

LONGITUDINAL STUDIES WITH MANCOVA

shapeAnalysisMANCOVA allows to test for differences between the surfaces of two different time points screenings in case of a same patient. This analytic approach is used first for paired longitudinal comparisons between the baseline measurement and the subsequent follow-up measurements of the same patient.

The first step consists in computing statistical features over each subject, using longitudinal information. For any subject-wise study, statistical features can be computed by using MeshMath:

Absolute distances In these color maps only the magnitude of the shape change is displayed, where green color shows no change from baseline to follow-up and red shows maximum change. The color gets darker as the magnitudes of the distance increase.

Vectors These maps intent to represent the directionality of the shape changes, displayed by means of vector maps that show the shape differences between the mean shape of the two groups tested.

Example to create Vector and Absolute Distance map features using MeshMath -subtract argument, for each subject:

```
MeshMath time2_mesh diff_feature.txt -subtract baseline_mesh
```

Signed distances In these color maps white color is used where the magnitudes are zero. The color gets darker as the magnitudes of the distance increase. The distance is positive if the mean surface of group A is protruding outside of the mean surface of group B; the distance is negative if the mean surface of group A is shrinking below the mean surface of group B. By default, positive distances are color-coded by blue and negative distances are color-coded by red.

Example to create Signed Distances using MeshMath and -magNormDir, for each subject:

```
MeshMath baseline_mesh signed_magn.txt -magNormDir diff_feature.txt
```

Vector files showing longitudinal changes can be input into MANCOVA instead of meshes, by including the flag `-KWMinput` in the command line. In case of analysis of distance maps (signed and unsigned) StatNonParaTestPDM can be used instead. Once any of those two features are obtained from that analysis, the next step consists in composing files with only raw features on it, the input file will be the same, but instead of containing meshes, it will contain point by point each feature for each point in each subject. That would produce long input subject lines. Thus, if we have M subject meshes and N points per subject meshes, the input file will be...

```
subjectID(1) groupindex(A) featurepoint(0) featurepoint (1) ... featurepoint(N)
```

```
subjectID(2) groupindex(A) featurepoint(0) featurepoint (1) ... featurepoint(N)
```

```
...
```

subjectID(M-1) groupindex(B) featurepoint(0) featurepoint (1) ... featurepoint(N)

subjectID(M) groupindex(B) featurepoint(0) featurepoint (1) ... featurepoint(N)

And then, once the input files have been formatted according to these guidelines, the last step is to input the right parameters for the program to compute the data needed. In case of distances, whether signed or unsigned, the input arguments for StatNonParamTestPDM will be:

-featgroupID X will specify the column that denotes the group indexes. It is zero based, in this case would be 1.

-featSelStart X will specify where your feature points start (in this case 2)

-featSelLen X, where X is the number of points to process (in this case N)

-log parameter will be required in case of Absolute (unsigned) Distances

Example of StatNonParamTestPDM command line for Absolute Distances:

```
StatNonParamTestPDM All_NOTsigned_magn.txt -featgroupID 0 -featSelStart 1 -featSelLen 102 -numPerms 20000 -log -signLevel 01 -signSteps 100 -v
```

Example of StatNonParamTestPDM command line for Signed Distances:

```
StatNonParamTestPDM All_signed_magn.txt -featgroupID 0 -featSelStart 1 -featSelLen 102 -numPerms 20000 -signLevel 01 -signSteps 100 -v
```

Visualization of the results obtained from the aforementioned tests provide three kinds of information at a specific location on the surface:

Average magnitude and direction of the shape changes between longitudinal groups:
Similarly to signed distance maps, white color is used where the magnitudes are zero. The distance is positive if the mean surface of group A is protruding outside of the mean surface of group B ; the distance is negative if the mean surface of group A is shrinking below the mean surface of group B. Positive distances are color-coded by blue and negative distances are color-coded by red.

Directionality of the shape changes: Displayed by means of vector maps that show the shape differences between the mean shape of the two groups tested.

Significance maps: Showing the areas in where the shape changes were considered to be statistically significant. The p-values are color-coded showing blue where the raw p-value exceeds 0.05, that is to say the change for that point is not significant regardless the magnitude of it, and red in those points where the changes are significant.