shapeAnalysisMANCOVA_Wizard

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University of North Carolina, Chapel Hill :
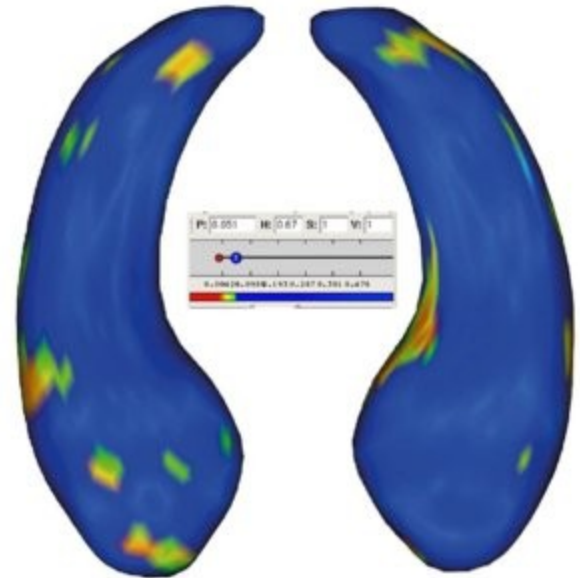Neuro Image Research and Analysis Lab

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NA-MIC Tutorial Contest: Summer 2011

Learning Objective

This tutorial shows how to perform statistical studies using :

➜ ShapeAnalysisMANCOVA

Prerequisites

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

The tutorial is available at:
http://www.slicer.org/slicerWiki/index.php/Slicer3.6:Training

This tutorial assumes that you have already completed the ShapeAnalysisModule Tutorial
(by Lucile Bompard)

The tutorial is available at:
http://www.nitrc.org/docman/index.php?group_id=308&selected_doc_group_id=758&language_id=1#folder

Material

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

They are available at the following locations:

➔ **Slicer3.6** download page

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

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

If you do not find it :

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

➔ **Tutorial dataset**:ShapeAnalysisMANCOVA_Wizard_TutorialData

http://www.nitrc.org/docman/index.php?
group_id=294&selected_doc_group_id=1966&language_id=1#folder

Platform

This tutorial has been developed and performed on Linux.

Prerequisites

➜ Use the View ⇀Extension Manager menu option ⇀Next

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

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

(The last release)

Overview

1- Input file

2- Pipeline description

3- Output images and organisation

4- Execution within Slicer / Qt

5- More details on the Wizard

6- Conclusion

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Input File

➜ A CSV file : **C**omma **S**eparated **V**alue
➜ Contains all the subjects information : age, group, MRI...
➜ Contains the path to the data.

```
Gender, SPHARM Surface in Original Space,
0,/.../data/groupA_01_hippo_pp_surfSPHARM_procalign.vtk
0,/.../data/groupA_02_hippo_pp_surfSPHARM_procalign.vtk
1,/.../data/groupB_01_hippo_pp_surfSPHARM_procalign.vtk
1,/.../data/groupB_02_hippo_pp_surfSPHARM_procalign.vtk
```

Fig: a CSV file.

The data set for this tutorial:
➜ Download and unzip :
ShapeAnalysisMANCOVA_Data_Example.zip

➜ All the hippocampus meshes needed are in the folder "/data"

➜ Modify the CSV file (4data) : replace the path of the data by yours.
   We will use the CSV with only 4 of the 40 hippocampus available, in order to increase the speed of the running

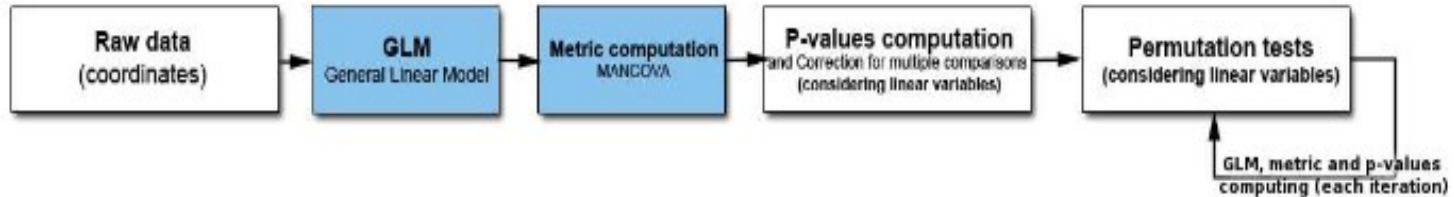**The first line of the CSV file, needs to be the headers of the columns**

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Pipeline Description

Workflow used for statistical analysis.

The blue squares highlight this new statistical analysis approach.
A **G**eneral **L**inear **M**odel is computing to test 2 group differences at every surface location

Overview
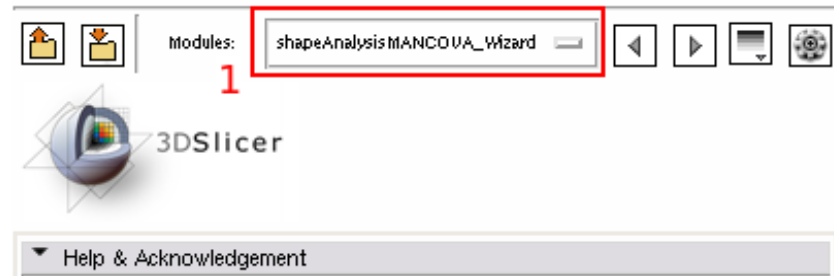
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Output files and organisation

All the output are in the same directory : where the input file is located.

There are some text files:
- ➜customLut_DiffMagnitude.txt   customLut_FDRP.txt   customLut_RawP.txt
- ➜distances_scaled.txt
- ➜commandline.txt
- ➜DiffMagnitude.txt
- ➜diffMesh.txt
- ➜mancovaBonferroniP.txt
- ➜mancovaFDRP.txt
- ➜mancovaRawP.txt
- ➜normDistance.txt
- ➜normProjections.txt

And some Mesh files:
- ➜meanAll uncorrected.meta
- ➜meanA.meta and meanB.meta
- ➜GLM corrected meanAll.meta

The meanings of all those files are explained on this link:
http://www.nitrc.org/plugins/mwiki/index.php/shape_mancova:MainPage

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Execution within Slicer :
Start ShapeAnalysisMANCOVA_Wizzard

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

1- Select the "ShapeAnalysisMANCOVA_Wizzard" in Modules ->Statistics.
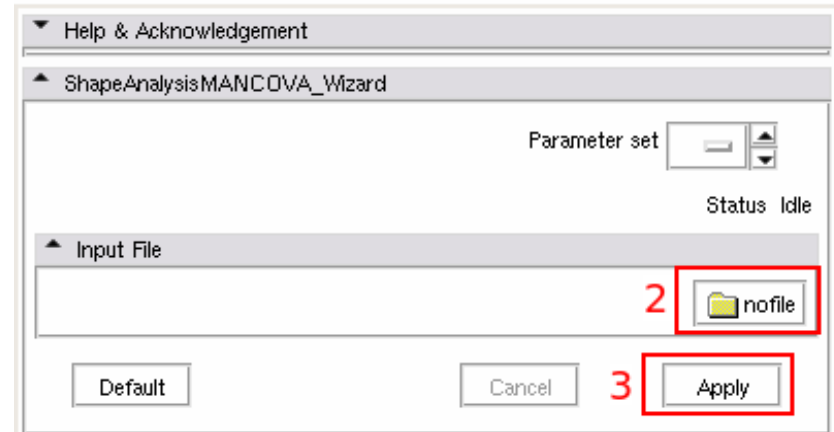
Execution within Slicer :
Load the Qt Window

1- Select the "ShapeAnalysisMANCOVA_Wizard" in Modules ->Statistics.

2- **You can select an input file (it will be display directly in the Wizard) or not.**

In this tutorial, we are selecting an input file : the one given with the data set.

3- Click on the "Apply" button to open the Wizard

Execution within Slicer :
The Wizard

Execution within Slicer :
Wizard : Choosing the type of the columns

Select the type of columns, to run a simple group test:

1- Check a checkbox
2- Doubleclick on one of the cells of the column

In this tutorial :

     * Just one group : Gender (column 0)
     * No scale, No independent variable
     * The inputfile column is the 2nd

Execution within Slicer :
Wizard : Choosing the statistical parameters

1- Check a checkbox
2- Doubleclick on one of the cells of the column

3- Got to the second tab

4- Check the box "Group test". The name of the header of the group test column chosen appeared (5-)

6- Click on the "Run" button

Execution within Slicer :
Wizard : End of the running

1- Check a checkbox
2- Doubleclick on on
3- Got to the second tab
4- Check the box "Group test".
6- Click on the "Run" button

If the path to Slicer is found, slicer3 is opening and you can see the mrml scene.
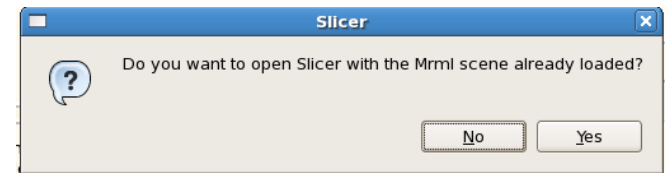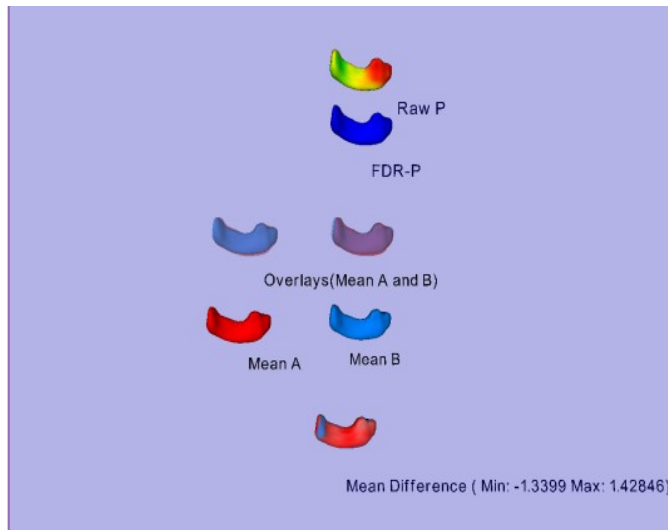
Execution within Slicer :
Wizard :After ShapeAnalysisModule

You can use the output file of ShapeAnalysisModule :

        in /OutputGroupFiles

The group column is the "Gender" one : the first one
We advice you to choose the column "*SPHARM Surface in Procaligned Space*" (the 10th) as the inputfile column

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More details on the Wizard:
Load an input File

1. Choose the checkBox : Load a file

2. Use the button « Load a file » to select it

3. The path to your file is written here

4. You can see if
  * your csv is ok
  * your csv have a problem (missing coma)
  * your file is not a cvs

5. You can change your file

6. The infile column is detected (by default it is the first which contains a path)

7. You can delete the last line

8. You can add a row (at the bottom)

9. You can delete a column (the last one)

10. You add a column (at the end), the header will be the one written

More details on the Wizard:
Create an input File

1. Choose the checkBox : new csv

2. Choose your numbers of lines and columns and then use the button « Apply»

> NB: you can add/delete lines/columns subsequently

3. Select the folder where your file (where all the shapeAnalysisMANCOVA outputs will be)

4. The path to the folder is written

5. Choose the name of your file. The end MUST be .csv
   NB : the name will be the base of the output names

You can **change the name of a header:**

6. Click on the button « modify a header entry » and click on the header (**7.**)

8. A pop-up window will appear, choose the name of this column

> NB: you have to click on the button every time you want to change a header name

More details on the Wizard:
Create an input File (2)

You can try to create an input file from scratch : by creating again the csv file from the example

1. Put 4 lines and 3 columns in your grid, then change the name and fill the first one with the number of groups.

2. Change the name and fill the second column with the scale factor.

3. Check "select the input file column", select the third, uncheck the box and change the name of the header

4. Thanks to the browser, you have to fill the 4 boxes with thoses datas available in the example zip

5. Then change the name and fill the description column (4th)

1

3

5

	group	scale	data	descritpion
1	0	1	/home…M.vtk	none
2	0	1	/home…M.vtk	none
3	1	1	/home…M.vtk	none
4	1	1	/home…M.vtk	none

2

	Group	scale
1	0	1
2	0	1
3	0	1
4	0	1

4

groupA_01_hippo_pp_surfSPHARM.vtk
groupA_02_hippo_pp_surfSPHARM.vtk
groupB_01_hippo_pp_surfSPHARM.vtk
groupB_02_hippo_pp_surfSPHARM.vtk

More details on the Wizard: choose the types of the columns

If there is a scale column,

You have to check the box « there is a scale column » and let the box checked. Then , as previously:

1. Choose the checkBox : Select scale column
2. Click on a square
3. The color of the header changes and the number of the column is written

You can unselect a group, an independent variables or the scale column :

* Choose the checkbox : « unselect a column »
* Click on a square
* The header will become black and the number of the column won't be written

You can change the type of a column by selecting le new type and clicking on a square
But the infile column have the priority ie, you can change the column only if its checkbox is checked

You can fill the square of the grid

Any of the 4 encircled checkboxs should be checked

If you fill a square of a non infile column, double click on the square and write the content

If you fill an infile column square, when you double click, a browser window is openning and you can choose the data
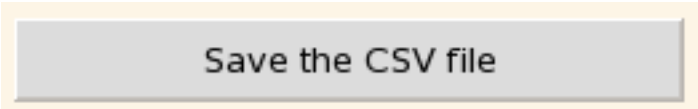
More details on the Wizard: Save the input File

If you have created a new file or made some changes on one loaded , you have to save it

Save the CSV file

By clicking on the button the file displayed in the grid will be save

If you are loading a file

└──────► It will be saved in stead of the one you have loaded

If you are creating a file

└──────► It will be save in the folder and with the name you have chosen

All the squares have to be filled before saving

More details on the Wizard: Group or Interaction test

Fig: headers

	group	infile	inde1	inde2	scale
1					

☑ group Test

☐ interaction Test

Test column

Group ▾

simple correlations (Spearman and Pearson) :

◉ test for trend correlation

◯ test for negative correlation

◯ test for positive correlation

Number of permutations: 10000

You have to choose between a group test or an interaction test

In the "input reading parameters" you will be able to choose the "test column".

ie: the name of the columns of the type you have chosen are displayed

If want to make an interaction test, you can chose your type of correlation

☐ group Test

☑ interaction Test

Test column

Indep1 ▾

Indep2 ▾

simple correlations (Spearman and Pearson) :

◉ test for trend correlation

◯ test for negative correlation

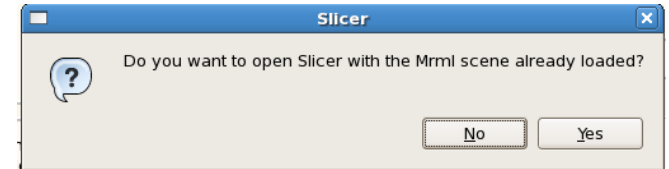◯ test for positive correlation

Number of permutations: 10000

With our example, you have to choose the group test and the test column will be the first

More details on the Wizard:
Opening Slicer3 with a mrml scene

At the end of the execution, the pop-up will appear

If you say « No » you will go on the previous window
you can leave it (Quit button)

If you say « Yes »

If the path to Slicer3 is found by the programme, Slicer3 is opening and you can see the output mrml scene.

If the path is not found, this pop-up will appear
Then though, you have to select the path before seeing the mrml scene in a Slicer 3 window
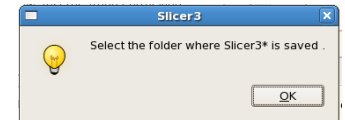
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Conclusion

The **shapeAnalysisMANCOVA** is a 3D Slicer module, readily usable with **shapeAnalysisMANCOVA_Wizard**. It is a 3D Slicer module that allows efficient computation of statistical shape analysis via the SPHARM-PDM_UNC pipeline including intuitive quality control visualizations. The versatility of the tool allows it to be applied in many different shape morphometry applications.

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

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