



SPHARM-PDM

User Tutorial

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at CHAPEL HILL



SPHARM-PDM Tool Description

Step 1: Post Process Segmentation

Step 2: Generate Mesh Parameters

Step 3: Parameters to SPHARM Mesh

Description of SPHARM-PDM

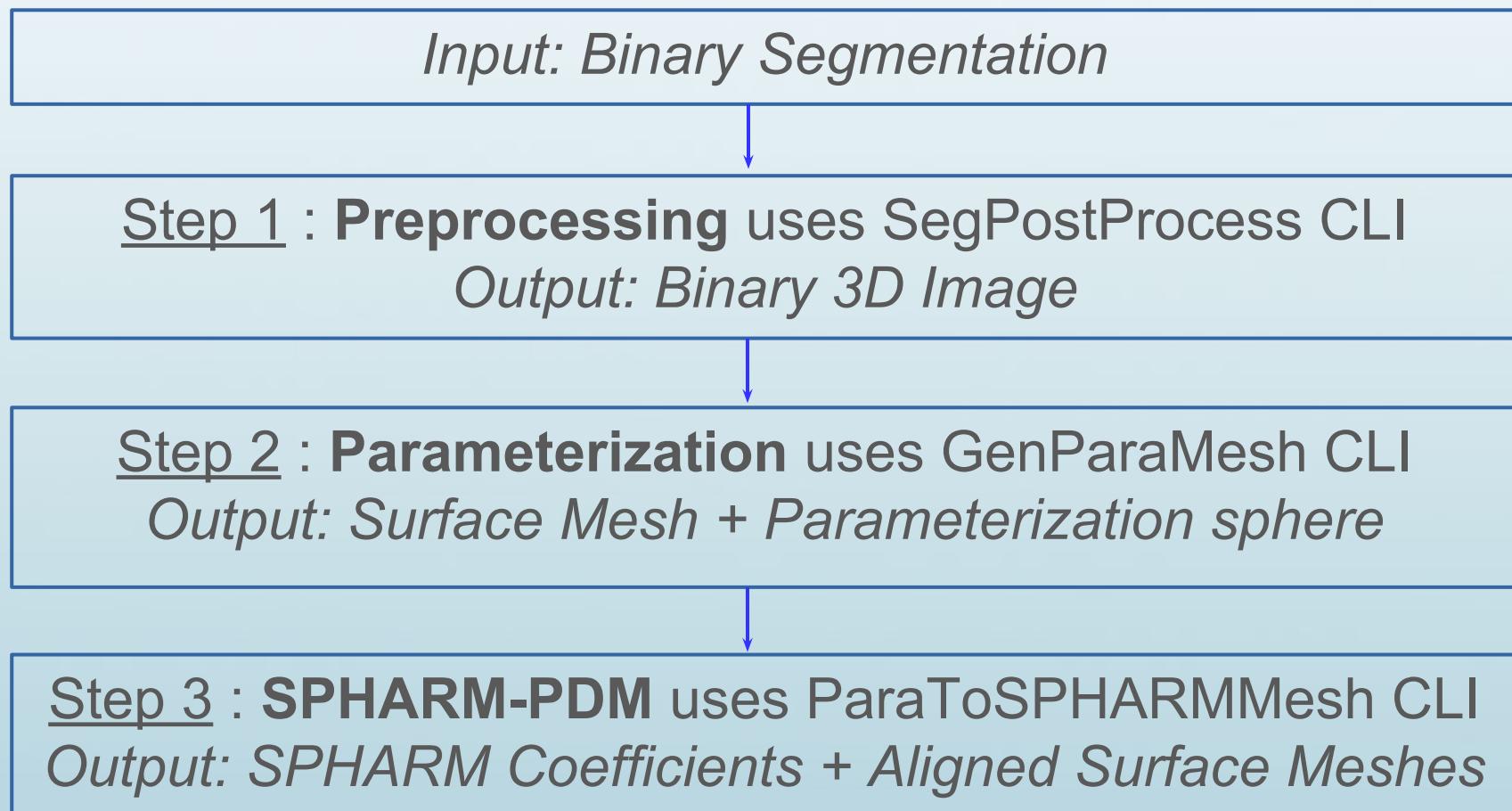
Shape Analysis allows to precisely locate morphological changes between healthy and pathological structures.

Spherical Harmonic Representation Point Distribution Models (SPHARM-PDM) tool is used to compute densely sampled correspondent point based models that allow performing 3D structural statistical shape analysis.

The inputs are binary segmentations which are converted into corresponding spherical harmonic descriptions (SPHARM) and then are sampled into triangulated surfaces (PDM)

Description of SPHARM-PDM

The SPHARM-PDM tool consists on three steps:



Step 1: Post Process Segmentation

This step will:

- Ensure spherical topology of the segmentations by filling any interior holes and by applying two smoothing operations
- Extract a single label or a label range
- Re-sample the label data to ensure an isotropic resolution and a relative fine resolution

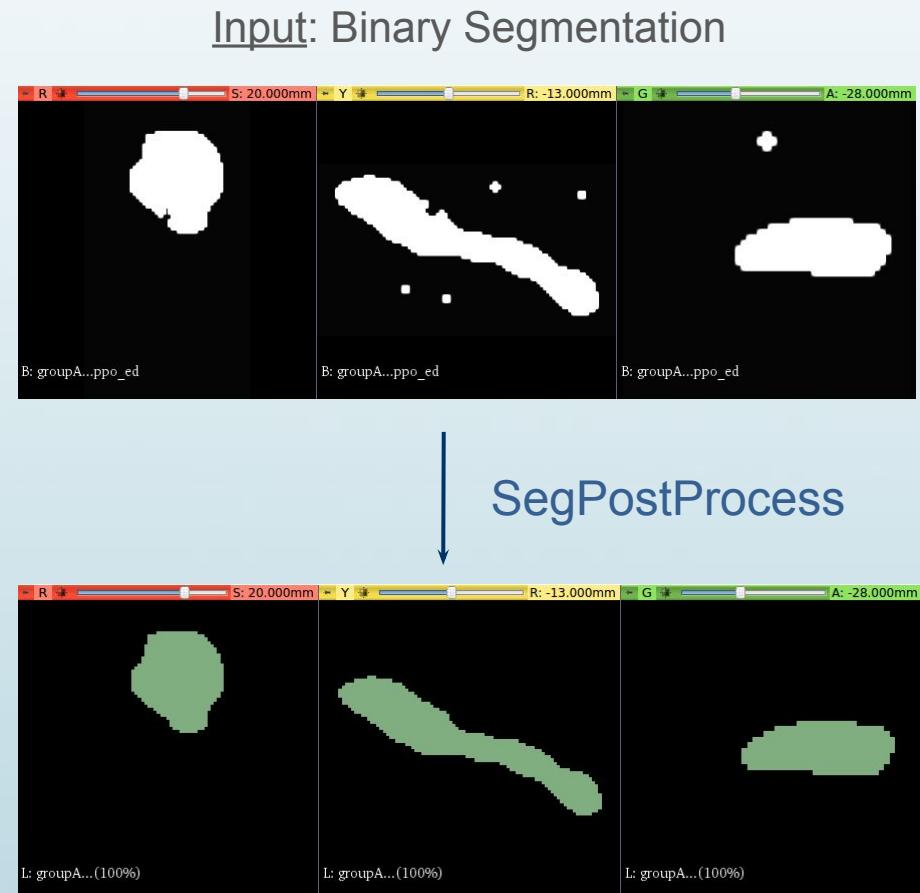
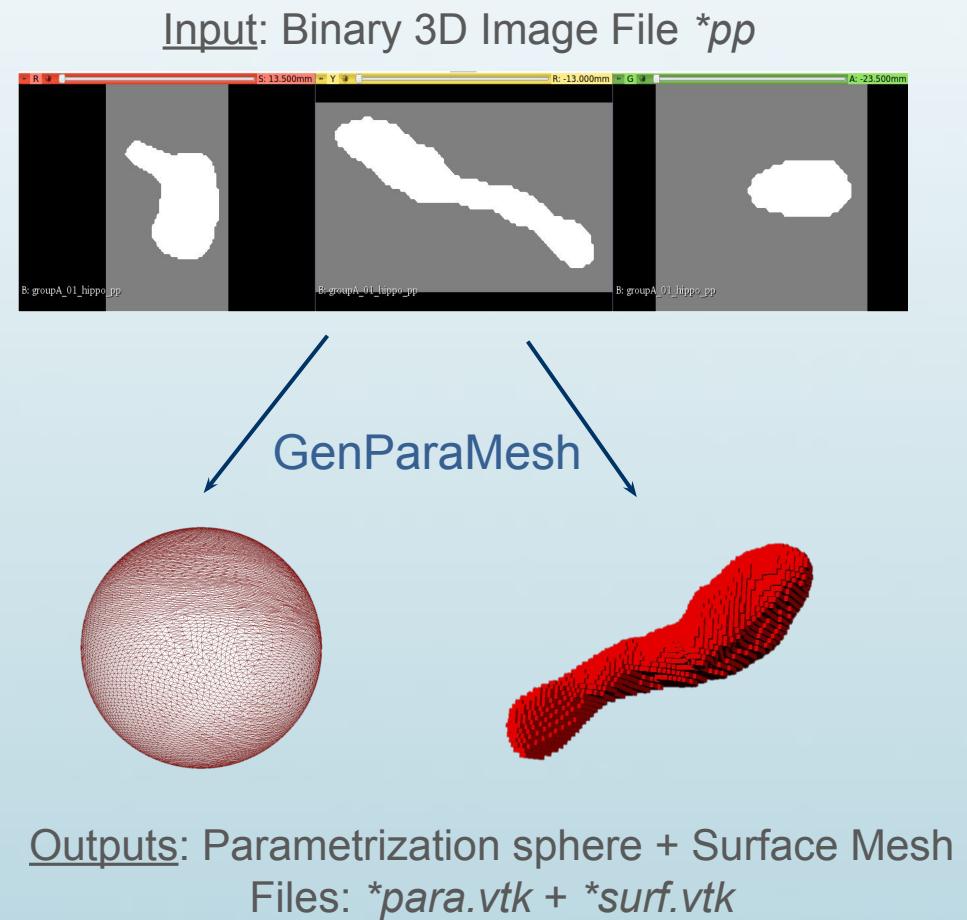


Figure: Input/Output of SegPostProcess CLI

Step 2: Generate Mesh Parameters

This step will:

1. Extract the surface of the input label segmentation
 2. Create an area conforming mapping of the surface mesh to a unit sphere
-
- Note: If this step reports bad Euler number, it will mean that the extracted surface is not a spherical topology. spherical topology has an Euler number of 2.



GenParaMesh

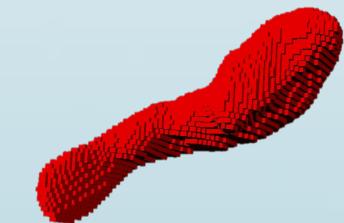
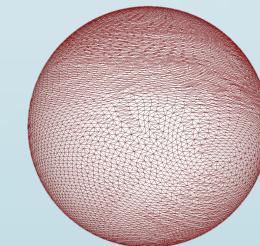


Figure: Input/Output of GenParaMesh CLI

Step 2: Generate Mesh Parameters

Outputs

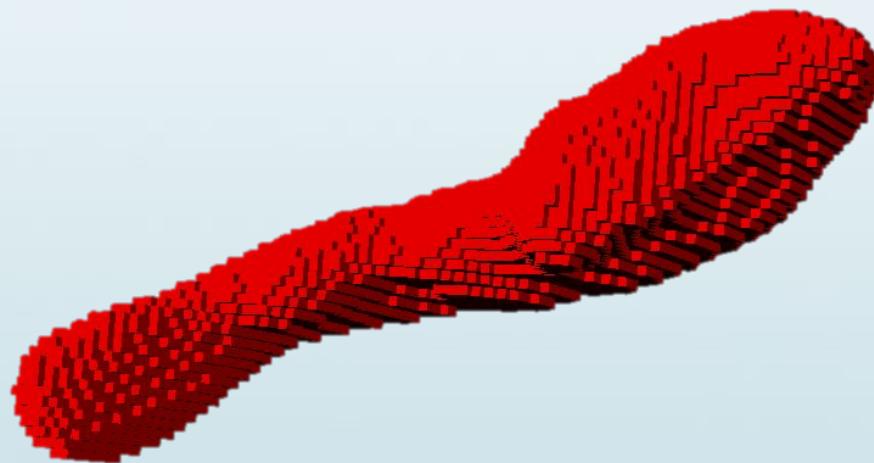


Figure: *surf.vtk is a surface approximation of the input file which represents the original voxel mesh: the cubes show the voxel delineation. The surface will appear blocky because of it is the result of a marching cubes algorithm.

Step 2: Generate Mesh Parameters

Outputs

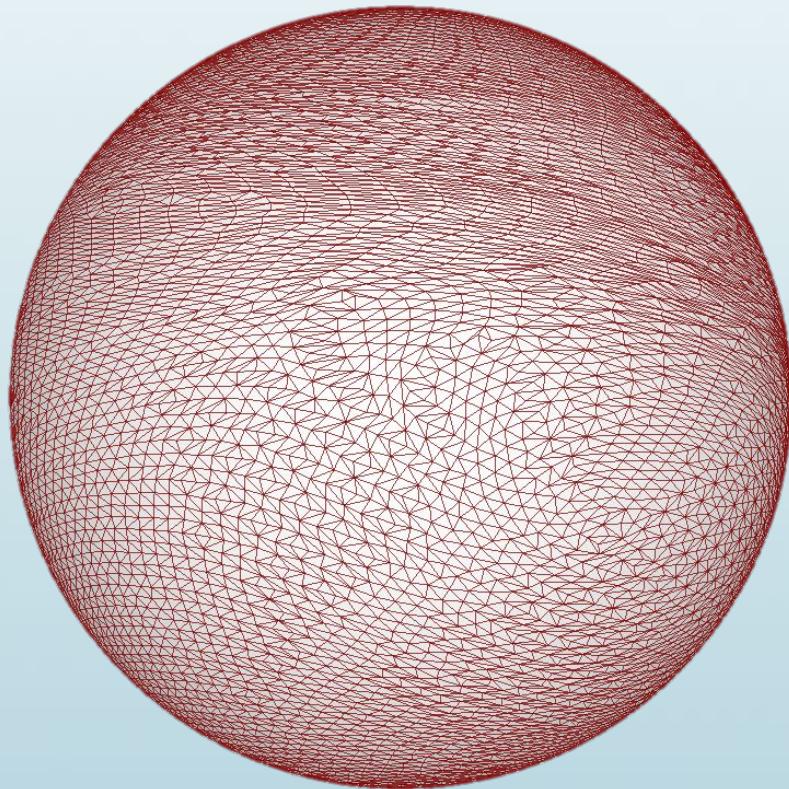


Figure: *para.vtk is a the spherical mapping of the *surf.vtk file. The sphere is an unit sphere (diameter = 1)

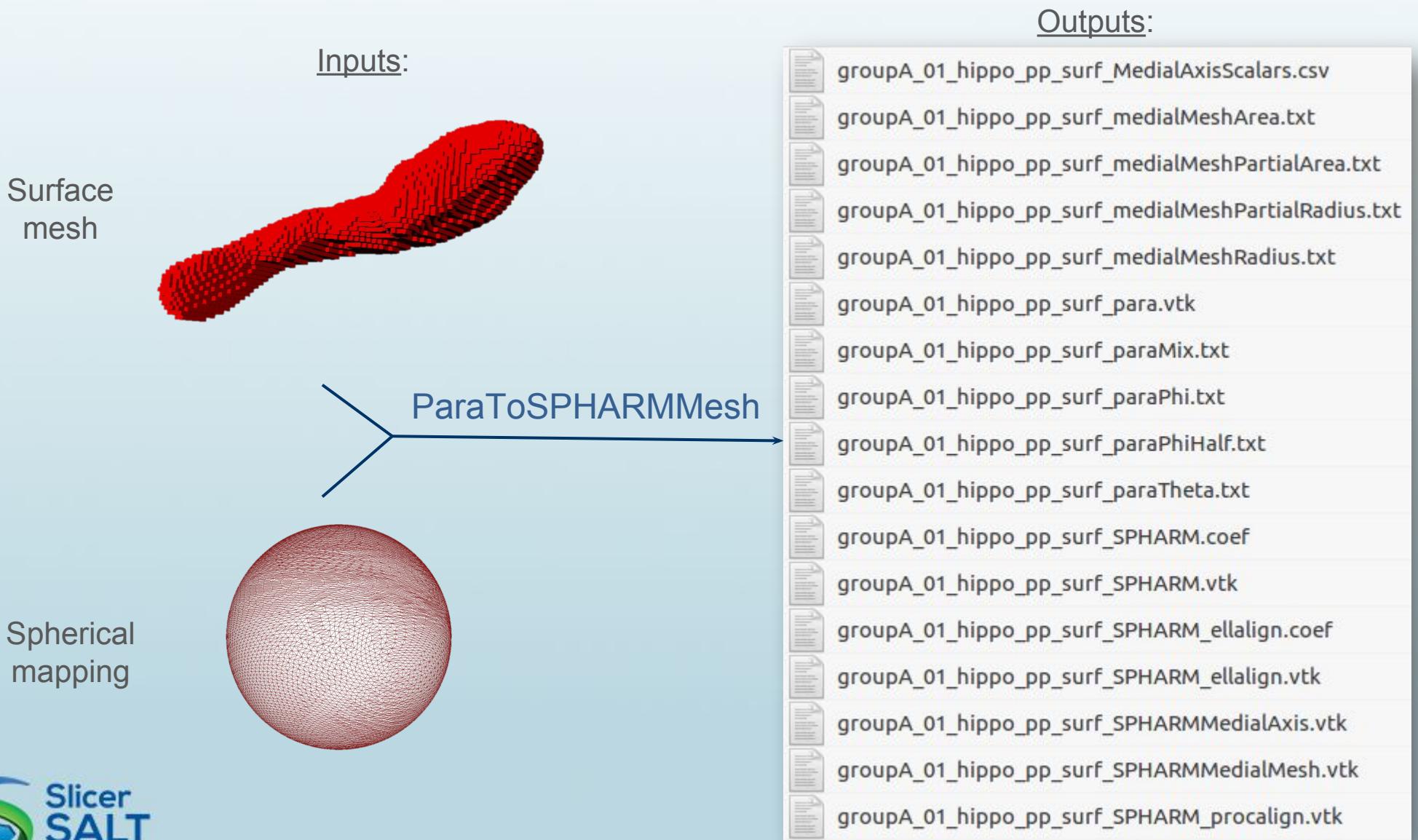
Step 3: Parameters to SPHARM Mesh

This step will:

- Compute the SPHARM-PDM representation
 - ◆ Compute the spherical harmonic description
 - ◆ Sample into a triangulated surface
 - ◆ The two main parameters for this step are:
 - The degree for SPHARM computation
 - The subdivision level for the icosahedron subdivision
 -
- Resolves issues of correspondence pose and alignment

Step 3: Parameters to SPHARM Mesh

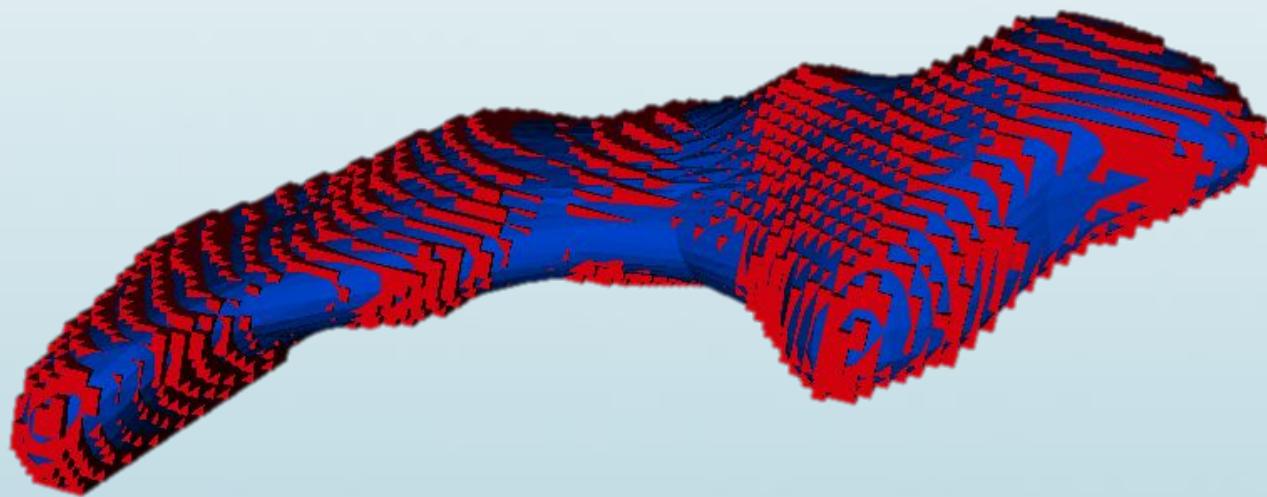
Figure: Input/Output of ParaToSPHARMMesh CLI



Step 3: Parameters to SPHARM Mesh

Outputs

Figure: Comparison between the surface mesh generated by the Generate Mesh Parameters step (red) and the SPHARM-PDM output **SPHARM.vtk* (blue):

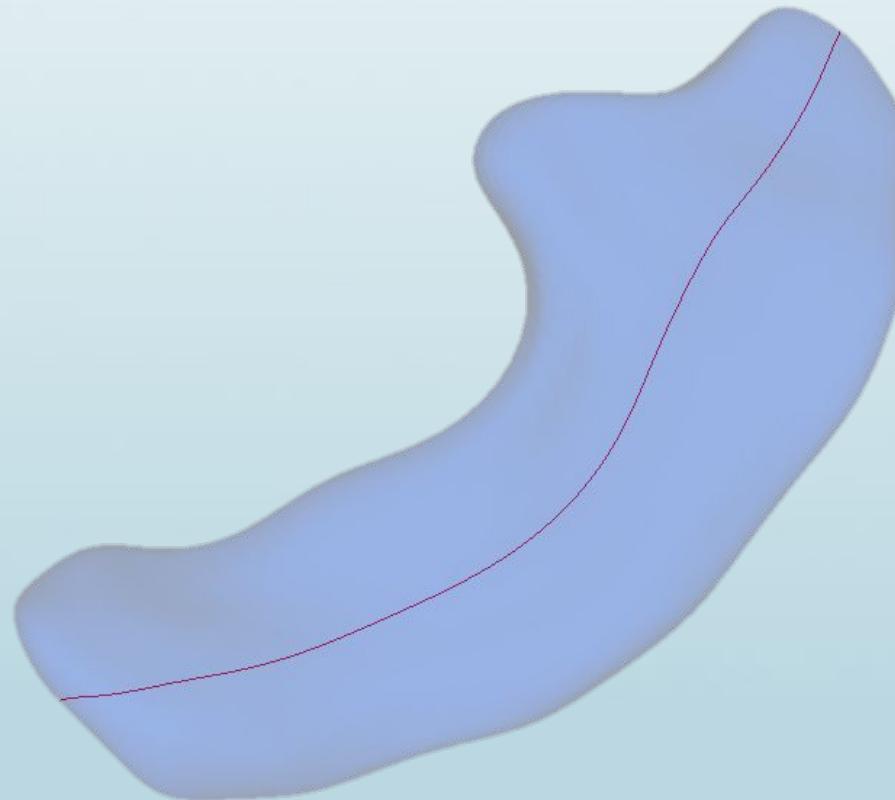


Note: This figure shows how the final correspondent PDM represents the geometry of the structure without fitting the voxel mesh obtained from the binary segmentation

Step 3: Parameters to SPHARM Mesh

Outputs

Figure: Visualization of **SPHARMMedialAxis.vtk* (red) and **SPHARMMedialMesh.vtk* (blue):



Step 3: Parameters to SPHARM Mesh

Outputs

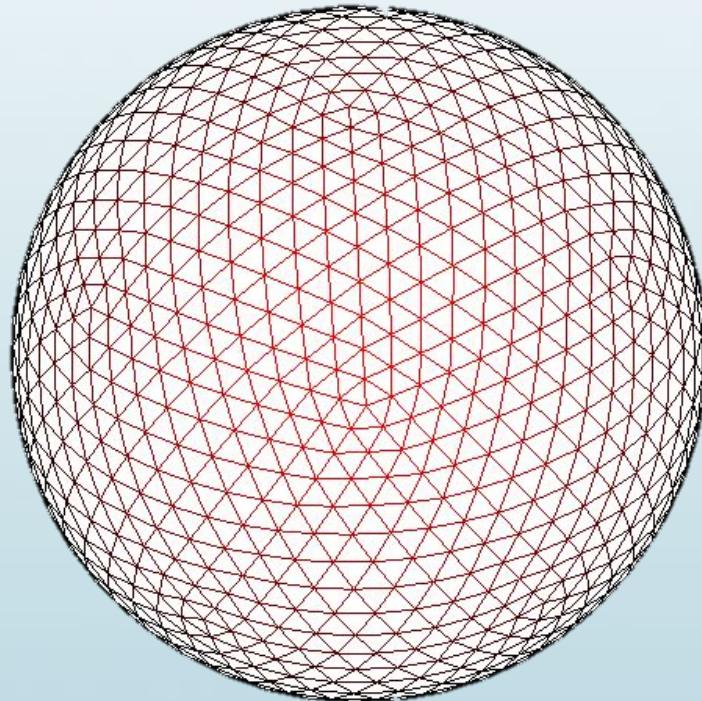


Figure: *para.vtk is a sphere with a icosahedron subdivision of 10.

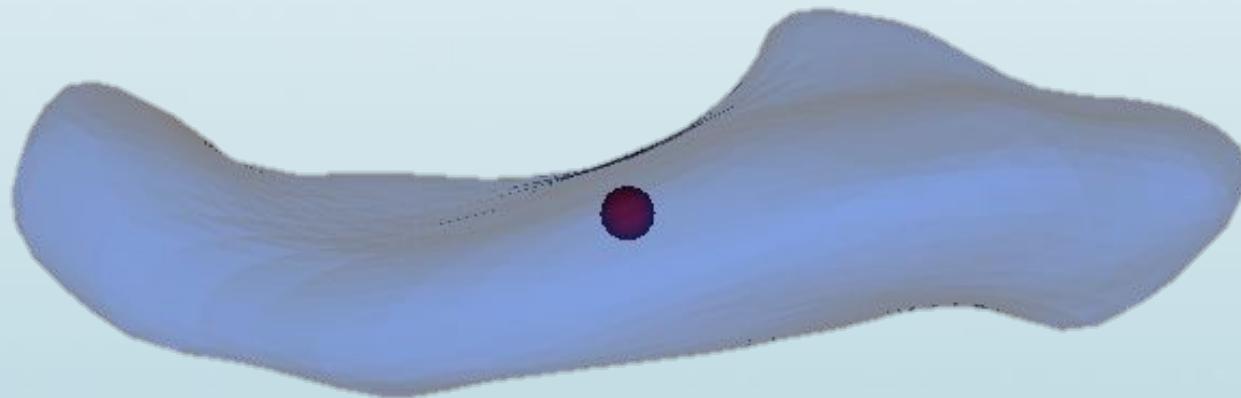
Note: The sphere has 1002 points and the triangulated surface generated will have the same number of points that this sphere. This file includes the spherical parameters (ϕ, θ) at each point.

This sphere is also a unit sphere
(diameter = 1)

Step 3: Parameters to SPHARM Mesh

Outputs

Figure: Visualization of **para.vtk* (blue) and **SPHARM_Ellalign.vtk* (red)
which is aligned with the **para.vtk* sphere:



Step 3: Parameters to SPHARM Mesh

Outputs

Spherical parameters color map files

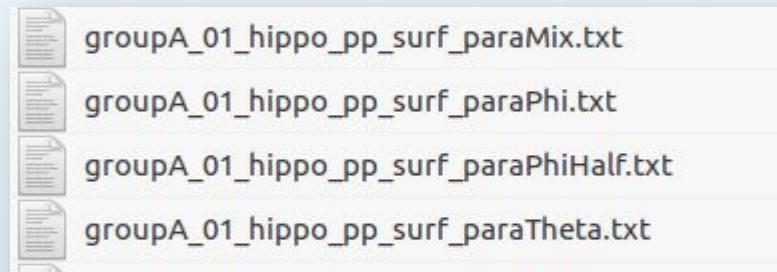
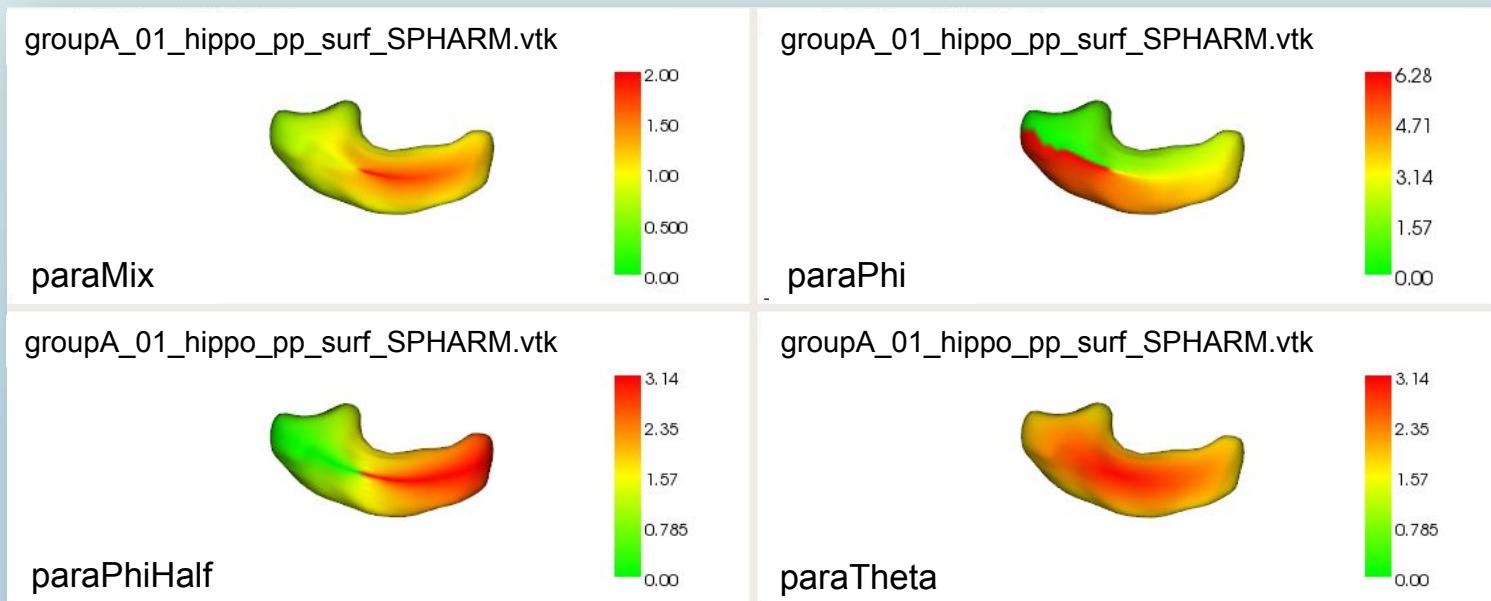


Figure: Comparison of the spherical parameters color maps containing in the *SPHARM.vtk in ShapePopulationViewer tool:



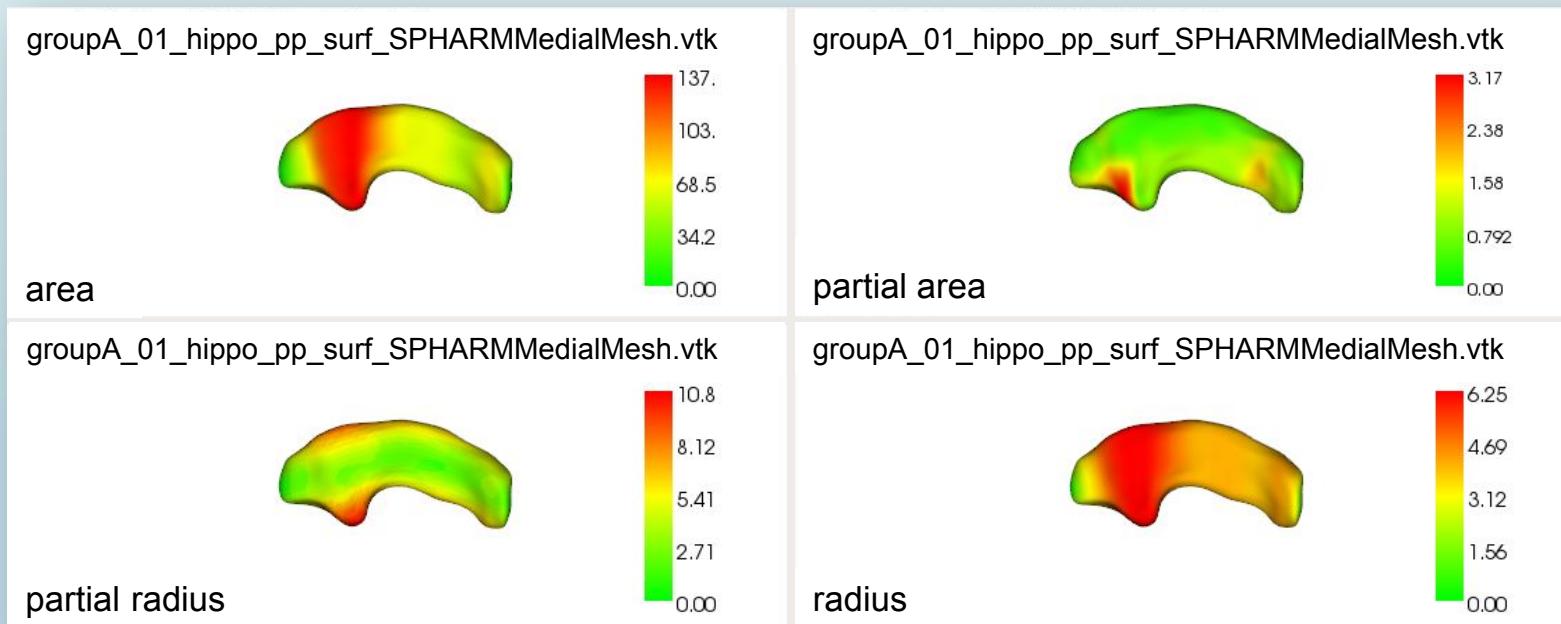
Step 3: Parameters to SPHARM Mesh

Outputs

Medial mesh parameter color map files



Figure: Comparison of the Medial mesh parameter color maps containing in the *SPHARMMedialMesh.vtk in ShapePopulationViewer tool:



Installation of SPHARM-PDM Tool

SPHARM-PDM tool can be used with two open-source software platforms:

- **SlicerSALT**: which is the dissemination vehicle of powerful shape analysis methodology. This software is a light-weight, customized version of 3D Slicer. It contains SPHARM-PDM as a module.
- **3D Slicer**: which is an open-source and free software platform for medical image informatics, image processing, and three-dimensional visualization. SPHARM-PDM can be downloaded as an extension.

SPHARM-PDM Installation on SlicerSALT

Download the SlicerSALT packages for your respective operating system from the [SlicerSALT website](#) and install it. SPHARM-PDM will be ready to use when

The screenshot shows the SlicerSALT website. At the top, there are navigation links: About, Citations, Documentation, and Download. The 'Download' link is highlighted with a red oval and a red arrow pointing to it from the left. Below the navigation, there is a large logo for 'Slicer SALT' with the subtitle 'Shape Analysis Toolbox'. Further down, there is a banner indicating 'Funded by NIBIB R01EB021391'. At the bottom, there are logos for The University of North Carolina at Chapel Hill, MD Anderson Cancer Center, NYU, Tandon School of Engineering, and Kitware.

The screenshot shows the Girder interface. On the left, there is a sidebar with 'Collections', 'Users', and 'Groups'. The main area displays a project titled 'NIH Shape Analysis Toolbox'. The description states: 'This project will develop a comprehensive software that will allow biomedical scientists to precisely locate shape changes in their imaging studies. This software called Shape AnaLysis Toolbox (SALT), will enhance the intuitiveness and ease of use for such studies, as well as allow researchers to find shape changes with higher statistical power. Altogether this constitutes a crucial resource for the imaging field that will enable many and important new findings in biomedical Imaging studies.' Below the description, there is a list of files under the 'SlicerSALT-Public-Packages' folder:

File	Size
SlicerSALT-0.1.0-34f95c7-linux-amd64.tar.gz	141.1 MB
SlicerSALT-0.1.0-34f95c7-macosx-amd64.dmg	92.66 MB
SlicerSALT-0.1.0-34f95c7-win-amd64.exe	83.14 MB

Powered by Girder



SPHARM-PDM Installation on 3D Slicer

1. Download 3D Slicer packages for your respective operating system on the [3D Slicer website](#) and install it.

The screenshot shows the official 3D Slicer website. At the top left is the 3D Slicer logo, which consists of a stylized 3D cube icon with a grid overlay. To its right, the text "3DSlicer" is written in a sans-serif font. In the center, there is a brief description: "A multi-platform, **free and open source** software package for **visualization** and **medical image computing**". Below this, there are three buttons: "Download" (with a red arrow pointing to it), "Slicer Training", and "Feedback". On the left side of the main content area, there is a sidebar with links: "Download Slicer", "Slicer Wiki", "About Slicer" (which is expanded to show "Introduction", "Acknowledgments", "News", "Contact Us", and "Licensing"). The main content area features a heading "Slicer 4.6 released" and a descriptive paragraph about the software's purpose and history.

A multi-platform, **free and open source** software package for **visualization** and **medical image computing**

[Download](#) [Slicer Training](#) [Feedback](#)

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[Slicer Wiki](#)

About Slicer

[Introduction](#)

[Acknowledgments](#)

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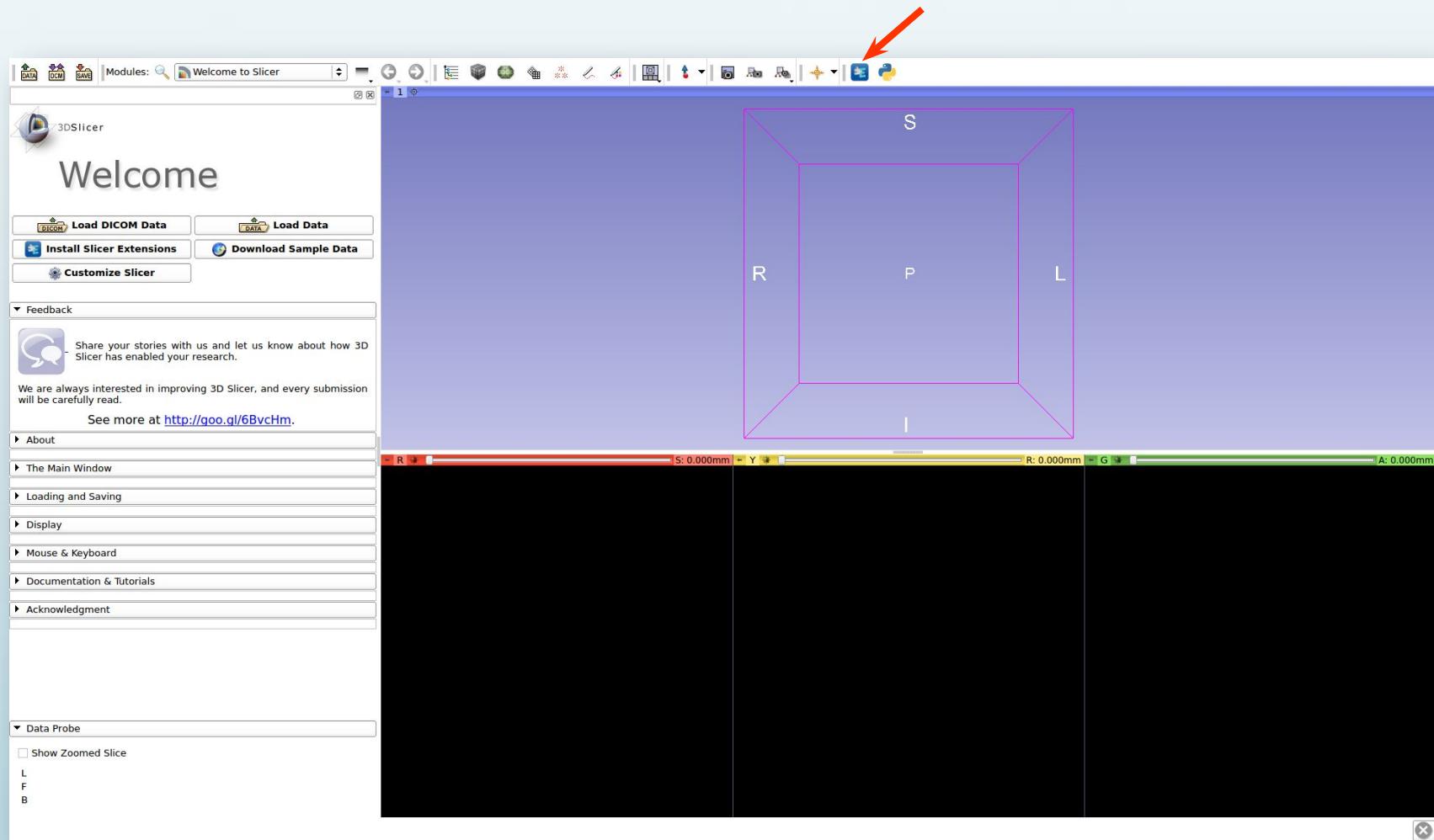
[Licensing](#)

Slicer 4.6 released

3D Slicer is an open source software platform for medical image informatics, image processing, and three-dimensional visualization. Built over two decades through support from the National Institutes of Health and a worldwide developer community, Slicer brings free, powerful cross-platform processing tools to physicians, researchers, and the general public.

SPHARM-PDM Installation on 3D Slicer

2. In 3D Slicer, open the Extension Manager



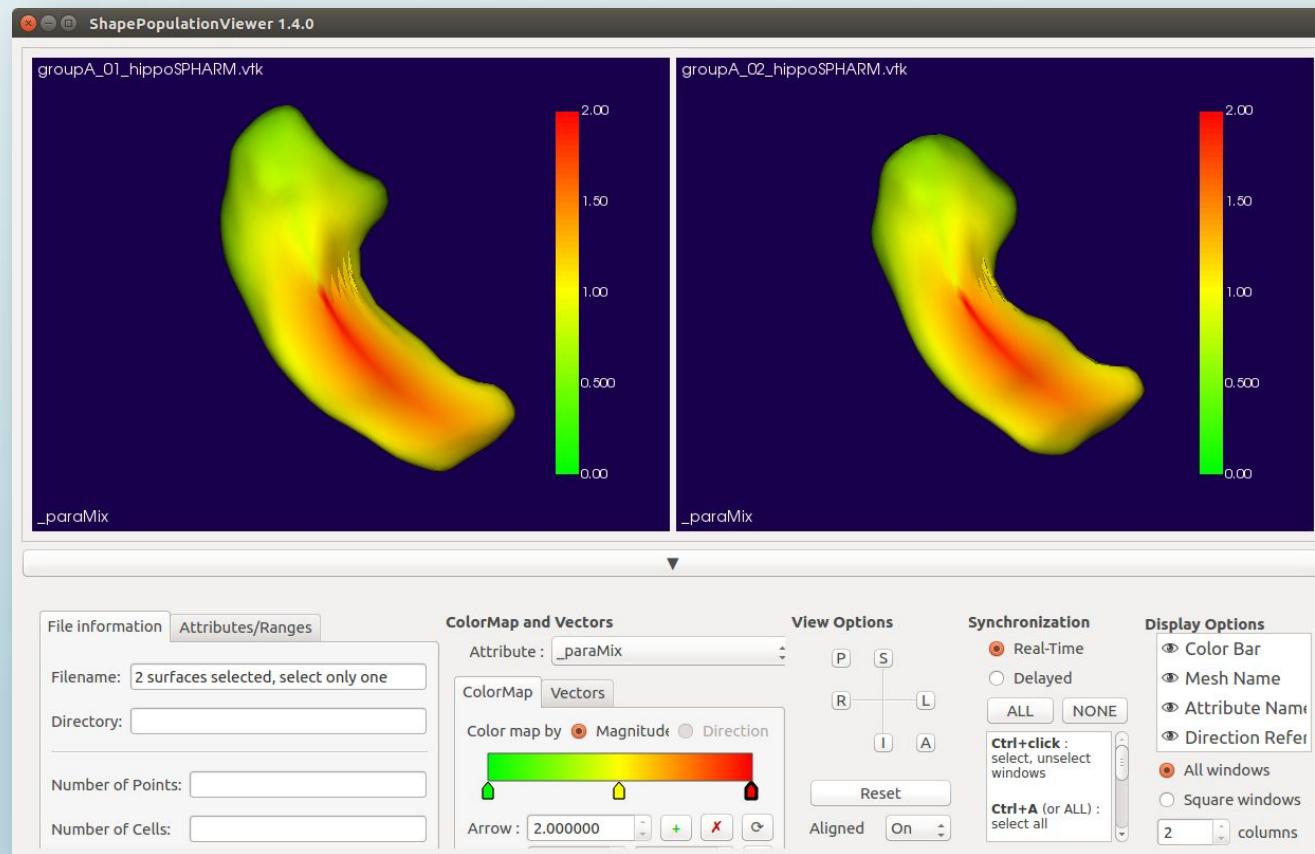
SPHARM-PDM Installation on 3D Slicer

3. In the *Install Extension* tab, select **SPHARM** under *Categories*
4. Under **SPHARM-PDM**, select the *Install* button and restart Slicer when prompted



SPHARM-PDM Installation on 3D Slicer

For quality control, we analyze our SPHARM-PDM outputs with **Shape Population Viewer** extension. Shape Population Viewer can be installed as a 3D Slicer extension or as an external binary. This module is included as part of the SlicerSALT package.



SPHARM-PDM Installation on 3D Slicer

To install **Shape Population Viewer** as a 3D Slicer extension:

- i. Open *Extension Manager*, in the *Install Extensions* tab,
select 'Shape Analysis' under *Categories*
- ii. Select the appropriate *Install* button and restart 3D Slicer
when prompted



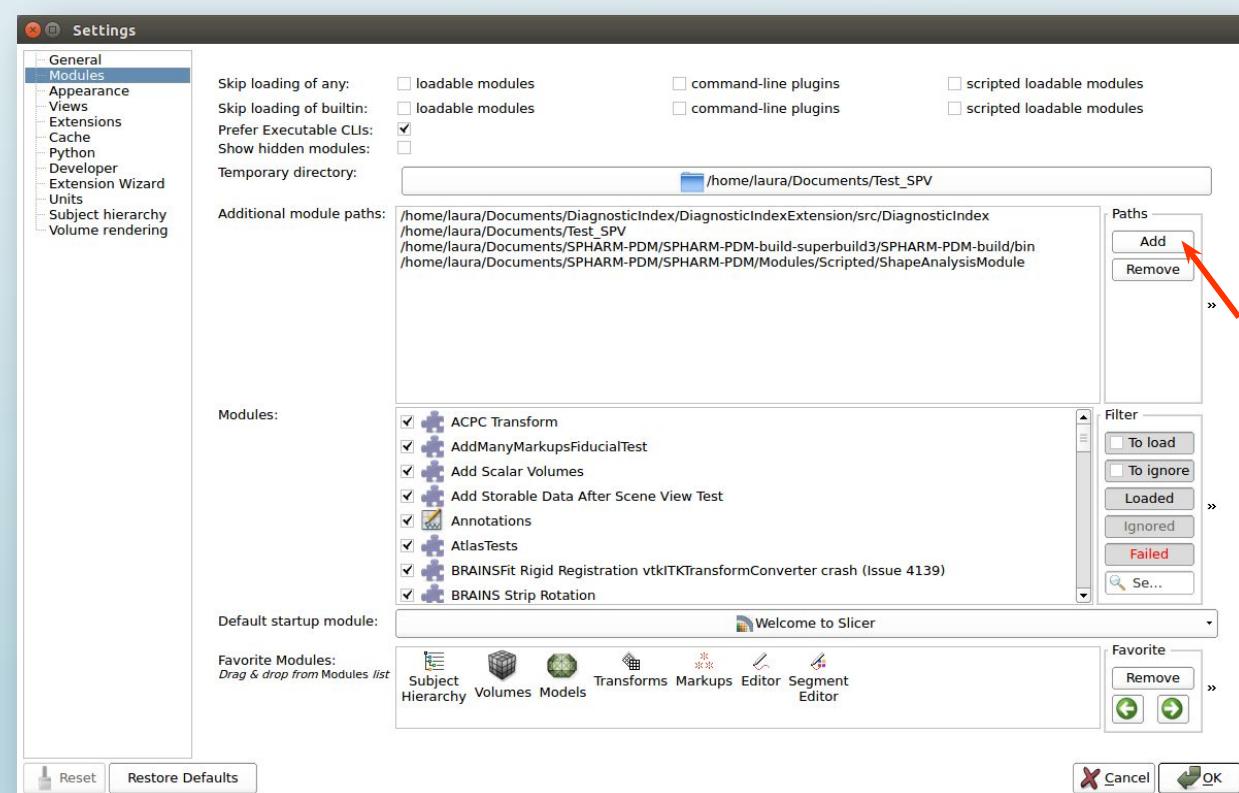
SPHARM-PDM Installation on 3D Slicer

To install **Shape Population Viewer** as an external binary:

- i. Download ShapePopulationViewer package for your respective operating system on [NITRC website](#)

- ii. In 3D Slicer, open *Application Settings* in the *Edit* Menu. On the tab *Modules*, Add the folder where ShapePopulationViewer is stored

- iii. Restart 3D Slicer



SPHARM-PDM Use

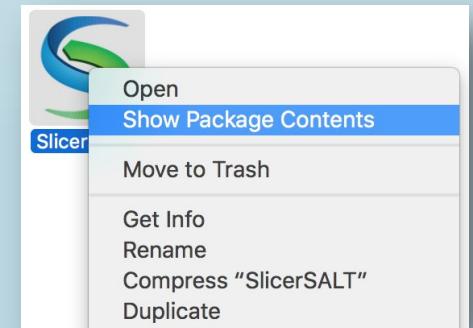
SPHARM-PDM tool can be used by two different ways:

- As **command-line tool** through the terminal thanks to SlicerSALT
- As a **module** of SlicerSALT or 3DSlicer

SPHARM-PDM Command-Line Tool

SPHARM-PDM method can be run on several cases through a terminal thanks to two files included in the SlicerSALT package:

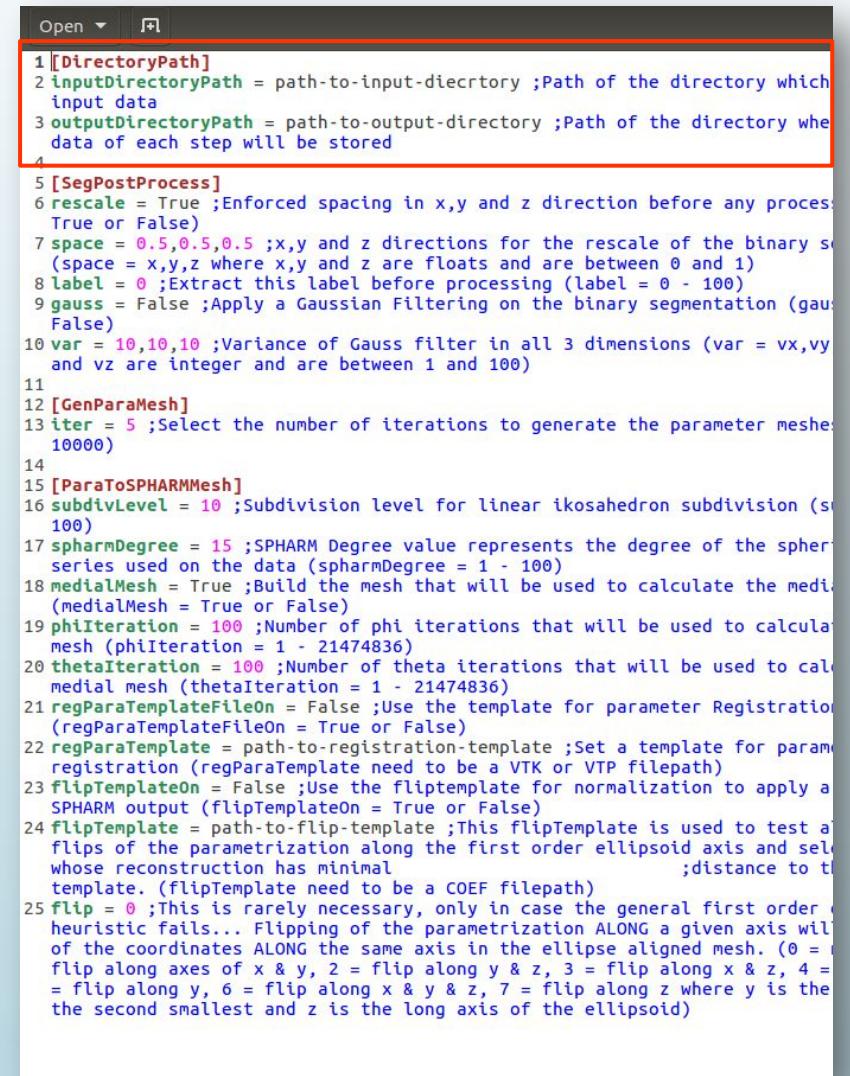
- SPHARM-PDM-parameters.ini which allows the user to specify the inputs, outputs and the parameters of the SPHARM-PDM tool
- SPHARM-PDM.py python script which will apply SPHARM-PDM method on the given input cases with the parameters specified in the SPHARM-PDM-parameters.ini file
- *Location of the SPHARM-PDM.py and SPHARM-PDM-parameters.ini files:*
 - *On Linux and Windows: share/Slicer-4.7/CommandLineTool*
 - *On MacOs: Open the SlicerSALT Contents → → Contents/share/Slicer-4.7/CommandLineTool*



SPHARM-PDM Command-Line Tool

Step 1: Modification of the *SPHARM-PDM-parameters.ini* file by specifying the **input directory path** containing the input cases and the **output directory path** where the SPHARM-PDM outputs will be stored.

The others parameters can also be modified to apply SPHARM-PDM to a particular case.



A screenshot of a Windows-style text editor window titled "Open". The file contains a configuration script for the SPHARM-PDM command-line tool. The code is color-coded, with comments in blue. A red box highlights the first three lines of the script, which define the input and output directory paths. The rest of the script includes parameters for segmentation, mesh generation, and registration.

```
1 [DirectoryPath]
2 inputDirectoryPath = path-to-input-diecrtry ;Path of the directory which
   input data
3 outputDirectoryPath = path-to-output-directory ;Path of the directory whe
   data of each step will be stored
4
5 [SegPostProcess]
6 rescale = True ;Enforced spacing in x,y and z direction before any proces
   True or False)
7 space = 0.5,0.5,0.5 ;x,y and z directions for the rescale of the binary se
   (space = x,y,z where x,y and z are floats and are between 0 and 1)
8 label = 0 ;Extract this label before processing (label = 0 - 100)
9 gauss = False ;Apply a Gaussian Filtering on the binary segmentation (gaus
   False)
10 var = 10,10,10 ;Variance of Gauss filter in all 3 dimensions (var = vx,vy
   and vz are integer and are between 1 and 100)
11
12 [GenParaMesh]
13 iter = 5 ;Select the number of iterations to generate the parameter meshes
   (10000)
14
15 [ParaToSPHARMMesh]
16 subdivLevel = 10 ;Subdivision level for linear ikosahedron subdivision (s
   100)
17 spharmDegree = 15 ;SPHARM Degree value represents the degree of the spherical
   series used on the data (spharmDegree = 1 - 100)
18 medialMesh = True ;Build the mesh that will be used to calculate the medial
   (medialMesh = True or False)
19 phiIteration = 100 ;Number of phi iterations that will be used to calculate
   the medial mesh (phiIteration = 1 - 21474836)
20 thetaIteration = 100 ;Number of theta iterations that will be used to calculate
   the medial mesh (thetaIteration = 1 - 21474836)
21 regParaTemplateFileOn = False ;Use the template for parameter Registration
   (regParaTemplateFileOn = True or False)
22 regParaTemplate = path-to-registration-template ;Set a template for parameter
   registration (regParaTemplate need to be a VTK or VTP filepath)
23 flipTemplateOn = False ;Use the flipTemplate for normalization to apply a
   SPHARM output (flipTemplateOn = True or False)
24 flipTemplate = path-to-flip-template ;This flipTemplate is used to test all
   flips of the parametrization along the first order ellipsoid axis and select
   whose reconstruction has minimal distance to the template. (flipTemplate need to be a COEF filepath)
25 flip = 0 ;This is rarely necessary, only in case the general first order
   heuristic fails... Flipping of the parametrization ALONG a given axis will
   of the coordinates ALONG the same axis in the ellipse aligned mesh. (0 =
   flip along axes of x & y, 2 = flip along y & z, 3 = flip along x & z, 4 =
   flip along y, 6 = flip along x & y & z, 7 = flip along z where y is the
   the second smallest and z is the long axis of the ellipsoid)
```

SPHARM-PDM Command-Line Tool

Step 2: Launch SPHARM-PDM method with the following command-lines:

- On Linux and Windows:

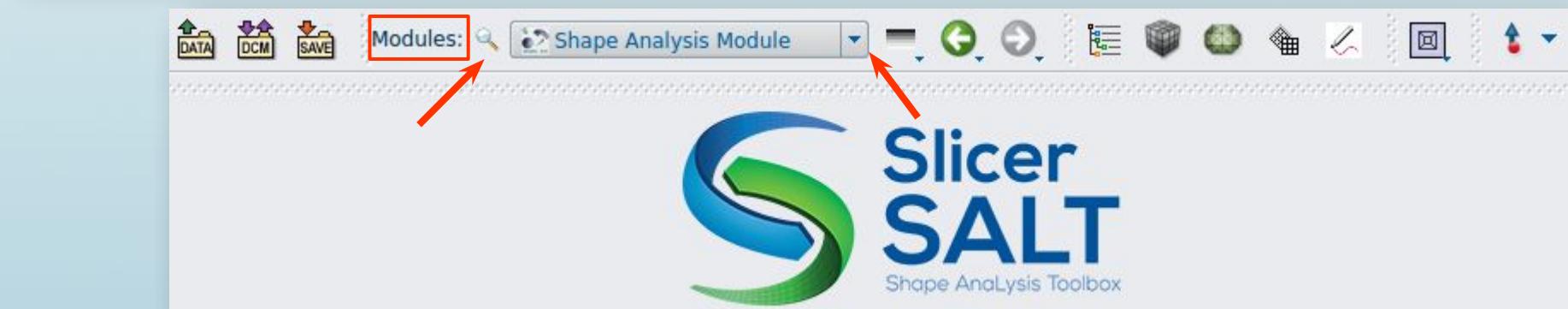
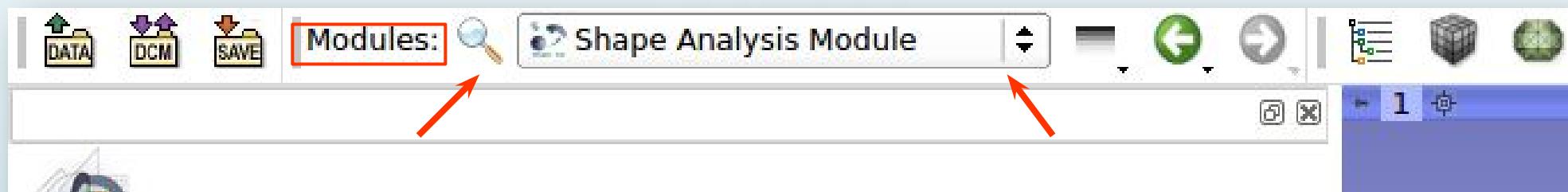
```
$cd path-to-the-SlicerSALT-package  
$./SlicerSALT --no-main-window --python-script  
share/Slicer-4.7/CommandLineTool/SPHARM-PDM.py  
share/Slicer-4.7/CommandLineTool/SPHARM-PDM-parameters.ini
```

- On MacOs:

```
$cd path-to-the-SlicerSALT-package/SlicerSALT.app/Contents/MacOS  
$./SlicerSALT --no-main-window --python-script  
..../share/Slicer-4.7/CommandLineTool/SPHARM-PDM.py  
..../share/Slicer-4.7/CommandLineTool/SPHARM-PDM-parameters.ini
```

SPHARM-PDM Module

In 3D Slicer or in SlicerSALT, select **Shape Analysis Module** from the *Modules* drop-down menu (Category: SPHARM) or on the Search bar.



Setting up Input/Output Directories

Group Project IO tab

- For ***Input Directory***, select the folder which contains the input data
- For ***Output Directory***, select the folder where the outputs of each step will be stored

▼ Group Project IO

Input Directory	 . /path/to/InputDirectory
Output Directory	 . /path/to/OutputDirectory
Verbose mode	<input type="checkbox"/>

Input/Output Data

The input directory contains the input data which can be:

- Label map volumes (.gpl, .gpl.gz, .nii, .nii.gz, .nrrd, .mgh, .mgh.gz, .mhd, or .hdr)
- Models (.vtk, or .vtpl)

The output directory will contain SPHARM output data sorted in three different folders for each of the three steps:

- ◆ **Step1_SegPostProcess** for the *Post Processed Segmentation* step
- ◆ **Step2_GenMeshPara** for the *Generate Mesh Parameters* step
- ◆ **Step3_ParaToSPHARMMesh** for the *Parameters to SPHARM Mesh* step



Features and Parameters

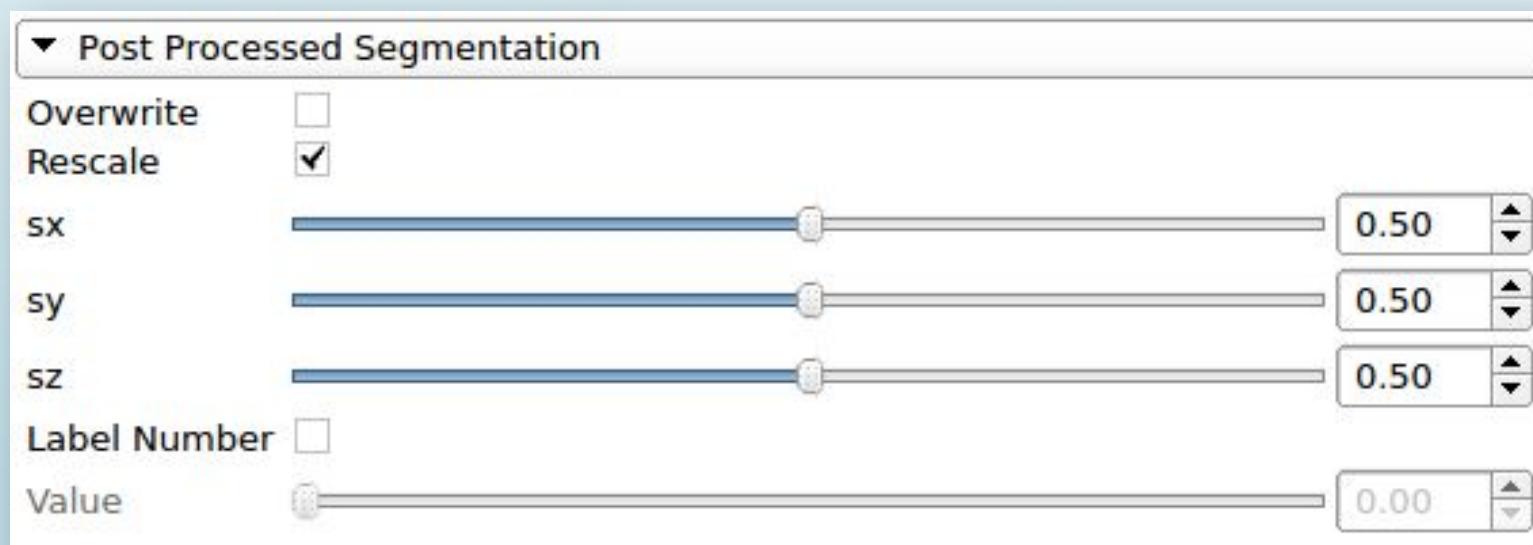
Common to all tabs

- ◆ The **Overwrite** option: this option is available for the three steps of *Shape Analysis Module*:
 - ◆ If this option **is not selected** for one step, it will skip the step if the output data were previously computed and stored in the output folder of this step:
 - ◆ Folder ***Step1_SegPostProcess*** for the *Post Processed Segmentation* step
 - ◆ Folder ***Step2_GenMeshPara*** for the *Generate Mesh Parameters* step
 - ◆ Folder ***Step3_ParaToSPHARMMesh*** for the *Parameters to SPHARM Mesh* step
 - ◆ If this option **is selected** for one step, all the files in the output folder of this step will be removed and the step won't be skipped.

Features and Parameters

Post Processed Segmentation tab

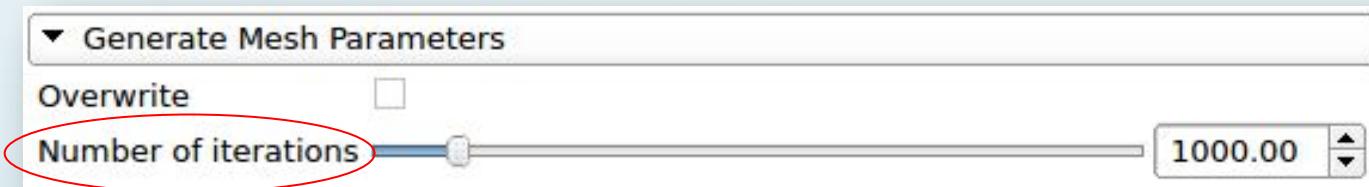
- Rescale option: The X, Y and Z spacing parameters ($s_x/s_y/s_z$) determine the resolution in which the data will be processed for each axis (in millimeters)
- Label Number option: First extraction of the specified label before to apply the post processing step



Features and Parameters

Generate Mesh Parameters tab

- Number of iterations: Higher number of iterations will improve the accuracy of the mapping of the surface mesh to a parameterization sphere



Number of iterations
5
1000

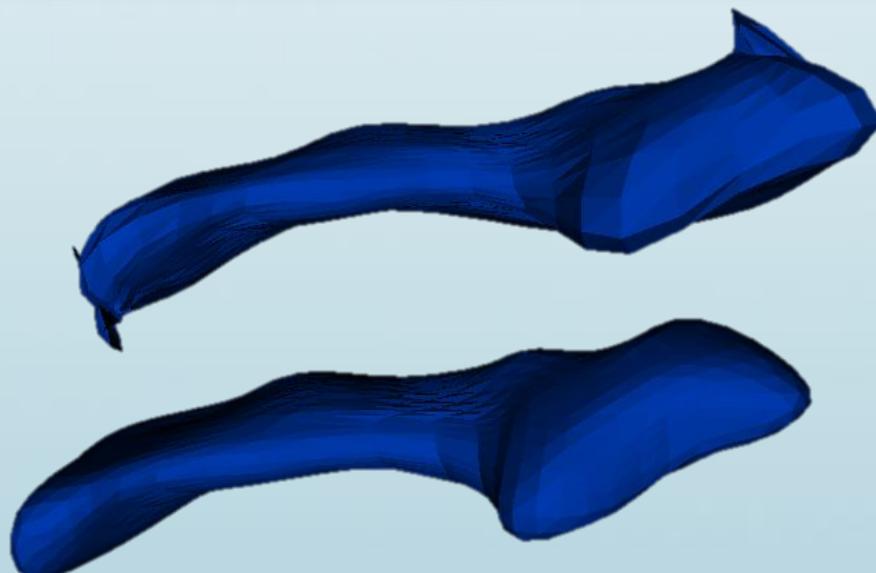


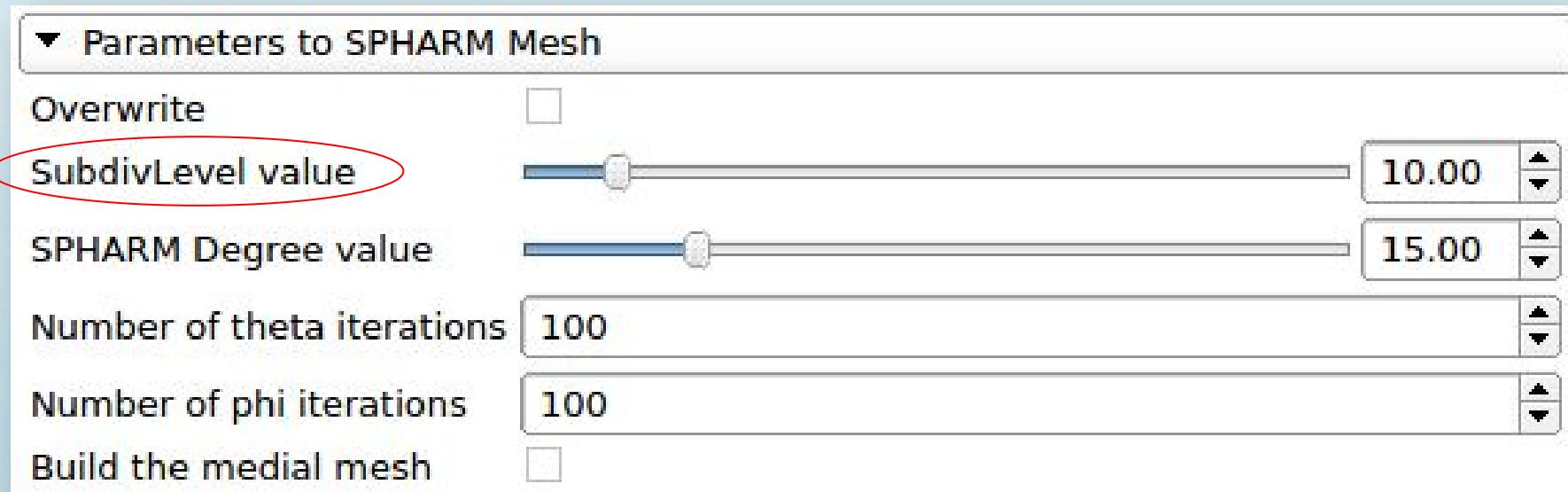
Figure: *SPHARM.vtk generated with 5 iterations (top) and 1000 iterations (bottom)

Note: Higher number of iterations will produce better representation results.

Features and Parameters

Parameters to SPHARM Mesh tab

- Subdivision Level value: Icosahedron subdivision allows for linear, uniform sampling of the object by referring to its spherical parameterization. The *SubdivLevel* value sets the level of the subdivision factor that will be used. Improving this value results in a SPHARM mesh with more points.

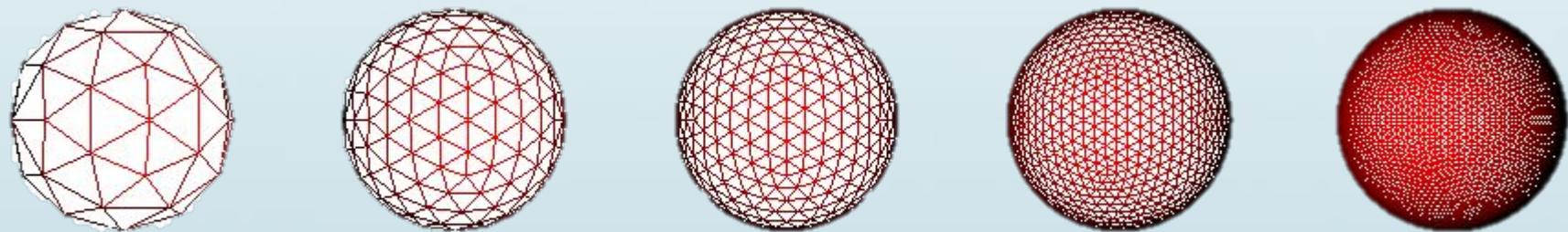


Features and Parameters

Parameters to SPHARM Mesh tab

Subdivision Level value:

Figure: *para.vtk generated with 5 subdivision different
(left to right : 2 – 4 – 6 – 10 - 20)



Subdivision Level	2	4	6	10	20
Number of Points	42	162	362	1002	4002

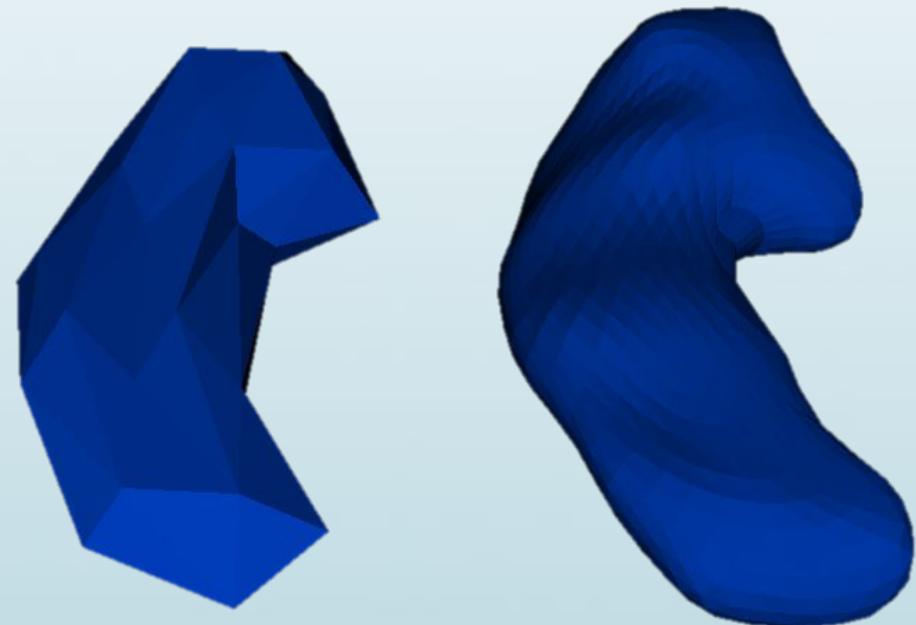
Features and Parameters

Parameters to SPHARM Mesh tab

Subdivision Level value:

Figure: *SPHARM.vtk generated with a subdivision level of 2 (left) and 10 (right)

Note: Higher subdivision level value will result in a smoother surface mesh.

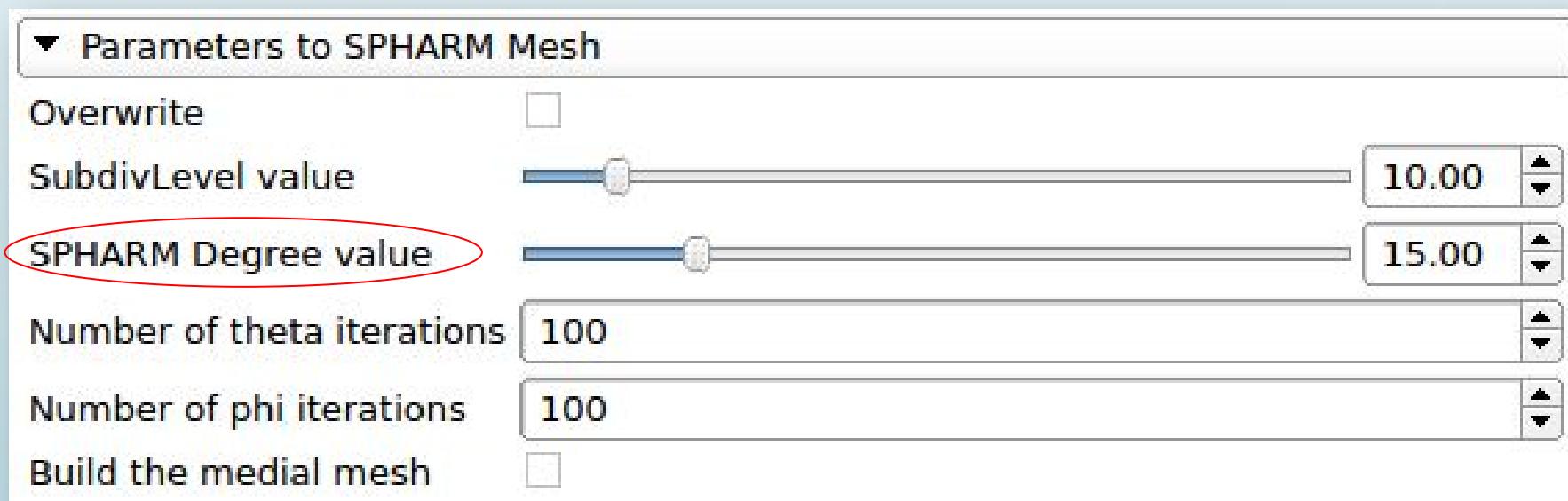


Subdivision Level	2	10
Number of points	42	1002

Features and Parameters

Parameters to SPHARM Mesh tab

- SPHARM Degree value represents the degree of the spherical harmonic series used on the data. Changing this value results in different levels of detail of the object.



Features and Parameters

Parameters to SPHARM Mesh tab

SPHARM Degree:

Figure: *SPHARM.vtk generated with different SPHARM degree (left to right: 1 – 3 – 5 – 10 – 25)

Note: A higher SPHARM degree value will result in a surface mesh with more details.



SPHARM degree
1
3
5
10
25

Features and Parameters

Parameters to SPHARM Mesh tab

- Build the medial mesh: This option will compute the mean latitude axis associated with the data if checked. The Number of theta/phi iterations corresponds to the number of samples used in the medial mesh computation¹.

▼ Parameters to SPHARM Mesh

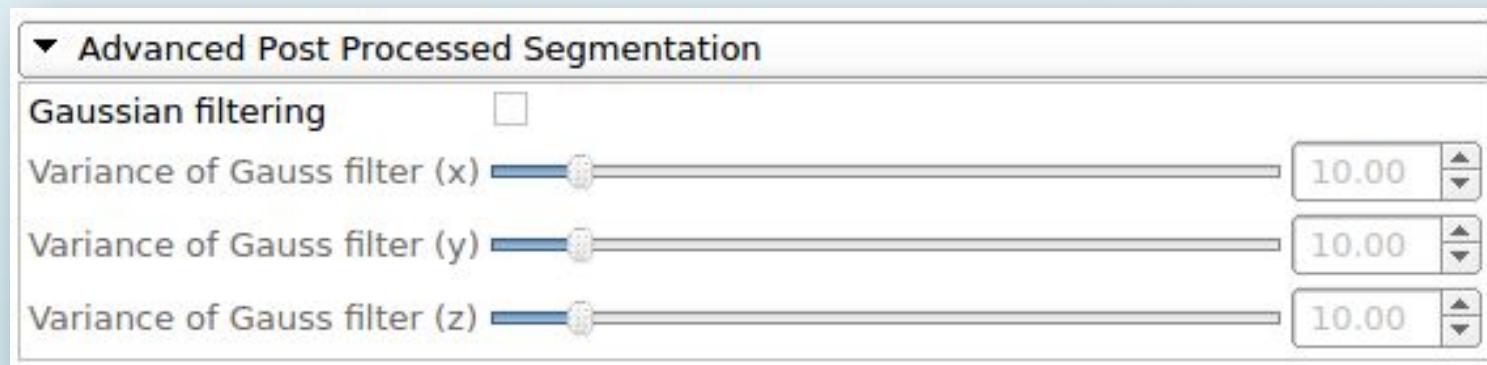
Overwrite	<input type="checkbox"/>
SubdivLevel value	<input type="range" value="10.00"/> 10.00
SPHARM Degree value	<input type="range" value="15.00"/> 15.00
Number of theta iterations	100
Number of phi iterations	100
Build the medial mesh	<input type="checkbox"/>

1. Paniagua B1, Lyall A, Berger JB, Vachet C, Hamer RM, Woolson S, Lin W, Gilmore J, Styner M. (2013). Lateral ventricle morphology analysis via mean latitude axis. Proc SPIE Int Soc Opt Eng. 2013 Mar 29;8672. pii: 2006846. <<http://www.ncbi.nlm.nih.gov/pubmed/23606800>>

Features and Parameters

Advanced Post Processed Segmentation tab

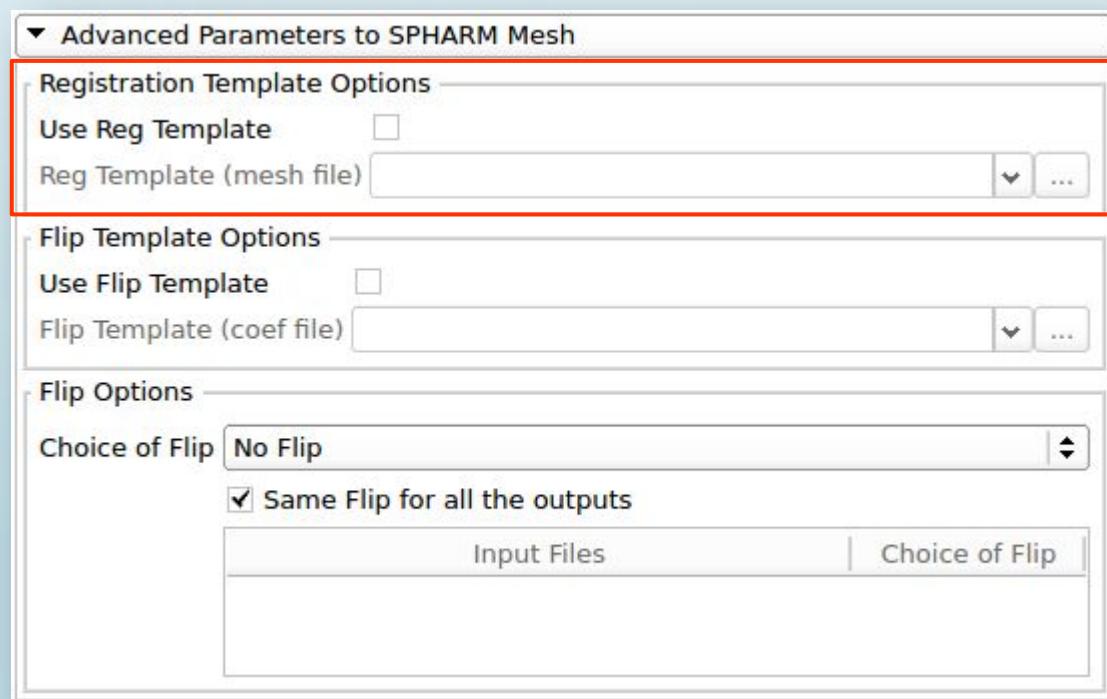
- Gaussian filtering: A Gaussian filter will be applied during the preprocessing step if this option is checked.



Features and Parameters

Advanced Parameters to SPHARM Mesh tab

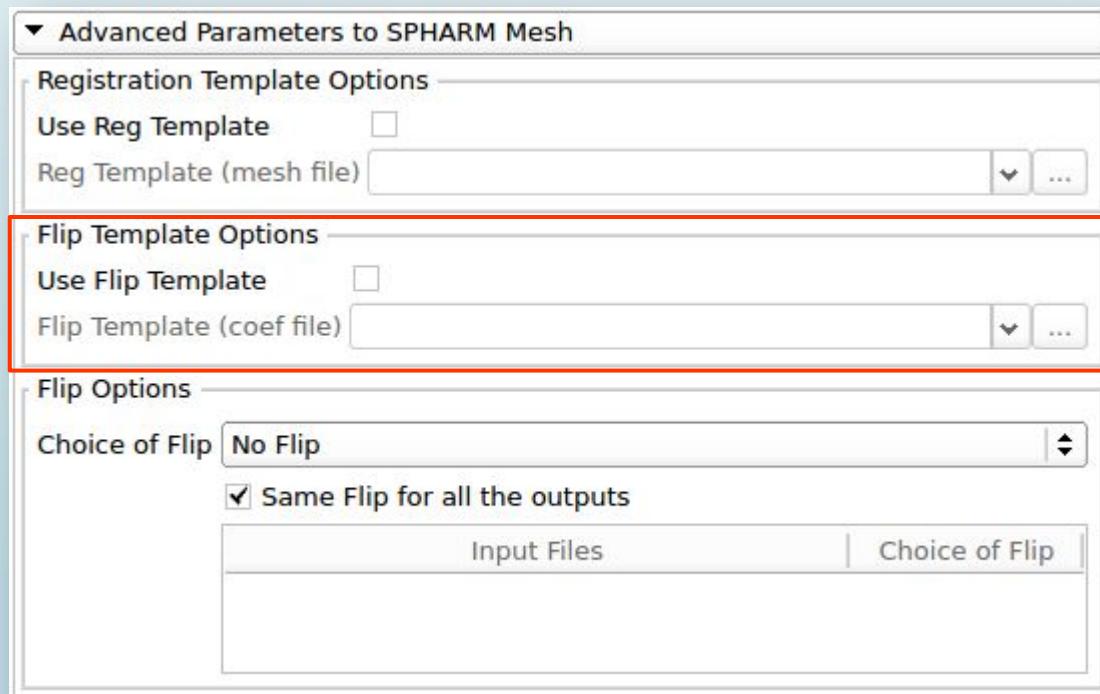
- Registration template Options: This option allows to have a rigid-body Procrustes alignment i.e. the **SPHARM_procalign* mesh generated by the tool will be aligned with the registration template (VTK file) by applying, if needed, a rigid transformation (which uses only translation and/or a rotation).



Features and Parameters

Advanced Parameters to SPHARM Mesh tab

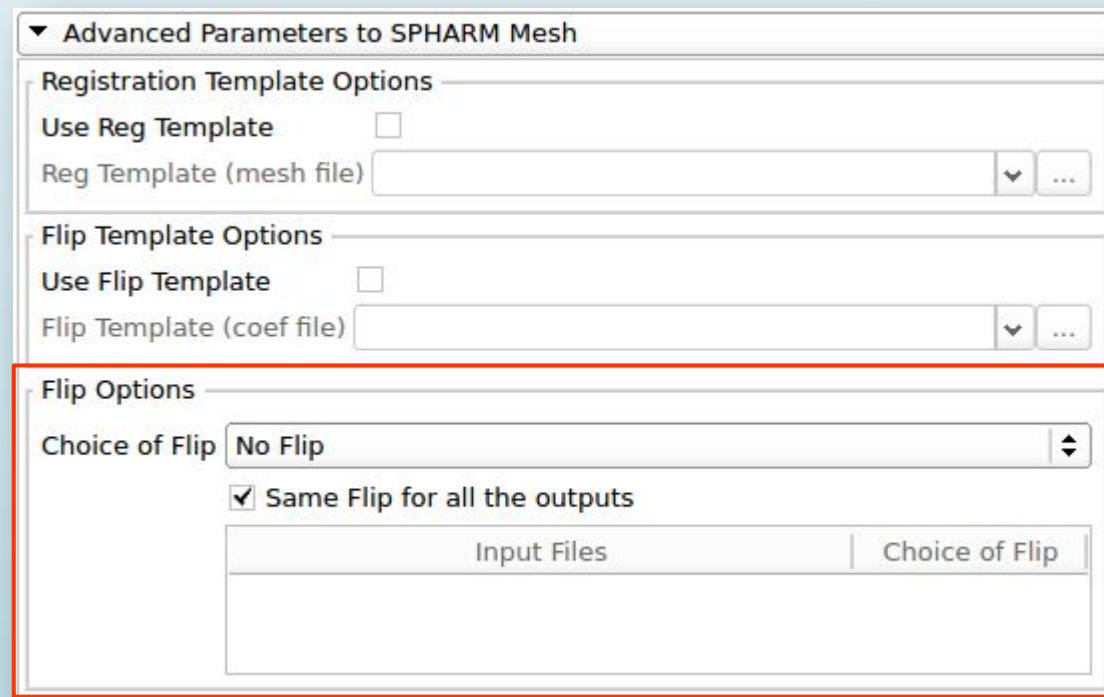
- Flip template Options: If *Use Flip Template* is checked, a *Flip Template* is used to test all possible flips of the parametrization along the first order ellipsoid axis and select the one whose reconstruction has minimal distance to the flip-template.



Features and Parameters

Advanced Parameters to SPHARM Mesh tab

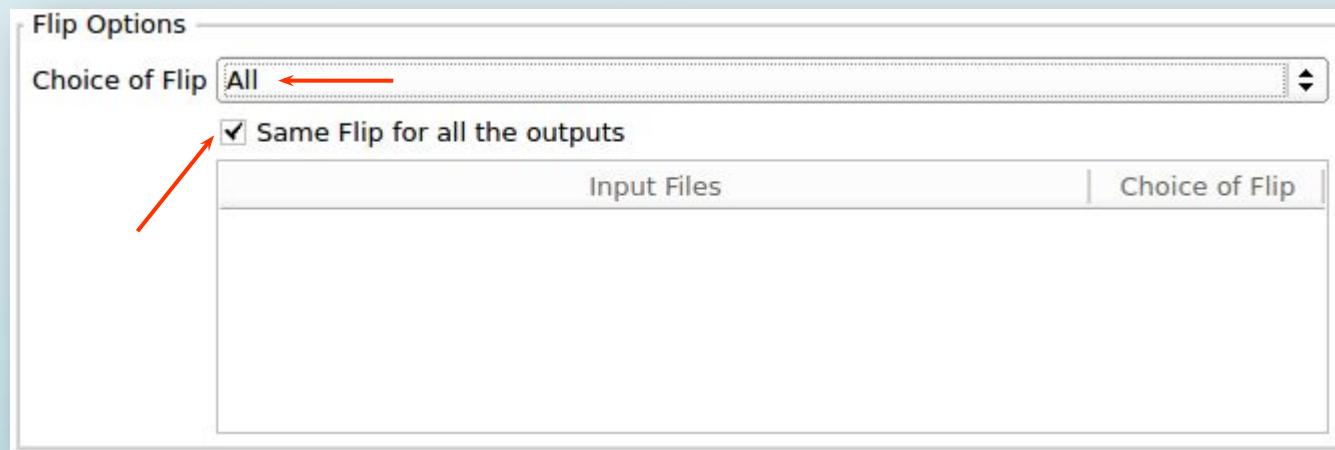
- Flip Options: This option allows an optional flipping of the parametrization specified by the user.



Features and Parameters

Advanced Parameters to SPHARM Mesh tab

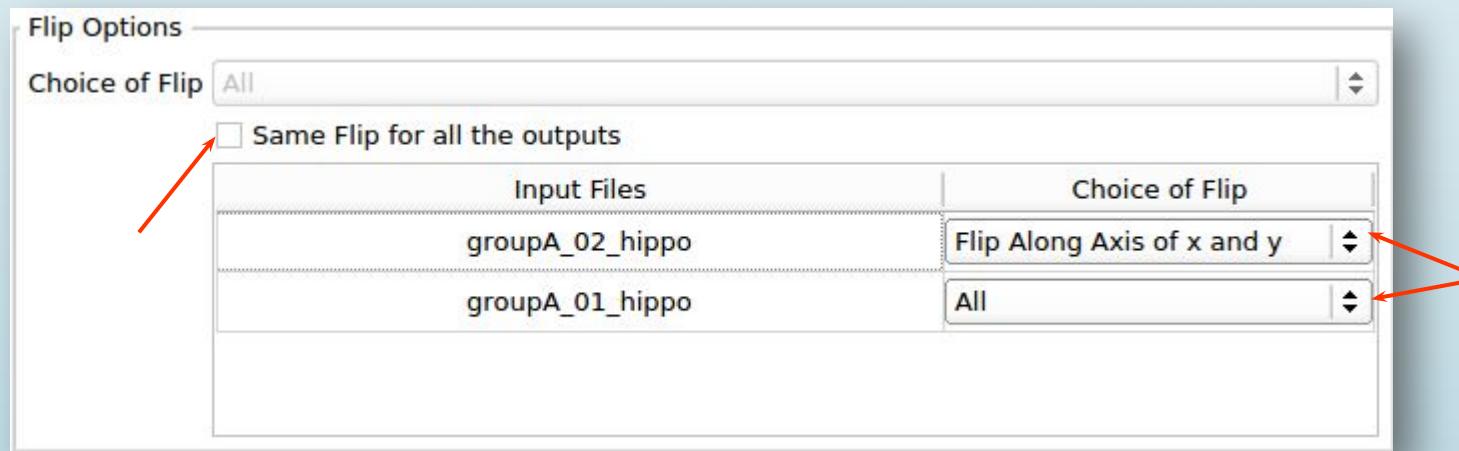
- Flip Options: To apply the same flip option for each case, check *Same Flip for all the outputs*.
- Select **one flip along an axis** or choose to apply **all the flips** to determine the best flip.



Features and Parameters

Advanced Parameters to SPHARM Mesh tab

- Flip Options: To apply different flip options for each case, uncheck *Same Flip for all the outputs*.
- As previously, select a flip option for each case.



Features and Parameters

Advanced Parameters to SPHARM Mesh tab

- Flip Options: Example of an application of all the flips on one case by iterating 7 times *ParaToSPHARMMesh* CLI. This figure shows a comparison of different flips in *Shape Population Viewer*.

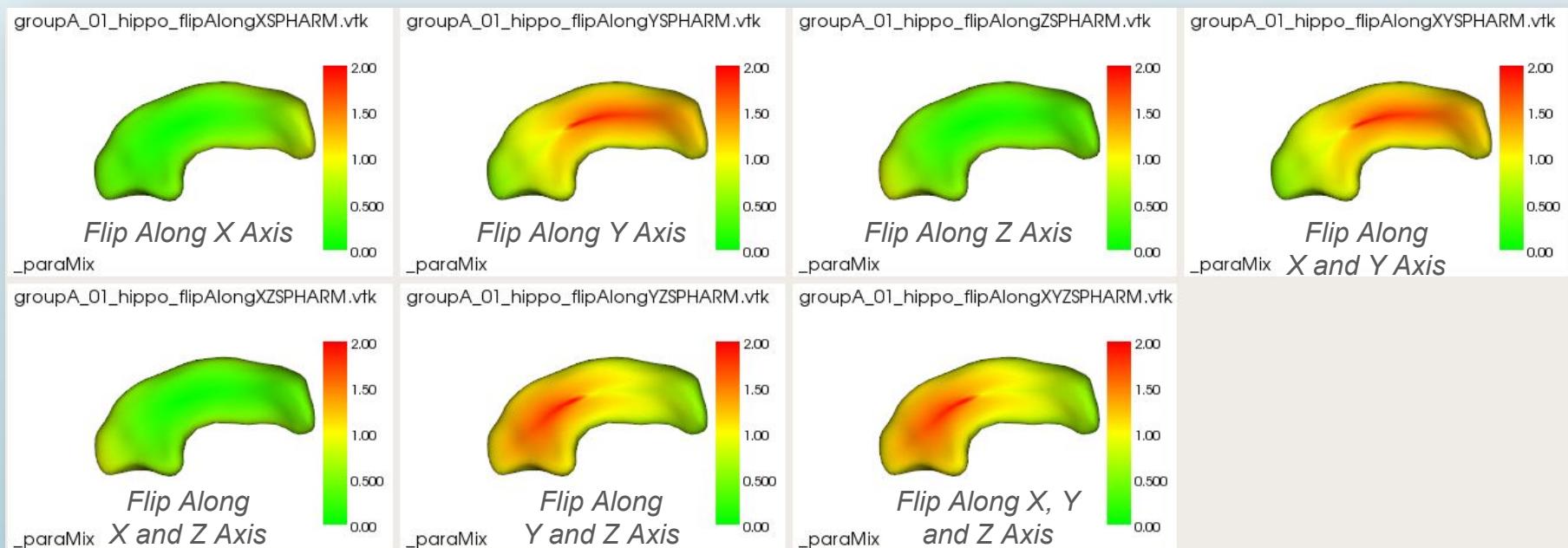
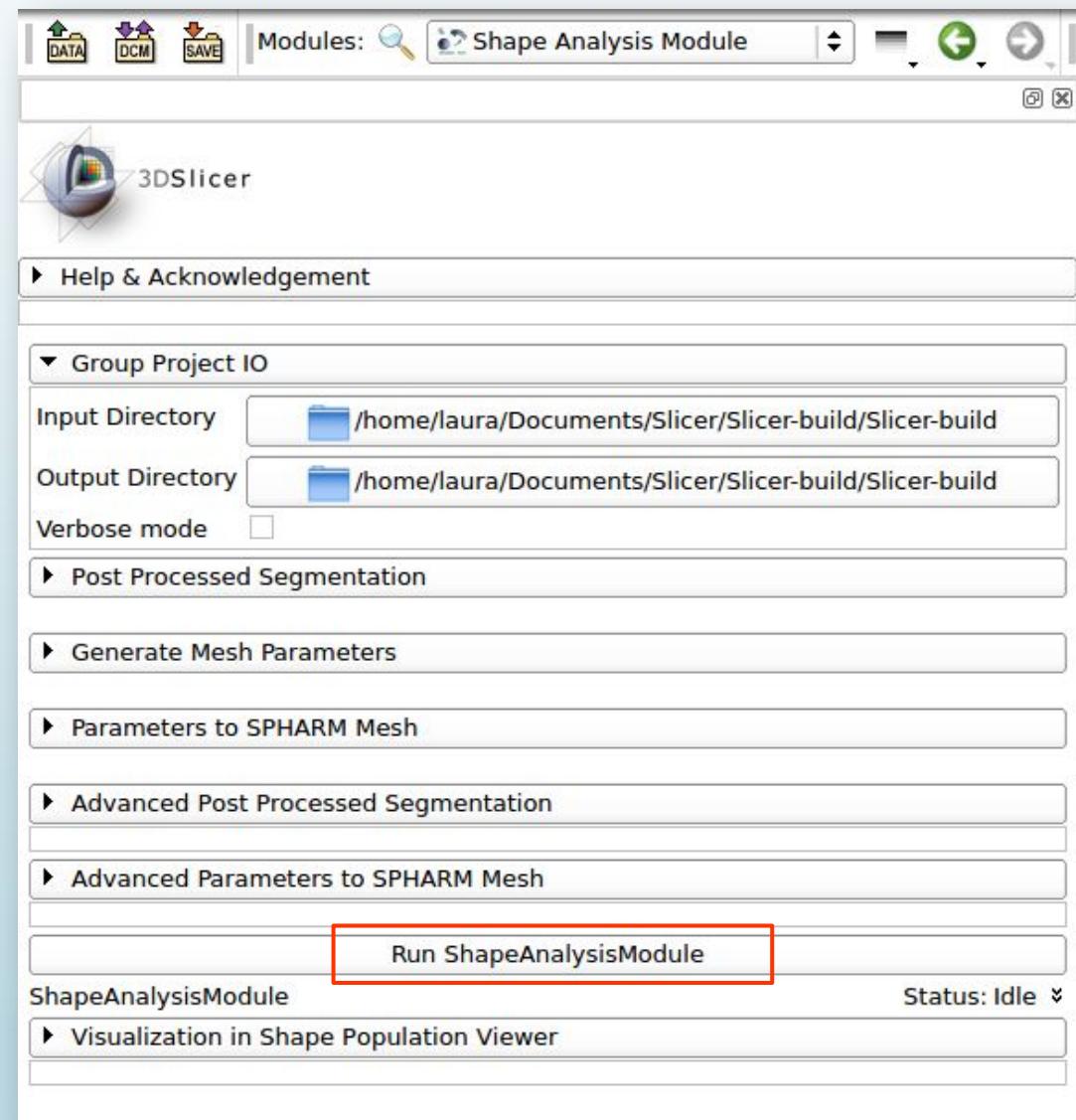


Figure: Visualization in ShapePopulationViewer of the different flips applied on *SPHARM model.

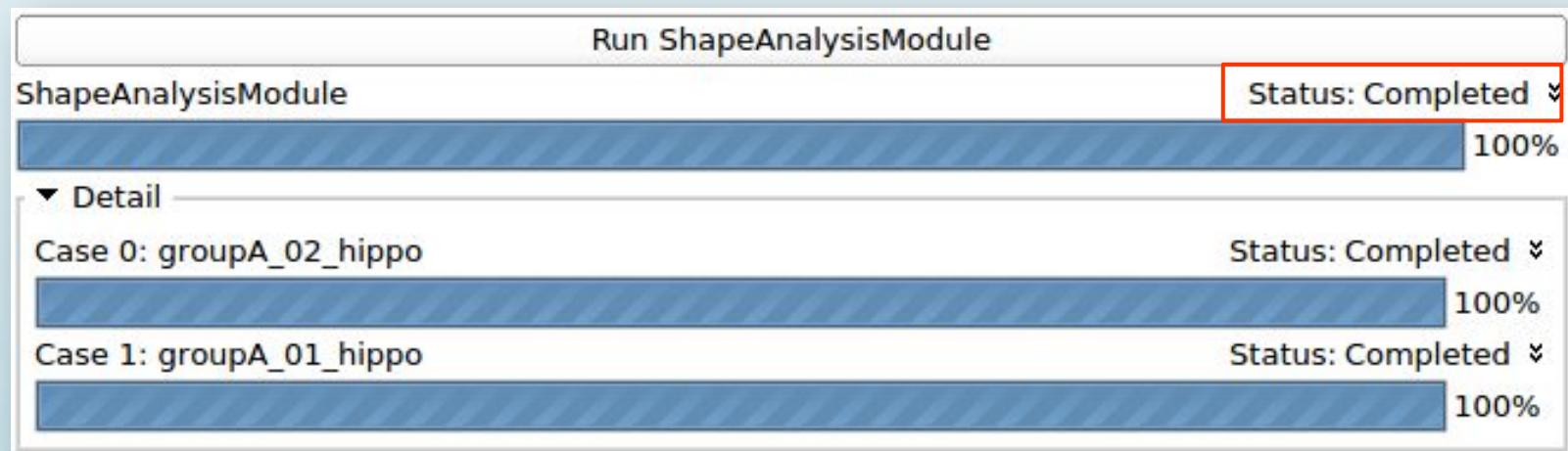
Running SPHARM-PDM

Click on the Run **ShapeAnalysisModule** button, to run the three steps on the provided inputs.



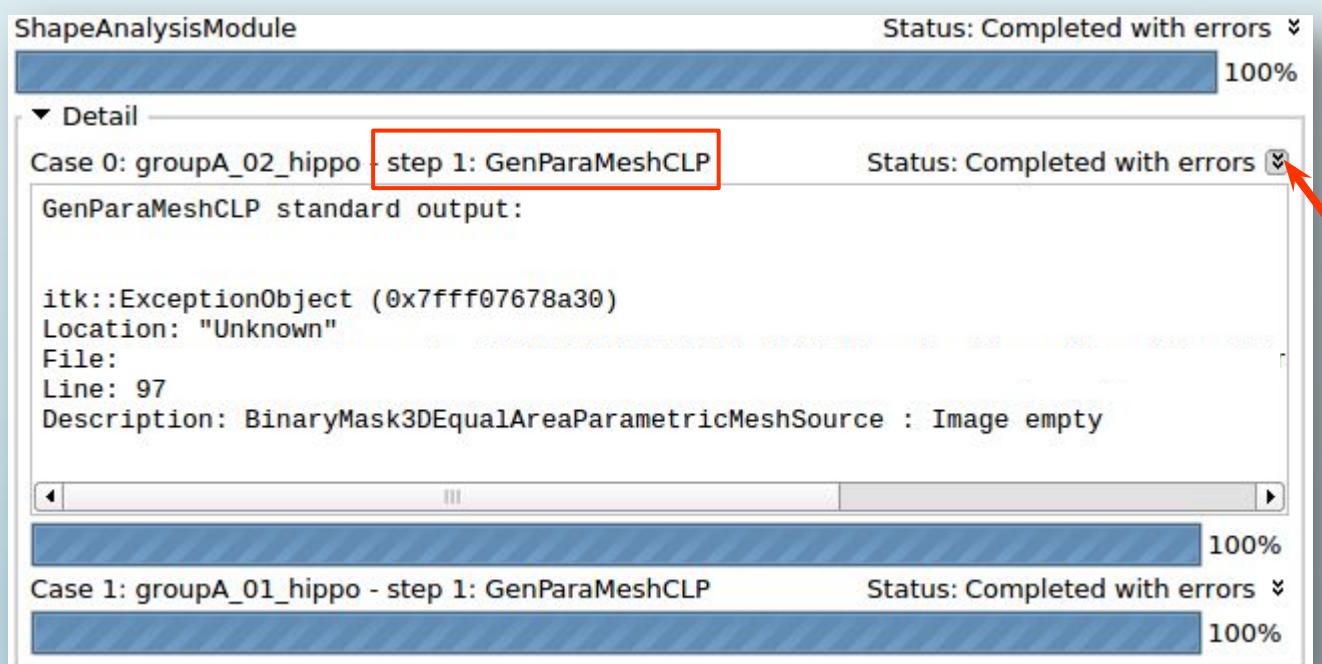
Running SPHARM-PDM

Progress bars will indicate when the computation is done and if the computation for each case was completed with or without error.



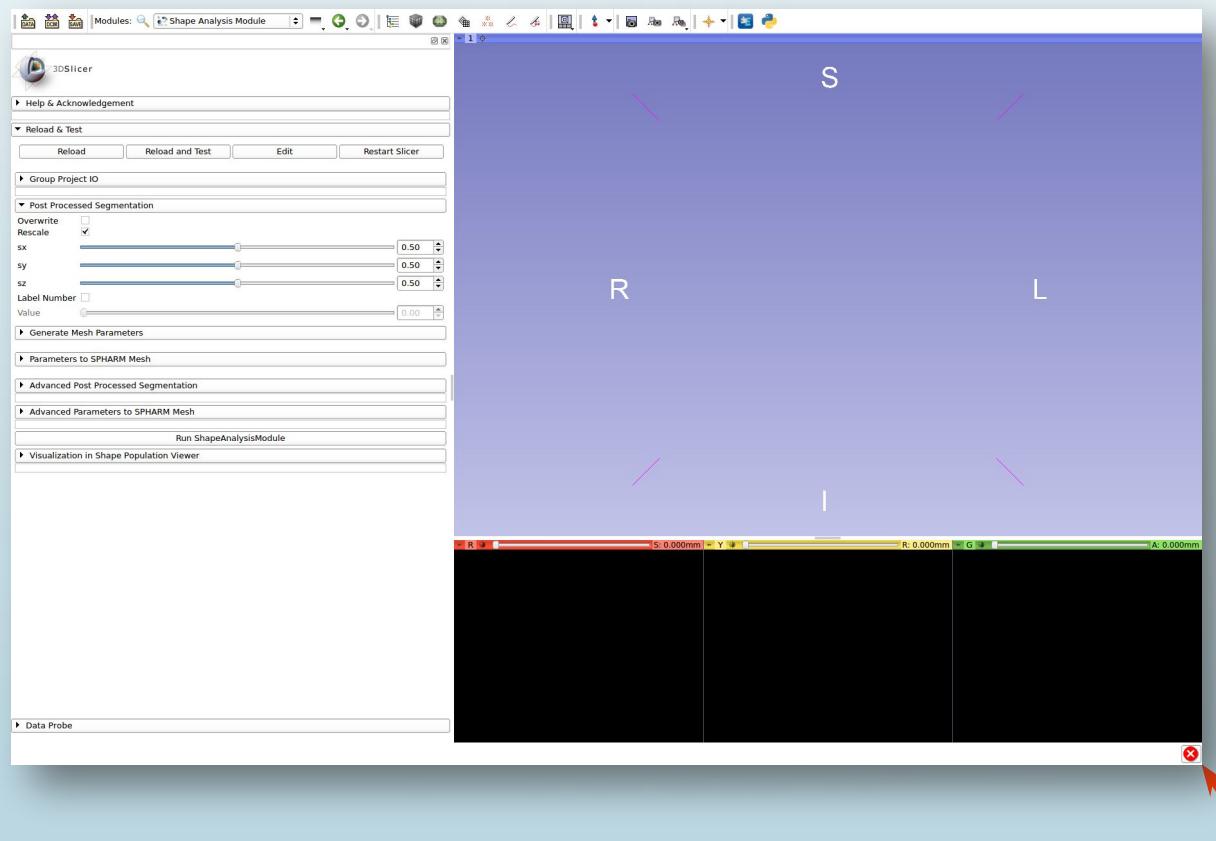
Debugging

If the module was completed with errors, the step which was completed with errors is indicated and the errors can be displayed by clicking on the little arrows:



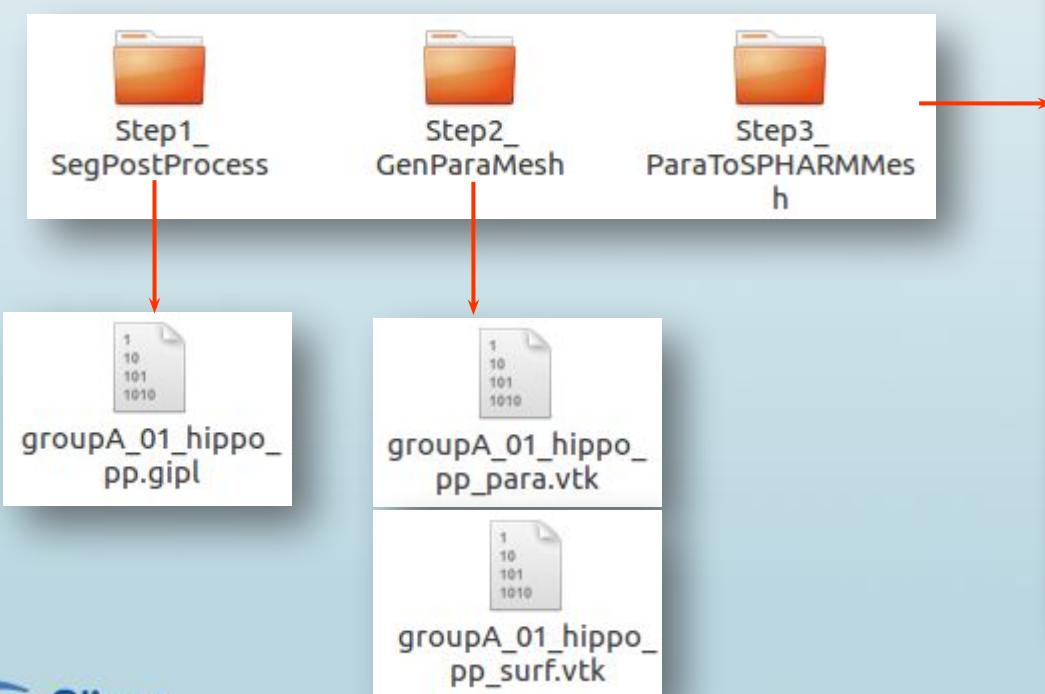
Debugging

3D Slicer's Error Log can also be used for debugging if the module was completed with errors. To open it, click on the red icon at the bottom right.



Output Files

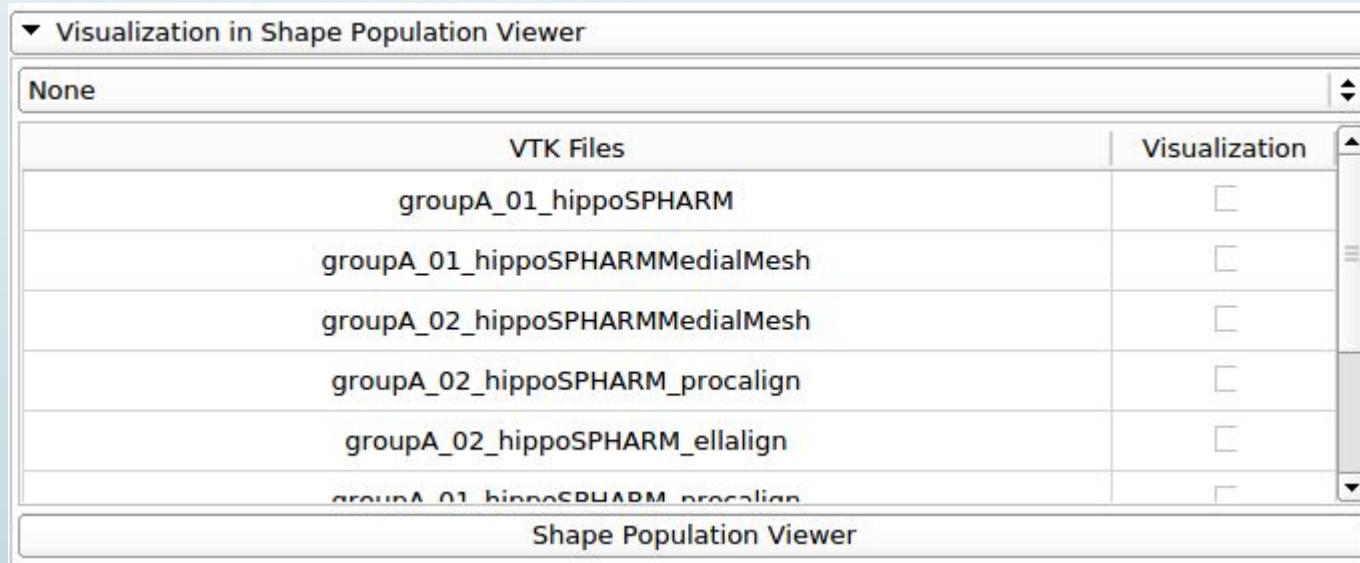
The outputs files for each step of SPHARM-PDM are stored in three folders in the output directory previously selected:



	<code>groupA_01_hippo_pp_surf_MedialAxisScalars.csv</code>
	<code>groupA_01_hippo_pp_surf_medialMeshArea.txt</code>
	<code>groupA_01_hippo_pp_surf_medialMeshPartialArea.txt</code>
	<code>groupA_01_hippo_pp_surf_medialMeshPartialRadius.txt</code>
	<code>groupA_01_hippo_pp_surf_medialMeshRadius.txt</code>
	<code>groupA_01_hippo_pp_surf_para.vtk</code>
	<code>groupA_01_hippo_pp_surf_paraMix.txt</code>
	<code>groupA_01_hippo_pp_surf_paraPhi.txt</code>
	<code>groupA_01_hippo_pp_surf_paraPhiHalf.txt</code>
	<code>groupA_01_hippo_pp_surf_paraTheta.txt</code>
	<code>groupA_01_hippo_pp_surf_SPHARM.coef</code>
	<code>groupA_01_hippo_pp_surf_SPHARM.vtk</code>
	<code>groupA_01_hippo_pp_surf_SPHARM_ellalign.coef</code>
	<code>groupA_01_hippo_pp_surf_SPHARM_ellalign.vtk</code>
	<code>groupA_01_hippo_pp_surf_SPHARMMedialAxis.vtk</code>
	<code>groupA_01_hippo_pp_surf_SPHARMMedialMesh.vtk</code>
	<code>groupA_01_hippo_pp_surf_SPHARM_procalign.vtk</code>

Quality control using ShapePopulationViewer

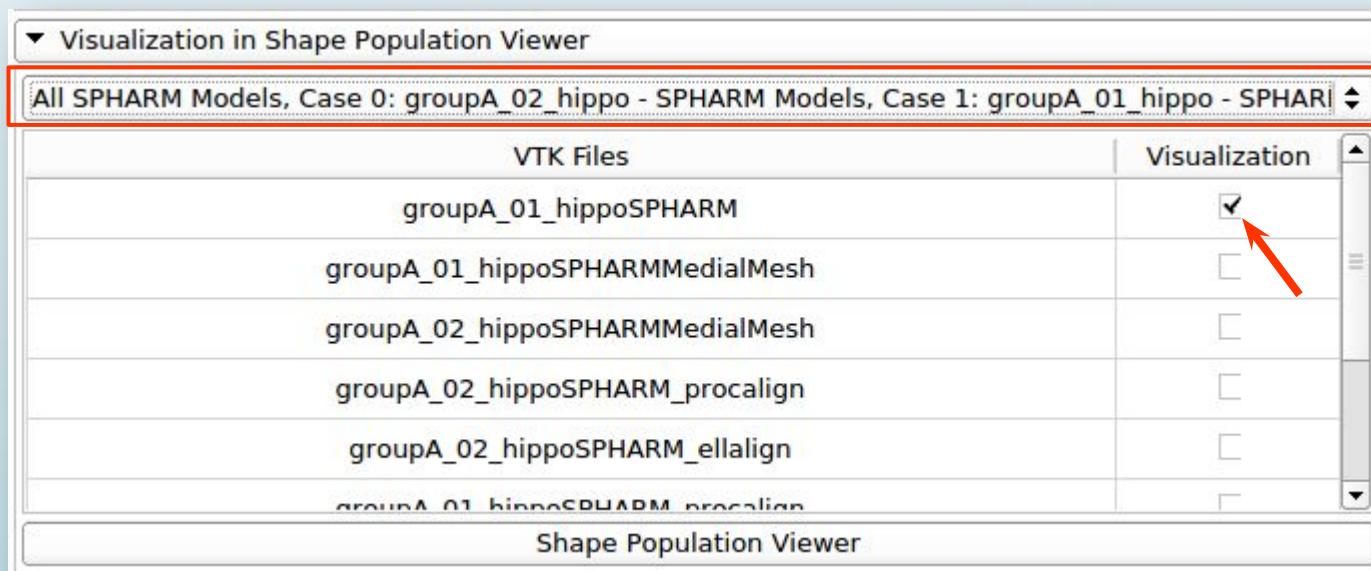
If *Shape Population Viewer* is installed, the Visualization tab will be enabled:



Note: *ShapePopulationViewer* is installed by default in SlicerSALT

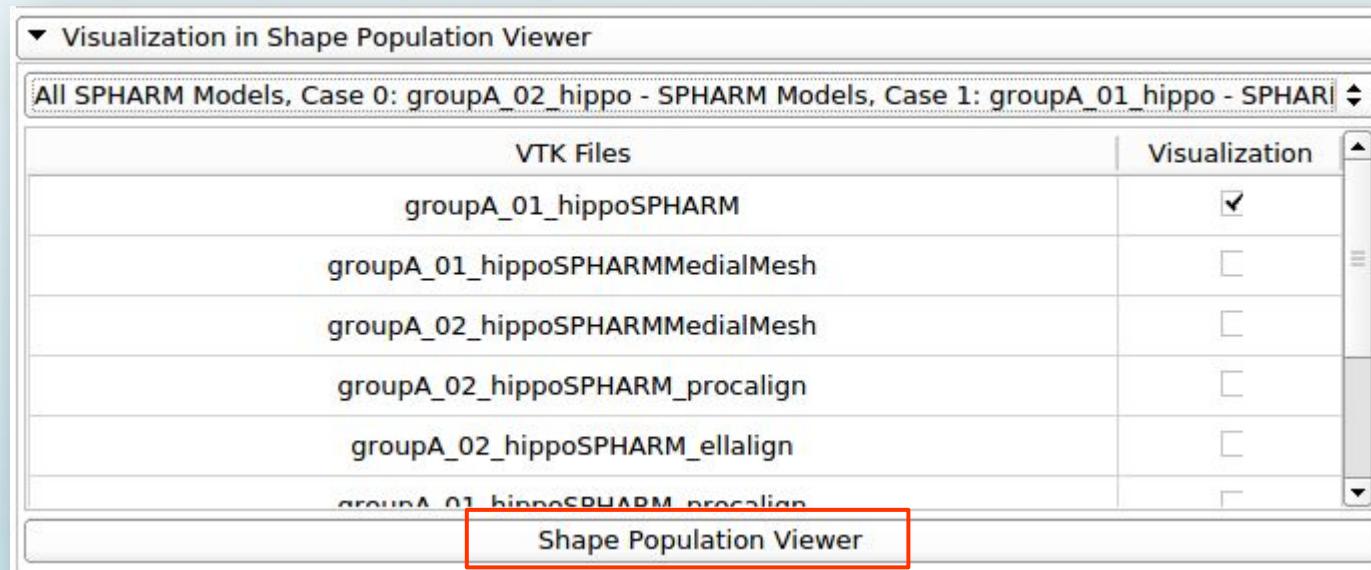
Quality control using ShapePopulationViewer

1 The selection of the SPHARM outputs which will be displayed in *Shape Population Viewer* can be done thanks to the checkable combobox or with the checkbox corresponding to them:



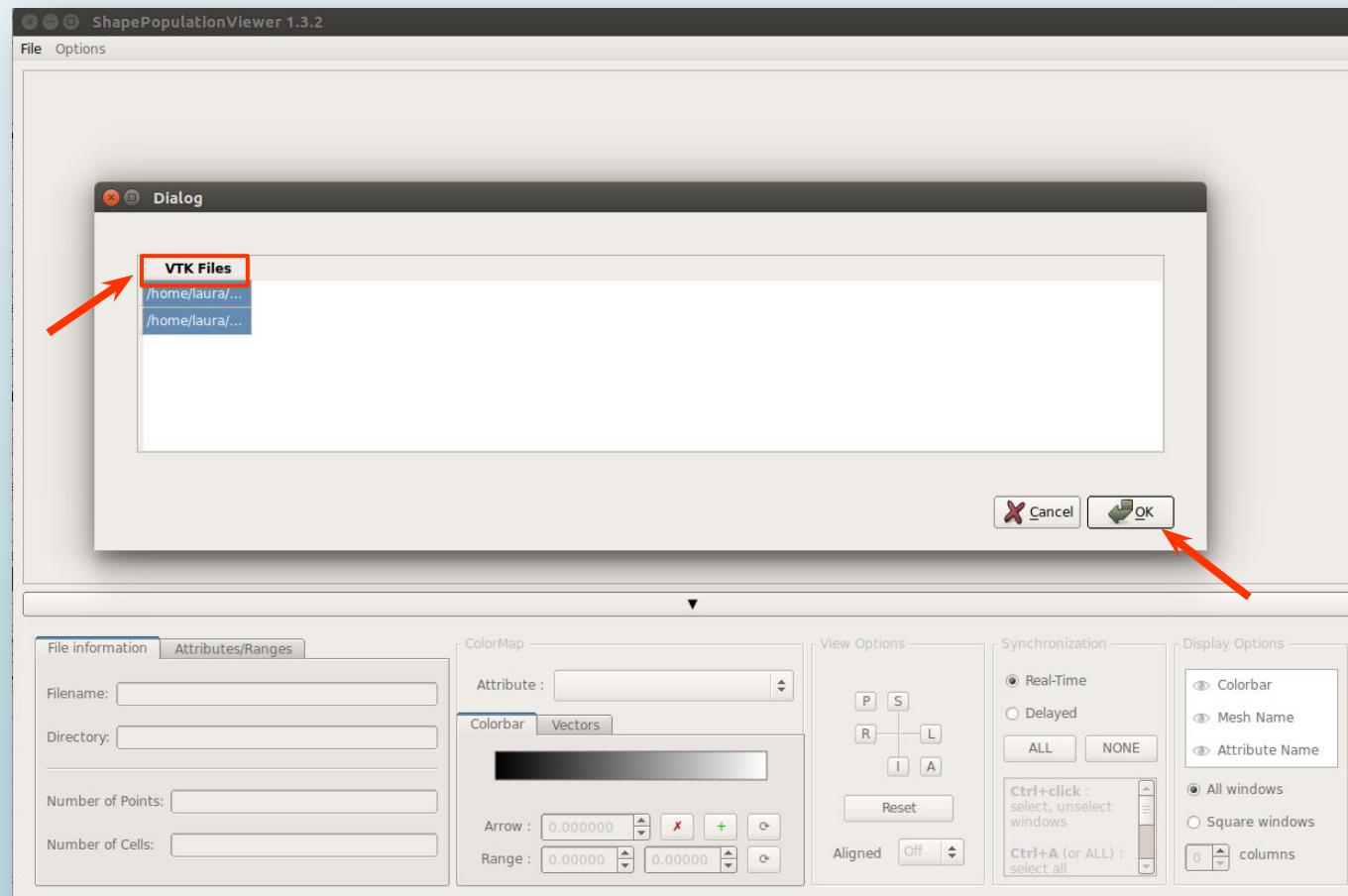
Quality control using ShapePopulationViewer

1 Run *Shape Population Viewer* by clicking on the *Shape Population Viewer* button:



Quality control using ShapePopulationViewer

To display the selected models in *Shape Population Viewer*, click on *VTK Files* and then *Ok*:



Quality control using ShapePopulationViewer

To display the different color maps on the meshes, use the comboBox Attributes:

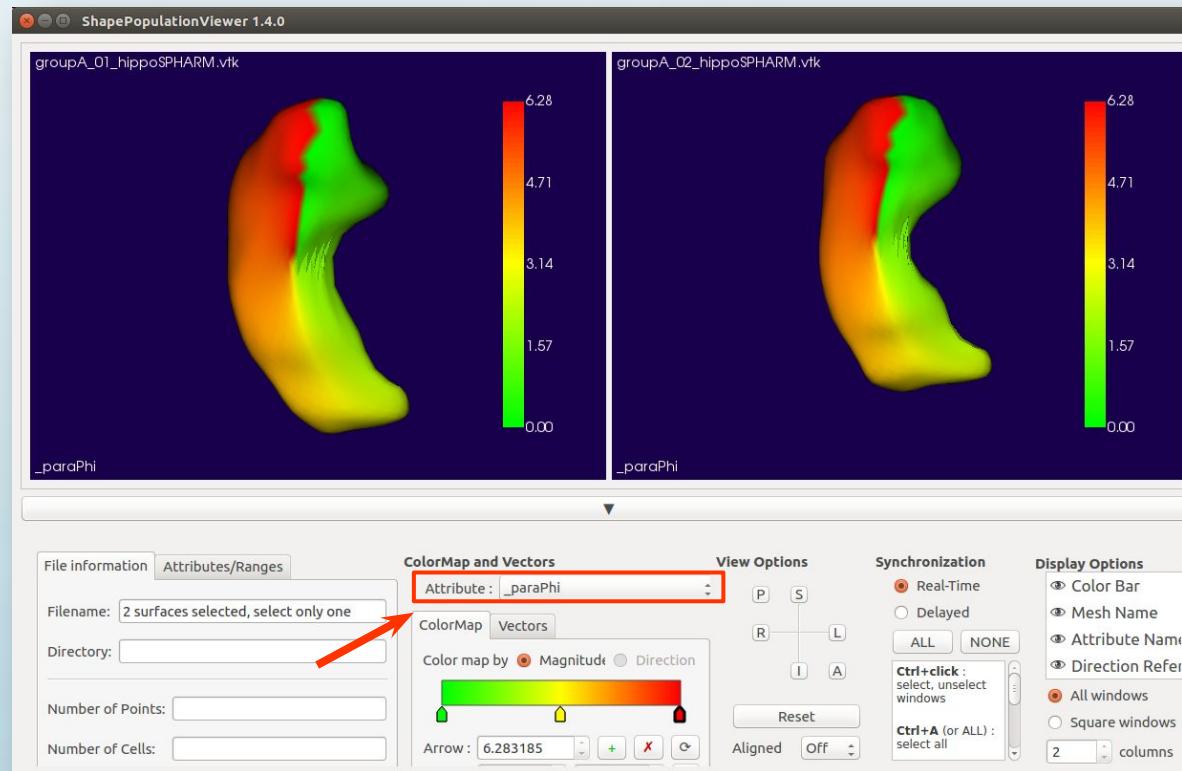


Figure: Visualization in ShapePopulationViewer of two *SPHARM models with the phi spherical parameter representation

Quality control using ShapePopulationViewer

Example: This view shows the phi correspondences between the files.

- Quality control of the correspondences is performed using the color-coded parameterization information.
- Equally colored areas represent equal corresponding area.

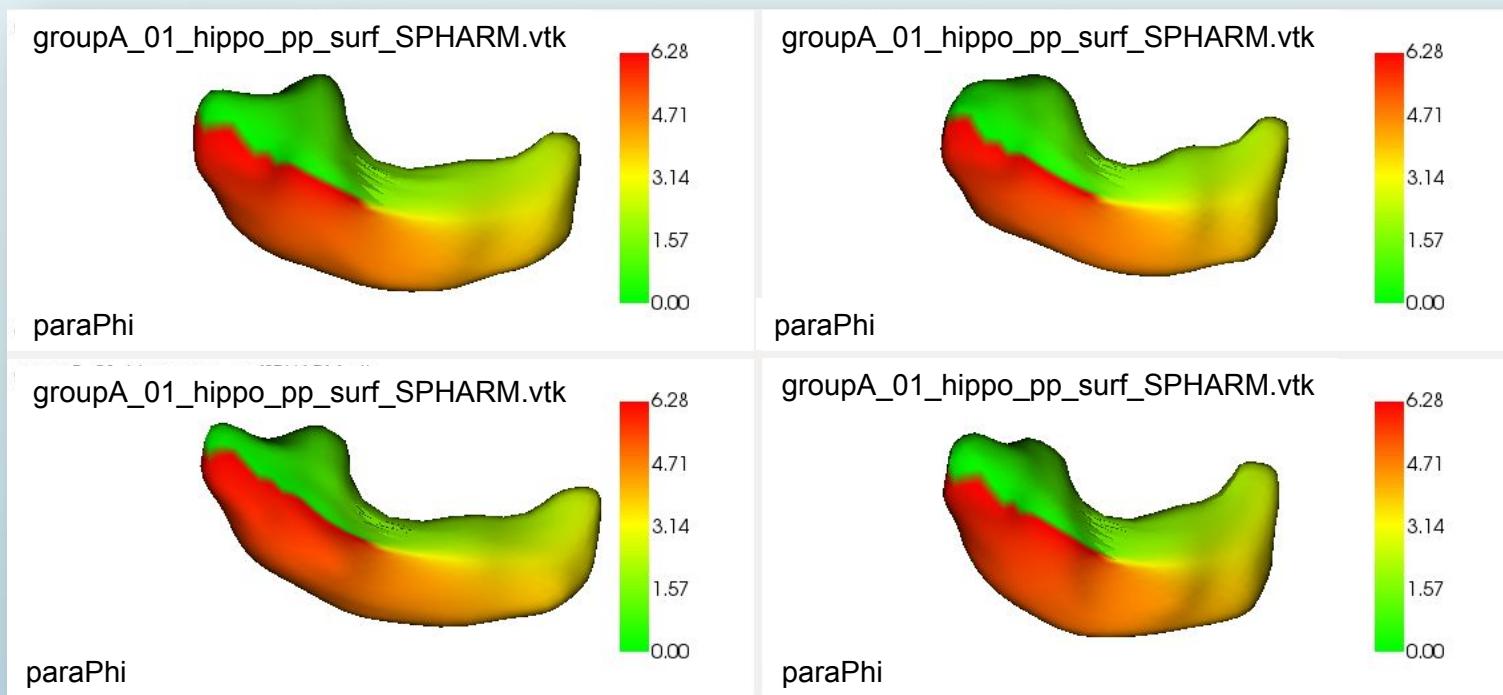


Figure: Visualization in ShapePopulationViewer of multiples *SPHARM shapes displaying paraPhi color map

Quality control using ShapePopulationViewer

Only data sets with Procrustes alignment information are automatically aligned in *Shape Population Viewer*.

For data sets without Procrustes alignment:

- Under *View Options*, set *Aligned* to **On** to align the data set using file information.



Quality control using ShapePopulationViewer

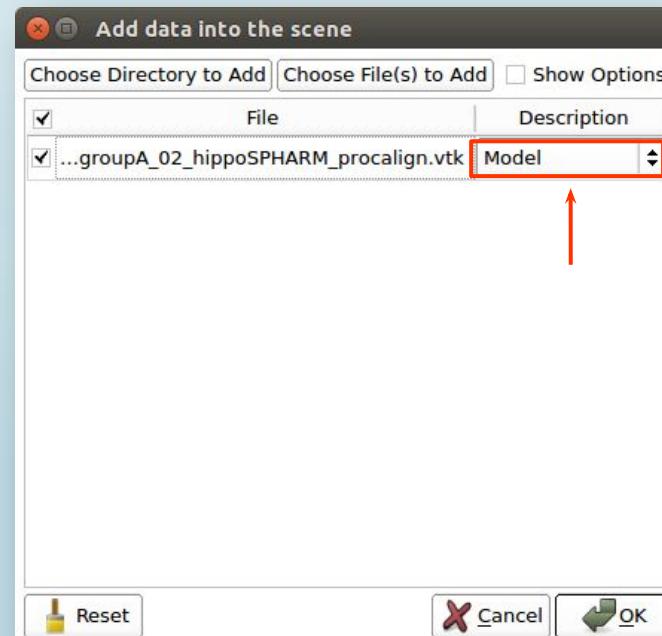
For more information about using *Shape Population Viewer* tool,
consult the [ShapePopulationViewer tutorial](#) by Alexis Girault.

Quality control using *Models* module

Models can be viewed in *3D Slicer* or *SlicerSALT* by dragging and dropping the files or by using the *Data* button in the toolbar to search for the file.



When importing the VTK file, select the *Model* Option :



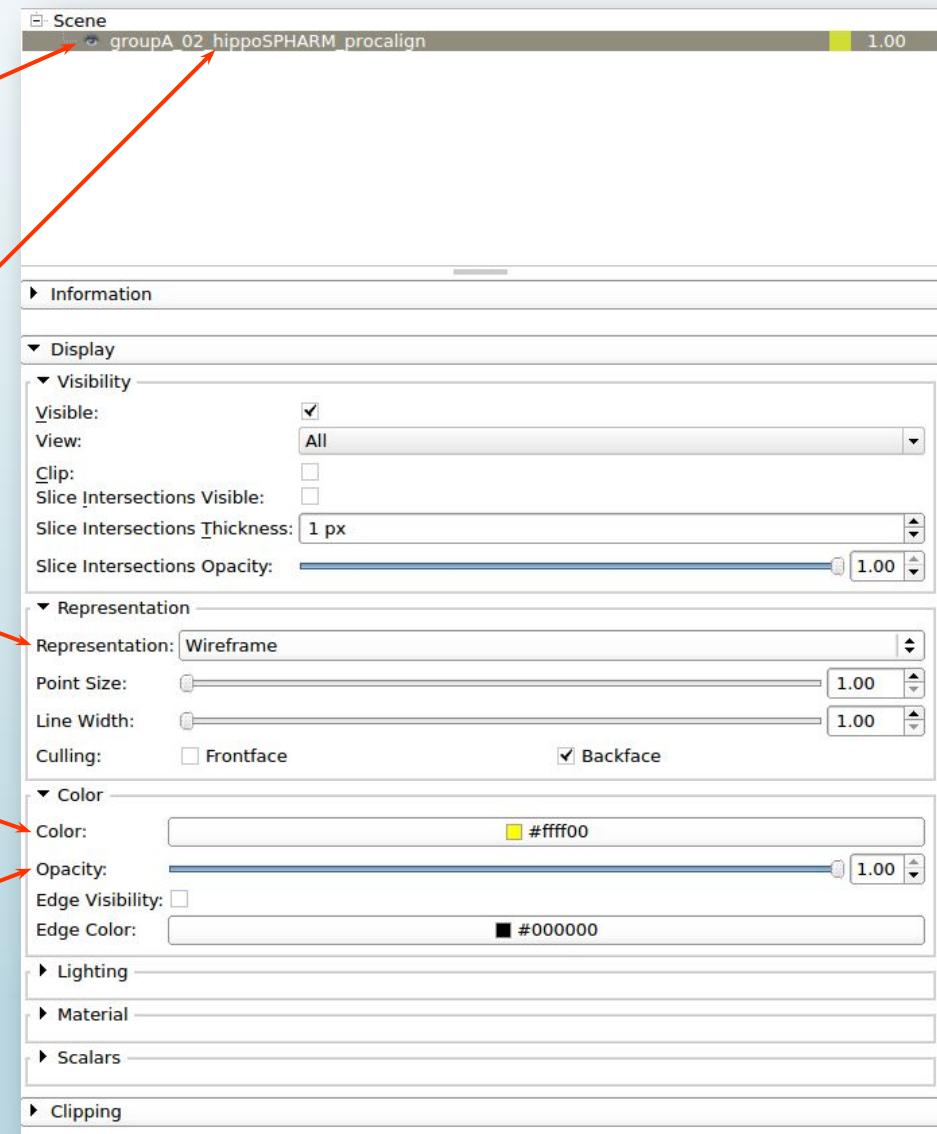
Quality control using *Models* module

When the VTK file has been imported, it will be visualized in the *Scene View* (or the *3D View*). Switch to the ***Models*** Module to change the display settings of the VTK model.



Quality control using Models module

- Hide/show the model by clicking on the eye icon
- To change the display properties of the VTK file, first select the file from the *Scene window* in the *Models Module*
- Change the representation of the model mesh. For example, *Wireframe* representation will display the meshing of the model
- Change the color of the mesh from the default gray color
- Change the opacity of the mesh



Acknowledgements - Resources - Questions

- The SPHARM-PDM developers gratefully acknowledge funding for this project provided by NIH NIBIB R01EB021391 (Shape Analysis Toolbox for Medical Image Computing Projects), as well as the Slicer community.
- Github repository:
 - [SPHARM-PDM](#)
 - [SlicerSALT](#)
 - [3D Slicer](#)
- Forums:
 - [SlicerSALT](#)
 - [3D Slicer](#)
- Papers:
 - [Lateral ventricle morphology analysis via mean latitude axis.](#)
 - [Framework for the Statistical Shape Analysis of Brain Structures using SPHARM-PDM](#)
- For other remarks or questions, please email:
 - laura.pascal@kitware.com

