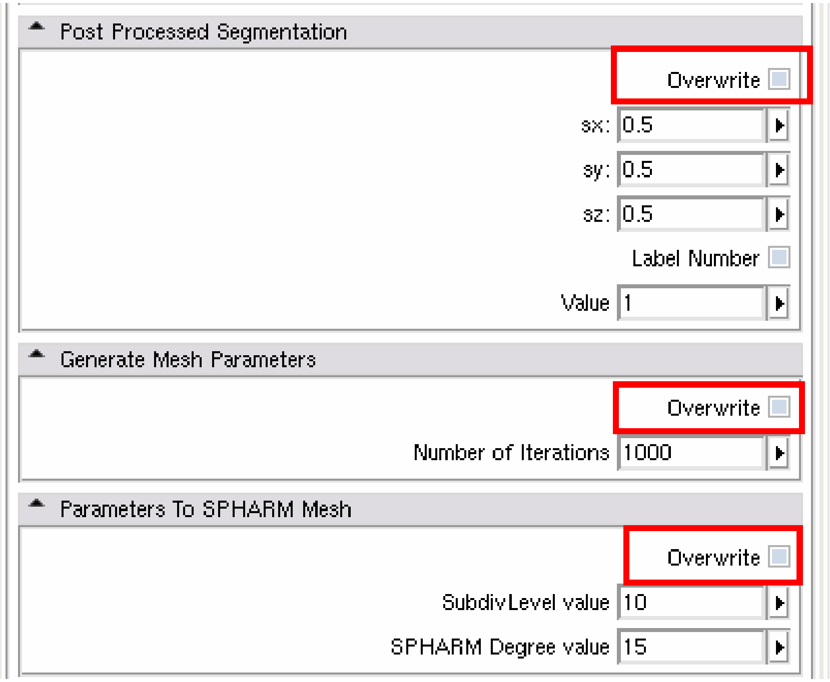


Execution within Slicer : Recompute

You can recompute the modules of the ShapeAnalysisModule pipeline:

Check one (or more) "Overwrite" box.

Click on the "Apply" button to recompute the module



Post Processed Segmentation

Overwrite ☐

sx: 0.5

sy: 0.5

sz: 0.5

Label Number ☐

Value 1

Generate Mesh Parameters

Overwrite ☐

Number of Iterations 1000

Parameters To SPHARM Mesh

Overwrite ☐

SubdivLevel value 10

SPHARM Degree value 15

Execution within Slicer : Advanced Parameters

Input file:

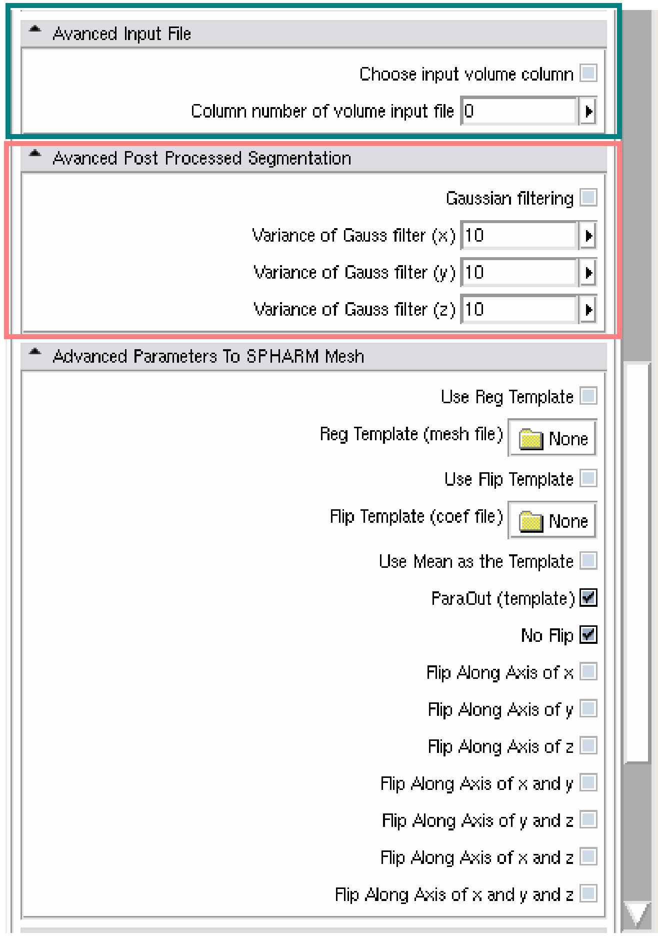
➜ By default the first column containing a volume file (.vtk, .meta etc..) is computed. But if you have multiple files in your CSV file, you can choose the column of the input data file

➜ 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



Avanced Input File

Choose input volume column ☐

Column number of volume input file 0

Avanced 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 : 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 alignement

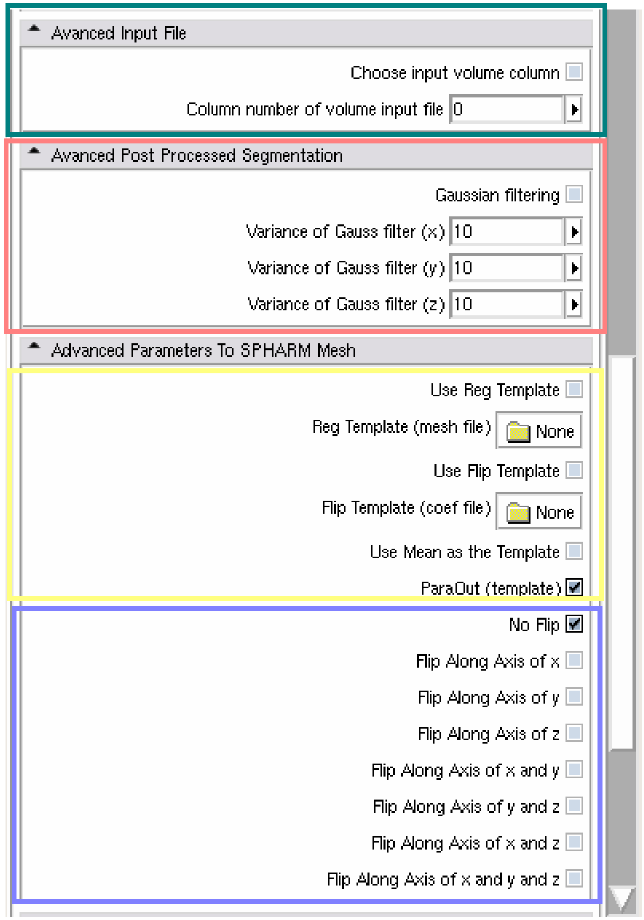
➜ Flip template is used to test all possible flips of the parametrization along the first order ellipsoid axis and select the one whose reconstruction has minimal distance to the flip-template

➜ 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.



Avanced Input File

Choose input volume column ☐

Column number of volume input file: 0

Avanced 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 ☐

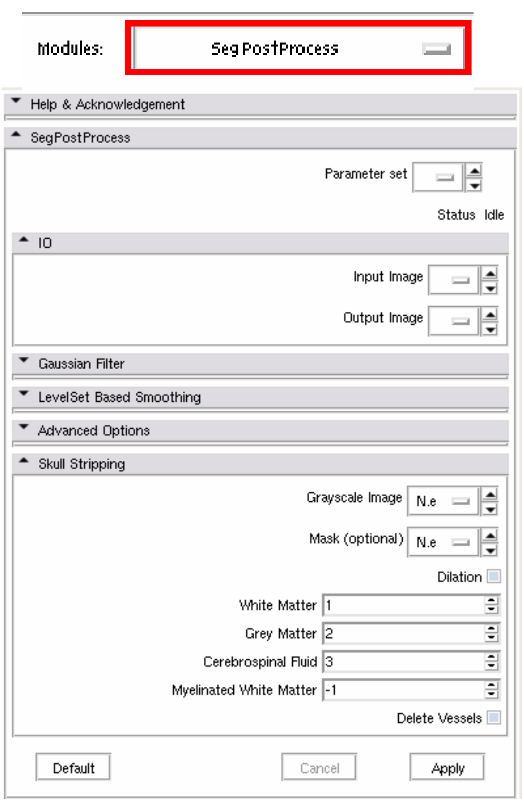
Flip Along Axis of y and z ☐

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.


Modules: SegPostProcess

Help & Acknowledgement

SegPostProcess

Parameter set

Status Idle

IO

Input Image

Output Image

Gaussian Filter

LevelSet Based Smoothing

Advanced Options

Skull Stripping

Grayscale Image N.e

Mask (optional) N.e

Dilation ☐

White Matter 1

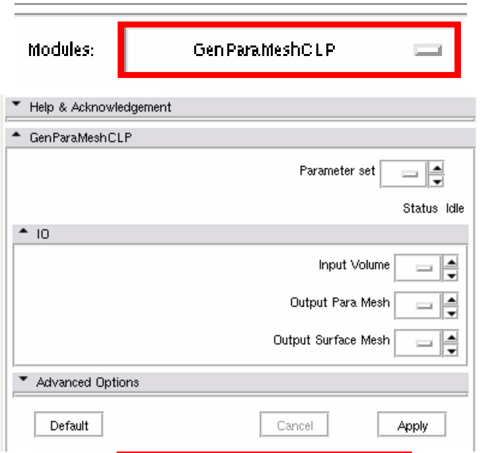
Grey Matter 2

Cerebrospinal Fluid 3

Myelinated White Matter -1

Delete Vessels ☐

Default Cancel Apply


Modules: GenParaMeshCLP

Help & Acknowledgement

GenParaMeshCLP

Parameter set

Status Idle

IO

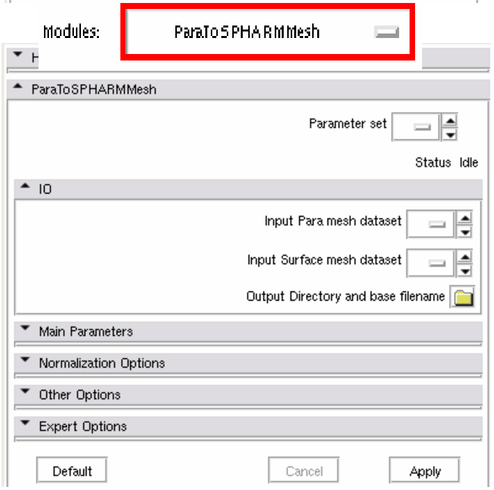
Input Volume

Output Para Mesh

Output Surface Mesh

Advanced Options

Default Cancel Apply


Modules: ParaToSPHARMMesh

ParaToSPHARMMesh

Parameter set

Status Idle

IO

Input Para mesh dataset

Input Surface mesh dataset

Output Directory and base filename

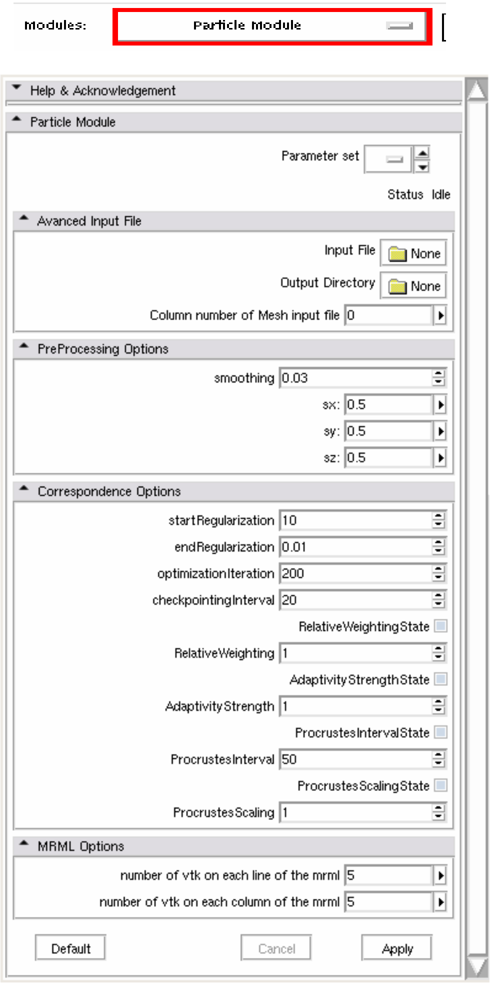
Main Parameters

Normalization Options

Other Options

Expert Options

Default Cancel Apply


Modules: Particle Module

Help & Acknowledgement

Particle Module

Parameter set

Status Idle

Avanced Input File

Input File None

Output Directory None

Column number of Mesh input file 0

PreProcessing Options

smoothing 0.03

sx: 0.5

sy: 0.5

sz: 0.5

Correspondence Options

startRegularization 10

endRegularization 0.01

optimizationIteration 200

checkpointingInterval 20

RelativeWeightingState ☐

RelativeWeighting 1

AdaptivityStrengthState ☐

AdaptivityStrength 1

ProcrustesIntervalState ☐

ProcrustesInterval 50

ProcrustesScalingState ☐

ProcrustesScaling 1

MRML Options

number of vtk on each line of the mrml 5

number of vtk on each column of the mrml 5

Default Cancel Apply

Overview

1- Input file

2- Pipeline description

3- Output images and organisation

4- Execution within Slicer

5- Command line execution

6- Conclusion

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 --columVolumeFile 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
```

Overview

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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 your are now able to perform shape analysis on your own dataset.

Acknowledgments

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