SPHARM-MAT Documentation

Release 1.0.0

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CONTENTS

CHAPTER

ONE

INTRODUCTION

1.1 License

SPHARM-MAT uses GNU General Public License (GPL). The license description is included in the software package. Please review and accept the license before installing SPHARM-MAT via any source.

1.2 Download and Installation

Software

Available at http://www.iu.edu/~spharm/.

Documentation

HTML: http://www.iu.edu/~spharm/SPHARM-docs/

PDF: http://www.iu.edu/~spharm/SPHARM-MAT.pdf

1.2.1 Install SPHARM-MAT

Download The SPHARM-MAT package is available at http://www.iu.edu/~spharm/.

Install Unzip the package and move the folder to an appropriate place, denoted as `SpharmMatDir` in the rest of the documentation. There are three subfolders under `SpharmMatDir`:

1. `SpharmMatDir/code/`: SPHARM-MAT code
2. `SpharmMatDir/code/license`: License description
3. `SpharmMatDir/data/`: Test data used in the tutorial
4. `SpharmMatDir/scripts/`: Command line scripts for running all the exercises under Matlab

Launch To start SPHARM-MAT, run `SpharmMatDir/code/SPHARM_MAT.m` under Matlab.

Build C mex (optional) The released package includes the precompiled mex files (“LocalSmoothing” and “simple”). However, they may not work on different computing environment from where they were compiled. Therefore, to make sure that they work on your computer, you can compile LocalSmoothing.c and simple.c, located in `SpharmMatDir/code/C_sources` and copy the mex files to `SpharmMatDir/code`.

How to compile simple.c

- On any platform

```
mex simple.c
```

How to compile LocalSmoothing.c

- If you are using the Lcc compiler that ships with MATLAB on MS Windows OS:

  ```
  mex LocalSmoothing.c matlabroot/extern/lib/win32/lcc/libmwlapack.lib
  matlabroot/extern/lib/win32/lcc/libmwblas.lib
  ```

- If you are using Microsoft Visual C++ as your C compiler on MS Windows OS:

  ```
  mex LocalSmoothing.c matlabroot/extern/lib/win32/microsoft/libmwlapack.lib
  matlabroot/extern/lib/win32/microsoft/libmwblas.lib
  ```

  or

  ```
  mex LocalSmoothing.c matlabroot/extern/lib/win64/microsoft/libmwlapack.lib
  matlabroot/extern/lib/win64/microsoft/libmwblas.lib
  ```

- On other platform:

  ```
  mex LocalSmoothing.c -lmwlapack -lmwblas
  ```

1.2.2 Install SPHARM-PDM

Recommended It is highly recommended to install SPHARM-PDM if you want to process voxel surfaces. Be aware of the difference in area distortion calculation between a voxel surface and its corresponding triangulation; see *ADC Calculation for Voxel Surface and Its Triangulation*.

Download SPHARM-PDM is available at http://www.nitrc.org/projects/spharm-pdm

Configure SPHARM-MAT for connecting it to SPHARM-PDM.

1. Run SPHARM_MAT.m
2. Select Tools->Config
3. In the "Configuration" window, set "PDM_path_pc" or "PDM_path_unix"
4. You only need to do this ONCE unless the PDM_path changes
5. You should make sure that SPHARM-PDM is working correctly

1.3 SPHARM-MAT Overview

1.3.1 SPHARM Method

SPHARM-MAT is implemented based on a powerful 3D Fourier surface representation method called SPHARM [Brechb1995], which creates parametric surface models using spherical harmonics. Spherical harmonics were first used as a type of parametric surface representation for radial or stellar surfaces $r(\theta, \phi)$. An extended method, called SPHARM, was proposed by [Brechb1995] to model more general shapes, where three functions of θ and ϕ were used to represent a surface. SPHARM is a widely used shape description method for arbitrarily shaped but simply connected 3D objects. It is suitable for surface comparison and can deal with protrusions and intrusions. It is a fine-scale global descriptor with several advantages, including inherent interpolation, accurate scaling, and implicit correspondence. It can be used to derive other widely used shape descriptors such as landmarks, deformation fields, and medical axes. In addition, SPHARM has been successfully applied to many applications in medical imaging.

SPHARM is essentially a Fourier transform technique that defines a 3D surface using three spherical functions and transforms them into three sets of Fourier coefficients in the frequency domain. Three steps are involved to obtain a SPHARM shape descriptor:

1. **Spherical parameterization** creates a continuous and uniform mapping from the object surface to the surface of a unit sphere, and its result is a bijective mapping between each point $\mathbf{v}$ on a surface and a pair of spherical coordinates θ and ϕ: $\mathbf{v}(\theta,\phi) = (x(\theta,\phi), y(\theta,\phi), z(\theta,\phi))^T$.
2. **SPHARM expansion** expands the object surface into a complete set of spherical harmonic basis functions Y_l^m, where Y_l^m denotes the spherical harmonic of degree l and order m and it is essentially a Fourier basis function defined on the sphere. The expansion takes the form: $\mathbf{v}(\theta,\phi) = \sum_{l=0}^{\infty}\sum_{m=-l}^{l} \mathbf{c}_l^m Y_l^m(\theta,\phi)$, where $\mathbf{v}(\theta,\phi) = (x(\theta,\phi), y(\theta,\phi), z(\theta,\phi))^T$ and $\mathbf{c}_l^m = (c_{xl}^m, c_{yl}^m, c_{zl}^m)^T$. The Fourier coefficients $\mathbf{c}_l^m$ up to a user-desired degree can be estimated by solving a linear system. The object surface can be reconstructed using these coefficients, and using more coefficients leads to a more detailed reconstruction.
3. **SPHARM alignment** creates a shape descriptor (i.e., excluding translation, rotation, and scaling) from a normalized set of SPHARM coefficients, which are comparable across objects. The first two steps are necessary for modeling an individual shape, while the third step is mainly for group analysis.

1.3.2 SPHARM-MAT, SPHARM-PDM, SurfStat

SPHARM-PDM [Styner2006] is an existing SPHARM shape analysis tool and is a part of the NA-MIC toolkit. SPHARM-MAT (SPHARM Modeling and Analysis Toolkit) is a synergistic effort to SPHARM-PDM. While SPHARM-PDM is implemented in C/C++, SPHARM-MAT is Matlab-based. The advantage of having an additional tool on a different platform is twofold: (1) flexibility for users to choose the platform they favor, and (2) opportunity for tool comparison and cross-validation. Compared with SPHARM-PDM, SPHARM-MAT has a few additional features summarized below.

1. **Spherical parameterization**: SPHARM-MAT implements the conventional spherical parameterization procedure proposed in [Brechb1995], which can be applied only to voxel surfaces. However, 3D surfaces are in general represented as triangular meshes. SPHARM-MAT implements a spherical parameterization algorithm that makes the SPHARM model applicable to general triangle meshes.
2. **SPHARM expansion**: The SPHARM coefficients computed by SPHARM-MAT are complex numbers. The SPHARM coefficients computed by SPHARM-PDM are real numbers, where the imaginary part of each coefficient is ignored.
3. **SPHARM alignment**: Typical SPHARM registration implemented in SPHARM-PDM uses the first order ellipsoid (FOE) for establishing surface correspondence and aligning objects, which may not be sufficient in some cases. In addition to FOE alignment, SPHARM-MAT implements SHREC, an efficient and general-purpose surface matching method for registering 3D SPHARM models.

SPHARM-MAT includes a few components (in both GUI and command line) that interface with SPHARM-PDM. It is highly recommended to install SPHARM-PDM if you want to parameterize voxel surfaces.

SPHARM-MAT contains two simple statistical components for group analysis. For more complicated statistical models, we suggest that SurfStat [Worsley2008] should be considered. Surfstat is a free software tool which performs statistical analysis of univariate and multivariate surface and volumetric data using linear mixed effects models and random field theory. Since SurfStat is also matlab-based, it is straightforward to integrate SurfStat with SPHARM-MAT for statistical surface analysis. For example, one can first use SPHARM-MAT to model and align surfaces and extract surface signals, and then use SurfStat for statistical inference on the surface.

1.4 Documentation Overview

1.4.1 Tutorial and Processing Pipeline

A set of exercises are provided in the following six chapters to serve as a tutorial for showing how to use SPHARM-MAT. While the last chapter shows a few miscellaneous functions, the first five chapters naturally form the processing pipeline of SPHARM-MAT.

- *Data Preparation*: Preprocess 3D binary image data.
- *Spherical Parameterization*: Map object surface onto sphere with distortion minimization.
- *SPHARM Expansion*: Expand the surface into spherical harmonic representation.
- *Surface Alignment*: Align all SPHARM models together for subsequent group analysis.
- *Statistical Analysis*: Perform statistical shape analysis.
- *Other Utilities*: Demonstrate a few other SPHARM-MAT utilities.

After completing all the exercises in these chapters, you should have a basic idea on how SPHARM-MAT works.

1.4.2 Command Line and Batch Processing

All the exercises are designed for using the graphical user interface (GUI). However, for each exercise, we have put together a command line script in `SpharmMatDir/scripts/`. Running this script completes the same task in the batch mode. So if you don't want to work with the GUI, you can modify these command line scripts to form your own batch processing task.

1.4.3 System Features

Besides the tutorial, we also provide the following chapters with system relevant features.

- *System Components and Features*: Organized based on GUI components.
- *Tips*: Useful tips.
- *Changes*: Keep track of changes.
- *Bibliography*: Reference information.

1.4.4 Data Structure

We summarize our naming convention for various data files as follows.

`*_bim.mat`: 3D binary objects

- bim: binary image
- origin: coordinates of voxel (1,1,1)
- vxsize: voxel size

`*_fix.mat`: 3D binary objects after topology fix

- bim: binary image
- origin: coordinates of voxel (1,1,1)
- vxsize: voxel size

`*_obj.mat`: original surface meshes

- vertices: vertices on the surface
- faces: mesh elements

`*_ini.mat`: surface mesh after initial parameterization

- vertices: vertices on the surface
- faces: mesh elements
- sph_verts: spherical mapping of vertices
- dateline: date line on the sphere ($\phi = 0$)
- landmarks: vertices of north, south, east, and west on the sphere

`*_smo.mat`: surface mesh after optimized parameterization

- vertices: vertices on the surface
- faces: mesh elements
- sph_verts: spherical mapping of vertices
- measure: distortion measures of the parameterization

`*_des.mat`: surface mesh with SPHARM coefficients

- vertices: vertices on the original surface (or vertices on the SPHARM-PDM reconstruction if the file is converted from SPHARM-PDM result)
- faces: mesh elements
- sph_verts: spherical mapping of vertices
- fvec: SPHARM coefficients (complex numbers)

`*_prm.mat`: surface mesh with SPHARM coefficients after FOE alignment in the parameter space

- vertices: vertices on the surface
- faces: mesh elements
- sph_verts: spherical mapping of vertices
- fvec: SPHARM coefficients (complex numbers)

`*_reg.mat`: surface mesh with SPHARM coefficients after registration

- vertices: vertices on the registered surface (not available for SHREC results)
- faces: mesh elements (not available for SHREC results)
- sph_verts: spherical mapping of vertices (not available for SHREC results)
- fvec: registered SPHARM coefficients (complex numbers)

`t_map*.mat`: Data and results for t-test

- atlas_vertices: vertices on the atlas surface
- faces: mesh elements
- sph_verts: spherical mapping of atlas_vertices
- grInfo: group ID for each subject
- groupID: annotation for each group ID
- pvalue: vertex-wise p values
- tstats: vertex-wise t values
- signal: description of the signal

- vtnorm: surface normals
- FWHM: size of heat kernel used for surface signal smoothing

`PCA_stat*.mat`: Data and results for PCA analysis

- eigenvals: eigenvalues
- eigenvecs: eigenvectors
- fvecs: a set of SPHARM coefficients
- groupID: group ID
- scores: principal component (PC) scores
- perc_variance_explained: percentage of data variance explained by each PC
- cum_percent_explained: cumulated percentage of data variance explained by the first n PCs

`*.gipl`: 3D binary objects in GIPL format

- Used by SPHARM-PDM: see *Exercise 2.2: SPHARM-PDM Topology Fix*
- See also *Format Conversion for Binary Objects*

`*.meta`: surface mesh in META format

- Used by SPHARM-PDM: see *Exercise 3.3 Voxel Surfaces (PDM)*
- See also *Format Conversion for Surface Meshes*
- See also *Format Conversion for SPHARM Models*

`*.coef`: SPHARM coefficients (real parts kept, imaginary parts ignored)

- Used by SPHARM-PDM: see *Exercise 4.2 SPHARM-PDM Expansion*
- See also *Format Conversion for SPHARM Models*

1.5 Team and Contact

The first release of SPHARM-MAT was primarily supported by the following award:

```
NIH/NIBIB R03 EB008674 SPHARM Shape Modeling and Analysis Toolkit for Brain Imaging
PI: Li Shen, Co-PI: Andrew J. Saykin
```

The project was developed at:

```
The IU Center for Neuroimaging (CfN)
The Center for Computational Biology and Bioinformatics (CCBB)
Indiana University School of Medicine (IUSM).
```

The following people contributed to the development, testing and documentation of various components of SPHARM-MAT:

```
Major developers: Li Shen, Sungeun Kim
Other contributors: Jing Wan, John D. West, Kiernan McCullough,
                    Thomas Councell, Andrew J. Saykin
Collaborators at UT Arlington: Heng Huang, Fillia Makedon
Collaborator at UW Madison: Moo K. Chung
```

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```

Question about SPHARM-MAT or bug reporting:

```
SpharmMat@gmail.com
```

CHAPTER

TWO

DATA PREPARATION

This step is designed for preprocessing 3D binary image data. If your data are surface meshes, you can ignore this step.

In medical imaging domain, many structures of interest are obtained by manual or automated segmentation from volumetric scans (e.g., MRI, CT, etc.), and are often described as 3D binary images. This data preparation step deals with how to remove noises (e.g., 3D holes, bad edge connectivity, bad vertex connectivity, etc) in a 3D binary object so that its voxel surface has a spherical topology. Note that SPHARM-MAT can be used to model arbitrarily shaped but simply connected 3D objects. That is, the object surface needs to have a spherical topology (i.e., genus-zero surface).

If there are small vacancies or discontinuities between image voxels, they can be repaired using the “TopologyFix” tool which will remove any possible sources of error without significantly altering the original image. SPHARM-MAT has two options to do the topology fix: (1) an in-house tool (see *Exercise 2.1: In-house Topology Fix* for a demo), and (2) an alternative tool integrated from SPHARM-PDM (see *Exercise 2.2: SPHARM-PDM Topology Fix* for a demo).

2.1 Exercise 2.1: In-house Topology Fix

This exercise was tested on a WinXP machine (3GHz CPU, 3.25G RAM) running Matlab 7.7.0 (R2008b). It took a few minutes to finish.

Major Steps

1. Topology Fix
2. Binary Object Visualization (Solid with Mesh)

2.1.1 Topology Fix

Task

Fix the topology of a set of 3D binary objects so that their voxel surfaces have a spherical topology

Input

`SpharmMatDir/data/Ex0201/hip01_bim/*_bim.mat`

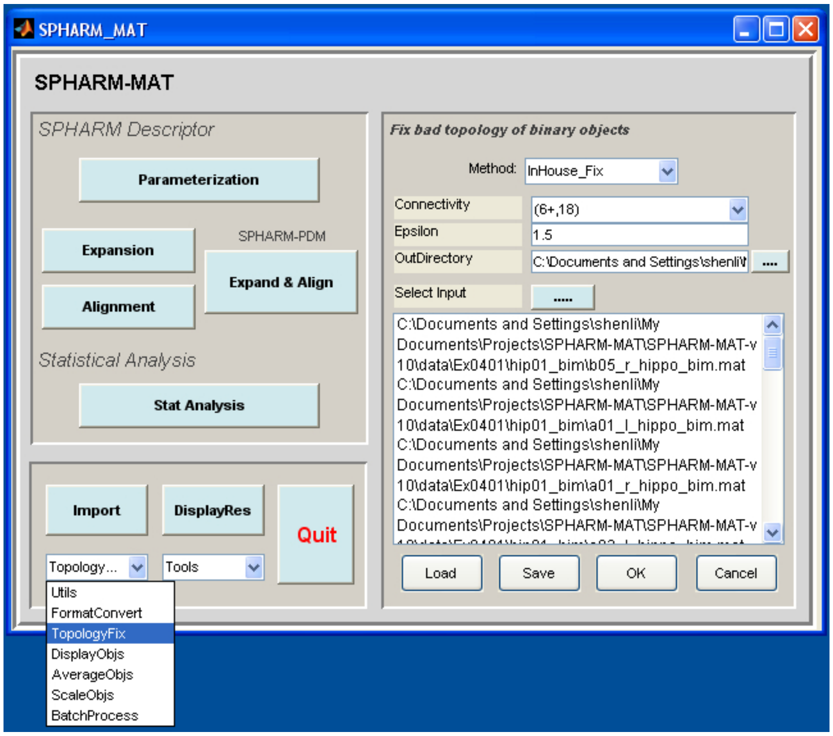
Output

`SpharmMatDir/data/Ex0201/hip02_fix/*_fix.mat`

Steps

1. Run **SPHARM_MAT.m** under Matlab
2. Select **TopologyFix** under the **Utils** pop-up menu (bottom-left corner)

3. In the right panel, let **Method** be *InHouse_Fix*
4. Make an output directory `SpharmMatDir/data/Ex0201/hip02_fix`
5. In the right panel, select `SpharmMatDir/data/Ex0201/hip02_fix` as **OutDirectory**
6. In the right panel, click `.....` button next to **Select Input**, and select all the *_bim.mat files under `SpharmMatDir/data/Ex0201/hip01_bim` as input files
7. Click **OK** button (See *Screen Capture for In-House Topology Fix*)



Method: InHouse_Fix

Connectivity: (6+,18)

Epsilon: 1.5

OutDirectory: C:\Documents and Settings\shenli\

Select Input: .....

C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0401\hip01_bim\b05_r_hippo_bim.mat
C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0401\hip01_bim\a01_l_hippo_bim.mat
C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0401\hip01_bim\a01_r_hippo_bim.mat
C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v

Figure 2.1: Screen Capture for In-House Topology Fix

2.1.2 Binary Object Visualization (Solid with Mesh)

Task

Visualize the binary objects before and after topology fix

Input

`SpharmMatDir/data/Ex0201/hip01_bim/*_bim.mat` or

`SpharmMatDir/data/Ex0201/hip02_fix/*_fix.mat`

Output

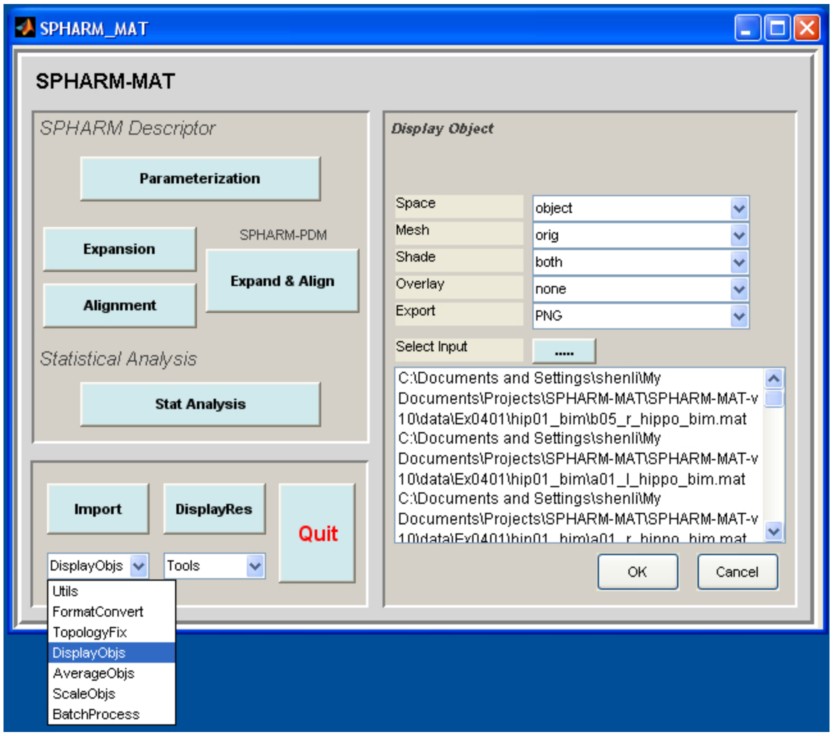
`SpharmMatDir/data/Ex0201/hip01_bim/PNG/*.png` or

`SpharmMatDir/data/Ex0201/hip02_fix/PNG/*.png`

Steps

1. Select **DisplayObjs** under the **Utils** pop-up menu (bottom-left corner)
2. In the right panel, let **Space** be *object*, **Mesh** be *orig*, **Shade** be *both*, **Overlay** be *none*, **Export** be *PNG*

3. In the right panel, click `.....` button next to **Select Input**, and select either all the `SpharmMatDir/data/Ex0201/hip01_bim/*_bim.mat` files or all the `SpharmMatDir/data/Ex0201/hip02_fix/*_fix.mat` as the input files
4. Click **OK** button (See *Screen Capture for Display Binary Objects (Solid with Mesh)*)



Space: object
Mesh: orig
Shade: both
Overlay: none
Export: PNG
Select Input: .....

```
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0401\hip01_bim\b05_r_hippo_bim.mat
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0401\hip01_bim\a01_l_hippo_bim.mat
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0401\hip01_bim\a01_r_hippo_bim.mat
```

Figure 2.2: Screen Capture for Display Binary Objects (Solid with Mesh)

Notes

- The visualization results are saved as PNG files under `SpharmMatDir/data/Ex0201/hip01_bim/PNG` and `SpharmMatDir/data/Ex0201/hip01_fix/PNG`.
- A couple of examples are shown in *Binary Object Visualization (Solid with Mesh)*.

2.1.3 Relevant Information

Useful Tips

- *TopologyFix InHouse_Fix Option*
- *DisplayObjs Shade Option*
- *DisplayObjs Export Option*
- *Data Structure*
- *File Selection*

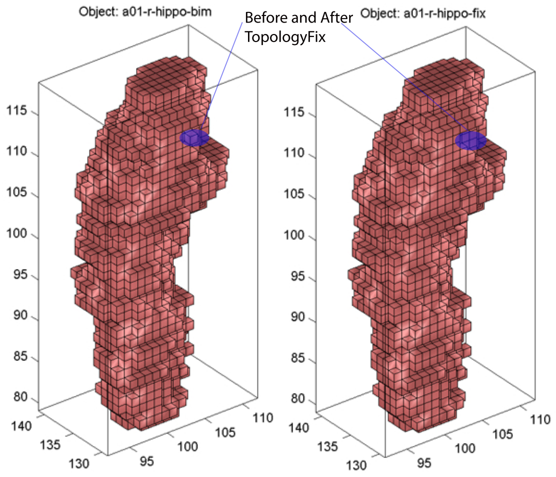


Figure 2.3: Binary Object Visualization (Solid with Mesh)

2.2 Exercise 2.2: SPHARM-PDM Topology Fix

This exercise was tested on a WinXP machine (3GHz CPU, 3.25G RAM) running Matlab 7.7.0 (R2008b) and SPHARM-PDM (WinXP-v1.3). It took a few minutes to finish. In order to run this exercise, you need to install the SPHARM-PDM package (see *Install SPHARM-PDM*).

Major Steps

1. Format Conversion bim2gipl
2. Topology Fix
3. Format Conversion gipl2bim
4. Binary Object Visualization (Mesh)

2.2.1 Format Conversion bim2gipl

Task

Convert matlab 3D binary image format to gipl format used by SPHARM-PDM

Input

`SpharmMatDir/data/Ex0202/hip01_bim/*_bim.mat`

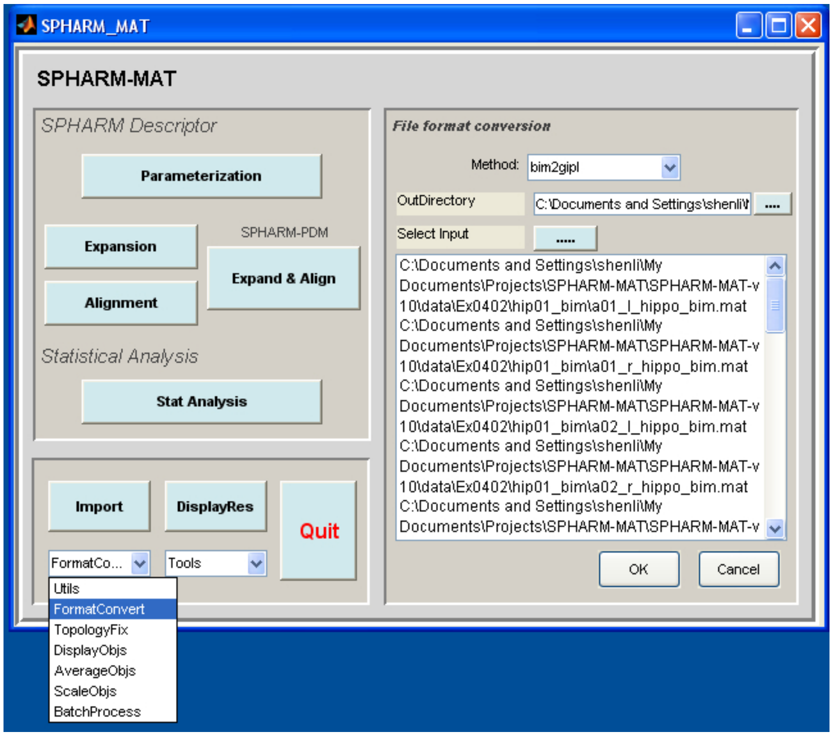
Output

`SpharmMatDir/data/Ex0202/hip02_gipl/*.gipl`

Steps

1. Run **SPHARM_MAT.m** under Matlab
2. Select **FormatConvert** under the **Utils** pop-up menu (bottom-left corner)
3. In the right panel, let **Method** be *bim2gipl*
4. Make an output directory `SpharmMatDir/data/Ex0202/hip02_gipl`
5. In the right panel, select `SpharmMatDir/data/Ex0202/hip02_gipl` as **OutDirectory**

6. In the right panel, click `.....` button next to **Select Input**, and select all the *_bim.mat files under `SpharmMatDir/data/Ex0202/hip01_bim` as input files
7. Click **OK** button (See *Screen shot for Format Conversion bim2gipl.*)



Method: bim2gipl

OutDirectory: C:\Documents and Settings\shenli\

Select Input

```
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0402\hip01_bim\a01_l_hippo_bim.mat
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0402\hip01_bim\a01_r_hippo_bim.mat
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0402\hip01_bim\a02_l_hippo_bim.mat
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0402\hip01_bim\a02_r_hippo_bim.mat
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
```

Figure 2.4: Screen shot for Format Conversion bim2gipl.

2.2.2 Topology Fix

Task

Fix the topology of a set of 3D binary objects so that their voxel surfaces have a spherical topology

Input

`SpharmMatDir/data/Ex0202/hip02_gipl/*.gipl`

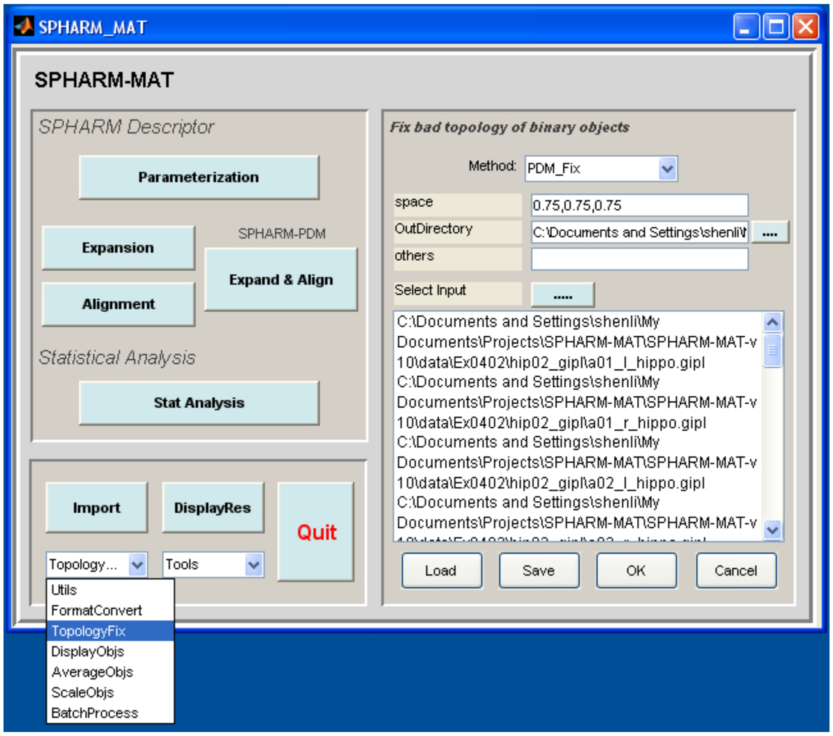
Output

`SpharmMatDir/data/Ex0202/hip03_gipl_fix/*_fix.gipl`

Steps

1. Run **SPHARM_MAT.m** under Matlab
2. Select **TopologyFix** under the **Utils** pop-up menu (bottom-left corner)
3. In the right panel, let **Method** be *PDM_Fix*
4. Make an output directory `SpharmMatDir/data/Ex0202/hip03_gipl_fix`
5. In the right panel, select `SpharmMatDir/data/Ex0202/hip03_gipl_fix` as **OutDirectory**
6. In the right panel, click `.....` button next to **Select Input**, and select all the *.gipl files under `SpharmMatDir/data/Ex0202/hip02_gipl` as input files

7. Click **OK** button (See *Screen Shot for SPHARM-PDM Topology Fix*)



Method: PDM_Fix

space: 0.75,0.75,0.75

OutDirectory: C:\Documents and Settings\shenli\

others:

C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0402\hip02_gipl\a01_l_hippo.gipl
C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0402\hip02_gipl\a01_r_hippo.gipl
C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0402\hip02_gipl\a02_l_hippo.gipl
C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v

Figure 2.5: Screen Shot for SPHARM-PDM Topology Fix

2.2.3 Format Conversion gipl2bim

Task

Convert gipl format used by SPHARM-PDM to matlab 3D binary image format

Input

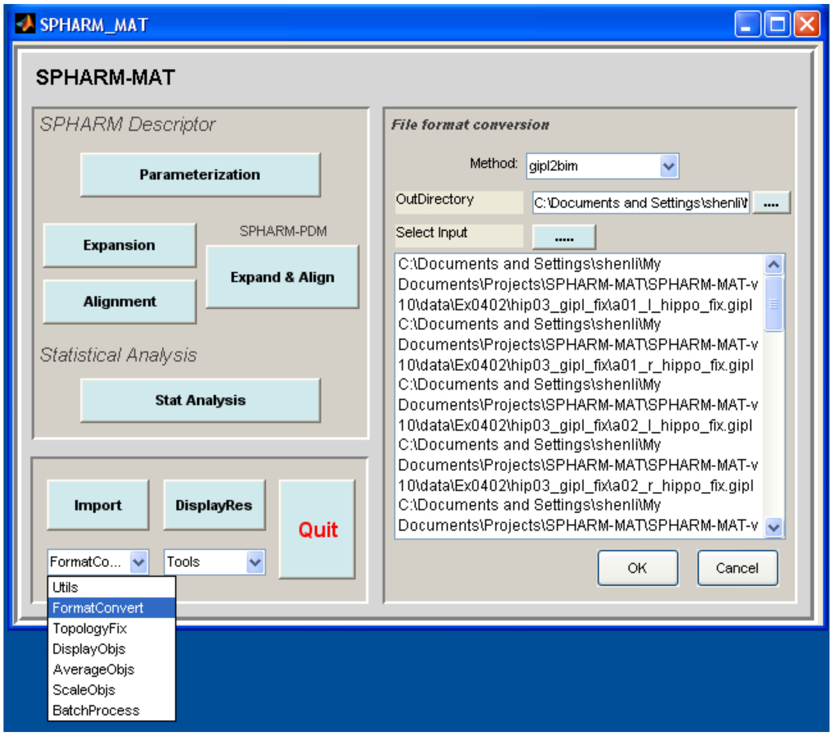
`SpharmMatDir/data/Ex0202/hip03_gipl_fix/*_fix.gipl`

Output

`SpharmMatDir/data/Ex0202/hip04_fix/*_fix.mat`

Steps

1. Run **SPHARM_MAT.m** under Matlab
2. Select **FormatConvert** under the **Utils** pop-up menu (bottom-left corner)
3. In the right panel, let **Method** be *gipl2bim*
4. Make an output directory `SpharmMatDir/data/Ex0202/hip04_fix`
5. In the right panel, select `SpharmMatDir/data/Ex0202/hip04_fix` as **OutDirectory**
6. In the right panel, click `.....` button next to **Select Input**, and select all the *_fix.gipl files under `SpharmMatDir/data/Ex0202/hip03_gipl_fix` as input files
7. Click **OK** button (See *Screen shot for Format Conversion gipl2bim*)



```
Method: gipl2bim
OutDirectory C:\Documents and Settings\shenli\
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0402\hip03_gipl_fix\a01_l_hippo_fix.gipl
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0402\hip03_gipl_fix\a01_r_hippo_fix.gipl
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0402\hip03_gipl_fix\a02_l_hippo_fix.gipl
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0402\hip03_gipl_fix\a02_r_hippo_fix.gipl
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
```

Figure 2.6: Screen shot for Format Conversion gipl2bim

2.2.4 Binary Object Visualization (Mesh)

Task

Visualize the binary objects before and after topology fix

Input

`SpharmMatDir/data/Ex0202/hip01_bim/*_bim.mat` or

`SpharmMatDir/data/Ex0202/hip04_fix/*_fix.mat`

Output

`SpharmMatDir/data/Ex0202/hip01_bim/PNG/*.png` or

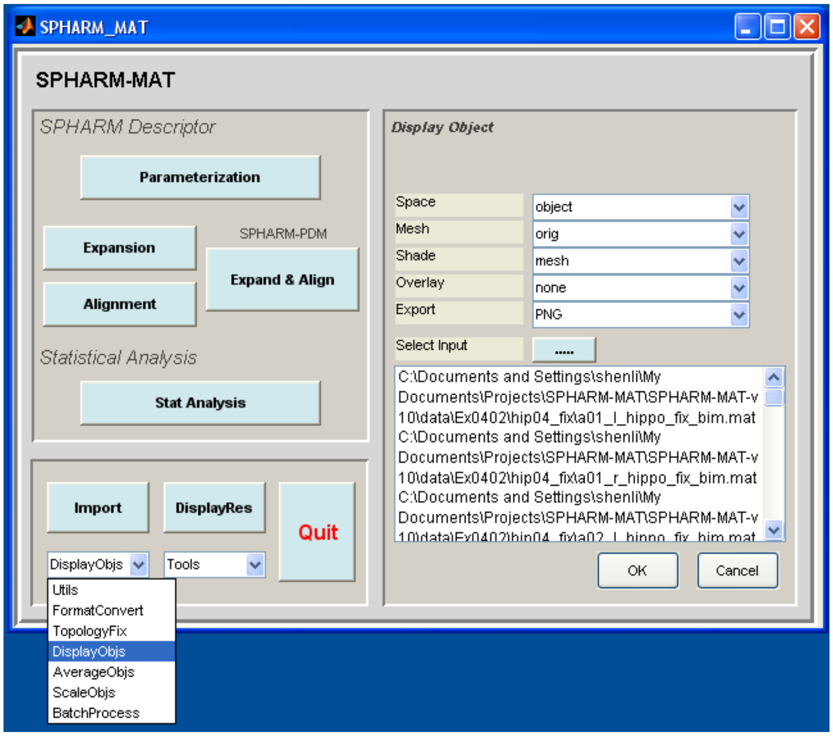
`SpharmMatDir/data/Ex0202/hip04_fix/PNG/*.png`

Steps

1. Select **DisplayObjs** under the **Utils** pop-up menu (bottom-left corner)
2. In the right panel, let **Space** be *object*, **Mesh** be *orig*, **Shade** be *both*, **Overlay** be *none*, **Export** be *PNG*
3. In the right panel, click `.....` button next to **Select Input**, and select either all the `SpharmMatDir/data/Ex0202/hip01_bim/*_bim.mat` files or all the `SpharmMatDir/data/Ex0202/hip04_fix/*_fix.mat` as the input files
4. Click **OK** button (See *Screen shot for Format Conversion gipl2bim*)

Notes

- The visualization results are saved as PNG files under `SpharmMatDir/data/Ex0202/hip01_bim/PNG` and `SpharmMatDir/data/Ex0201/hip04_fix/PNG`.



Space: object
Mesh: orig
Shade: mesh
Overlay: none
Export: PNG

```
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0402\hip04_fix\a01_l_hippo_fix_bim.mat
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0402\hip04_fix\a01_r_hippo_fix_bim.mat
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0402\hip04_fix\a02_l_hippo_fix_bim.mat
```

Figure 2.7: Display binary objects (mesh)

- A couple of examples are available in *Binary Object Visualization (Mesh)*.

2.2.5 Relevant Information

Notes

- In *Screen Shot for SPHARM-PDM Topology Fix*, the *space* option is set as *0.75 0.75 0.75* , meaning the voxel size for each resulting binary volume is 0.75-by-0.75-by-0.75. Therefore, these binary volumes are not only topologically fixed but also re-sliced by SPHARM-PDM; see *Binary Object Visualization (Mesh)* for a sample comparison before and after topology fix and reslicing.

Useful Tips

- *Format Conversion for Binary Objects*
- *TopologyFix PDM_Fix Option*
- *DisplayObjs Shade Option*
- *DisplayObjs Export Option*
- *Data Structure*
- *File Selection*

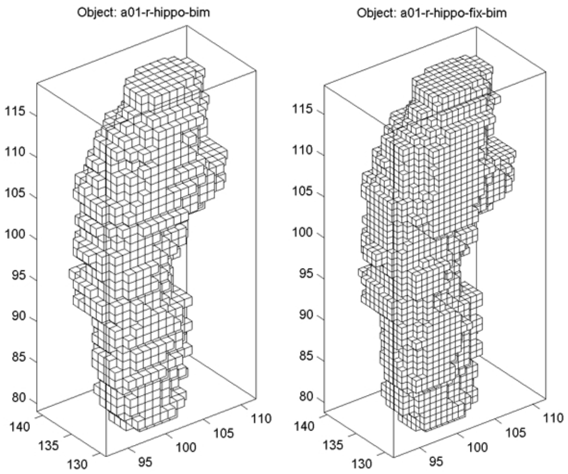


Figure 2.8: Binary Object Visualization (Mesh)

CHAPTER

THREE

SPHERICAL PARAMETERIZATION

Spherical parameterization creates a continuous and uniform mapping from the object surface to the surface of a unit sphere, and its result is a bijective mapping between each point $\mathbf{v}$ on a surface and a pair of spherical coordinates θ and ϕ:

$$\mathbf{v}(\theta, \phi) = (x(\theta, \phi), y(\theta, \phi), z(\theta, \phi))^T. \tag{3.1}$$

The spherical parameterization method proposed with the original SPHARM paper [Brechb1995] aimed to create an equal area mapping as well as minimize angle distortions by solving a constrained optimization problem, which was implemented in SPHARM-PDM [Styner2006]. This traditional method has been very effective in analyzing small and moderately-sized structures extracted from volumetric images (e.g., MRI, CT). However, it is applicable only to voxel surfaces. CALD [Shen2006] is a newer method that extends the traditional method and can be applied to general triangular meshes. In SPHARM-MAT, an enhanced version of CALD method is available for analyzing triangular meshes (see *Exercise 3.1 Surface Meshes (CALD)* and *Exercise 3.2 Voxel Surfaces (CALD)*). In addition, SPHARM-PDM can also be called from SPHARM-MAT for analyzing voxel surfaces (see *Exercise 3.3 Voxel Surfaces (PDM)*).

3.1 Area Distortion Cost

The concept of area distortion cost introduced by [Shen2006] is employed as the performance measure in the following exercises. Let $M = \{t_i\}$ be a surface mesh in the object space and let Ψ be its spherical parameterization, which maps M to the unit sphere $\Psi(M) = \{\Psi(t_i)\}$.

$A(\cdot)$ is used to denote the relative area of a triangle or a spherical triangle:

- For a triangle, its relative area is defined as its area divided by the total area of the object surface.
- For a spherical triangle, its relative area is defined as its area divided by 4π, the surface area of the unit sphere.

The area distortion cost (ADC) C_a with respect to Ψ is defined as follows:

- For each triangle $t_i \in M$,

  $$C_a(t_i, \Psi) = \frac{A(\Psi(t_i))}{A(t_i)}. \tag{3.2}$$

  This measures the local ADC of a single triangle.

- For the whole parametric mesh M,

  $$C_a(M, \Psi) = \frac{\sum_{t_i \in M} max(C_a(t_i, \Psi), \frac{1}{C_a(t_i, \Psi)})A(\Psi(t_i))}{A(\Psi(M))}. \tag{3.3}$$

This measures the overall ADC for the whole mesh. By taking

$$max\left(C_a(t_i,\Psi),\frac{1}{C_a(t_i,\Psi)}\right) \tag{3.4}$$

as the ADC contribution from each triangle, we treat contraction and expansion equally, and so always have $C_a(M,\Psi) \geq 1$.

3.2 Exercise 3.1 Surface Meshes (CALD)

This exercise was tested on a WinXP machine (3GHz CPU, 3.25G RAM) running Matlab 7.7.0 (R2008b). It took a few minutes to finish.

Major Steps

1. CALD Parameterization for Surface Meshes
2. Surface Visualization (ADC_ParaMap, Solid with Mesh)

3.2.1 CALD Parameterization for Surface Meshes

Task

Create spherical parameterization for surface meshes

Input

`SpharmMatDir/data/Ex0301/mesh01_obj/*_obj.mat`: An input surface needs to be genus zero (i.e., with spherical topology), and can be represented by a triangulation or a quadrilateral mesh.

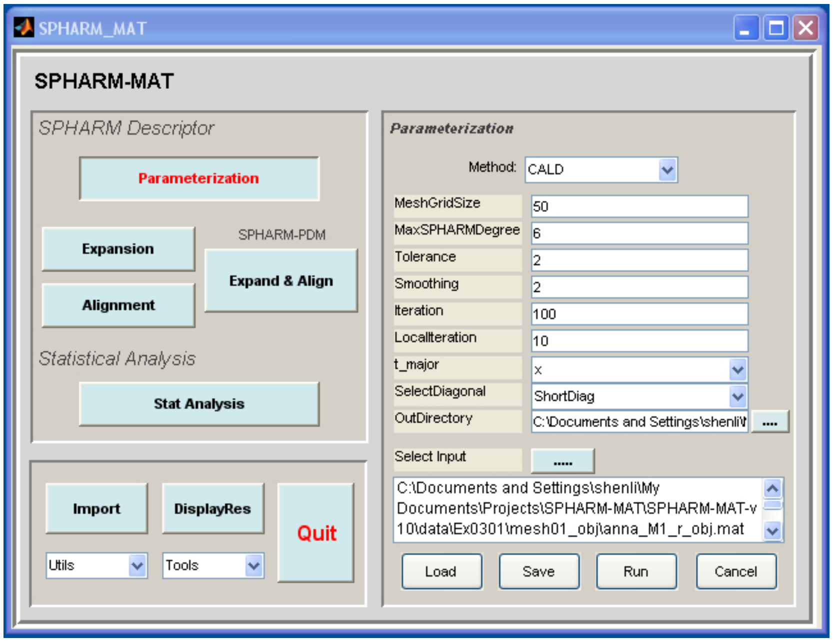
Output

`SpharmMatDir/data/Ex0301/mesh02_smo/initParamCALD/*_ini.mat`: Results of initial parameterization

`SpharmMatDir/data/Ex0301/mesh02_smo/*_smo.mat`: Results of optimized parameterization

Steps

1. Make an output directory `SpharmMatDir/data/Ex0301/mesh02_smo`
2. Run **SPHARM_MAT.m** under Matlab
3. Click **Parameterization** button
4. In the right panel, let **Method** be *CALD*
5. In the right panel, let **MeshGridSize** be *50*, **MaxSPHARMDegree** be *6*, **Tolerance** be *2*, **Smoothing** be *2*, **Iteration** be *100*, **LocalIteration** be *10*, **t_major** be *x*, **SelectDiagonal** be *ShortDiag*.
6. In the right panel, select `SpharmMatDir/data/Ex0301/mesh02_smo` as **OutDirectory**
7. In the right panel, click `.....` button next to **Select Input**, and select all the `*_obj.mat` files under `SpharmMatDir/data/Ex0301/mesh01_obj` as input files
8. Click **OK** button (See *Screen Capture for CALD Parameterization (Surface Mesh)*)



Method: CALD
MeshGridSize 50
MaxSPHARMDegree 6
Tolerance 2
Smoothing 2
Iteration 100
LocalIteration 10
t_major x
SelectDiagonal ShortDiag
OutDirectory C:\Documents and Settings\shenli\

C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v 10\data\Ex0301\mesh01_obj\anna_M1_r_obj.mat

Figure 3.1: Screen Capture for CALD Parameterization (Surface Mesh)

3.2.2 Surface Visualization (ADC_ParaMap, Solid with Mesh)

Task

Visualize surface meshes in both object and parameter spaces

Input

`SpharmMatDir/data/Ex0301/mesh02_smo/*_smo.mat` or

`SpharmMatDir/data/Ex0301/mesh02_smo/initParamCALD/*_ini.mat`

Output

`SpharmMatDir/data/Ex0301/mesh02_smo/PNG/*.png` or

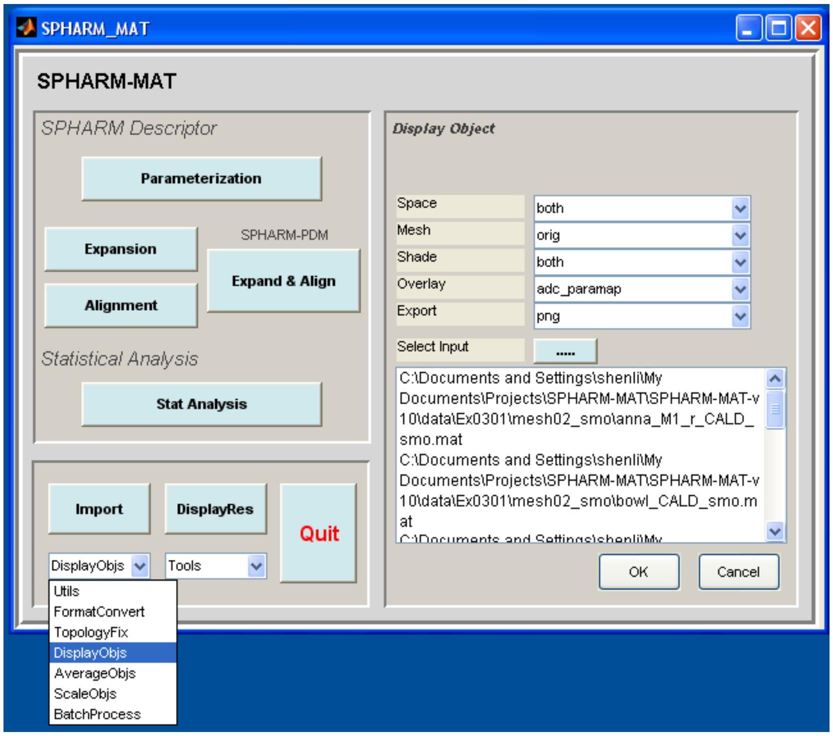
`SpharmMatDir/data/Ex0301/mesh02_smo/initParamCALD/PNG/*.png`

Steps

1. Select **DisplayObjs** under the **Utils** pop-up menu (bottom-left corner)
2. In the right panel, let **Space** be *both*, **Mesh** be *orig*, **Shade** be *both*, **Overlay** be *adc_paramap*, **Export** be *PNG*
3. In the right panel, click `.....` button next to **Select Input**, and select either all the `SpharmMatDir/data/Ex0301/mesh02_smo/PNG/*.png` files or all the `SpharmMatDir/data/Ex0301/mesh02_smo/initParamCALD/PNG/*.png` as the input files
4. Click **OK** button (See *Screen Capture for Surface Visualization (ADC_ParaMap, Solid with Mesh)*)

Notes

- The visualization results are saved as PNG files under `SpharmMatDir/data/Ex0301/mesh02_smo/PNG` and `SpharmMatDir/data/Ex0301/mesh02_smo/initParamCALD/PNG`.
- The results of initial parameterization and optimized parameterization for the head model are shown in *Surface Visualization (ADC_ParaMap, Solid with Mesh)*, where the ADC (area distortion cost) is defined in *Area Distortion Cost*.



Space: both
Mesh: orig
Shade: both
Overlay: adc_paramap
Export: png

C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0301\mesh02_smo\anna_M1_r_CALD_smo.mat
C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0301\mesh02_smo\bowl_CALD_smo.mat
C:\Documents and Settings\shenli\My

Figure 3.2: Screen Capture for Surface Visualization (ADC_ParaMap, Solid with Mesh)

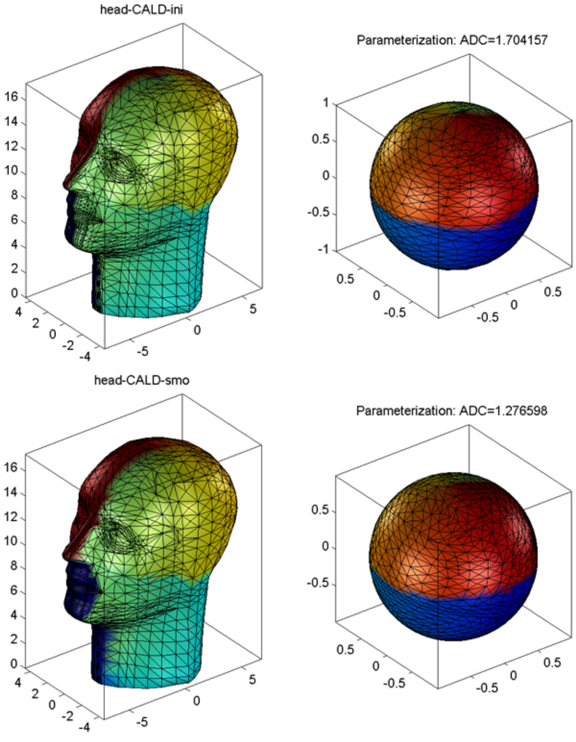


Figure 3.3: Surface Visualization (ADC_ParaMap, Solid with Mesh)

3.2.3 Relevant Information

Useful Tips

- *Parameterization CALD Input and Output*
- *Parameterization CALD Parameters*
- *DisplayObjs Space Option*
- *DisplayObjs Shade Option*
- *DisplayObjs Overlay Option*
- *DisplayObjs Export Option*
- *Data Structure*
- *File Selection*

3.3 Exercise 3.2 Voxel Surfaces (CALD)

This exercise was tested on a WinXP machine (3GHz CPU, 3.25G RAM) running Matlab 7.7.0 (R2008b). It took 10-20 minutes to finish.

Major Steps

1. CALD Parameterization for Voxel Surfaces
2. Surface Visualization (ADC_ParaMap, Mesh)

3.3.1 CALD Parameterization for Voxel Surfaces

Task

> Create spherical parameterization for voxel surfaces using CALD

Input

> `SpharmMatDir/data/Ex0302/hip02_fix/*_fix.mat`: This folder is a copy of `SpharmMatDir/data/Ex0201/hip02_fix/*_fix.mat`. The surface of an input binary object needs to be genus zero (i.e., with spherical topology).

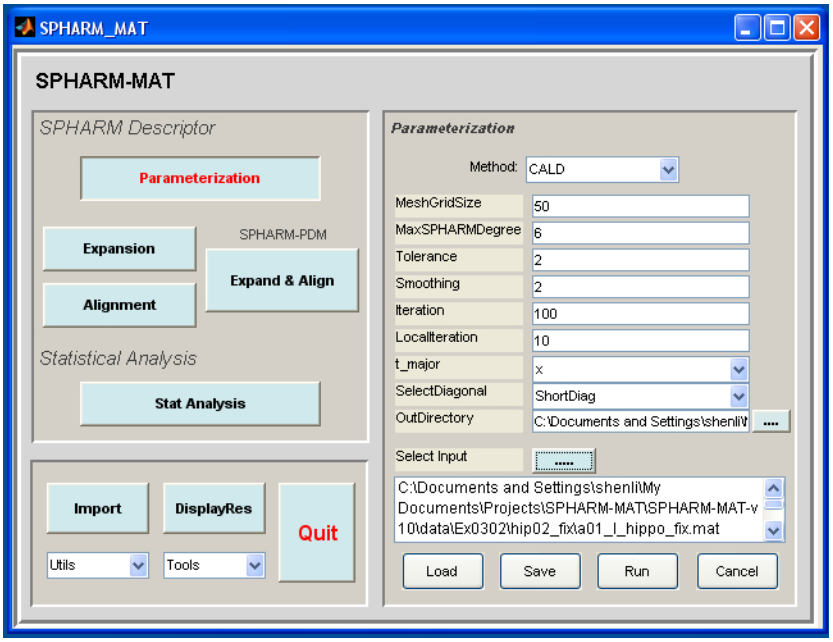
Output

> `SpharmMatDir/data/Ex0302/hip03_smo/initParamCALD/*_ini.mat`: Results of initial parameterization
>
> `SpharmMatDir/data/Ex0302/hip03_smo/*_smo.mat`: Results of optimized parameterization

Steps

1. Make an output directory `SpharmMatDir/data/Ex0302/hip03_smo`
2. Run **SPHARM_MAT.m** under Matlab
3. Click **Parameterization** button
4. In the right panel, let **Method** be *CALD*
5. In the right panel, let **MeshGridSize** be *50*, **MaxSPHARMDegree** be *6*, **Tolerance** be *2*, **Smoothing** be *2*, **Iteration** be *100*, **LocalIteration** be *10*, **t_major** be *x*, **SelectDiagonal** be *ShortDiag*.

6. In the right panel, select `SpharmMatDir/data/Ex0302/hip03_smo` as **OutDirectory**
7. In the right panel, click `.....` button next to **Select Input**, and select all the `*_fix.mat` files under `SpharmMatDir/data/Ex0302/hip02_fix` as input files
8. Click **OK** button (See *Screen Capture for CALD Parameterization (Voxel Surface)*)



Method: CALD
MeshGridSize 50
MaxSPHARMDegree 6
Tolerance 2
Smoothing 2
Iteration 100
LocalIteration 10
t_major x
SelectDiagonal ShortDiag
OutDirectory C:\Documents and Settings\shenli\M

C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0302\hip02_fix\a01_l_hippo_fix.mat

Figure 3.4: Screen Capture for CALD Parameterization (Voxel Surface)

3.3.2 Surface Visualization (ADC_ParaMap, Mesh)

Task

Visualize surface meshes in both object and parameter spaces

Input

`SpharmMatDir/data/Ex0302/hip03_smo/*_smo.mat` or

`SpharmMatDir/data/Ex0302/hip03_smo/initParamCALD/*_ini.mat`

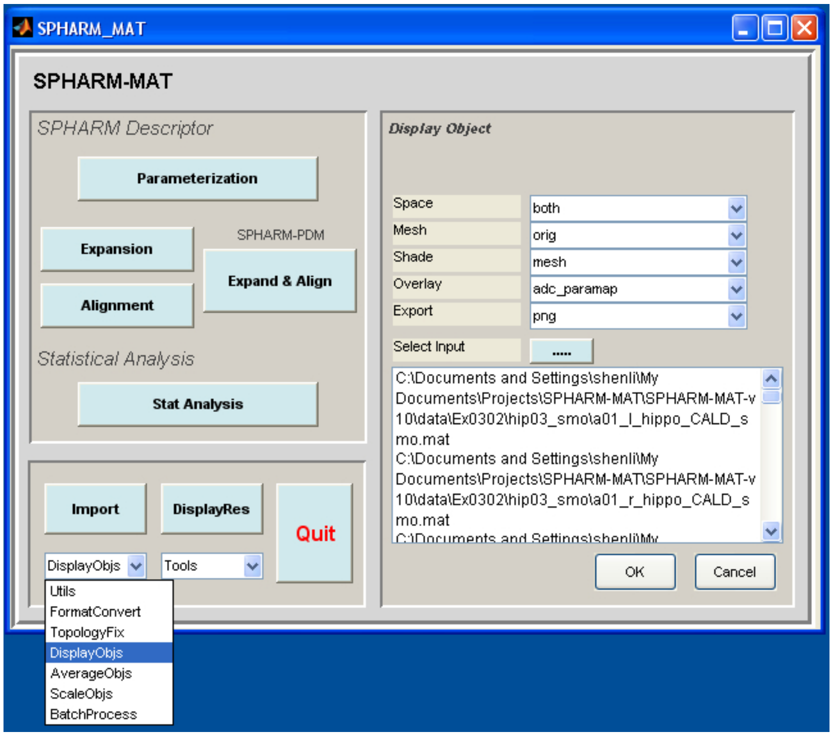
Output

`SpharmMatDir/data/Ex0302/hip03_smo/PNG/*.png` or

`SpharmMatDir/data/Ex0302/hip03_smo/initParamCALD/PNG/*.png`

Steps

1. Select **DisplayObjs** under the **Utils** pop-up menu (bottom-left corner)
2. In the right panel, let **Space** be *both*, **Mesh** be *orig*, **Shade** be *mesh*, **Overlay** be *adc_paramap*, **Export** be *PNG*
3. In the right panel, click `.....` button next to **Select Input**, and select either all the `SpharmMatDir/data/Ex0302/hip03_smo/PNG/*.png` files or all the `SpharmMatDir/data/Ex0302/hip03_smo/initParamCALD/PNG/*.png` as the input files
4. Click **OK** button (See *Screen Capture for Surface Visualization (ADC_ParaMap, Mesh)*)



Space: both
Mesh: orig
Shade: mesh
Overlay: adc_paramap
Export: png

C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0302\hip03_smo\a01_l_hippo_CALD_smo.mat
C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0302\hip03_smo\a01_r_hippo_CALD_smo.mat
C:\Documents and Settings\shenli\My

Figure 3.5: Screen Capture for Surface Visualization (ADC_ParaMap, Mesh)

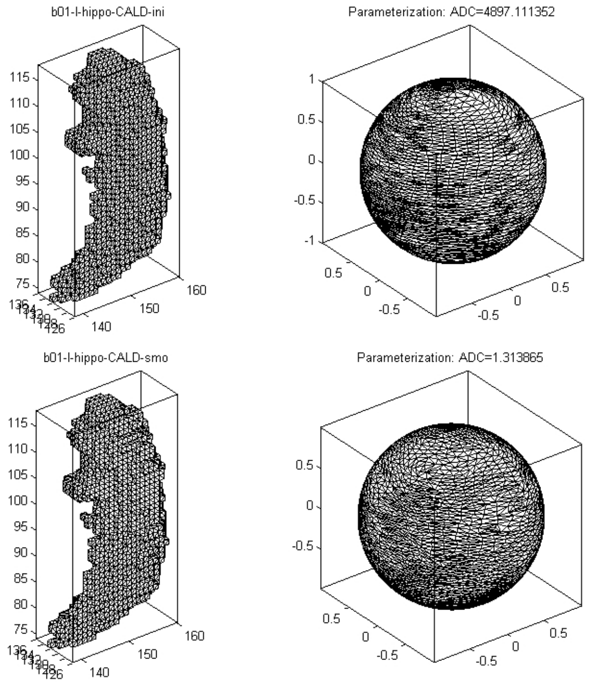
Notes

- The visualization results are saved as PNG files under `SpharmMatDir/data/Ex0302/hip03_smo/PNG` and `SpharmMatDir/data/Ex0302/hip03_smo/initParamCALD/PNG`.
- The results of initial parameterization and optimized parameterization for a hippocampus are shown in *Surface Visualization (ADC_ParaMap, Mesh)*, where the ADC (area distortion cost) is defined in *Area Distortion Cost*.

3.3.3 Relevant Information

Useful Tips

- *Parameterization CALD Input and Output*
- *Parameterization CALD Parameters*
- *DisplayObjs Space Option*
- *DisplayObjs Shade Option*
- *DisplayObjs Overlay Option*
- *DisplayObjs Export Option*
- *Data Structure*
- *File Selection*


b01-l-hippo-CALD-ini

Parameterization: ADC=4897.111352

b01-l-hippo-CALD-smo

Parameterization: ADC=1.313865

Figure 3.6: Surface Visualization (ADC_ParaMap, Mesh)

3.4 Exercise 3.3 Voxel Surfaces (PDM)

This exercise was tested on a WinXP machine (3GHz CPU, 3.25G RAM) running Matlab 7.7.0 (R2008b) and SPHARM-PDM (WinXP-v1.3). It took 30-40 minutes to parameterize all 40 objects.

Major Steps

1. PDM Parameterization for Voxel Surfaces
2. Format Conversion surf_para_meta2smo
3. Surface Visualization (ADC_ParaMap, Solid with Mesh)

3.4.1 PDM Parameterization for Voxel Surfaces

Task

Create spherical parameterization for voxel surfaces using SPHARM-PDM

Input

`SpharmMatDir/data/Ex0303/hip03_gipl_fix/*_fix.gipl`: This folder is a copy of `SpharmMatDir/data/Ex0202/hip03_gipl_fix/*_fix.gipl`. The surface of an input binary object needs to be genus zero (i.e., with spherical topology).

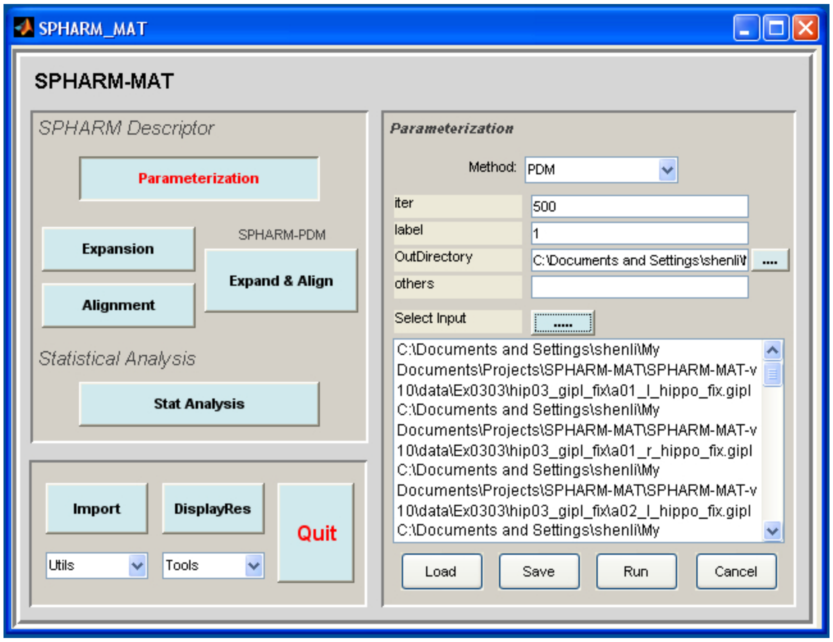
Output

`SpharmMatDir/data/Ex0303/hip04_meta/*.meta`: Object and parameter meshes are stored in `*_surf.meta` and `*_para.meta` respectively.

Steps

1. Make an output directory `SpharmMatDir/data/Ex0303/hip04_meta`

2. Run **SPHARM_MAT.m** under Matlab
3. Click **Parameterization** button
4. In the right panel, let **Method** be *PDM*
5. In the right panel, let **iter** be *500*, **label** be *1*, **others** be *empty*.
6. In the right panel, select `SpharmMatDir/data/Ex0303/hip04_meta` as **OutDirectory**
7. In the right panel, click `.....` button next to **Select Input**, and select all the `*_fix.gipl` files under `SpharmMatDir/data/Ex0303/hip03_gipl_fix` as input files
8. Click **OK** button (See *Screen Capture for PDM Parameterization (Voxel Surface)*)



Method: PDM

iter: 500

label: 1

OutDirectory: C:\Documents and Settings\shenli\M

others:

Select Input: .....

```
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0303\hip03_gipl_fix\a01_l_hippo_fix.gipl
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0303\hip03_gipl_fix\a01_r_hippo_fix.gipl
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0303\hip03_gipl_fix\a02_l_hippo_fix.gipl
C:\Documents and Settings\shenli\My
```

Figure 3.7: Screen Capture for PDM Parameterization (Voxel Surface)

3.4.2 Format Conversion surf_para_meta2smo

Task

Convert META surface format generated by SPHARM-PDM to matlab format

Input

`SpharmMatDir/data/Ex0303/hip04_meta/*.meta`

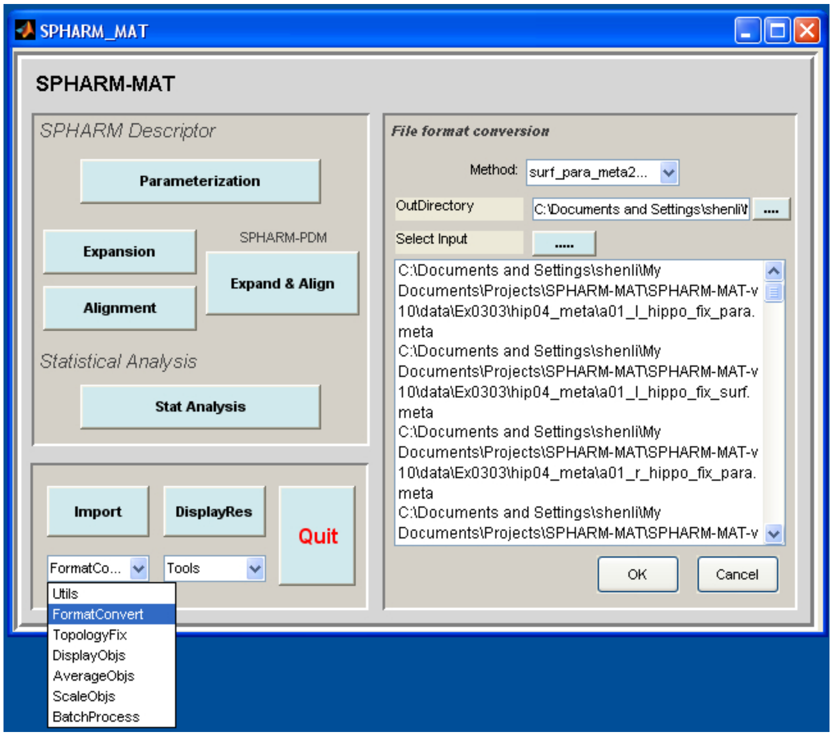
Output

`SpharmMatDir/data/Ex0303/hip05_smo/*_smo.mat`

Steps

1. Make an output directory `SpharmMatDir/data/Ex0303/hip05_smo/`
2. Run **SPHARM_MAT.m** under Matlab
3. Select **FormatConvert** under the **Utils** pop-up menu (bottom-left corner)
4. In the right panel, let **Method** be *surf_para_meta2smo*

5. In the right panel, select `SpharmMatDir/data/Ex0303/hip05_smo/` as **OutDirectory**
6. In the right panel, click `.....` button next to **Select Input**, and select all the `*.meta` files under `SpharmMatDir/data/Ex0303/hip04_meta/` as input files
7. Click **OK** button (See *Screen shot for Format Conversion surf_para_meta2smo.*)



Method: surf_para_meta2...

OutDirectory C:\Documents and Settings\shenli\

Select Input

```
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0303\hip04_meta\a01_l_hippo_fix_para.
meta
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0303\hip04_meta\a01_l_hippo_fix_surf.
meta
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0303\hip04_meta\a01_r_hippo_fix_para.
meta
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
```

Figure 3.8: Screen shot for Format Conversion surf_para_meta2smo.

3.4.3 Surface Visualization (ADC_ParaMap, Solid with Mesh)

Task

Visualize surface meshes in both object and parameter spaces

Input

`SpharmMatDir/data/Ex0303/hip05_smo/*_smo.mat`

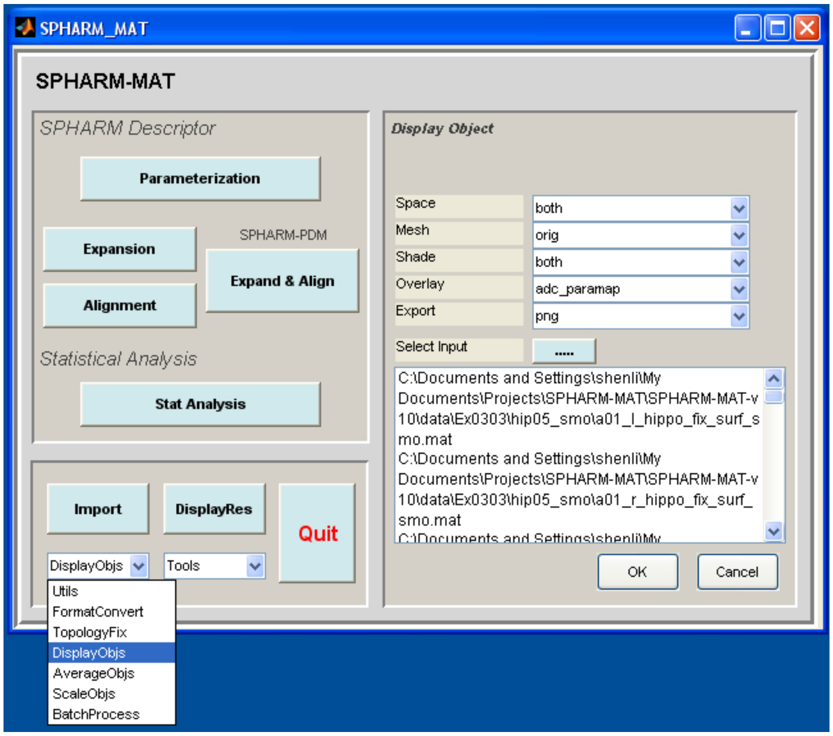
Output

`SpharmMatDir/data/Ex0303/hip05_smo/PNG/*.png`

Steps

1. Select **DisplayObjs** under the **Utils** pop-up menu (bottom-left corner)
2. In the right panel, let **Space** be *both*, **Mesh** be *orig*, **Shade** be *both*, **Overlay** be *adc_paramap*, **Export** be *PNG*
3. In the right panel, click `.....` button next to **Select Input**, and select all the `SpharmMatDir/data/Ex0303/hip05_smo/PNG/*.png` files as the input files
4. Click **OK** button (See *Screen Capture for Surface Visualization (ADC_ParaMap, Solid with Mesh)*)

Notes



Space: both
Mesh: orig
Shade: both
Overlay: adc_paramap
Export: png

C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0303\hip05_smo\a01_l_hippo_fix_surf_smo.mat
C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0303\hip05_smo\a01_r_hippo_fix_surf_smo.mat
C:\Documents and Settings\shenli\My

Figure 3.9: Screen Capture for Surface Visualization (ADC_ParaMap, Solid with Mesh)

- The visualization results are saved as PNG files under `SpharmMatDir/data/Ex0303/hip05_smo/PNG`.
- The parameterization result for a hippocampus is shown in *Surface Visualization (ADC_ParaMap, Solid with Mesh)*, where the ADC (area distortion cost) is defined in *Area Distortion Cost*.
- To understand why ADC is so high in this example, see *ADC Calculation for Voxel Surface and Its Triangulation*.

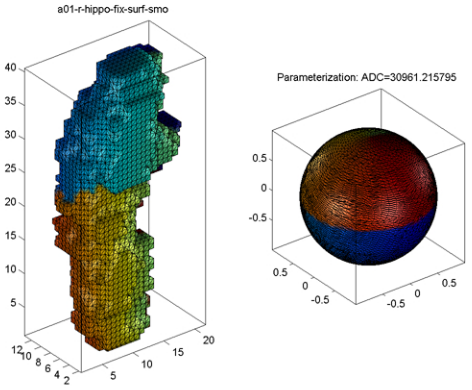


Figure 3.10: Surface Visualization (ADC_ParaMap, Solid with Mesh)

3.4.4 Relevant Information

Useful Tips

- *ADC Calculation for Voxel Surface and Its Triangulation*
- *Parameterization PDM Input*
- *Parameterization PDM Parameters*
- *Format Conversion for Surface Meshes*
- *DisplayObjs Space Option*
- *DisplayObjs Shade Option*
- *DisplayObjs Overlay Option*
- *DisplayObjs Export Option*
- *Data Structure*
- *File Selection*

CHAPTER FOUR

SPHARM EXPANSION

SPHARM expansion expands the object surface into a complete set of spherical harmonic basis functions Y_l^m, where Y_l^m denotes the spherical harmonic of degree l and order m and it is essentially a Fourier basis function defined on the sphere. The expansion takes the form:

$$\mathbf{v}(\theta, \phi) = \sum_{l=0}^{\infty} \sum_{m=-l}^{l} \mathbf{c}_l^m Y_l^m(\theta, \phi), \tag{4.1}$$

where

$$\mathbf{v}(\theta, \phi) = (x(\theta, \phi), y(\theta, \phi), z(\theta, \phi))^T \tag{4.2}$$

and

$$\mathbf{c}_l^m = (c_{xl}^m, c_{yl}^m, c_{zl}^m)^T. \tag{4.3}$$

The Fourier coefficients $\mathbf{c}_l^m$ up to a user-desired degree can be estimated by solving a linear system. The object surface can be reconstructed using these coefficients, and using more coefficients leads to a more detailed reconstruction.

A sample reconstruction case is shown in *Surface Visualization (icosa4, Solid with Mesh)*: The original model is shown in the left panel and its SPHARM reconstructions using coefficients up to degrees 5 and 15 are shown in the middle and right panels, respectively.

Different spherical sampling schemes can be used to reconstruct the object. In *Surface Visualization (quad64, Mesh)*, the reconstruction shown in the right panel is created using a regular mesh grid on the sphere, and the one shown in the left panel is created using a level 4 icosahedral subdivision.

In SPHARM-MAT, a standard expansion method as described above is implemented for creating the SPHARM descriptors (see *Exercise 4.1 SPHARM-MAT Expansion*). In addition, SPHARM-PDM can also be integrated for performing SPHARM expansion (see *Exercise 4.2 SPHARM-PDM Expansion* and *SPHARM Expansion PDM Difference*).

4.1 Exercise 4.1 SPHARM-MAT Expansion

This exercise was tested on a WinXP machine (3GHz CPU, 3.25G RAM) running Matlab 7.7.0 (R2008b). It took a few minutes to finish.

Major Steps

1. SPHARM-MAT Expansion
2. Surface Visualization (icosa4, Solid with Mesh)

4.1.1 SPHARM-MAT Expansion

Task

Calculate SPHARM coefficients

Input

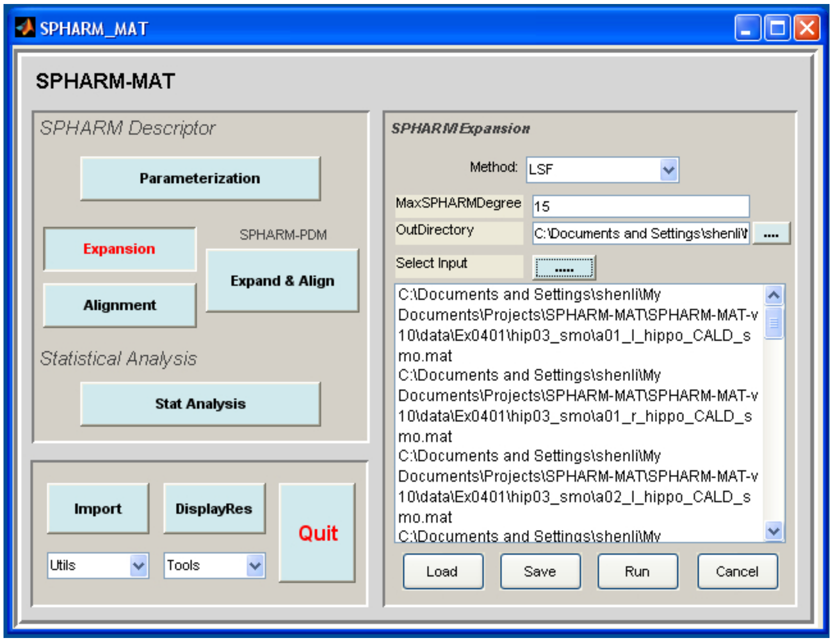
`SpharmMatDir/data/Ex0401/hip03_smo/*_smo.mat`: This folder is a copy of `SpharmMatDir/data/Ex0302/hip03_smo/*_smo.mat`.

Output

`SpharmMatDir/data/Ex0401/hip04_des/*_des.mat`

Steps

1. Make an output directory `SpharmMatDir/data/Ex0401/hip04_des`
2. Run **SPHARM_MAT.m** under Matlab
3. Click **Expansion** button
4. In the right panel, let **Method** be *LSF*
5. In the right panel, let **MaxSPHARMDegree** be *15*
6. In the right panel, select `SpharmMatDir/data/Ex0401/hip04_des` as **OutDirectory**
7. In the right panel, click `.....` button next to **Select Input**, and select all the `*_smo.mat` files under `SpharmMatDir/data/Ex0401/hip03_smo` as input files
8. Click **OK** button (See *Screen Capture for SPHARM-MAT Expansion*)



Method: LSF

MaxSPHARMDegree 15

OutDirectory C:\Documents and Settings\shenli\M

```
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0401\hip03_smo\a01_l_hippo_CALD_s
mo.mat
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0401\hip03_smo\a01_r_hippo_CALD_s
mo.mat
C:\Documents and Settings\shenli\My
Documents\Projects\SPHARM-MAT\SPHARM-MAT-v
10\data\Ex0401\hip03_smo\a02_l_hippo_CALD_s
mo.mat
C:\Documents and Settings\shenli\My
```

Figure 4.1: Screen Capture for SPHARM-MAT Expansion

4.1.2 Surface Visualization (icosa4, Solid with Mesh)

Task

Visualize SPHARM reconstruction in object space

Input

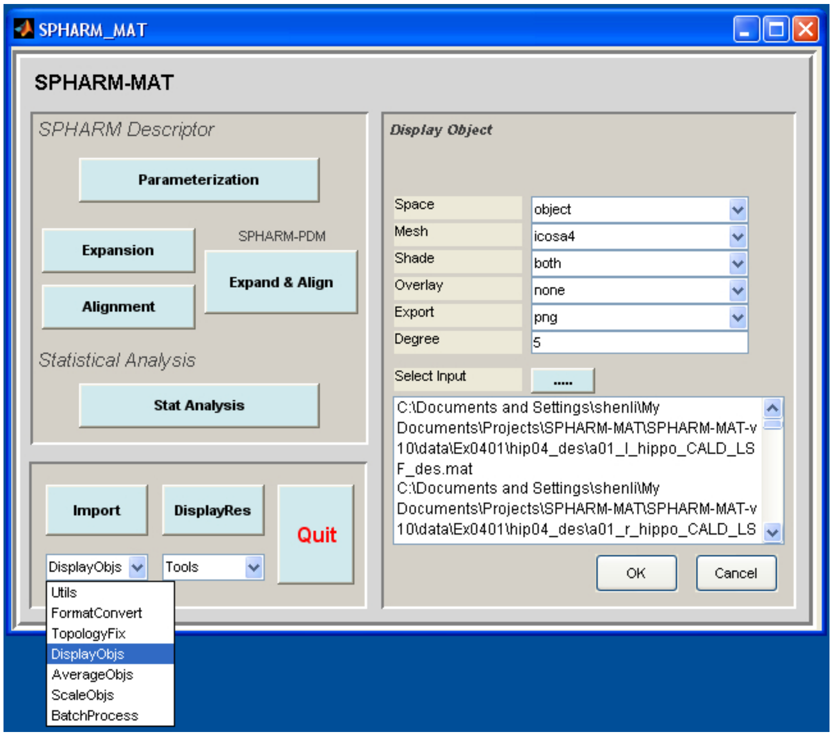
`SpharmMatDir/data/Ex0401/hip04_des/*_des.mat`

Output

`SpharmMatDir/data/Ex0401/hip04_des/*_des.mat/PNG/*.png`

Steps

1. Select **DisplayObjs** under the **Utils** pop-up menu (bottom-left corner)
2. Be sure to run this experiments three times by setting different configurations in the right panel as follows
   - Run 1 (original surfaces): let **Space** be *object*, **Mesh** be *orig*, **Shade** be *both*, **Overlay** be *none*, **Export** be *png*, **Degree** be *empty*
   - Run 2 (SPHARM reconstruction up to degree 5): let **Space** be *object*, **Mesh** be *icosa4*, **Shade** be *both*, **Overlay** be *none*, **Export** be *png*, **Degree** be *5*
   - Run 3 (SPHARM reconstruction up to degree 15): let **Space** be *object*, **Mesh** be *icosa4*, **Shade** be *both*, **Overlay** be *none*, **Export** be *png*, **Degree** be *15*
3. In the right panel, click ..... button next to **Select Input**, and select all the `SpharmMatDir/data/Ex0401/hip04_des/*_des.mat` files as input files
4. Click **OK** button (See *Screen Capture for Surface Visualization (icosa4, Solid with Mesh)*)



Space: object
Mesh: icosa4
Shade: both
Overlay: none
Export: png
Degree: 5
Select Input: .....

C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0401\hip04_des\a01_l_hippo_CALD_LSF_des.mat
C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0401\hip04_des\a01_r_hippo_CALD_LS

Figure 4.2: Screen Capture for Surface Visualization (icosa4, Solid with Mesh)

Notes

- The visualization results are saved as PNG files under `SpharmMatDir/data/Ex0401/hip04_des/*_des.mat/PNG`

- Sample original surface and its SPHARM reconstructions using coefficients up to degree 5 and degree 15 are shown in *Surface Visualization (icosa4, Solid with Mesh)*.

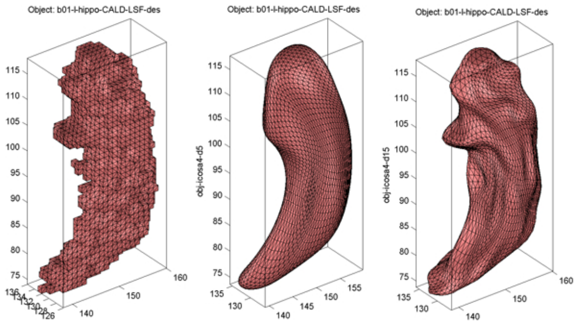


Figure 4.3: Surface Visualization (icosa4, Solid with Mesh)

4.1.3 Relevant Information

Useful Tips

- *SPHARM Expansion Degree*
- *DisplayObjs Space Option*
- *DisplayObjs Shade Option*
- *DisplayObjs Export Option*
- *DisplayObjs Degree Option*
- *Data Structure*
- *File Selection*

4.2 Exercise 4.2 SPHARM-PDM Expansion

Step 1 of this exercise was tested on a Linux machine (3GHz CPU, 8G RAM) running Matlab 7.5.0 (R2007b) and SPHARM-PDM (Linux64-v1.7), since the windows version of this function is not available. Steps 2-3 of this exercise were tested on a WinXP machine (3GHz CPU, 3.25G RAM) running Matlab 7.7.0 (R2008b) and SPHARM-PDM (WinXP-v1.3). It took a few minutes to finish.

Major Steps

1. SPHARM-PDM Expansion
2. Format Conversion meta_coef2des
3. Surface Visualization (quad64, Mesh)

4.2.1 SPHARM-PDM Expansion

Task

Calculate SPHARM coefficients using SPHARM-PDM

Input

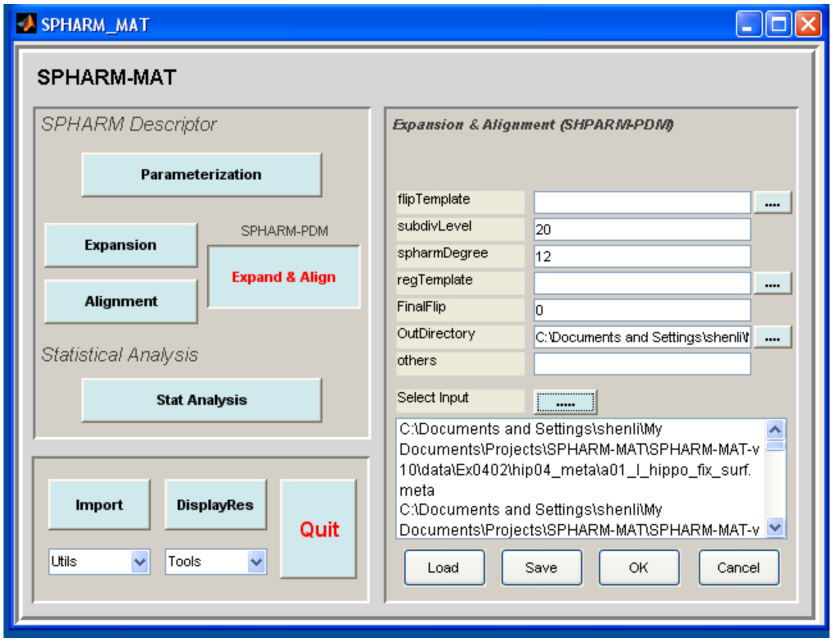
`SpharmMatDir/data/Ex0402/hip04_meta/*.meta`: This folder is a copy of `SpharmMatDir/data/Ex0303/hip04_meta/*.meta`.

Output

`SpharmMatDir/data/Ex0402/hip05_coef/*.*`: SPHARM coefficients are stored in `*.coef` and SPHARM reconstructions are stored in `*.meta`.

Steps

1. Be sure to run this on a Linux machine, since the window version does not support this function
2. Make an output directory `SpharmMatDir/data/Ex0402/hip05_coef/`
3. Run **SPHARM_MAT.m** under Matlab
4. Click **Expand & Align** button
5. In the right panel, let **subdivLevel** be *20*, **spharmDegree** be *12*, **FinalFlip** be *0*, and other options be *empty*.
6. In the right panel, select `SpharmMatDir/data/Ex0402/hip05_coef` as **OutDirectory**
7. In the right panel, click `.....` button next to **Select Input**, and select all the `*.meta` files under `SpharmMatDir/data/Ex0402/hip04_meta` as input files
8. Click **OK** button (See *Screen Capture for SPHARM-PDM Expansion*)



flipTemplate

subdivLevel 20

spharmDegree 12

regTemplate

FinalFlip 0

OutDirectory C:\Documents and Settings\shenli\

others

Select Input

C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0402\hip04_meta\a01_l_hippo_fix_surf.meta
C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v

Figure 4.4: Screen Capture for SPHARM-PDM Expansion

4.2.2 Format Conversion meta_coef2des

Task

Convert COEF coefficient format and META surface format generated by SPHARM-PDM to matlab format

Input

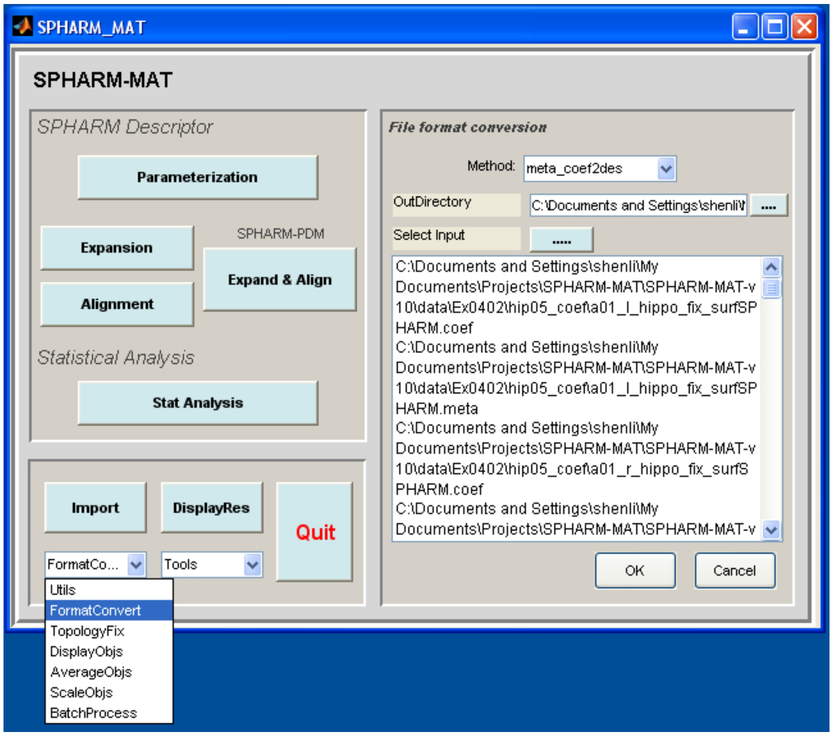
`SpharmMatDir/data/Ex0402/hip05_coef/*.coef` and `SpharmMatDir/data/Ex0402/hip05_coef/*.met`

Output

`SpharmMatDir/data/Ex0402/hip06_des/*_des.mat`

Steps

1. Make an output directory `SpharmMatDir/data/Ex0402/hip06_des/`
2. Run **SPHARM_MAT.m** under Matlab
3. Select **FormatConvert** under the **Utils** pop-up menu (bottom-left corner)
4. In the right panel, let **Method** be *meta_coef2des*
5. In the right panel, select `SpharmMatDir/data/Ex0402/hip06_des/` as **OutDirectory**
6. In the right panel, click `.....` button next to **Select Input**, and select all the `*_surfSPHARM.coef` `*_surfSPHARM.meta` files under `SpharmMatDir/data/Ex0402/hip05_coef/` as input files
7. Click **OK** button (See *Screen shot for Format Conversion meta_coef2des.*)



Method: meta_coef2des

OutDirectory: C:\Documents and Settings\shenli\

Select Input:

C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0402\hip05_coef\a01_l_hippo_fix_surfSPHARM.coef
C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0402\hip05_coef\a01_l_hippo_fix_surfSPHARM.meta
C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0402\hip05_coef\a01_r_hippo_fix_surfSPHARM.coef
C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v

Figure 4.5: Screen shot for Format Conversion meta_coef2des.

Notes

- This conversion packages `*.coef` (SPHARM coefficents) and `*.meta` (Surface reconstruction created by SPHARM-PDM) into a single `*_des.mat` file. Therefore, the surface in the resulting `*_des.mat` file is a SPHARM reconstruction generated by SPHARM-PDM instead of the original object surface. See also *Data Structure*.
- SPHARM-PDM stores only real parts of the coefficients in `*.coef` files. See also *SPHARM Expansion PDM Difference*.

4.2.3 Surface Visualization (quad64, Mesh)

Task

Visualize SPHARM reconstructions in the object space

Input

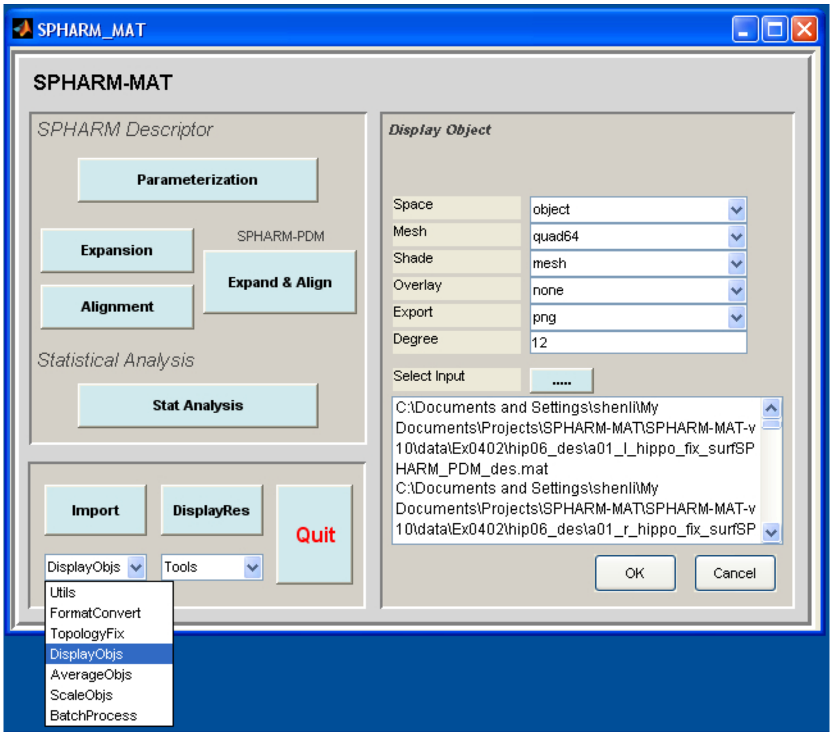
`SpharmMatDir/data/Ex0402/hip06_des/*_des.mat`

Output

`SpharmMatDir/data/Ex0402/hip06_des/PNG/*.png`

Steps

1. Select **DisplayObjs** under the **Utils** pop-up menu (bottom-left corner)
2. Be sure to run this experiments twice by setting different configurations in the right panel as follows
    - Run 1 (SPHARM-PDM reconstructions converted from `*.meta` files): let **Space** be *object*, **Mesh** be *orig*, **Shade** be *mesh*, **Overlay** be *none*, **Export** be *png*, **Degree** be *empty*
    - Run 2 (SPHARM reconstruction using coefficients up to degree 12): let **Space** be *object*, **Mesh** be *quad64*, **Shade** be *mesh*, **Overlay** be *none*, **Export** be *png*, **Degree** be *12*
3. In the right panel, click `.....` button next to **Select Input**, and select all the `SpharmMatDir/data/Ex0402/hip06_des/*_des.mat` files as the input files
4. Click **OK** button (See *Screen Capture for Surface Visualization (quad64, Mesh)*)



Space: object
Mesh: quad64
Shade: mesh
Overlay: none
Export: png
Degree: 12

C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0402\hip06_des\a01_l_hippo_fix_surfSPHARM_PDM_des.mat
C:\Documents and Settings\shenli\My Documents\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0402\hip06_des\a01_r_hippo_fix_surfSP

Figure 4.6: Screen Capture for Surface Visualization (quad64, Mesh)

Notes

- The visualization results are saved as PNG files under `SpharmMatDir/data/Ex0402/hip06_des/PNG/`.

- The surface reconstruction generated by SPHARM-PDM and then converted into `*_des.mat` is shown as the left panel of *Surface Visualization (quad64, Mesh)*, where the underlying mesh used in reconstruction is an icosahedron subdivision. The surface reconstructed using coefficients up to degree 12 is shown as the right panel of *Surface Visualization (quad64, Mesh)*, where the underlying mesh used in reconstruction is a 64-by-64 spherical mesh.

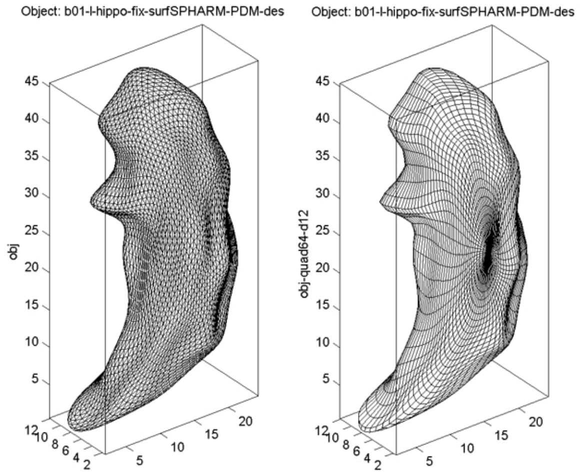


Figure 4.7: Surface Visualization (quad64, Mesh)

4.2.4 Relevant Information

Useful Tips

- *Expand and Align Parameters*
- *SPHARM Expansion PDM Difference*
- *SPHARM Expansion Degree*
- *Format Conversion for SPHARM Models*
- *DisplayObjs Space Option*
- *DisplayObjs Shade Option*
- *DisplayObjs Export Option*
- *DisplayObjs Degree Option*
- *Data Structure*
- *File Selection*

CHAPTER

FIVE

SURFACE ALIGNMENT

Surface alignment is an important operation allowing for pairwise processing or group analysis across different surface models and is a critical step in many applications. The traditional SPHARM registration method ([Styner2006], [Brechb1995]) uses the first order ellipsoid (FOE) for alignment, and works when this ellipsoid is a real ellipsoid. When FOE is not a real ellipsoid, SHREC [Shen2008], a newer SPHARM registration method can be used. SHREC minimizes the mean square distance between corresponding surface parts and is designed for general cases.

In SPHARM-MAT, both FOE alignment and SHREC are available for registering SPHARM models (see *Exercise 5.1 FOE Alignment* and *Exercise 5.2 SHREC Alignment*). In addition, SPHARM-PDM can also be integrated for performing FOE alignment (see *Exercise 5.3 SPHARM-PDM FOE Alignment*).

5.1 Exercise 5.1 FOE Alignment

This exercise was tested on a WinXP machine (3GHz CPU, 3.25G RAM) running Matlab 7.7.0 (R2008b). It took a few minutes to finish.

Major Steps

1. FOE Alignment
2. Surface Visualization (quad64, Solid with Mesh)

5.1.1 FOE Alignment

Task

Use first order ellipsoids (FOE) to register SPHARM models so that each FOE has a canonical orientation in both object and parameter space.

Input

`SpharmMatDir/data/Ex0501/hip04_des/*_des.mat`: This folder is a copy of `SpharmMatDir/data/Ex0401/hip04_des/*_des.mat`.

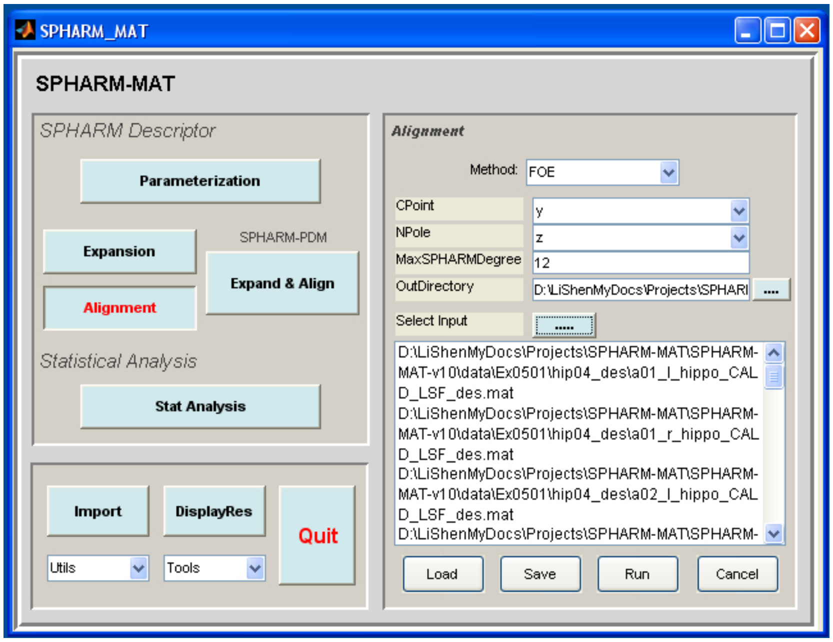
Output

`SpharmMatDir/data/Ex0501/hip05_reg/alignParam/*_prm.mat`: intermediate results after alignment in parameter space

`SpharmMatDir/data/Ex0501/hip05_reg/*_reg.mat`: final results after alignment in both object and parameter space

Steps

1. Make an output directory `SpharmMatDir/data/Ex0501/hip05_reg/`
2. Run **SPHARM_MAT.m** under Matlab
3. Click **Alignment** button
4. In the right panel, let **Method** be *FOE*
5. In the right panel, let **CPoint** be *y*, **NPole** be *z*, **MaxSPHARMDegree** be *12*
6. In the right panel, select `SpharmMatDir/data/Ex0501/hip05_reg/` as **OutDirectory**
7. In the right panel, click `.....` button next to **Select Input**, and select all the `*_des.mat` files under `SpharmMatDir/data/Ex0501/hip04_des` as input files
8. Click **OK** button (See *Screen Capture for FOE Alignment*)



Method: FOE

CPoint: y

NPole: z

MaxSPHARMDegree: 12

OutDirectory: D:\LiShenMyDocs\Projects\SPHARI

D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0501\hip04_des\a01_l_hippo_CALD_LSF_des.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0501\hip04_des\a01_r_hippo_CALD_LSF_des.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0501\hip04_des\a02_l_hippo_CALD_LSF_des.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-

Figure 5.1: Screen Capture for FOE Alignment

5.1.2 Surface Visualization (quad64)

Task

Visualize SPHARM reconstruction before and after FOE alignment

Input

`SpharmMatDir/data/Ex0501/hip04_des/*_des.mat`

`SpharmMatDir/data/Ex0501/hip05_reg/alignParam/*_prm.mat`

`SpharmMatDir/data/Ex0501/hip05_reg/*_reg.mat`

Output

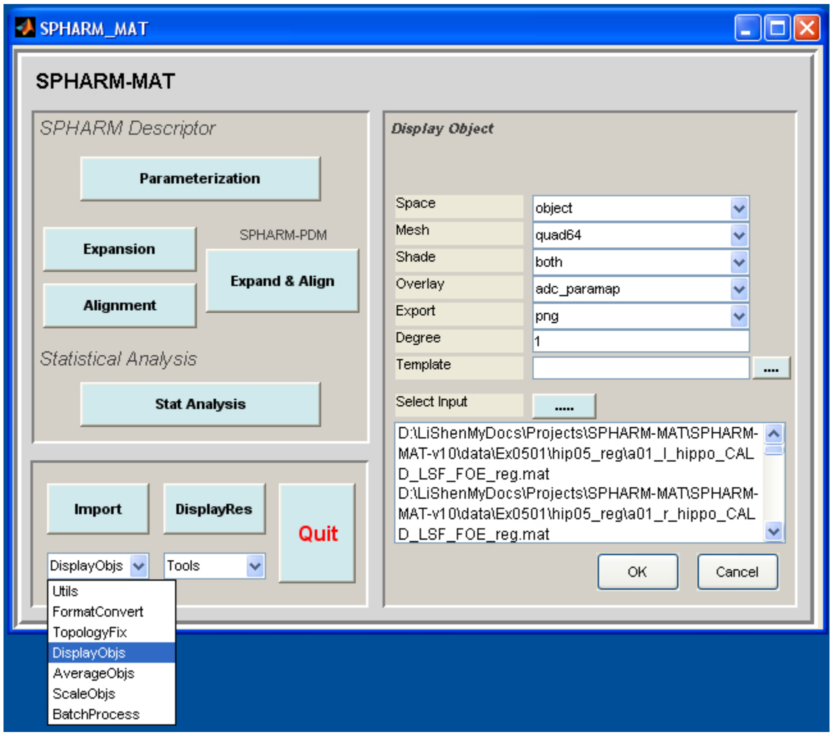
`SpharmMatDir/data/Ex0501/hip04_des/PNG/*.png`

`SpharmMatDir/data/Ex0501/hip05_reg/alignParam/PNG/*.png`

`SpharmMatDir/data/Ex0501/hip05_reg/PNG/*.png`

Steps

1. Select **DisplayObjs** under the **Utils** pop-up menu (bottom-left corner)
2. Be sure to run this experiments six times by setting different configurations in the right panel as follows
    - Runs 1-3 (SPHARM reconstruction up to degree 1): let **Space** be *object*, **Mesh** be *quad64*, **Shade** be *both*, **Overlay** be *adc_paramap*, **Export** be *png*, **Degree** be *1*
    - Runs 4-6 (SPHARM reconstruction up to degree 12): let **Space** be *object*, **Mesh** be *quad64*, **Shade** be *both*, **Overlay** be *adc_paramap*, **Export** be *png*, **Degree** be *12*
3. In the right panel, click `.....` button next to **Select Input**, and select the following files in six different runs respectively
    - Run 1 and Run 4: `SpharmMatDir/data/Ex0501/hip04_des/*_des.mat`
    - Run 2 and Run 5: `SpharmMatDir/data/Ex0501/hip05_reg/alignParam/*_prm.mat`
    - Run 3 and Run 6: `SpharmMatDir/data/Ex0501/hip05_reg/*_reg.mat`
4. Click **OK** button (See *Screen Capture for Surface Visualization (quad64)*)



Space: object
Mesh: quad64
Shade: both
Overlay: adc_paramap
Export: png
Degree: 1
Template:
Select Input:
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0501\hip05_reg\a01_l_hippo_CALD_LSF_FOE_reg.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0501\hip05_reg\a01_r_hippo_CALD_LSF_FOE_reg.mat

Figure 5.2: Screen Capture for Surface Visualization (quad64)

Notes

- The visualization results are saved as PNG files under the PNG folder of the input directories
- Sample alignment procedure is shown below (from left to right: original, intermediate result after aligning parameter net, final result)
    - *Surface Visualization (quad64, Degree 1)*: SPHARM reconstructions using coefficients up to degree 1 (i.e., FOE)
    - *Surface Visualization (quad64, Degree 12)*: SPHARM reconstructions using coefficients up to degree 12

- See *DisplayObjs Overlay Option* for information about color-coded visualization of the underlying parameterization.

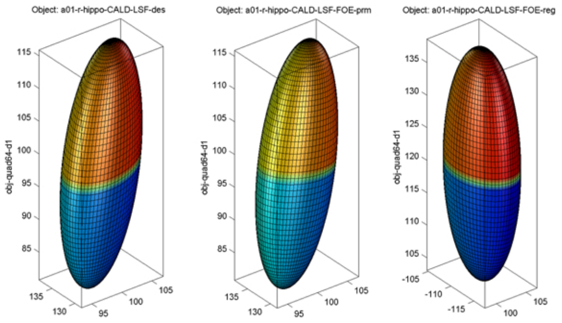


Figure 5.3: Surface Visualization (quad64, Degree 1)

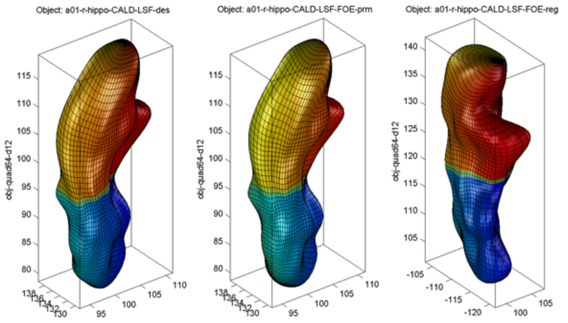


Figure 5.4: Surface Visualization (quad64, Degree 12)

5.1.3 Relevant Information

Useful Tips

- *Alignment FOE Parameters*
- *DisplayObjs Overlay Option*
- *DisplayObjs Mesh Option*
- *DisplayObjs Export Option*
- *DisplayObjs Degree Option*
- *Data Structure*
- *File Selection*

5.2 Exercise 5.2 SHREC Alignment

This exercise was tested on a WinXP machine (3GHz CPU, 3.25G RAM) running Matlab 7.7.0 (R2008b). It took about 20 minutes to finish.

Major Steps

1. SHREC Alignment

2. Surface Visualization (quad64, template)

5.2.1 SHREC Alignment

Task

Use SHREC to register SPHARM models to a template model for minimizing root mean square distance (RMSD)

Input

`SpharmMatDir/data/Ex0502/hip05_prm/*_prm.mat`: This folder is a subset of `SpharmMatDir/data/Ex0501/hip05_reg/alignParam/*_prm.mat`, where only right hippocampi are included.

Output

`SpharmMatDir/data/Ex0502/hip06_reg/*_reg.mat`

Steps

1. Make an output directory `SpharmMatDir/data/Ex0502/hip06_reg/`
2. Run **SPHARM_MAT.m** under Matlab
3. Click **Alignment** button
4. In the right panel, let **Method** be *SHREC*
5. In the right panel, let **Template** be `SpharmMatDir/data/Ex0502/hip05_prm/a01_r_hippo_CALD_LSF_FOE_prm.` **MaxSPHARMDegree** be *12*, **GroupAlpha** be *100*, **NormalizeSize** be *No*, **BaseRes** be *1*, **HierarchyStep** be *1*, **HierarchyDepth** be *3*, **Top_K** be *1*, **GammaRes** be *2*
6. In the right panel, select `SpharmMatDir/data/Ex0502/hip06_reg/` as **OutDirectory**
7. In the right panel, click `.....` button next to **Select Input**, and select all the `*_prm.mat` files under `SpharmMatDir/data/Ex0502/hip05_prm/` as input files
8. Click **OK** button (See *Screen Capture for SHREC Alignment*)

Notes

- See *Alignment SHREC Parameters* for more information about parameters.
- See *Alignment SHREC Initial Models* for notes about selection of initial SPHARM models.
- See *Alignment SHREC Template* for notes about selection of the template.
- SHREC saves only `fvec` in the results.

5.2.2 Surface Visualization (quad64, template)

Task

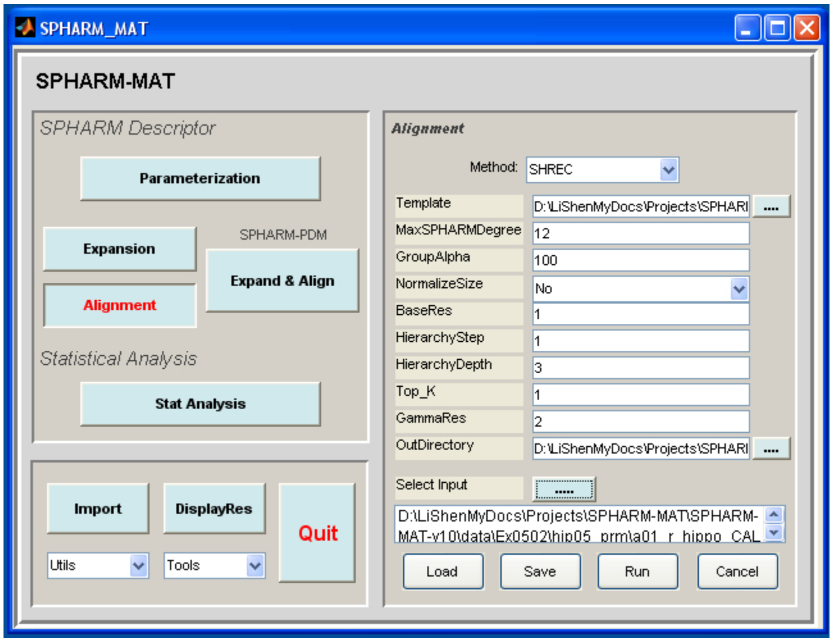
Visualize SPHARM reconstruction in object space

Input

`SpharmMatDir/data/Ex0502/hip05_prm/*_prm.mat`

`SpharmMatDir/data/Ex0502/hip06_reg/*_reg.mat`

Output



Method: SHREC
Template: D:\LiShenMyDocs\Projects\SPHARI
MaxSPHARMDegree: 12
GroupAlpha: 100
NormalizeSize: No
BaseRes: 1
HierarchyStep: 1
HierarchyDepth: 3
Top_K: 1
GammaRes: 2
OutDirectory: D:\LiShenMyDocs\Projects\SPHARI
Select Input: .....

D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10\data\Ex0502\hip05_prm\a01_r_hippo_CAL

Figure 5.5: Screen Capture for SHREC Alignment

`SpharmMatDir/data/Ex0502/hip05_prm/PNG/*.png`

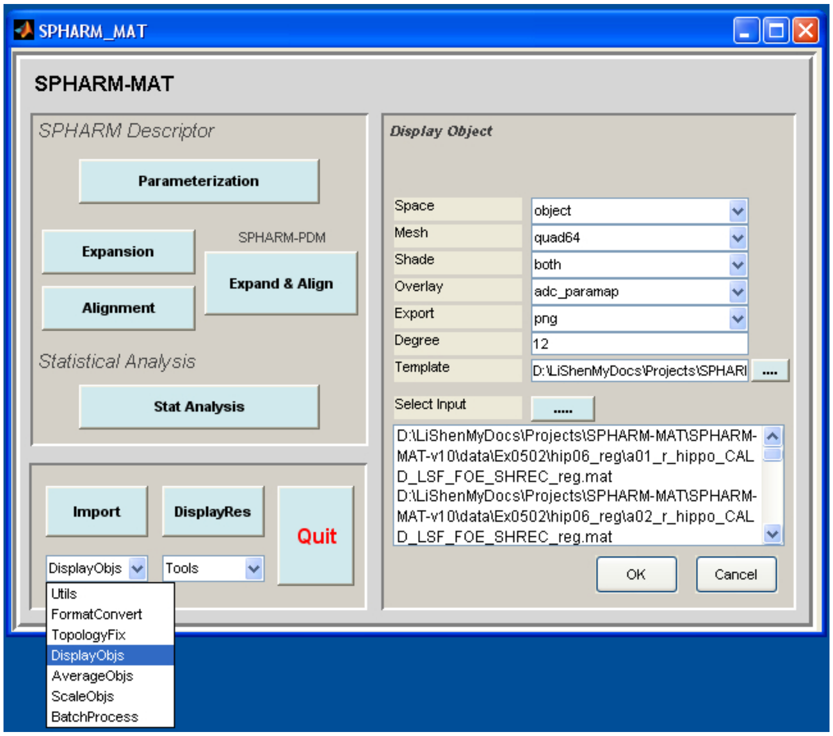
`SpharmMatDir/data/Ex0502/hip06_reg/*_reg.mat/PNG/*.png`

Steps

1. Select **DisplayObjs** under the **Utils** pop-up menu (bottom-left corner)
2. In the right panel, let **Space** be *object*, **Mesh** be *quad64*, **Shade** be *both*, **Overlay** be *adc_paramap*, **Export** be *png*, **Degree** be *12*, **Template** be *SpharmMatDir/data/Ex0502/hip05_prm/a01_r_hippo_CALD_LSF_FOE_prm.mat*
3. In the right panel, click `.....` button next to **Select Input**, and select the following files in two different runs respectively
    - Run 1: `SpharmMatDir/data/Ex0502/hip05_prm/*_prm.mat`
    - Run 2: `SpharmMatDir/data/Ex0502/hip06_reg/*_reg.mat`
4. Click **OK** button (See *Screen Capture for Surface Visualization (quad64, template)*)

Notes

- The visualization results are saved as PNG files under the PNG folder of the input directories
- Sample alignment procedure is shown in *Surface Visualization (quad64, template)*, where the template, the individual before alignment, and the individual after alignment are shown from left to right. The root mean square distance (RMSD) between an individual and the template is plot on the z axis.
- See *DisplayObjs Template Option* for information about template and RMSD.
- See *DisplayObjs Overlay Option* for information about color-coded visualization of the underlying parameterization.



Space: object

Mesh: quad64

Shade: both

Overlay: adc_paramap

Export: png

Degree: 12

Template: D:\LiShenMyDocs\Projects\SPHARI

Select Input:

D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v1.0\data\Ex0502\hip06_reg\a01_r_hippo_CALD_LSF_FOE_SHREC_reg.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v1.0\data\Ex0502\hip06_reg\a02_r_hippo_CALD_LSF_FOE_SHREC_reg.mat

Figure 5.6: Screen Capture for Surface Visualization (quad64, template)

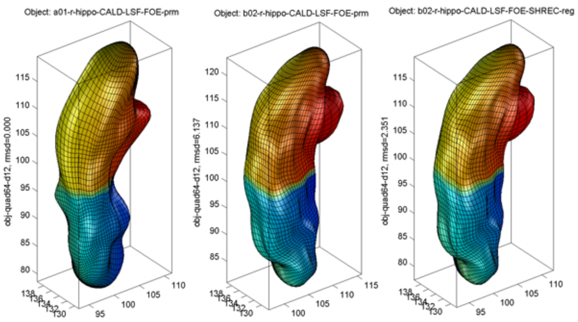


Figure 5.7: Surface Visualization (quad64, template)

5.2.3 Relevant Information

Useful Tips

- *Alignment SHREC Parameters*
- *Alignment SHREC Initial Models*
- *Alignment SHREC Template*
- *DisplayObjs Template Option*
- *DisplayObjs Overlay Option*
- *DisplayObjs Mesh Option*
- *DisplayObjs Export Option*
- *DisplayObjs Degree Option*
- *Data Structure*
- *File Selection*

5.3 Exercise 5.3 SPHARM-PDM FOE Alignment

Step 1 of this exercise was tested on a Linux machine (3GHz CPU, 8G RAM) running Matlab 7.5.0 (R2007b) and SPHARM-PDM (Linux64-v1.7), since the windows version of this function is not available. Steps 2-3 of this exercise were tested on a WinXP machine (3GHz CPU, 3.25G RAM) running Matlab 7.7.0 (R2008b) and SPHARM-PDM (WinXP-v1.3). It took a few minutes to finish.

Major Steps

1. SPHARM-PDM FOE Alignment
2. Format Conversion ellalign_meta_coef2reg
3. Surface Visualization (quad64)

5.3.1 SPHARM-PDM FOE Alignment

Task

> Use first order ellipsoids (FOE) to register SPHARM models so that each FOE has a canonical orientation in both object and parameter space.

Input

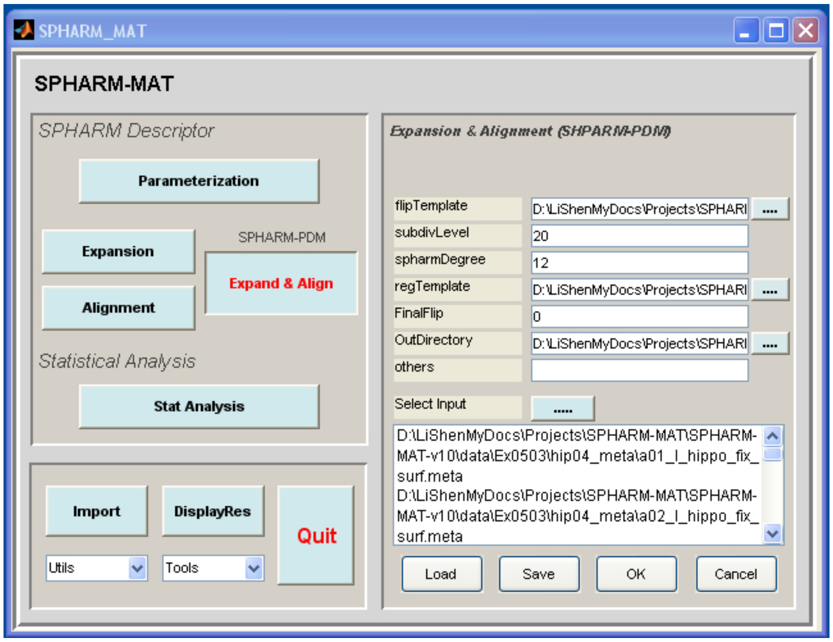
> `SpharmMatDir/data/Ex0503/hip04_meta/*.meta`: This folder is a subset of `SpharmMatDir/data/Ex0402/hip04_meta/*.meta`, where only left hippocampi are included
>
> `SpharmMatDir/data/Ex0503/hip05_temp/a01_l_hippo_fix_surfSPHARM_ellalign.*`: These two files are copied from `SpharmMatDir/data/Ex0402/hip05_coef/` and are used as flipTemplate and regTemplate (see *Expand and Align Parameters*)

Output

> `SpharmMatDir/data/Ex0503/hip06_coef/*.*`: SPHARM coefficients are stored in `*.coef` and SPHARM reconstructions are stored in `*.meta` (see also *Format Conversion for SPHARM Models*).

Steps

1. Be sure to run this on a Linux machine, since the window version does not support this function
2. Make an output directory `SpharmMatDir/data/Ex0503/hip06_coef/`
3. Run **SPHARM_MAT.m** under Matlab
4. Click **Expand & Align** button
5. In the right panel, let **flipTemplate** be *SpharmMatDir/data/Ex0503/hip05_temp/a01_l_hippo_fix_surfSPHARM_ellalign.coef*, **subdivLevel** be *20*, **spharmDegree** be *12*, **regTemplate** be *SpharmMatDir/data/Ex0503/hip05_temp/a01_l_hippo_fix_surfSPHARM_ellalign.meta*, **FinalFlip** be *0*, and other options be *empty*.
6. In the right panel, select `SpharmMatDir/data/Ex0503/hip06_coef` as **OutDirectory**
7. In the right panel, click `.....` button next to **Select Input**, and select all the `*.meta` files under `SpharmMatDir/data/Ex0503/hip04_meta/*.meta` as input files
8. Click **OK** button (See *Screen Capture for SPHARM-PDM FOE Alignment*)



flipTemplate: D:\LiShenMyDocs\Projects\SPHARI

subdivLevel: 20

spharmDegree: 12

regTemplate: D:\LiShenMyDocs\Projects\SPHARI

FinalFlip: 0

OutDirectory: D:\LiShenMyDocs\Projects\SPHARI

others:

D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v1 0\data\Ex0503\hip04_meta\a01_l_hippo_fix_surf.meta
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v1 0\data\Ex0503\hip04_meta\a02_l_hippo_fix_surf.meta

Figure 5.8: Screen Capture for SPHARM-PDM FOE Alignment

5.3.2 Format Conversion ellalign_meta_coef2reg

Task

Convert COEF coefficient format and META surface format generated by SPHARM-PDM to matlab format

Input

`SpharmMatDir/data/Ex0503/hip06_coef/*.coef` and `SpharmMatDir/data/Ex0503/hip06_coef/*.met`

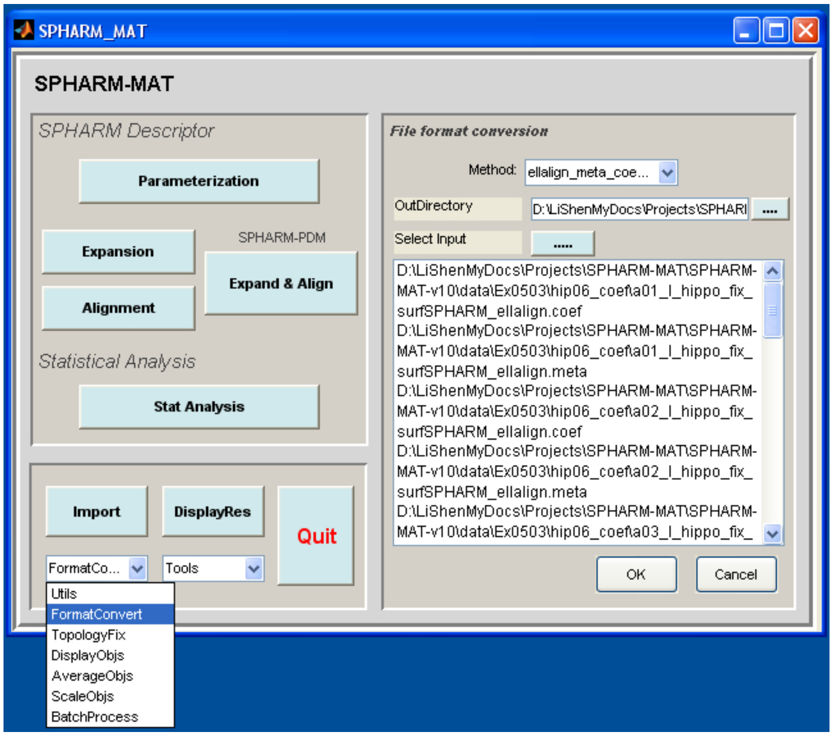
Output

`SpharmMatDir/data/Ex0503/hip07_reg/*_des.mat`: SPHARM models in original coordinate system

`SpharmMatDir/data/Ex0503/hip07_reg/*_reg.mat`: SPHARM models in FOE aligned coordinate system

Steps

1. Make an output directory `SpharmMatDir/data/Ex0503/hip07_reg/`
2. Run **SPHARM_MAT.m** under Matlab
3. Select **FormatConvert** under the **Utils** pop-up menu (bottom-left corner)
4. Be sure to run this experiments twice by setting different configurations in the right panel as follows
    - Run 1: let **Method** be *meta_coef2des*
    - Run 2: let **Method** be *ellalign_meta_coef2reg*
5. In the right panel, select `SpharmMatDir/data/Ex0503/hip07_des/` as **OutDirectory**
6. In the right panel, click `.....` button next to **Select Input**, and select all the `*.coef` `*.meta` files under `SpharmMatDir/data/Ex0503/hip06_coef/` as input files
7. Click **OK** button (See *Screen shot for Format Conversion ellalign_meta_coef2reg.*)



Method: ellalign_meta_coe...

OutDirectory: D:\LiShenMyDocs\Projects\SPHARI

```
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-
MAT-v10\data\Ex0503\hip06_coef\a01_l_hippo_fix_
surfSPHARM_ellalign.coef
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-
MAT-v10\data\Ex0503\hip06_coef\a01_l_hippo_fix_
surfSPHARM_ellalign.meta
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-
MAT-v10\data\Ex0503\hip06_coef\a02_l_hippo_fix_
surfSPHARM_ellalign.coef
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-
MAT-v10\data\Ex0503\hip06_coef\a02_l_hippo_fix_
surfSPHARM_ellalign.meta
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-
MAT-v10\data\Ex0503\hip06_coef\a03_l_hippo_fix_
```

Figure 5.9: Screen shot for Format Conversion ellalign_meta_coef2reg.

Notes

- This conversion packages `*.coef` (SPHARM coefficents) and `*.meta` (Surface reconstruction created by SPHARM-PDM) into a single `*.mat` file: either (1) `*_des.mat` for SPHARM models in the original coordinate system, or (2) `*_reg.mat` for SPHARM models in the FOE aligned coordinate system. Therefore, the surface in the resulting `*_des.mat` or `*_reg.mat` file is a SPHARM reconstruction generated by SPHARM-PDM instead of the original object surface. See also *Data Structure* and *Format Conversion for SPHARM Models*.

- SPHARM-PDM stores only real parts of the coefficients in `*.coef` files. See also *SPHARM Expansion PDM Difference*.

5.3.3 Surface Visualization (quad64)

Task

Visualize SPHARM reconstructions before and after FOE alignment

Input

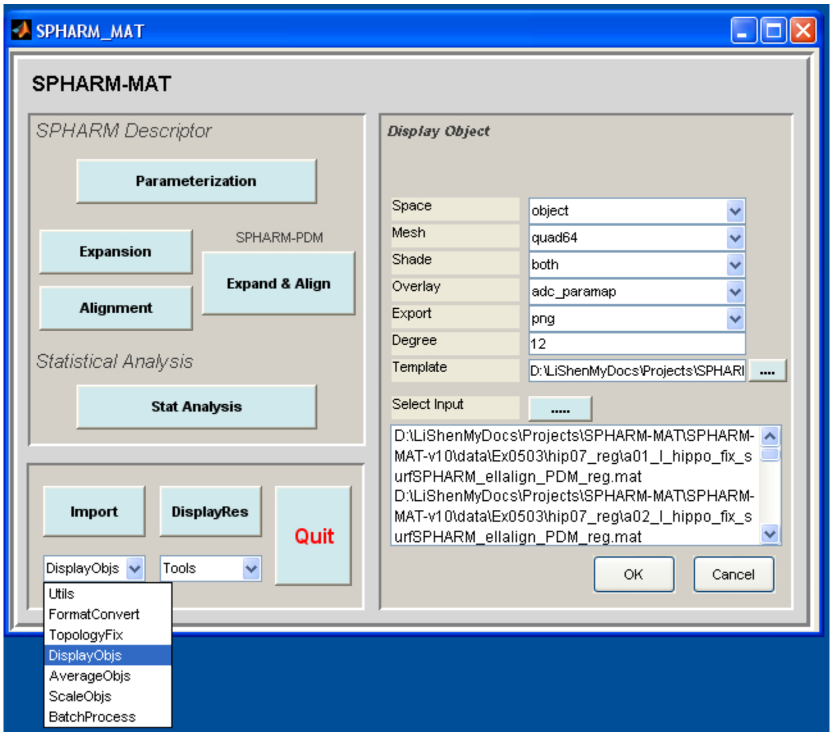
`SpharmMatDir/data/Ex0503/hip07_reg/*.mat`

Output

`SpharmMatDir/data/Ex0503/hip07_reg/PNG/*.png`

Steps

1. Select **DisplayObjs** under the **Utils** pop-up menu (bottom-left corner)
2. Be sure to run this experiments twice by setting different configurations in the right panel as follows
    - Run 1 (SPHARM reconstruction using coefficients up to degree 1): let **Space** be *object*, **Mesh** be *quad64*, **Shade** be *both*, **Overlay** be *adc_paramap*, **Export** be *png*, **Degree** be *1*
    - Run 2 (SPHARM reconstruction using coefficients up to degree 12): let **Space** be *object*, **Mesh** be *quad64*, **Shade** be *both*, **Overlay** be *adc_paramap*, **Export** be *png*, **Degree** be *12*
3. In the right panel, click `.....` button next to **Select Input**, and select all the `SpharmMatDir/data/Ex0503/hip07_reg/*.mat` files as the input files
4. Click **OK** button (See *Screen Capture for Surface Visualization (quad64)*)



Space: object
Mesh: quad64
Shade: both
Overlay: adc_paramap
Export: png
Degree: 12
Template: D:\LiShenMyDocs\Projects\SPHARI
Select Input: .....

D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v1 0\data\Ex0503\hip07_reg\a01_l_hippo_fix_surfSPHARM_ellalign_PDM_reg.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v1 0\data\Ex0503\hip07_reg\a02_l_hippo_fix_surfSPHARM_ellalign_PDM_reg.mat

Figure 5.10: Screen Capture for Surface Visualization (quad64)

Notes

- The visualization results are saved as PNG files under `SpharmMatDir/data/Ex0503/hip07_reg/PNG/`.
- Sample alignment results are shown below: original model on the left and FOE aligned model on the right
  - *Surface Visualization (quad64, Degree 1)*: SPHARM reconstructions using coefficients up to degree 1 (i.e., FOE)
  - *Surface Visualization (quad64, Degree 12)*: SPHARM reconstructions using coefficients up to degree 12
- See *DisplayObjs Overlay Option* for information about color-coded visualization of the underlying parameterization.

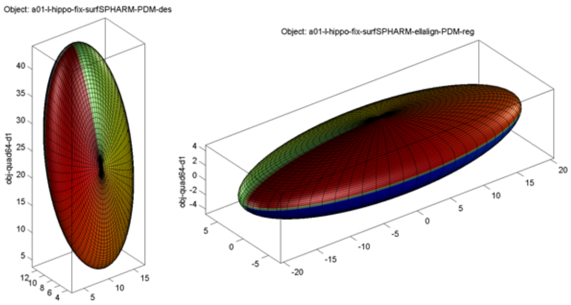


Figure 5.11: Surface Visualization (quad64, Degree 1)

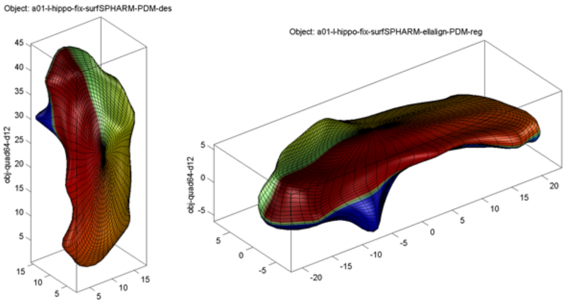


Figure 5.12: Surface Visualization (quad64, Degree 12)

5.3.4 Relevant Information

Useful Tips

- *Expand and Align Parameters*
- *Format Conversion for SPHARM Models*
- *SPHARM Expansion PDM Difference*
- *SPHARM Expansion Degree*
- *DisplayObjs Overlay Option*
- *DisplayObjs Space Option*
- *DisplayObjs Shade Option*
- *DisplayObjs Export Option*

- *DisplayObjs Degree Option*
- *Data Structure*
- *File Selection*

CHAPTER

SIX

STATISTICAL ANALYSIS

After registering all the individual SPHARM models to a template model, all the SPHARM coefficients are normalized and comparable across objects, and then group analysis can be performed. In SPHARM-MAT, two simple statistical components are implemented to demonstrate its capability for group analysis.

The first component (see *Exercise 6.1 T Test*) aims to quantify and localize shape changes between two groups of objects. The basic processing pipeline includes the following steps: (1) uniformly sample each SPHARM surface to create a landmark representation; (2) surface signal extraction using different schemes (see [Shen2006b]); (3) perform a t-test on surface signals and visualize the result (e.g., t-map, uncorrected p-map) on the surface.

The second component (see *Exercise 6.2 PCA*) aims to establish a statistical shape model for one group of 3D objects by characterizing the mean and variability of the population. An ideal model should involve a small number of variables (i.e., simple) but capture major characteristics of the group (i.e., representative). Principal component analysis (PCA) is applied to SPHARM coefficients and characterize the shape group using the PCA eigenmodes. The first few principal components often explain most of the data variance and can be used to create a good statistical shape model that summarizes the whole group. Visualization can also be created for intuitive understanding of the group characteristics.

For more complicated statistical models, we suggest that SurfStat [Worsley2008] should be considered. Surfstat is a free software tool which performs statistical analysis of univariate and multivariate surface and volumetric data using linear mixed effects models and random field theory. Since SurfStat is also matlab-based, it is straightforward to integrate SurfStat with SPHARM-MAT for statistical surface analysis. For example, one can first use SPHARM-MAT to model and align surfaces and extract surface signals, and then use SurfStat for statistical inference on the surface.

6.1 Exercise 6.1 T Test

This exercise was tested on a WinXP machine (3GHz CPU, 3.25G RAM) running Matlab 7.7.0 (R2008b). It took a few minutes to finish.

Major Steps

1. T Test
2. Stat Visualization

6.1.1 T Test

Task

Perform a vertex-by-vertex t test on a surface manifold.

Input

`SpharmMatDir/data/Ex0601/hip06_reg/*_reg.mat`: This folder is a copy of `SpharmMatDir/data/Ex0502/hip06_reg/*_reg.mat`. Group 1 contains `a*_reg.mat` objects and Group 2 contains `b*_reg.mat` objects

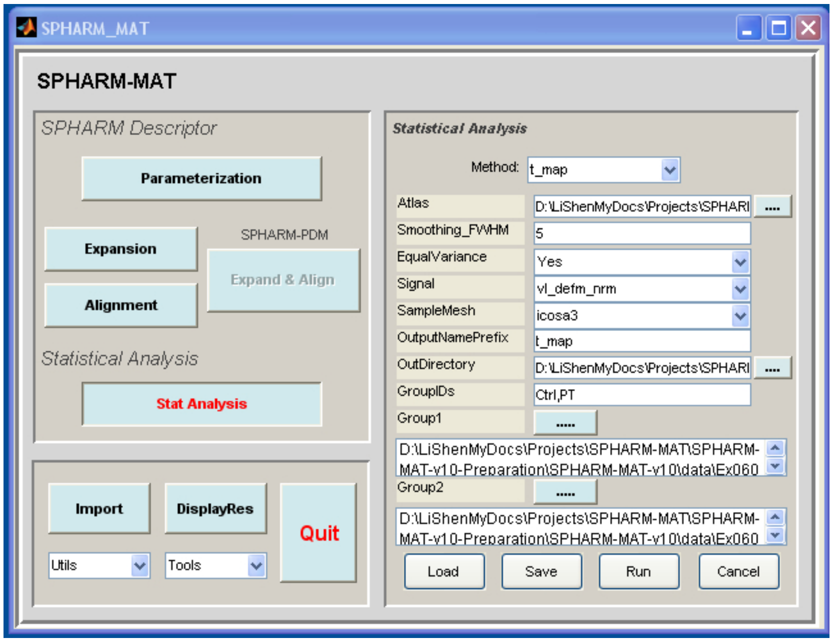
`SpharmMatDir/data/Ex0601/hip07_atlas/atlas.mat`: The template surface or atlas

Output

`SpharmMatDir/data/Ex0601/hip08_stat/*.mat`: Resulting statistics

Steps

1. Make an output directory `SpharmMatDir/data/Ex0601/hip08_stat/`
2. Run **SPHARM_MAT.m** under Matlab
3. Click **Stat Analysis** button
4. In the right panel, let **Method** be *t_map*
5. In the right panel, let **Atlas** be `SpharmMatDir/data/Ex0601/hip07_atlas/atlas.mat`, **Smoothing_FWHM** be *5*, **EqualVariance** be *Yes*, **Signal** be *vl_defm_nrm*, **SampleMesh** be *icosa3*, **OutputNamePrefix** be *t_map*, **OutDirectory** be `SpharmMatDir/data/Ex0601/hip08_stat`, **GroupIDs** be *Ctrl,PT*,
6. In the right panel, click `.....` button next to **Group1**, and select all the `a*_reg.mat` files under `SpharmMatDir/data/Ex0601/hip06_reg` as Group 1 files
7. In the right panel, click `.....` button next to **Group2**, and select all the `b*_reg.mat` files under `SpharmMatDir/data/Ex0601/hip06_reg` as Group 2 files
8. Click **OK** button (See *Screen Capture for T Test*)



Method: t_map
Atlas: D:\LiShenMyDocs\Projects\SPHARI
Smoothing_FWHM: 5
EqualVariance: Yes
Signal: vl_defm_nrm
SampleMesh: icosa3
OutputNamePrefix: t_map
OutDirectory: D:\LiShenMyDocs\Projects\SPHARI
GroupIDs: Ctrl,PT
Group1: D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v1.0-Preparation\SPHARM-MAT-v1.0\data\Ex060
Group2: D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v1.0-Preparation\SPHARM-MAT-v1.0\data\Ex060

Figure 6.1: Screen Capture for T Test

6.1.2 Stat Visualization

Task

Visualize statistical maps: t-map and p-map

Input

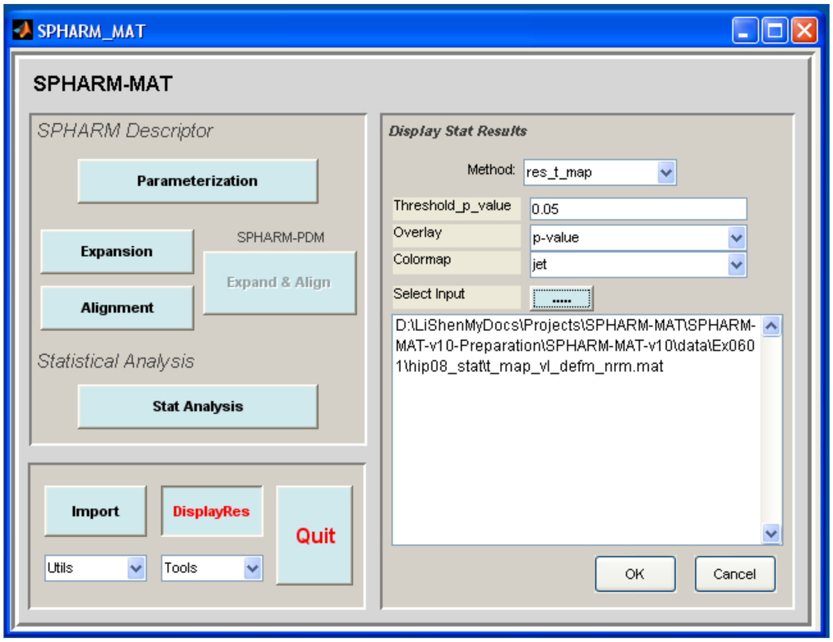
`SpharmMatDir/data/Ex0601/hip08_stat/t_map*.mat`

Output

Figure on the screen

Steps

1. Click **DisplayRes** button
2. In the right panel, let **Method** be *res_t_map*, **Threshold_p_value** be *0.05*, **Colormap** be *jet*
3. **Be sure to run this experiments twice by setting different configurations in the right panel as follows**
    - Run 1: let **Overlay** be *t-map*
    - Run 2: let **Overlay** be *p-value*
4. In the right panel, click `.....` button next to **Select Input**, and select the `t_map*.mat` files under `SpharmMatDir/data/Ex0601/hip08_stat`
5. Click **OK** button (See *Screen Capture for Stat Visualization*)



Method: res_t_map
Threshold_p_value 0.05
Overlay p-value
Colormap jet
Select Input

D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex0601\hip08_stat\t_map_vl_defm_nrm.mat

Figure 6.2: Screen Capture for Stat Visualization

Notes

- The visualization results are rendered on the screen (see *Stat Visualization (t-map, p-map)*)
- Only significant regions (uncorrected p<0.05) are color-mapped
- For getting corrected p values, see [Worsley2008] and [Chung2005]

6.1.3 Relevant Information

Useful Tips

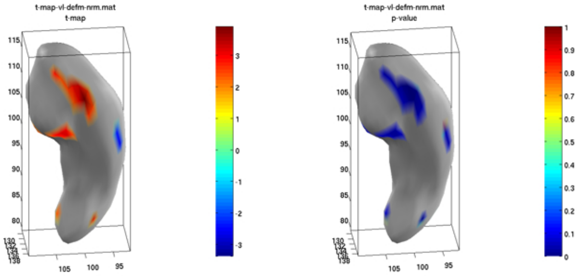


Figure 6.3: Stat Visualization (t-map, p-map)

- *Stat Analysis T Map Parameters*
- *DisplayRes T-Map Parameters*
- *Data Structure*
- *File Selection*

6.2 Exercise 6.2 PCA

This exercise was tested on a WinXP machine (3GHz CPU, 3.25G RAM) running Matlab 7.7.0 (R2008b). It took a few minutes to finish.

Major Steps

1. PCA
2. PCA Visualization

6.2.1 PCA

Task

Perform principal component analysis on SPHARM coefficients.

Input

`SpharmMatDir/data/Ex0602/hip06_reg/*_reg.mat`: This folder is a copy of `SpharmMatDir/data/Ex0502/hip06_reg/*_reg.mat`

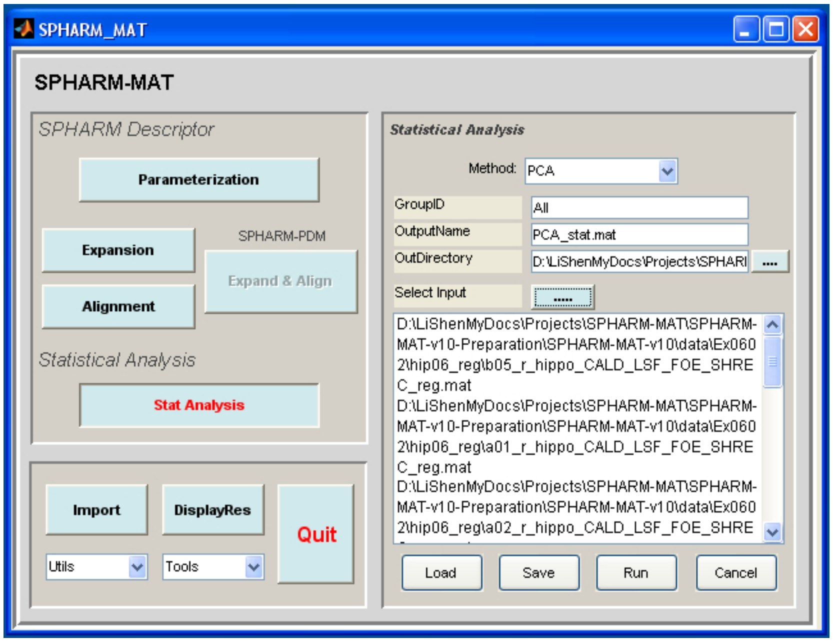
Output

`SpharmMatDir/data/Ex0602/hip07_stat/PCA_stat*.mat`: Resulting statistics

Steps

1. Make an output directory `SpharmMatDir/data/Ex0602/hip07_stat/`
2. Run **SPHARM_MAT.m** under Matlab
3. Click **Stat Analysis** button
4. In the right panel, let **Method** be *PCA*
5. In the right panel, let **GroupID** be *All*, **OutputName** be *PCA_stat.mat*, **OutDirectory** be `SpharmMatDir/data/Ex0602/hip07_stat`

6. In the right panel, click `.....` button next to **Select Input**, and select all the `*_reg.mat` files under `SpharmMatDir/data/Ex0602/hip06_reg` as input files
7. Click **OK** button (See *Screen Capture for PCA*)



Method: PCA

GroupID: All

OutputName: PCA_stat.mat

OutDirectory: D:\LiShenMyDocs\Projects\SPHARI

Select Input

```
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-
MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex060
2\hip06_reg\b05_r_hippo_CALD_LSF_FOE_SHRE
C_reg.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-
MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex060
2\hip06_reg\a01_r_hippo_CALD_LSF_FOE_SHRE
C_reg.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-
MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex060
2\hip06_reg\a02_r_hippo_CALD_LSF_FOE_SHRE
```

Figure 6.4: Screen Capture for PCA

6.2.2 PCA Visualization

Task

Visualize PCA modes

Input

`SpharmMatDir/data/Ex0602/hip07_stat/PCA_stat*.mat`

Output

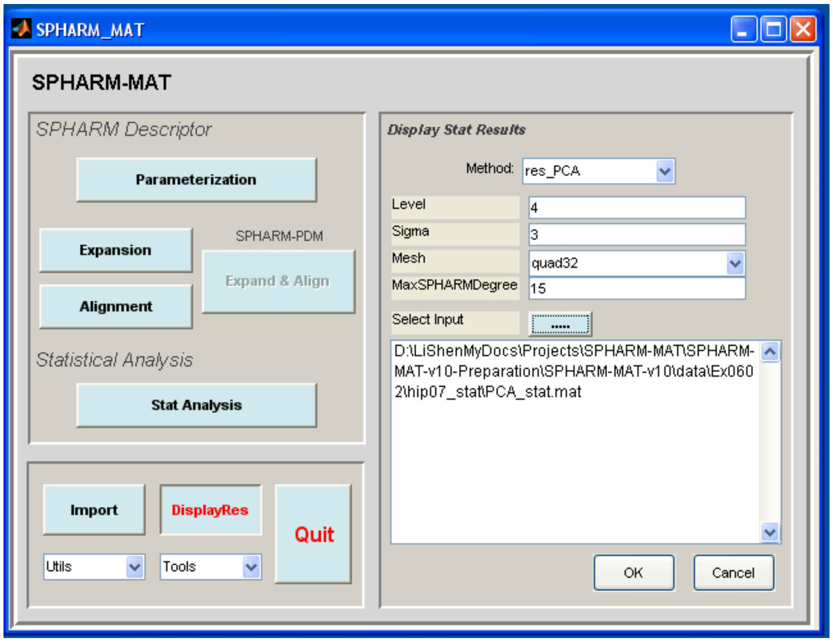
Figure on the screen

Steps

1. Click **DisplayRes** button
2. In the right panel, let **Method** be *res_PCA*
3. In the right panel, let **Level** be *4*, **Sigma** be *3*, **Mesh** be *quad32*, **MaxSPHARMDegree** be *15*,
4. In the right panel, click `.....` button next to **Select Input**, and select the `PCA_stat*.mat` files under `SpharmMatDir/data/Ex0602/hip07_stat`
5. Click **OK** button (See *Screen Capture for PCA Visualization*)

Notes

- The visualization results are rendered on the screen (see *PCA Visualization*)
- For details about such a visualization, see [Shen2008]



Method: res_PCA

Level: 4

Sigma: 3

Mesh: quad32

MaxSPHARMDegree: 15

Select Input: D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex0602\hip07_stat\PCA_stat.mat

Figure 6.5: Screen Capture for PCA Visualization

Figure 6.6: PCA Visualization

6.2.3 Relevant Information

Useful Tips

- *Stat Analysis T Map Parameters*
- *DisplayRes T-Map Parameters*
- *Data Structure*
- *File Selection*

CHAPTER SEVEN

OTHER UTILITIES

This chapter demonstrates three SPHARM-MAT utilities.

Exercise 7.1 Import shows how to import (1) binary images stored as nifti and analyze files and (2) surface objects stored as stl and Amira matlab files.

Exercise 7.2 Average Objects shows how to create an average surface, which can be used as the atlas in group analysis. In a typical study, you can select a set of control objects and run this utility to create an atlas that represents an average normal surface. This utility implements the following steps: (1) let the atlas be the first model; (2) align each model to the atlas using SHREC; (3) let the atlas be the mean of all the data; and (4) repeat (2) and (3) until the atlas converges. See *Surface Visualization (icosa4)* for an example atlas. Once the atlas is created, you can use SHREC to register all the individual objects to the atlas (instead of using an individual object as the template, which was used in *Exercise 5.2 SHREC Alignment*).

Exercise 7.3 Scale Objects shows how to scale a set of SPHARM objects. The scaling factors need to be pre-computed by users and provided as a csv file as an input file.

7.1 Exercise 7.1 Import

This exercise was tested on a WinXP machine (3GHz CPU, 3.25G RAM) running Matlab 7.7.0 (R2008b). It took a few minutes to finish.

Major Steps

1. Import
2. Surface Visualization (Solid with Mesh)

7.1.1 Import

Task

Import surface meshes and binary objects of various different formats

Input

`SpharmMatDir/data/Ex0701/hip00_org/*_surf.m`: Amira matlab surface mesh

`SpharmMatDir/data/Ex0701/hip00_org/*_bim.*`: Analyze binary objects

`SpharmMatDir/data/Ex0701/hip00_org/*_surf.stl`: STL surface mesh

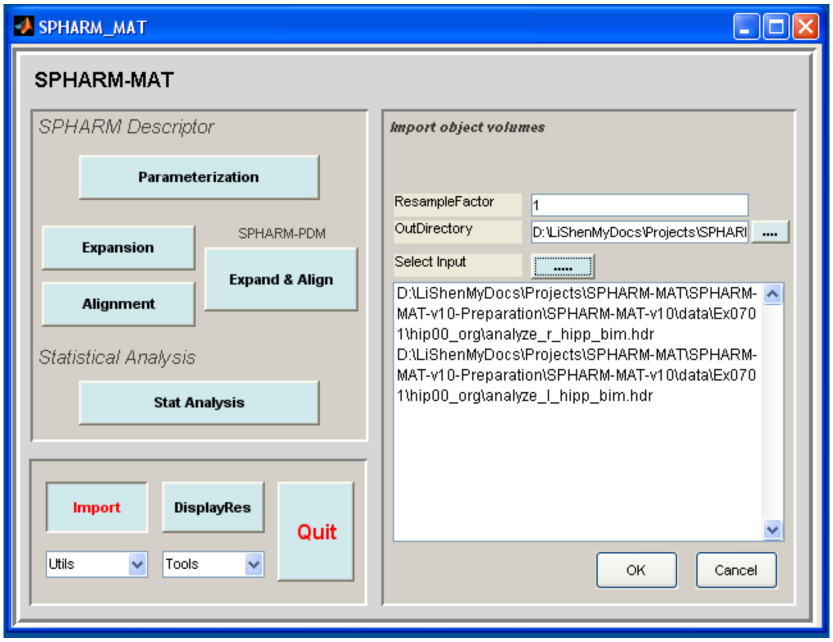
Output

`SpharmMatDir/data/Ex0701/hip01_res/*_obj.mat`: Surface meshes

`SpharmMatDir/data/Ex0701/hip01_res/*_bim.mat`: Binary objects

Steps

1. Make an output directory `SpharmMatDir/data/Ex0701/hip01_res`
2. Run **SPHARM_MAT.m** under Matlab
3. Click **Import** button
4. In the right panel, let **ResampleFactor** be *1*
5. In the right panel, select `SpharmMatDir/data/Ex0701/hip01_res` as **OutDirectory**
6. Be sure to run this experiment three times by selecting the following files as input files
    - `*_surf.m` files under `SpharmMatDir/data/Ex0701/hip00_org`
    - `*_bim.hdr` files under `SpharmMatDir/data/Ex0701/hip00_org`
    - `*_surf.stl` files under `SpharmMatDir/data/Ex0701/hip00_org`
7. Click **OK** button (See *Screen Capture for Import*)



ResampleFactor: 1

OutDirectory: D:\LiShenMyDocs\Projects\SPHARI

Select Input:

D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex0701\hip00_org\analyze_r_hipp_bim.hdr
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex0701\hip00_org\analyze_l_hipp_bim.hdr

Figure 7.1: Screen Capture for Import

7.1.2 Surface Visualization (Solid with Mesh)

Task

Visualize binary objects or surface meshes

Input

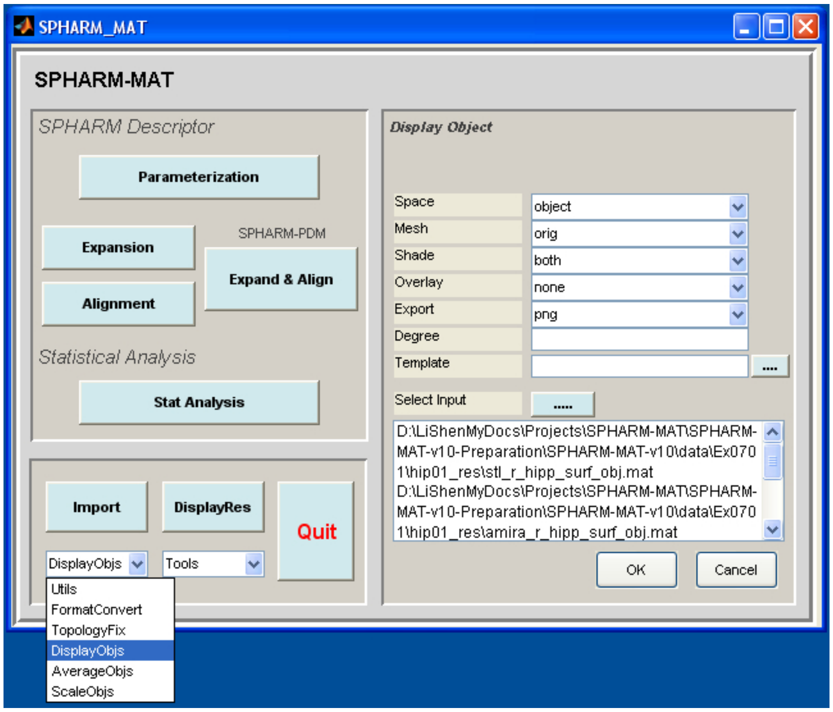
`SpharmMatDir/data/Ex0701/hip01_res/*.mat`

Output

```
SpharmMatDir/data/Ex0701/hip01_res/PNG/*.png
```

Steps

1. Select **DisplayObjs** under the **Utils** pop-up menu (bottom-left corner)
2. In the right panel, let **Space** be *object*, **Mesh** be *orig*, **Shade** be *both*, **Overlay** be *none*, **Export** be *png*, **Degree** be *empty*
3. In the right panel, click `.....` button next to **Select Input**, and select all the `SpharmMatDir/data/Ex0701/hip01_res/*.mat` files as input files
4. Click **OK** button (See *Screen Capture for Surface Visualization (Solid with Mesh)*)



Space: object
Mesh: orig
Shade: both
Overlay: none
Export: png
Degree:
Template:
Select Input: .....

D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex0701\hip01_res\stl_r_hipp_surf_obj.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex0701\hip01_res\amira_r_hipp_surf_obj.mat

Figure 7.2: Screen Capture for Surface Visualization (Solid with Mesh)

Notes

- The visualization results are saved as PNG files under `SpharmMatDir/data/Ex0701/hip01_res/PNG`
- Sample visualization results are shown in *Surface Visualization (Solid with Mesh)*.

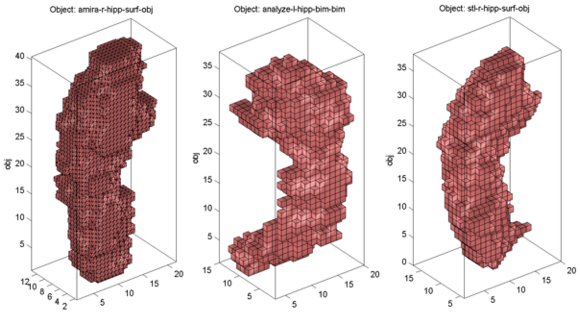


Figure 7.3: Surface Visualization (Solid with Mesh)

7.1.3 Relevant Information

Useful Tips

- *Import Parameters*
- *DisplayObjs Space Option*
- *DisplayObjs Shade Option*
- *DisplayObjs Export Option*
- *DisplayObjs Degree Option*
- *Data Structure*
- *File Selection*

7.2 Exercise 7.2 Average Objects

This exercise was tested on a WinXP machine (3GHz CPU, 3.25G RAM) running Matlab 7.7.0 (R2008b). It took a few minutes to finish.

Major Steps

1. Average Objects
2. Surface Visualization (icosa4)

7.2.1 Average Objects

Task

> Create an average by iteratively aligning all the individual objects together

Input

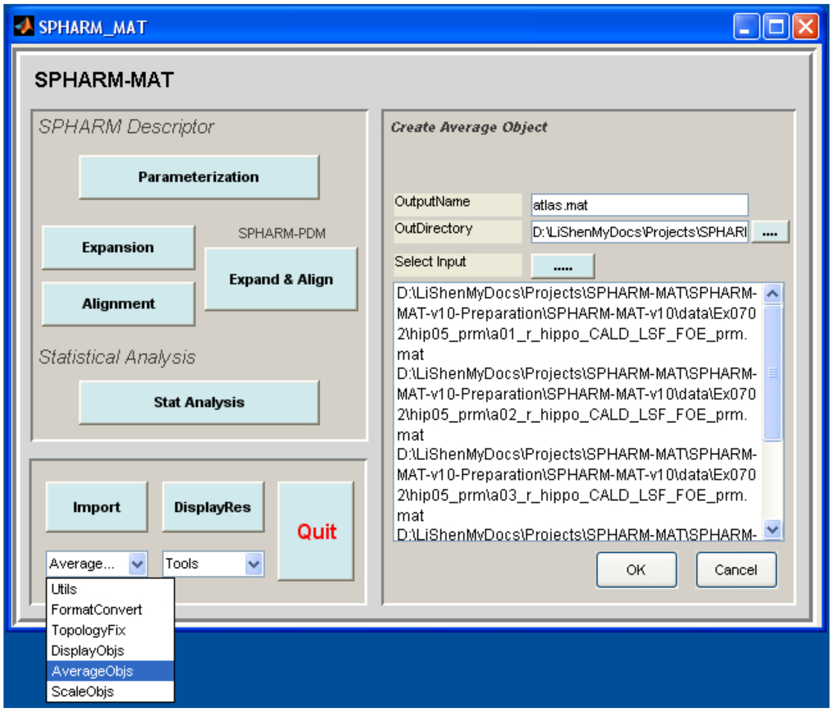
> `SpharmMatDir/data/Ex0702/hip05_prm/*_prm.mat`: This folder is a subset of `SpharmMatDir/data/Ex0501/hip05_reg/alignParam/*_prm.mat`, where only right hippocampi of controls are included.

Output

> `SpharmMatDir/data/Ex0702/hip06_reg/*.*`: `atlas.mat` is the average, `*_als.mat` files are individuals registered to the atlas.

Steps

1. Make an output directory `SpharmMatDir/data/Ex0702/hip05_prm/`
2. Run **SPHARM_MAT.m** under Matlab
3. Select **AverageObjs** under the **Utils** pop-up menu (bottom-left corner)
4. In the right panel, let **OutputName** be *atlas*.
5. In the right panel, select `SpharmMatDir/data/Ex0702/hip06_reg` as **OutDirectory**
6. In the right panel, click `.....` button next to **Select Input**, and select all the `*_prm.mat` files under `SpharmMatDir/data/Ex0702/hip05_prm` as input files
7. Click **OK** button (See *Screen Capture for Average Objects*)



OutputName: atlas.mat

OutDirectory: D:\LiShenMyDocs\Projects\SPHARI

D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex0702\hip05_prm\a01_r_hippo_CALD_LSF_FOE_prm.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex0702\hip05_prm\a02_r_hippo_CALD_LSF_FOE_prm.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex0702\hip05_prm\a03_r_hippo_CALD_LSF_FOE_prm.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-

Figure 7.4: Screen Capture for Average Objects

7.2.2 Surface Visualization (icosa4)

Task

Visualize SPHARM reconstructions in the object space

Input

`SpharmMatDir/data/Ex0702/hip06_reg/*_alt.mat`

Output

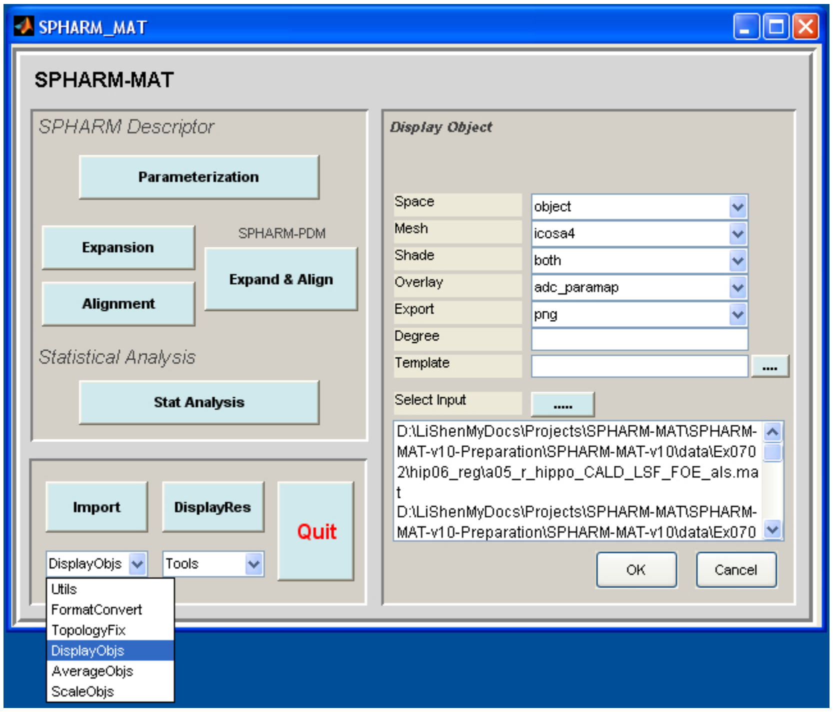
`SpharmMatDir/data/Ex0702/hip06_reg/PNG/*.png`

Steps

1. Select **DisplayObjs** under the **Utils** pop-up menu (bottom-left corner)
2. In the right panel, let **Space** be *object*, **Mesh** be *icosa4*, **Shade** be *both*, **Overlay** be *adc_paramap*, **Export** be *png*, **Degree** be *empty*
3. In the right panel, click `.....` button next to **Select Input**, and select all the `SpharmMatDir/data/Ex0702/hip06_reg/*_des.mat` files as the input files
4. Click **OK** button (See *Screen Capture for Surface Visualization (icosa4)*)

Notes

- The visualization results are saved as PNG files under `SpharmMatDir/data/Ex0702/hip06_reg/PNG/`.
- In *Surface Visualization (icosa4)*, the average object (i.e., the atlas) is shown in the left panel, while two sample individuals registered to the atlas are shown in the middle and right panels respectively.



Space	object
Mesh	icosa4
Shade	both
Overlay	adc_paramap
Export	png
Degree	
Template	
Select Input	.....

D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex0702\hip06_reg\a05_r_hippo_CALD_LSF_FOE_als.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex070

Figure 7.5: Screen Capture for Surface Visualization (icosa4)

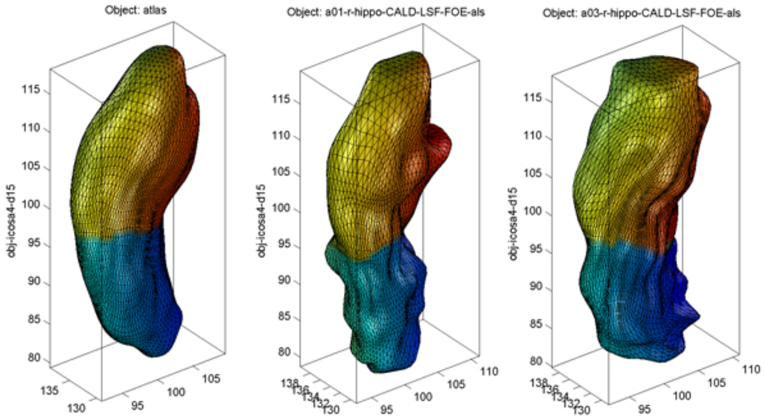


Figure 7.6: Surface Visualization (icosa4)

7.2.3 Relevant Information

Useful Tips

- *AverageObjs Parameters*
- *DisplayObjs Space Option*
- *DisplayObjs Shade Option*
- *DisplayObjs Export Option*
- *DisplayObjs Degree Option*
- *Data Structure*
- *File Selection*

7.3 Exercise 7.3 Scale Objects

This exercise was tested on a WinXP machine (3GHz CPU, 3.25G RAM) running Matlab 7.7.0 (R2008b). It took a few minutes to finish.

Major Steps

1. Scale Objects
2. Surface Visualization (orig, icosa4)

7.3.1 Scale Objects

Task

Scale objects using user-specified scaling information

Input

`SpharmMatDir/data/Ex0703/hip04_des/*_des.mat`: This folder is a copy of `SpharmMatDir/data/Ex0401/hip04_des/*_des.mat`.

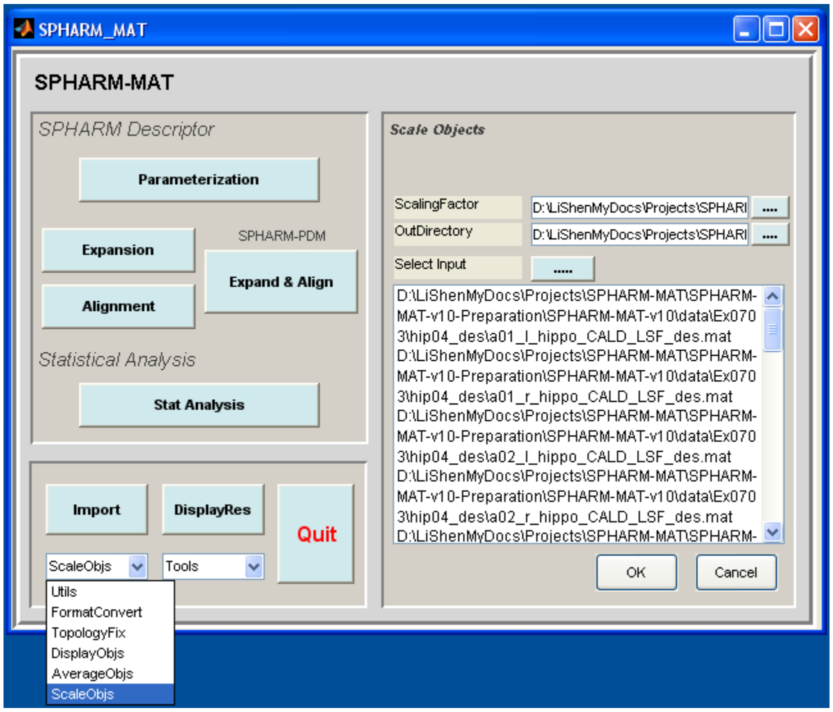
`SpharmMatDir/data/Ex0703/hip05_scl/volume_sf.csv`: User-specified scaling factors

Output

`SpharmMatDir/data/Ex0703/hip05_scl/*_scl_des.mat`

Steps

1. Make an output directory `SpharmMatDir/data/Ex0703/hip05_scl/`
2. Run **SPHARM_MAT.m** under Matlab
3. Select **ScaleObjs** under the **Utils** pop-up menu (bottom-left corner)
4. In the right panel, let **ScalingFactor** be `SpharmMatDir/data/Ex0703/hip05_scl/volume_sf.csv`.
5. In the right panel, select `SpharmMatDir/data/Ex0703/hip05_scl` as **OutDirectory**
6. In the right panel, click `.....` button next to **Select Input**, and select all the `*_des.mat` files under `SpharmMatDir/data/Ex0703/hip04_des` as input files
7. Click **OK** button (See *Screen Capture for Scale Objects*)



ScalingFactor: D:\LiShenMyDocs\Projects\SPHARI

OutDirectory: D:\LiShenMyDocs\Projects\SPHARI

Select Input

```
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-
MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex070
3\hip04_des\a01_l_hippo_CALD_LSF_des.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-
MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex070
3\hip04_des\a01_r_hippo_CALD_LSF_des.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-
MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex070
3\hip04_des\a02_l_hippo_CALD_LSF_des.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-
MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex070
3\hip04_des\a02_r_hippo_CALD_LSF_des.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-
```

Figure 7.7: Screen Capture for Scale Objects

7.3.2 Surface Visualization (orig, icosa4)

Task

Visualize original surface and SPHARM reconstructions in the object space

Input

`SpharmMatDir/data/Ex0703/hip04_des/*_des.mat`: before scaling

`SpharmMatDir/data/Ex0703/hip05_scl/*_scl_des.mat`: after scaling

Output

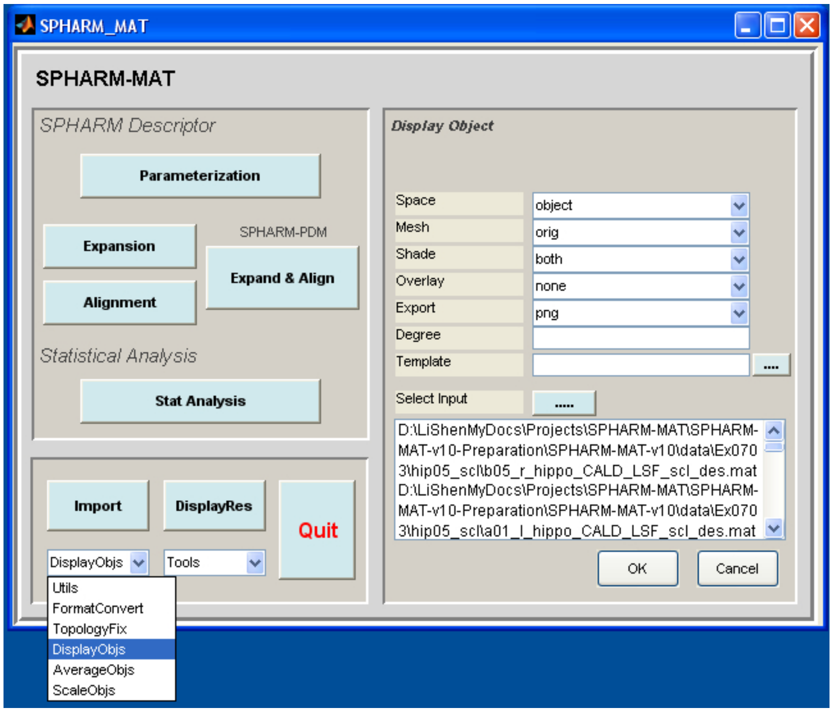
`SpharmMatDir/data/Ex0703/hip04_des/PNG/*.png`

`SpharmMatDir/data/Ex0703/hip05_scl/PNG/*.png`

Steps

1. Select **DisplayObjs** under the **Utils** pop-up menu (bottom-left corner)
2. Be sure to run this experiments four times by setting different configurations in the right panel as follows
   - Run 1 and Run 3: let **Space** be *object*, **Mesh** be *orig*, **Shade** be *both*, **Overlay** be *adc_paramap*, **Export** be *png*, **Degree** be *empty*
   - Run 2 and Run 4: let **Space** be *object*, **Mesh** be *icosa4*, **Shade** be *both*, **Overlay** be *adc_paramap*, **Export** be *png*, **Degree** be *empty*
3. In the right panel, click `.....` button next to **Select Input**, and select the following files in four different runs respectively
   - Run 1 and Run 2: `SpharmMatDir/data/Ex0703/hip04_des/*_des.mat`
   - Run 3 and Run 4: `SpharmMatDir/data/Ex0703/hip05_scl/*_scl_des.mat`

4. Click **OK** button (See *Screen Capture for Surface Visualization (orig, icosa4)*)



Space: object
Mesh: orig
Shade: both
Overlay: none
Export: png
Degree:
Template:
Select Input:
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex0703\hip05_scl\b05_r_hippo_CALD_LSF_scl_des.mat
D:\LiShenMyDocs\Projects\SPHARM-MAT\SPHARM-MAT-v10-Preparation\SPHARM-MAT-v10\data\Ex0703\hip05_scl\a01_l_hippo_CALD_LSF_scl_des.mat

Figure 7.8: Screen Capture for Surface Visualization (orig, icosa4)

Notes

- The visualization results are saved as PNG files under `SpharmMatDir/data/Ex0703/hip04_des/PNG` and `SpharmMatDir/data/Ex0703/hip05_scl/PNG`.
- In *Surface Visualization (orig, icosa4)*, the original surface and its SPHARM reconstruction before scaling are shown in the left two panels, while the results after scaling are shown in the right panels. Although the shapes are the same, the scales on the axes are different.

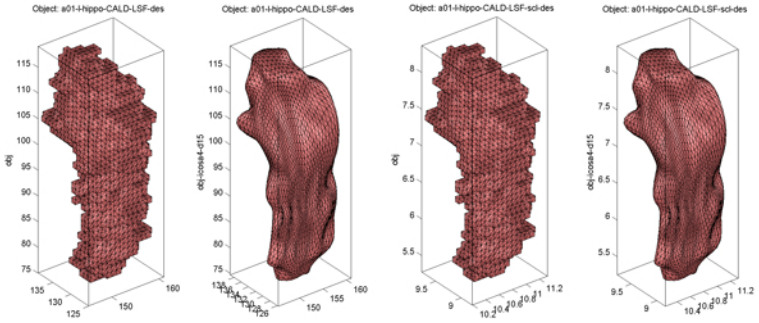


Figure 7.9: Surface Visualization (orig, icosa4)

7.3.3 Relevant Information

Useful Tips

- *ScaleObjs Parameters*

CHAPTER

EIGHT

SYSTEM COMPONENTS AND FEATURES

SPHARM-MAT is a multifaceted computational analysis tool which allows for the in-depth application of SPHARM expansion techniques to accurately describe the morphometric features of the brain, its various components or other 3D structures. By using a graphical user interface, the toolkit is easy to utilize and allows for enhanced user control in order to specify settings appropriate for each unique study; see *Tutorial and Processing Pipeline*. Matlab command line scripts are also provided to help users write their own batch scripts; see *Command Line and Batch Processing*. This chapter organizes relevant information according to the functional components arranged on the GUI.

8.1 Parameterization

Relevant chapters

- *Spherical Parameterization*

Relevant exercises

- *Exercise 3.1 Surface Meshes (CALD)*
- *Exercise 3.2 Voxel Surfaces (CALD)*
- *Exercise 3.3 Voxel Surfaces (PDM)*

Relevant tips

- *Parameterization CALD Input and Output*
- *Parameterization CALD Parameters*
- *Parameterization PDM Input*
- *Parameterization PDM Parameters*

8.2 Expansion

Relevant chapters

- *SPHARM Expansion*

Relevant exercises

- *Exercise 4.1 SPHARM-MAT Expansion*

- *Exercise 4.2 SPHARM-PDM Expansion*

Relevant tips

- *SPHARM Expansion Degree*
- *SPHARM Expansion PDM Difference*
- *Expand and Align Parameters*

8.3 Alignment

Relevant chapters

- *SPHARM Expansion*
- *Surface Alignment*

Relevant exercises

- *Exercise 5.1 FOE Alignment*
- *Exercise 5.2 SHREC Alignment*
- *Exercise 5.3 SPHARM-PDM FOE Alignment*

Relevant tips

- *Alignment FOE Parameters*
- *Alignment SHREC Parameters*
- *Expand and Align Parameters*

8.4 Expand & Align

Relevant chapters

- *Surface Alignment*

Relevant exercises

- *Exercise 4.2 SPHARM-PDM Expansion*
- *Exercise 5.3 SPHARM-PDM FOE Alignment*

Relevant tips

- *Expand and Align Parameters*

8.5 Stat Analysis

Relevant chapters

- *Statistical Analysis*

Relevant exercises

- *Exercise 6.1 T Test*
- *Exercise 6.2 PCA*

Relevant tips

- *Stat Analysis T Map Parameters*
- *Stat Analysis PCA Parameters*

8.6 Import

Relevant chapters

- *Other Utilities*

Relevant exercises

- *Exercise 7.1 Import*

Relevant tips

- *Import Parameters*

8.7 Display Res

Relevant chapters

- *Statistical Analysis*

Relevant exercises

- *Exercise 6.1 T Test*
- *Exercise 6.2 PCA*

Relevant tips

- *DisplayRes T-Map Parameters*
- *DisplayRes PCA Parameters*

8.8 Utils

8.8.1 FormatConvert

Relevant exercises

- *Exercise 2.2: SPHARM-PDM Topology Fix*
- *Exercise 3.3 Voxel Surfaces (PDM)*
- *Exercise 4.2 SPHARM-PDM Expansion*
- *Exercise 5.3 SPHARM-PDM FOE Alignment*

Relevant tips

- *Format Conversion for Binary Objects*
- *Format Conversion for Surface Meshes*
- *Format Conversion for SPHARM Models*

8.8.2 TopologyFix

Relevant chapters

- *Data Preparation*

Relevant exercises

- *Exercise 2.1: In-house Topology Fix*
- *Exercise 2.2: SPHARM-PDM Topology Fix*

Relevant tips

- *TopologyFix InHouse_Fix Option*
- *TopologyFix PDM_Fix Option*

8.8.3 DisplayObjs

Relevant exercises

- *Exercise 2.1: In-house Topology Fix*
- *Exercise 2.2: SPHARM-PDM Topology Fix*
- *Exercise 3.1 Surface Meshes (CALD)*
- *Exercise 3.2 Voxel Surfaces (CALD)*
- *Exercise 3.3 Voxel Surfaces (PDM)*
- *Exercise 4.1 SPHARM-MAT Expansion*
- *Exercise 5.1 FOE Alignment*
- *Exercise 5.2 SHREC Alignment*
- *Exercise 5.3 SPHARM-PDM FOE Alignment*

Relevant tips

- *DisplayObjs Space Option*
- *DisplayObjs Mesh Option*
- *DisplayObjs Shade Option*
- *DisplayObjs Overlay Option*
- *DisplayObjs Export Option*
- *DisplayObjs Degree Option*
- *DisplayObjs Template Option*

8.8.4 AverageObjs

Relevant chapters

- *Other Utilities*

Relevant exercises

- *Exercise 7.2 Average Objects*

Relevant tips

- *AverageObjs Parameters*

8.8.5 ScaleObjs

Relevant chapters

- *Other Utilities*

Relevant exercises

- *Exercise 7.3 Scale Objects*

Relevant tips

- *ScaleObjs Parameters*

8.9 Tools

- CD - Change directory
- PWD - Show current directory
- Config - Define SPHARM-PDM path for PC and UNIX

8.10 Quit

- Quit SPHARM-MAT.

CHAPTER

NINE

TIPS

This chapter provides a list of tips that address various SPHARM-MAT issues, including strengths, limitations, parameter settings, options, etc.

9.1 File Selection

Matlab starts navigation for file selection from the current directory. Thus, to minimize the effort of finding your data, you can change matlab current directory to your data directory if you want to work on the same data for a while.

9.2 ADC Calculation for Voxel Surface and Its Triangulation

We notice that the ADC values of SPHARM-PDM results are often extremely high; see *Surface Visualization (ADC_ParaMap, Solid with Mesh)* for an example. Some relevant discussion is provided below.

- First of all, the spherical parameterization created by SPHARM-PDM is a very high quality area preserving mapping for voxel surfaces, where each square face is mapped to a spherical quadrilateral with the same relative area.
- The major reason here is that our area distortion cost is calculated based on triangles instead of quadrilaterals. SPHARM-PDM creates an equal area mapping between quadrilaterals on the object space and parameter space. However, this area preserving property no longer holds for a triangulation of the same surface, where the triangulation is created by splitting each quadrilateral into two triangles. On the object surface, each quadrilateral (a square for the voxel surface case) always splits into two triangles with the same area, while this is not true on the parameter surface. Consequently, higher ADC values are generated from triangulation-based calculation for area distortion.
- In particular, for very slim quadrilaterals on the sphere, if the long diagonal happens to be selected for generating triangles, some of these triangles might have an area close to zero or even flipped. In these cases, very high ADCs are introduced.
- As mentioned in [Quicken2000], imposing constraints on area preservation results in only two degrees of freedom for distortion minimization for triangular meshes. However, for quadrilateral meshes, there are n degrees of freedom available, where n is the number of vertices on the surface. As a result, in terms of spherical parameterization, it is much more difficult to generate an area preserving map for a triangular mesh than a quadrilateral mesh of the same surface. This is another reason why an equal area mapping for a quadrilateral mesh does not imply an equal area mapping for the corresponding triangulation.
- Finally, even though the ADCs are high, SPHARM-PDM is still highly recommended for parameterizing voxel surfaces. Based on visual inspection, the PDM results usually preserve the area better than CALD ones; see *Surface Visualization (icosa4, Solid with Mesh)* and *Surface Visualization (quad64, Mesh)*.

9.3 Parameterization CALD Input and Output

Input

> Parameterization using *CALD* as **Method** can take a binary object, a triangular mesh, or a quadrilateral mesh as an input. For a binary object, SPHARM-MAT extracts its voxel surface and describes it as a triangular mesh. For a quadrilateral mesh, SPHARM-MAT converts it to a triangular mesh. In any case, the resulting triangular mesh needs to be a genus zero surface (i.e., with a spherical topology). If you work with binary images, be sure to run topology fix first (see *Data Preparation*).

Output

> Results of both initial parameterization and optimized parameterization are saved. See *Surface Visualization (ADC_ParaMap, Solid with Mesh)* for an example.

9.4 Parameterization CALD Parameters

Spherical parameterization using CALD has a few adjustable parameters shown below. In most cases, you can just use the default setting; see *Exercise 3.1 Surface Meshes (CALD)* and *Exercise 3.2 Voxel Surfaces (CALD)*.

- **MeshGridSize**: Used in global smoothing for creating regular meshes
- **MaxSPHARMDegree**: Used in global smoothing for interpolating the area scaling ratio functions
- **Tolerance**: Used in global smoothing for reducing extreme values
- **Smoothing**: Used in global smoothing for smoothing the area scaling ratio functions
- **Iteration**: Max number of iterations for global smoothing
- **LocalIteration**: Number of iterations in each local smoothing step
- **t_major**: x major smooths latitude first and longitude second, y major does the opposite. *This option was used in a previous implementation. It should be ignored in the current release.*
- **SelectDiagonal**: Used for converting quadrilaterals to triangles. ShortDiag uses the short diagonal to split the quadrilateral, LongDiag uses the long one for splitting. *This option was used in a previous implementation. It should be ignored in the current release.*

9.5 Parameterization PDM Input

Parameterization using *PDM* as **Method** takes a binary object as input. The surface of the binary object needs to be genus zero (i.e., with a spherical topology). To meet this requirement, be sure to run topology fix first (see *Data Preparation*).

9.6 Parameterization PDM Parameters

Parameterization using *PDM* as **Method** has a few adjustable parameters shown below. In most cases, you can just use the default setting; see *Exercise 3.3 Voxel Surfaces (PDM)*.

See Also:

SPHARM-PDM manual for further details about these parameters.

- **iter**: Max number of iterations (default 500)

- **label**: Binary volume is formed by all the voxels with value equal to the specified label (default 1)
- **others: Other command line parameters used in SPHARM-PDM**
  - *-outbase <basefile>*: base filename for output
  - *-initParam meshfile*: initialization of parameterization, file has to be a mesh of same triangle topology as the one extracted from the image
  - *-v*: verbose mode
  - *-vxml*: Display an XML description on the standard output

9.7 SPHARM Expansion Degree

The SPHARM coefficients $\mathbf{c}_l^m$ up to a user-desired degree are computed in SPHARM expansion step. The object surface can be reconstructed using these coefficients, and using more coefficients leads to a more detailed reconstruction; see *Surface Visualization (icosa4, Solid with Mesh)*.

SPHARM Expansion has the following parameter for users to specify the maximum degree; see *Exercise 4.1 SPHARM-MAT Expansion*.

- **MaxSPHARMDegree**: SPHARM coefficients up to this degree are stored in the model

9.8 SPHARM Expansion PDM Difference

The SPHARM coefficients computed by SPHARM-MAT (see *Exercise 4.1 SPHARM-MAT Expansion*) are complex numbers. The SPHARM coefficients computed by SPHARM-PDM (see *Exercise 4.2 SPHARM-PDM Expansion*) are real numbers, where the imaginary part of each coefficient is ignored.

9.9 Alignment FOE Parameters

Alignment using FOE has a few adjustable parameters shown below. In most cases, you can just use the default setting; see *Exercise 5.1 FOE Alignment*.

- **CPoint** {x/y/z}: CPoint is the crossing point of equator and zero meridian it should be on the positive side of x, y, or z axis in the object space
- **NPole** {x/y/z}: NPole is the north pole and it should be on the positive side of x, y, or z axis in the object space
- **MaxSPHARMDegree**: SPHARM coefficients up to this degree are stored in the results

9.10 Alignment SHREC Parameters

Alignment using SHREC has a few adjustable parameters shown below. In most cases, you can just use the default setting; see *Exercise 5.2 SHREC Alignment*.

- **Template**: To which all the SPHARM models are registered
- **MaxSPHARMDegree**: SPHARM coefficients up to this degree are stored in the results
- **GroupAlpha**: Number of rotations to be processed together (i.e., matrix operation instead of loop)
- **NormalizeSize** (Yes/No): If yes, do the scaling for normalizing the centroid size

- **BaseRes**: Base resolution of icosahedral subdivision to hierarchically sample the Euler rotation angles from icosahedral mesh.
- **HierarchyStep**: Step of hierarchical sampling scheme of Euler rotation angles (use 1 for now, >1 seems to be very slow, improvement needed).
- **HiderarchyDepth**: Depth of hierarchical sampling scheme of Euler rotation angles.
- **Top_K**: Number of selected angles at each iteration.
- **GammaRes**: Sampling resolution of gamma angles.

9.11 Alignment SHREC Initial Models

Initial SPHARM models for SHREC alignment: If the FOE of your data is a real ellipsoid having three distinct axes (e.g., like hippocampus), you may want to run FOE alignment first before doing SHREC. Note that the final results of FOE alignment do not preserve the original geometric information in the object space. Therefore, be sure to apply SHREC only to the intermediate results (i.e., `*_prm.mat` files in *Exercise 5.2 SHREC Alignment*) of FOE alignment. For these intermediate results, the orientation and the location of the objects have not been transformed in the object space; however, their parameter nets have been aligned to the canonical position so that an initial surface correspondence has been established among then.

9.12 Alignment SHREC Template

In SHREC alignment, a template needs to be specified so that all the individual SPHARM models can be registered to it. This template should be carefully picked or prepared. For a case-control group study, it could be an individual control object or the mean shape of a set of typical control objects (see *Exercise 7.2 Average Objects*). In addition, its underlying parameterization should be oriented to a canonical position. If the FOE of the template is a real ellipsoid, FOE alignment can be applied to achieve this goal, as described in *Alignment SHREC Initial Models*; otherwise, manual adjustment could be used to rotate the parameter net to a user-desired position.

9.13 Expand and Align Parameters

The `Expand & Align` button is provided for performing SPHARM expansion and FOE alignment using SPHARM-PDM. It has a few adjustable parameters shown below. In most cases, you can just use the default setting; see *Exercise 4.2 SPHARM-PDM Expansion* and *Exercise 5.3 SPHARM-PDM FOE Alignment*.

See Also:

SPHARM-PDM manual for further details about these parameters.

- **flipTemplate**: Set a fliptemplate for normalization of axis-flips (could be empty)
- **subdivLevel**: Set subdivision level for linear icosahedron subdivision
- **spharmDegree**: Set the degree of spherical harmonic expansion
- **regTemplate**: Specify a registration template (could be empty)
- **FinalFlip: Allows an optional additional flipping of the parameterization**
    - This is rarely necessary, only in case the general first order ellipsoid heuristic fails. Flipping of the parameterization ALONG a given axis will lead to a flip of the coordinates ALONG the same axis in the ellipse aligned mesh

  - There are 7 possibilities (1..7, 0 = no flip) of parameterization flipping along an axis
  - 1 = flip along axes of x & y, 2 = flip along y & z, 3 = flip along x & z, 4 = flip along x, 5 = flip along y, 6 = flip along x & y & z, 7 = flip along z, where y is the smallest, x is the second smallest and z is the long axis of the ellipsoid

- **Others:**
  - *-outbase <basefile>*: Set base filename for output (`*_surfSPHARM.coef`, `*_surfSPHARM.meta`, `*_surfSPHARM_ellalign.coef`, `*_surfSPHARM_ellalign.meta`, `*_surfSPHARM_procalign.meta`)
  - *-flipRegTemplate <meshfile>*: Set a template for parameter normalization and registration
  - *-flipRegPoints <points.samp>*: Set sample points on flipRegTemplate for parameter alignment
  - *-paraOut*: Write sphere parameterization and coloring to file
  - *-NoParaAlign*: Do not do any alignment/correspondence of the parameterization using the first order ellipsoid
  - *-v*: Verbose mode
  - *-vxml*: Display an XML description on the standard output

9.14 Stat Analysis T Map Parameters

Statistical analysis using t-map as method has a few adjustable parameters shown below. In most cases, you can just use the default setting; see *Exercise 6.1 T Test*.

- **Atlas**: The template surface used for extracting surface signals and for visualizing results
- **Smoothing_FWHM**: Size of kernel for surface signal smoothing using heat kernel method (see [Chung2005])
- **EqualVariance**: Equal variance assumption for t-test
- **Signal**: vl_defm_org, length of the deformation vector; vl_defm_nrm, deformation along normal direction of the atlas; vl_defm_pca, deformation component along PCA direction; vl_defm_fld, deformation component along FLD direction; see [Shen2006b] for details
- **SampleMesh**: Underlying mesh for SPHARM reconstruction
- **OutputNamePrefix**: Prefix of the name of the output statistics file
- **GroupIDs**: Group 1 ID and Group 2 ID separated by comma

9.15 Stat Analysis PCA Parameters

Statistical analysis using PCA as method has a few adjustable parameters shown below. In most cases, you can just use the default setting; see *Exercise 6.2 PCA*.

- **GroupID**: Group ID for selected objects
- **OutputName**: File name of output statistics

9.16 DisplayRes T-Map Parameters

DisplayRes using res-t-map as method has a few adjustable parameters shown below. In most cases, you can just use the default setting; see *Exercise 6.1 T Test*.

- **Threshold_p_value**: Regions with uncorrected p<threshold_p_value are color-mapped
- **Overlay**: Selection of p-value or t-map for display.
- **Colormap**: Selection of colormap, jet/hot/summer/cool/autumn/winter/spring.

9.17 DisplayRes PCA Parameters

DisplayRes using res-PCA as method has a few adjustable parameters shown below. In most cases, you can just use the default setting; see *Exercise 6.2 PCA*.

- **Level**: Number of principal components to display
- **Sigma**: Number of standard deviations in each principal component axis to display
- **Mesh**: Underlying mesh for SPHARM reconstruction, quad32/quad64/../quad512/icosa1/.../icosa6
- **MaxSPHARMDegree**: Maximum degree of SPHARM coefficients used for reconstruction

9.18 Import Parameters

Import utility does the following conversion (see *Exercise 7.1 Import*)

- Read in binary images in nifti and/or analyze formats and convert them to `*_bim.mat` files
- Read in surface meshes in stl and/or Amira matlab formats and convert them to `*_obj.mat` files

Import has the following parameter to adjust

- **ResampleFactor**: For upsampling (>1) or downsampling (<1) the input binary volumes (nifti and analyze); no effect on surface meshes (stl and Amira matlab).

9.19 Format Conversion for Binary Objects

SPHARM-MAT uses matlab format to store 3D binary objects (before topology fix: `*_bim.mat`; after topology fix: `*_fix.mat`). SPHARM-PDM uses gipl format to store 3D binary objects (`*.gipl`). **FormatConvert** under the **Utils** pop-up menu can be used for performing format conversion with the following three options:

- *bim2gipl*: Convert `*_bim.mat` to `*.gipl`; see *Screen shot for Format Conversion bim2gipl.*.
- *fix2gipl*: Convert `*_fix.mat` to `*.gipl`.
- *gipl2bim*: Convert `*.gipl` to `*_bim.mat`; see *Screen shot for Format Conversion gipl2bim*.

9.20 Format Conversion for Surface Meshes

SPHARM-MAT uses matlab format to store surfaces (original: `*_obj.mat`; after initial parameterization: `*_fix.mat`; after parameterization optimization: `*_smo.mat`). SPHARM-PDM uses META format to store object meshes (`*_surf.meta`) and parameter meshes (`*_para.meta`). **FormatConvert** under the **Utils** pop-up menu can be used for performing conversion between these formats:

- *surf_para_meta2smo*: Convert `*.meta` to `*_smo.mat`; see *Screen shot for Format Conversion surf_para_meta2smo.*.
- *smo2surf_para_meta*: Convert `*_smo.mat` to `*.meta`.

9.21 Format Conversion for SPHARM Models

SPHARM-MAT uses matlab format to store SPHARM models:

- in the original coordinate system: `*_des.mat`
- in the FOE/SHREC aligned coordinate system: `*_reg.mat`

SPHARM-PDM uses META format (i.e., surface meshes) and COEF format (i.e., SPHARM coefficients) to store SPHARM models:

- in the original coordinate system: `*_surfSPHARM.meta` and `*_surfSPHARM.coef`
- in the FOE aligned coordinate system: `*_surfSPHARM_ellalign.meta` and `*_surfSPHARM_ellalign.coef`
- in the Procrustes aligned coordinate system: `*_surfSPHARM_procalign.meta` (only reconstructed surface meshes available)

FormatConvert under the **Utils** pop-up menu can be used for performing conversion between these formats:

- *meta_coef2des*: Convert `*_surfSPHARM.meta` and `*_surfSPHARM.coef` to `*_des.mat`; see *Screen shot for Format Conversion meta_coef2des.*.
- *des2meta_coef*: Convert `*_des.mat` to `*.meta` and `*.coef`.
- *ellalign_meta_coef2reg*: Convert `*_surfSPHARM_ellalign.meta` and `*_surfSPHARM_ellalign.coef` to `*_reg.mat`; see *Screen shot for Format Conversion ellalign_meta_coef2reg.*.
- *reg2proalign_meta*: Convert `*_reg.mat` to `*_proalign.meta` and `*.coef`.

9.22 TopologyFix InHouse_Fix Option

TopologyFix under the **Utils** pop-up menu has two options for customizing 3D hole filing process if *Inhouse_Fix* is selected as **Method**:

- *Connectivity*: Neighborhood connectivity can be defined by one of the four options 1=(6+,18), 2=(18,6+), 3=(6,26), 4=(26,6). More details are available in http://dx.doi.org/10.1016/S0167-8655(01)00152-0.
- *Epsilon*: Hole size can be specified by voxel count so that holes bigger than Epsilon won't be filled.

See *Screen Capture for In-House Topology Fix*.

9.23 TopologyFix PDM_Fix Option

TopologyFix under the **Utils** pop-up menu has two options for customizing 3D hole filing process if *PDM_Fix* is selected as **Method**:

- *space*: You can define voxel size and SPHARM-PDM will re-slice the volume.
- *other*: You can define other command line options used by SPHARM-PDM.

See *Screen Shot for SPHARM-PDM Topology Fix*.

9.24 DisplayObjs Space Option

DisplayObjs under the **Utils** pop-up menu has three options for selection of visualizing the surface in object and/or parameter spaces:

- *object*: A surface is rendered in the object space (e.g., *Binary Object Visualization (Solid with Mesh)*).
- *param*: A surface is rendered in the parameter space.
- *both*: A surface is rendered in both object and parameter spaces (e.g., *Surface Visualization (ADC_ParaMap, Solid with Mesh)*).

9.25 DisplayObjs Mesh Option

DisplayObjs under the **Utils** pop-up menu has a few options for selecting mesh structures:

- *orig*: A original surface mesh is selected for rendering (e.g., *Binary Object Visualization (Solid with Mesh)*).
- *quad32-quad512*: A SPHARM reconstruction based on a regular 32-by-32, ... , or 512-by-512 mesh is rendered.
- *icosa1-icosa6*: A SPHARM reconstruction based on an icosahedral mesh at level 1, ... , or 6 is rendered.

9.26 DisplayObjs Shade Option

DisplayObjs under the **Utils** pop-up menu has three options for shading the surface:

- *solid*: A solid surface is rendered (e.g., *Screen Capture for Surface Visualization (ADC_ParaMap, Solid with Mesh)*).
- *mesh*: A surface mesh is rendered (e.g., *Binary Object Visualization (Mesh)*).
- *both*: A solid surface with mesh is rendered (e.g., *Binary Object Visualization (Solid with Mesh)*).

9.27 DisplayObjs Overlay Option

DisplayObjs under the **Utils** pop-up menu has an option for showing additional information

- *none*: No additional information is shown.
- ***adc_paramap*: This option has two functions.**
    1. If **Space** is set as *both*, the ADC (see *Area Distortion Cost*) will be calculated and displayed.
    2. If **Shade** is set as *solid* or *both*, a color map will be displayed on the surface to visualize the underlying parameterization. For north hemisphere (i.e., $0 \leq \theta \leq \pi/2$), the color goes from green (i.e., $\phi = 0$) to red (i.e., $\phi = 2\pi$); for south hemisphere (i.e., $\pi/2 \leq \theta \leq \pi$), the color goes from green (i.e., $\phi = 0$) to blue (i.e., $\phi = 2\pi$).

  The option could be used in the following scenarios.

  - To check the quality of spherical parameterization: See *Surface Visualization (ADC_ParaMap, Solid with Mesh)*, *Surface Visualization (ADC_ParaMap, Mesh)*, *Screen Capture for Surface Visualization (ADC_ParaMap, Solid with Mesh)* for a few examples.
  - To visualize the correspondence between SPHARM models: See *Surface Visualization (quad64, Degree 1)*, *Surface Visualization (quad64, template)*, *Screen Capture for Surface Visualization (quad64)* for a few examples.

9.28 DisplayObjs Export Option

DisplayObjs under the **Utils** pop-up menu has three options for exporting the figure:

- *screen*: The figure is displayed on screen.
- *png*: The figure is saved as a png file.
- *both*: The figure is displayed on screen and saved as a png file.

9.29 DisplayObjs Degree Option

DisplayObjs under the **Utils** pop-up menu has an option called `Degree` for specifying the user-desired degree for SPHARM reconstruction. If empty, all the available coefficients are used for SPHARM reconstruction; otherwise, the reconstructed surface is generated only using those coefficients up to the user-specified degree. See *Surface Visualization (icosa4, Solid with Mesh)*.

9.30 DisplayObjs Template Option

DisplayObjs under the **Utils** pop-up menu has an option called `Template` for specifying a template. This is often used when you want to display registered SPHARM models. If the template file exists, the root mean square distance between each input SPHARM model and the specified template model will be calculated and displayed on the z-axis. See *Surface Visualization (quad64, template)*.

9.31 AverageObjs Parameters

AverageObjs under the **Utils** pop-up menu aims to create an average surface, which can be used as the atlas in group analysis. In a typical study, you can select a set of control objects and run this utility to create an atlas that represents an average normal surface. The method is the following: (1) let the atlas be the first model; (2) align each model to the atlas using SHREC; (3) let the atlas be the mean of all the data; and (4) repeat (2) and (3) until the atlas converges. See *Surface Visualization (icosa4)*: for an example atlas. Once the atlas is created, you can use SHREC to register all the individual objects to the atlas (instead of using an individual object as the template, as shown in *Exercise 5.2 SHREC Alignment*). **AverageObjs** has the following parameter to adjust

- *OutputName*: Name of the output average surface.

9.32 ScaleObjs Parameters

ScaleObjs under the **Utils** pop-up menu can be used to scale a set of SPHARM objects. The scaling factors need to be pre-computed by users and provided as a csv file as an input file. See *Exercise 7.2 Average Objects*: for an example.

ScaleObjs has the following parameter to adjust

- *ScalingFactor*: A csv file specifying a scaling factor for each input file.

CHAPTER TEN

CHANGES

10.1 Release 1.0.0 (June 18, 2010)

Major features of this first release of SPHARM_MAT include

- Implementation of the SPHARM-MAT processing pipeline: data preparation, spherical parameterization, SPHARM expansion, surface alignment, and statistical analysis.
- Tutorial containing a set of exercises covering the entire processing pipeline: both GUI step-by-step instructions and command line batch scripts are available for all the exercises.

Known issues

- **DO NOT** use `.` as a part of your directory name (e.g., a directory called `SPHARM-MAT-v1.0.0`). Otherwise, *Exercise 3.3 Voxel Surfaces (PDM)* won't work.

CHAPTER

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BIBLIOGRAPHY

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