Introduction to statistical shape analysis II: Semi-landmarks and beyond

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2/19/20

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Outline

- How many landmarks are enough?
- Semi-landmarks
- Deformable Analysis
- Spherical Harmonic Representation

How many landmarks are enough to characterize shape and size variation?

- Criteria for landmarks to be homologous and reproducible results in very sparse data from images
- For many data sets, this may not be sufficient to capture shape changes, especially along curves or smooth surfaces
- Point-landmark too stringent for effective biometrics in many 3D applications

Watanabe, Akinobu. "How many landmarks are enough to characterize shape and size variation?." PloS one 13.6 (2018): e0198341.

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Image data provides rich phenotype descriptions – how can this be leveraged?

Watanabe, Akinobu. "How many landmarks are enough to characterize shape and size variation?." PloS one 13.6 (2018): e0198341.

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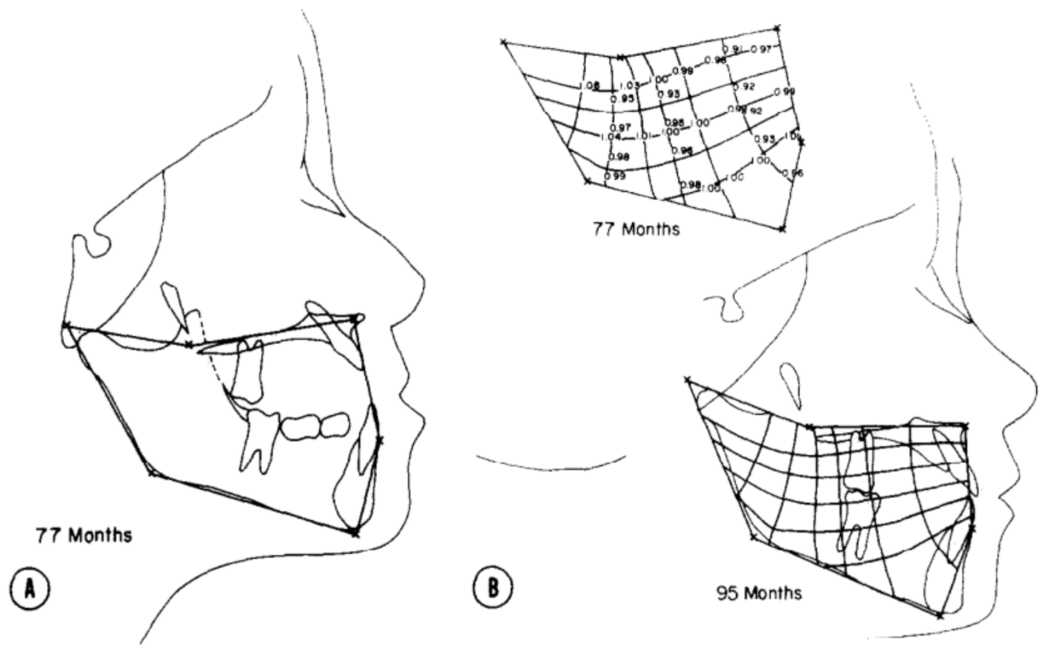
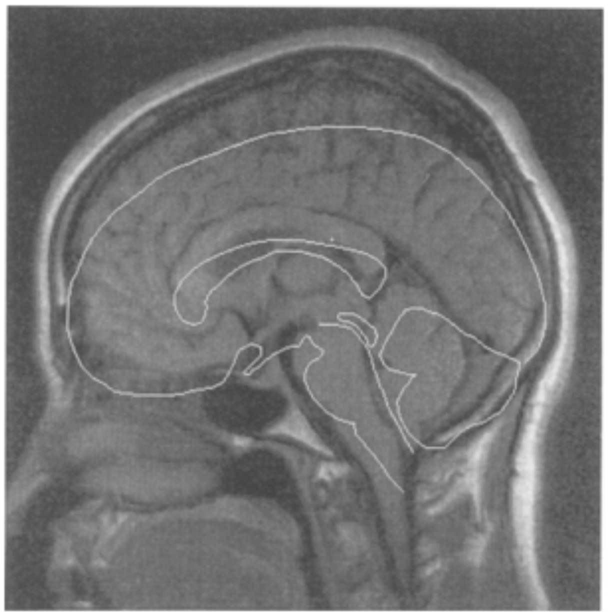
Constructed landmarks

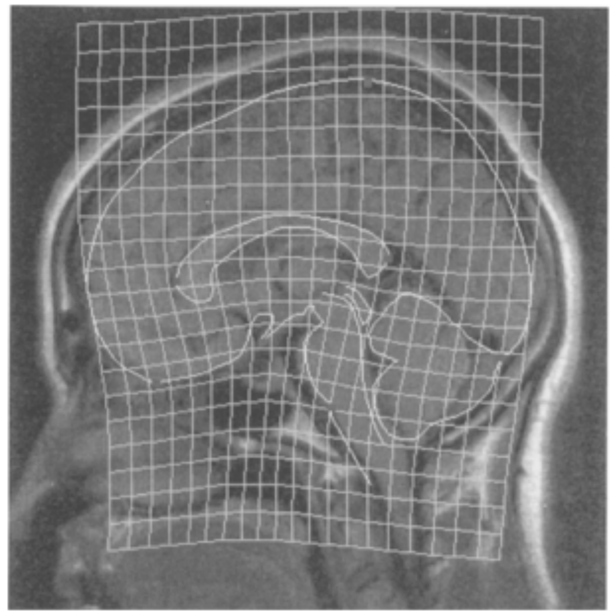


Geometric combinations of defined landmarks along lines erected at specific angles to define new landmarks

Moyers, Robert E., and Fred L. Bookstein. "The inappropriateness of conventional cephalometrics." *American Journal of Orthodontics and Dentofacial Orthopedics* 75.6 (1979): 599-617.

Extensions of TPS to include curvature





Bookstein, Fred L., and William DK Green. "A feature space for edgels in images with landmarks." *Journal of Mathematical imaging and vision* 3.3 (1993): 231-261.

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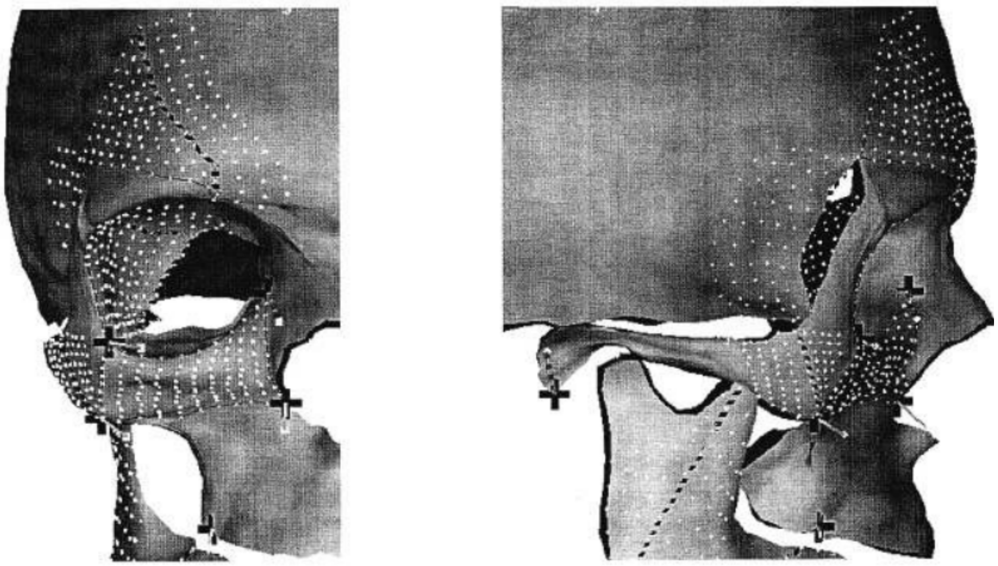
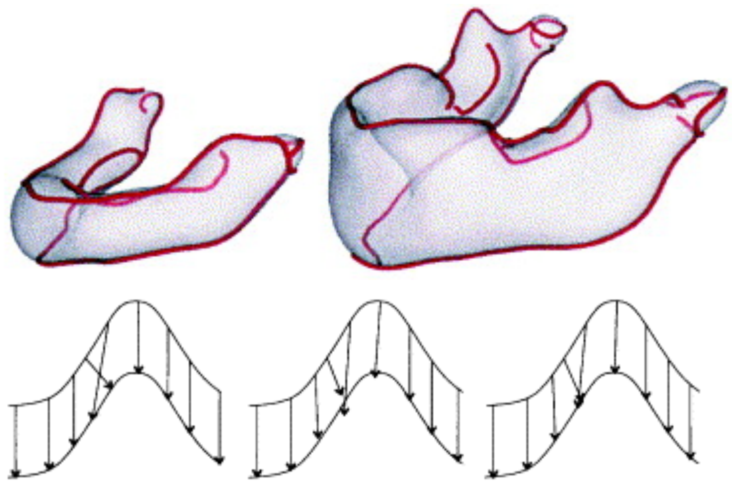
Smooth surface analysis

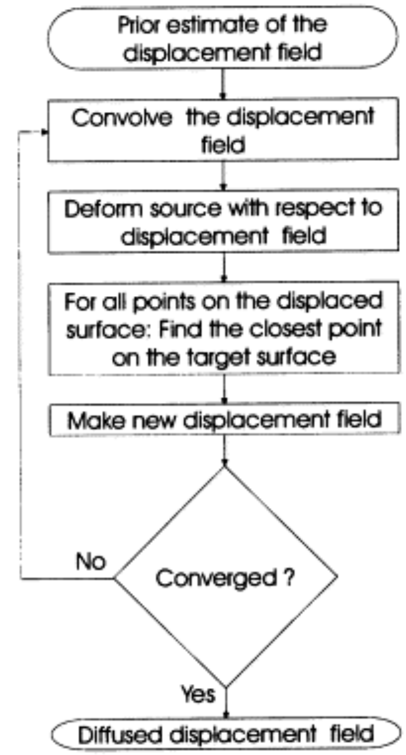


- Thin-plate spline unwarping to the Procrustes mean configuration
- Equally spaced points are declared homologous along curves
- Evenly spaced points are declared homologous on surface patches derived from these

Cutting, Court, et al. "A three-dimensional smooth surface analysis of untreated Crouzon's syndrome in the adult." *The Journal of craniofacial surgery* 6.6 (1995): 444-453.

Geometry constrained diffusion





- Ridge lines are automatically extracted from surface curvature
- Curves are matched in order to establish object correspondence
- Semilandmarks are mapped into Procrustes space for analysis

Andresen, Per Rønsholt, and Mads Nielsen. "Non-rigid registration by geometry-constrained diffusion." *Medical Image Analysis* 5.2 (2001): 81-88.

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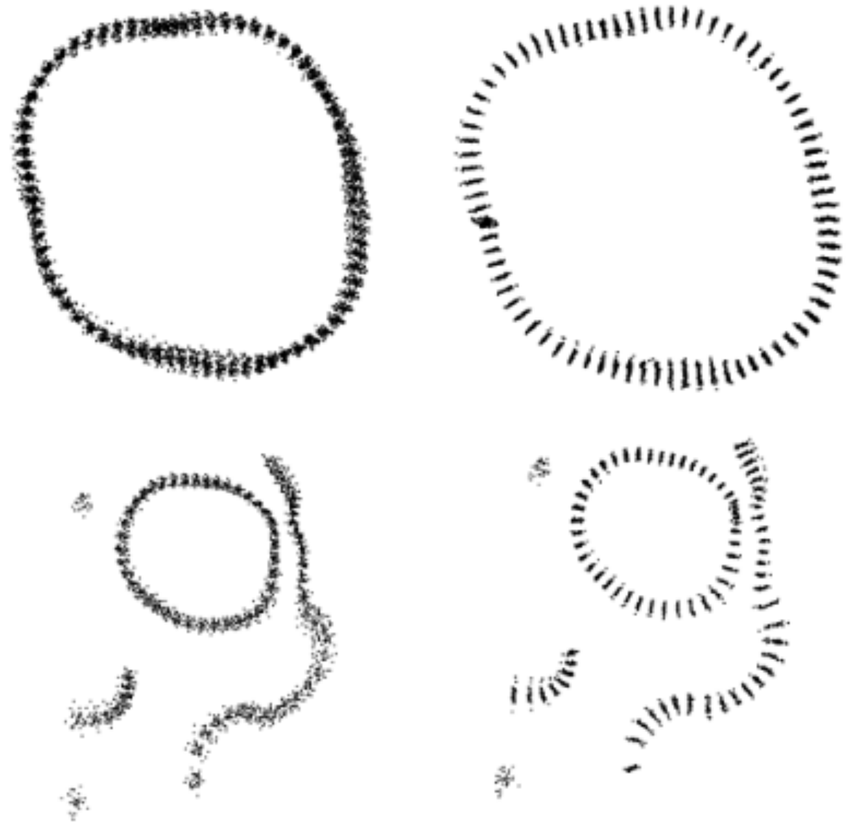
Sliding semi-landmarks

- Begin with structures that are known to correspond as parts (classical homology)
- Represents them by geometric curves or surfaces that generate reasonable mapping functions
- After Procrustes superimposition, semi-landmarks are slid along the surface to optimize correspondences



Before and after semi-landmark alignment of skull

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What is wrong with equidistant samples?

Produce spacing as a by-product of the analysis since the analysis is ignorant of the actual spacing.

Figure 3. (a) Form with one true landmark in the lower left corner and 31 other points equally spaced along the outline. (b) Bent form with one true landmark (1) and 31 other points in equal spacing. (c) The position of the points now optimizes bending energy.

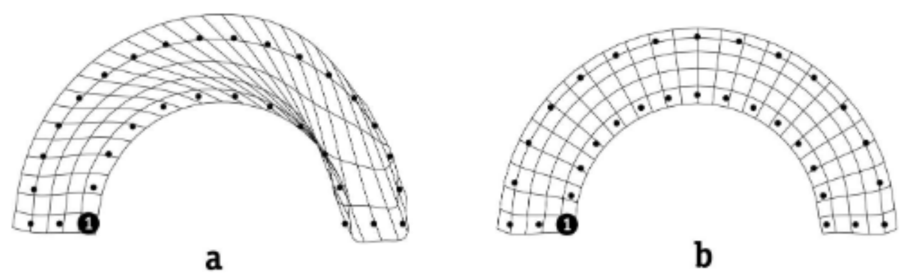

Figure 4. Splines corresponding to Figure 3. (a) Deformation grid from the form in Figures 3a and 3b. (b) Deformation grid from the form in Figures 3a and 3c.

Gunz, Philipp, Philipp Mitteroecker, and Fred L. Bookstein. "Semilandmarks in three dimensions." *Modern morphometrics in physical anthropology*. Springer, Boston, MA, 2005. 73-98.

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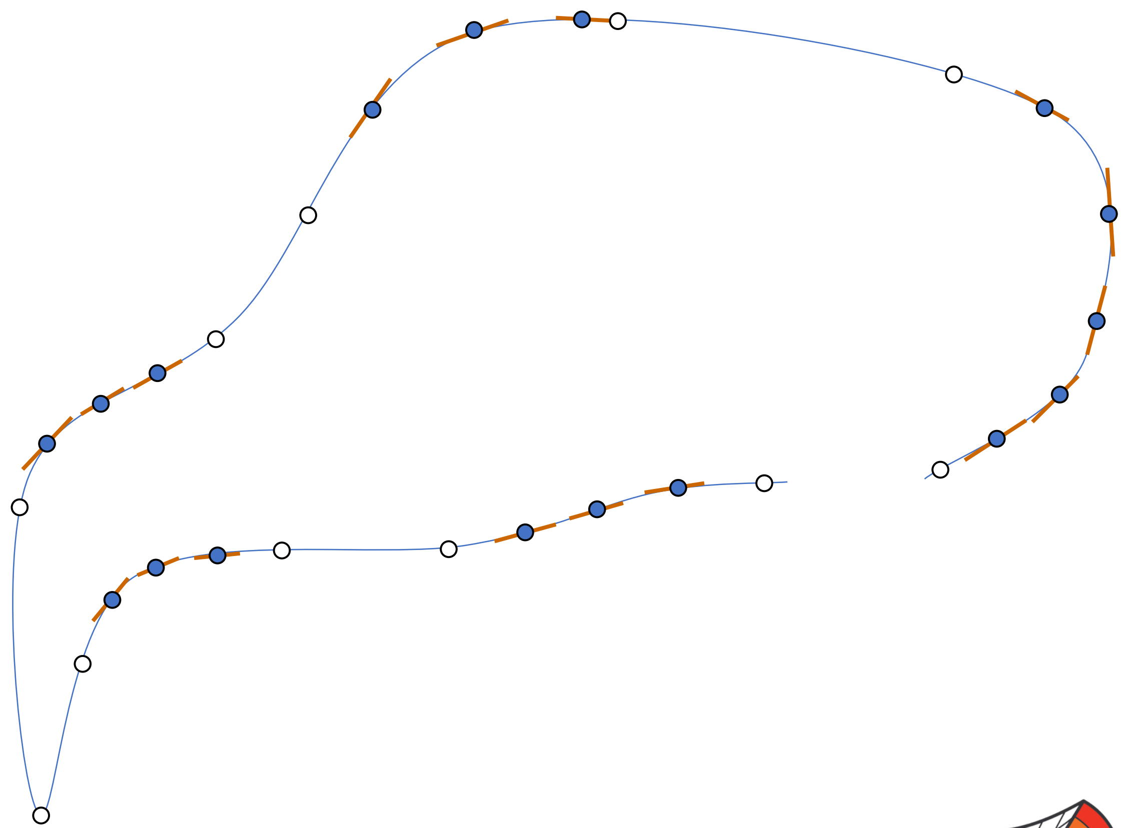
Sliding semi-landmark method

1) Find optimal Procrustes alignment of samples using landmark points
2) Slide semi-landmark points along the surface until they satisfy matching criteria with a single reference specimen
3) Calculate Procrustes average shape
4) Slide semi-landmark points along the surface until they satisfy matching criteria with the Procrustes average
5) Repeat steps 3 and 4 until convergence



Bookstein, Fred L. "Landmark methods for forms without landmarks: morphometrics of group differences in outline shape." *Medical image analysis* 1.3 (1997): 225-243.

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Determining position of sliding semi-landmarks

1) **Minimum bending energy criterion:** select semi-landmark positions that result in the smoothest possible transformation to the mean shape

2) **Procrustes distance criterion:** estimate the tangent to the mean surface for each semi-landmark point and remove the component of the difference between the mean and each specimen that lies along this tangent.

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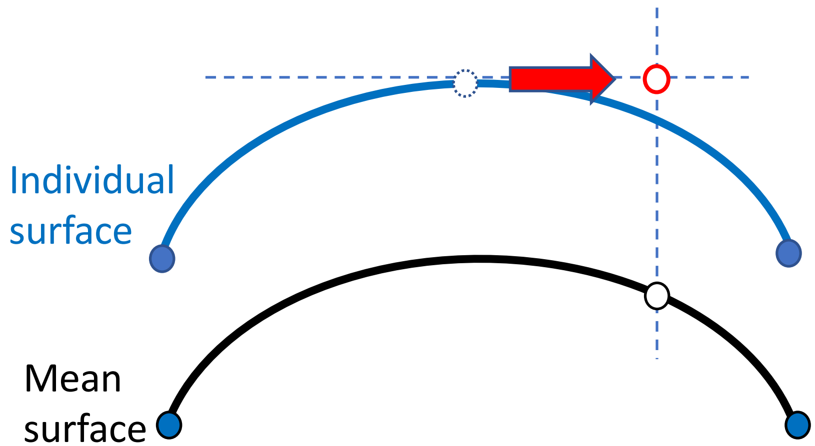
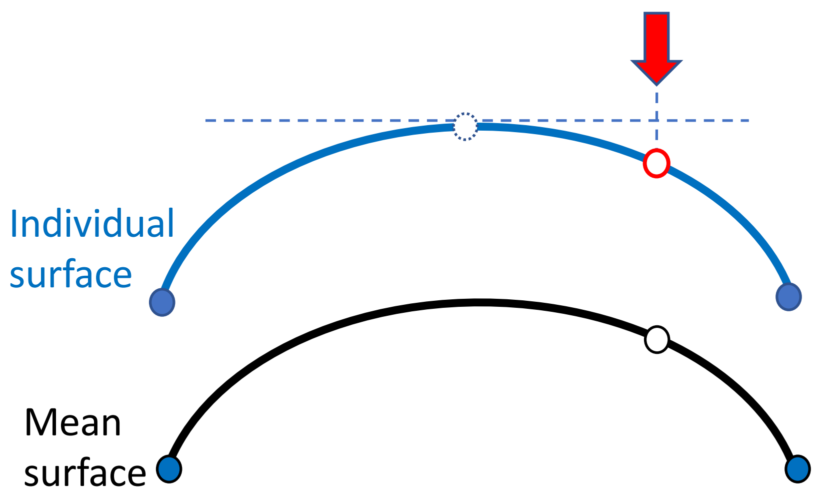
Minimum bending energy criteria



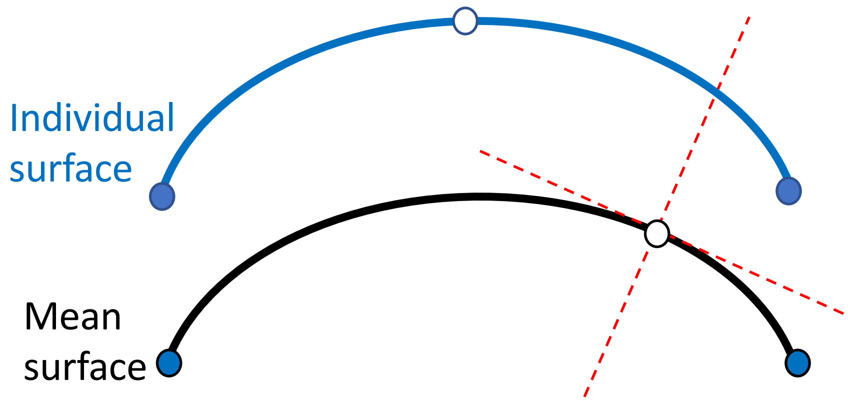
Slide along the surface's tangent structure to the position minimizing the bending energy of the transform between the individual and mean shape.

Minimum bending energy criteria

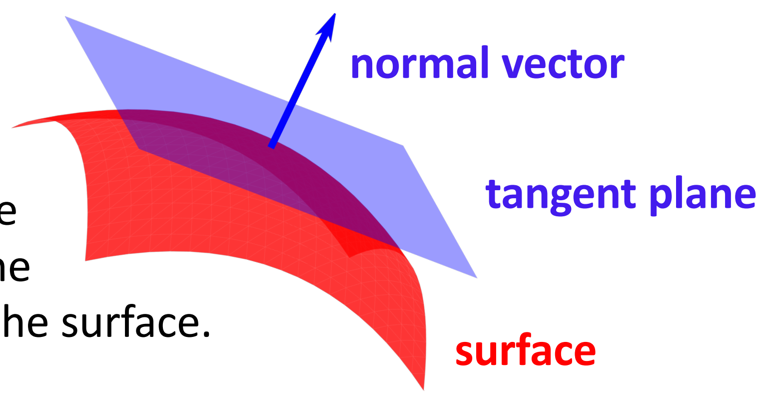


Project the point back to the point back to the surface.

Procrustes distance criteria



Find the normal vector of the reference surface at the landmark point.



A **normal vector** points in the direction perpendicular to the tangent plane at a point on the surface.

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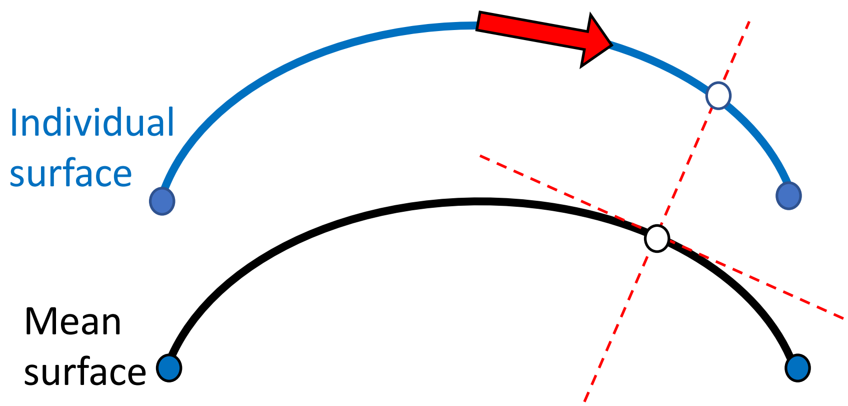
Procrustes distance criteria



Slide the semi-landmark towards the reference surface normal vector.

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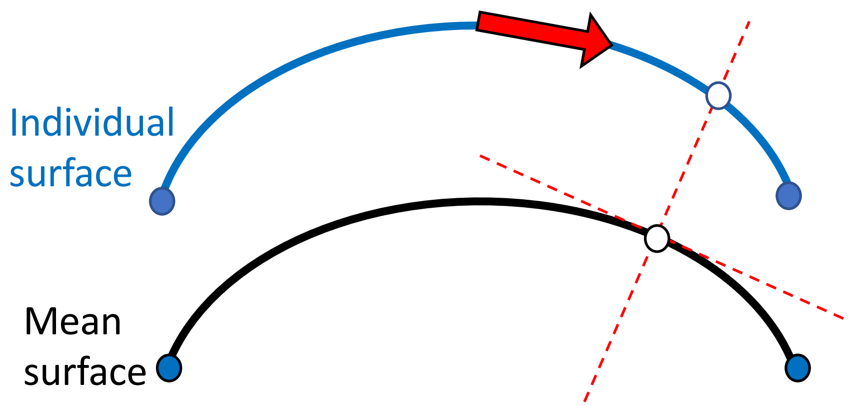
Procrustes distance criteria



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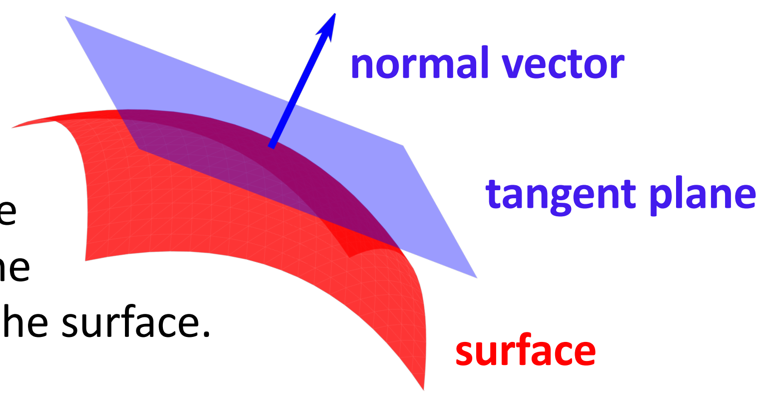

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Minimum bending energy or Procrustes distance?

- Use different background assumptions
- The difference between the criteria can alter the results when morphological variation in the sample is low
- More noticeable with smaller numbers of semi-landmarks

Perez, S. Ivan, Valeria Bernal, and Paula N. Gonzalez. "Differences between sliding semi-landmark methods in geometric morphometrics, with an application to human craniofacial and dental variation." *Journal of anatomy* 208.6 (2006): 769-784.

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Limitations of semi-landmarks

- Limited homology
- The method of handling semi-landmarks can influence the results
- The number of semi-landmarks may also influence the results
- Sliding semi-landmark positions are dependent on the dataset. Not possible to compare new shapes without recalculating

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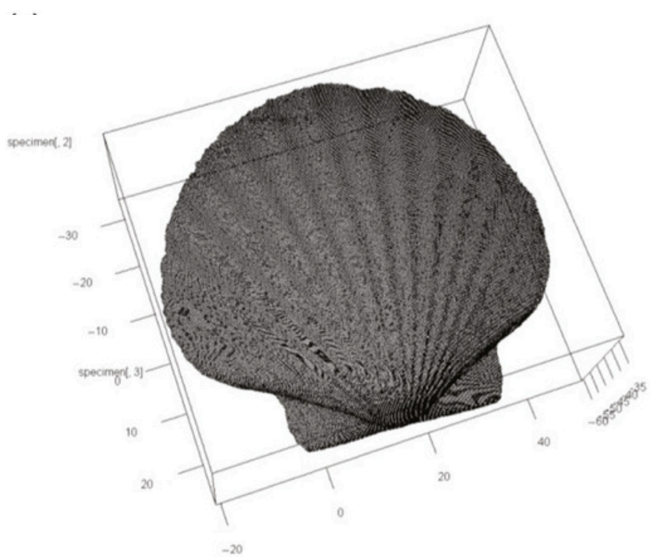
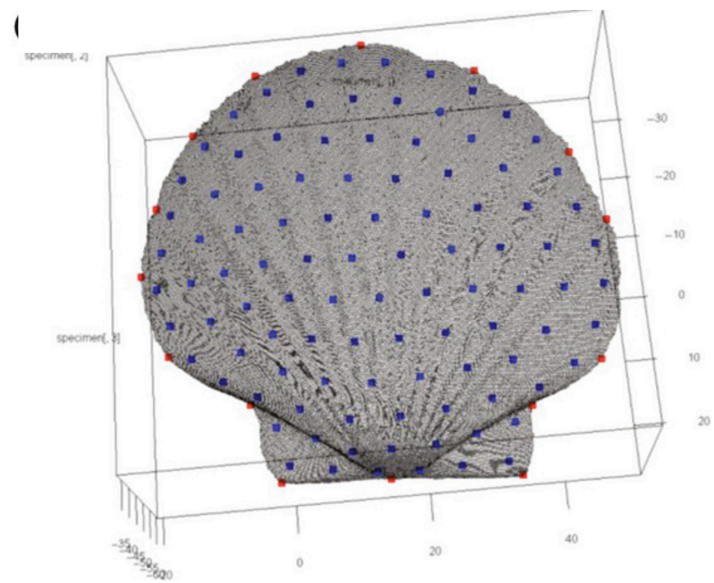
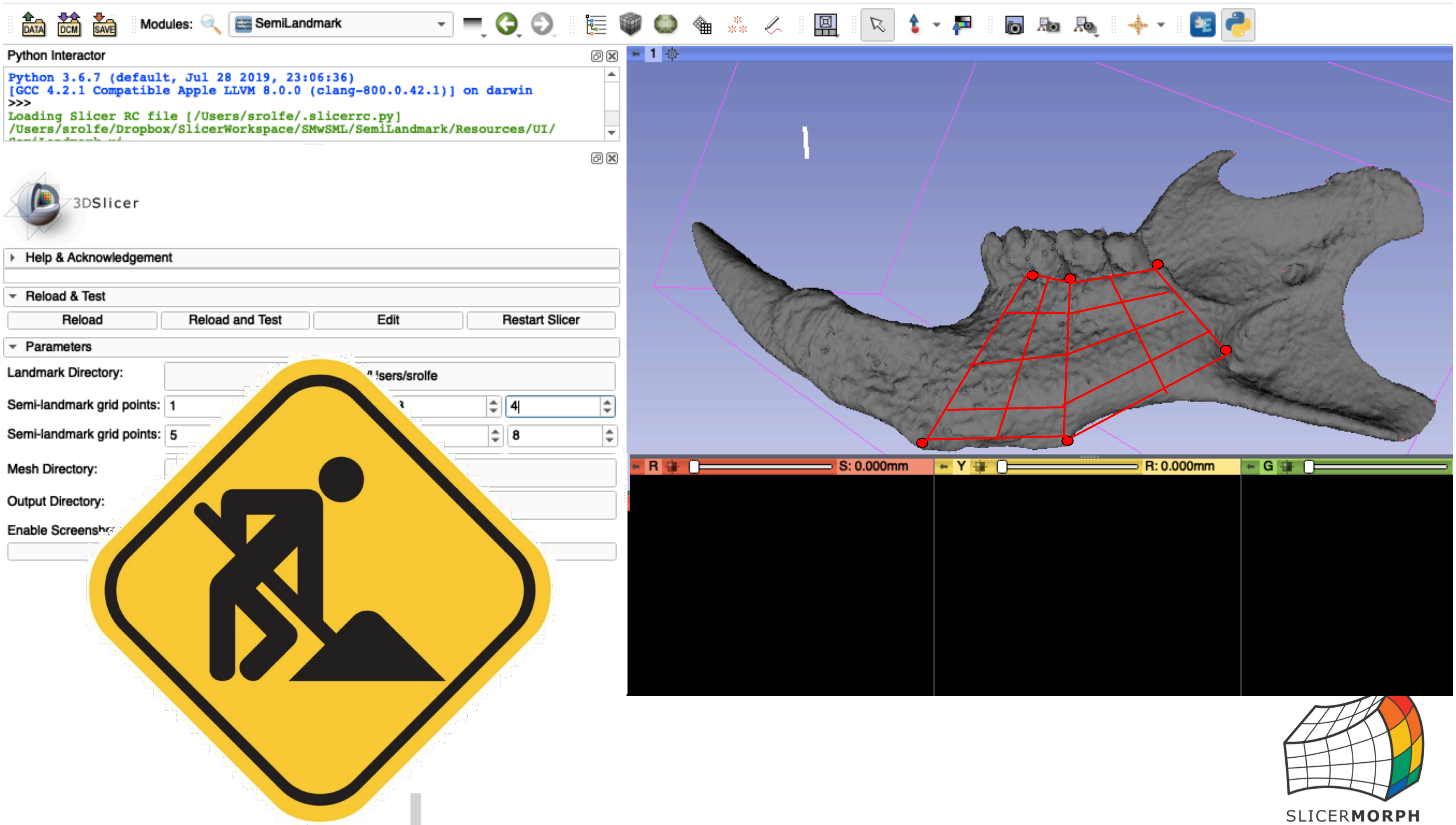
Semi-landmarks in R: Morpho

R Toolboxes [Morpho](#) and [Geomorph](#) for morphometric analysis provide support for capturing and analyzing semi-landmarks





Coming soon



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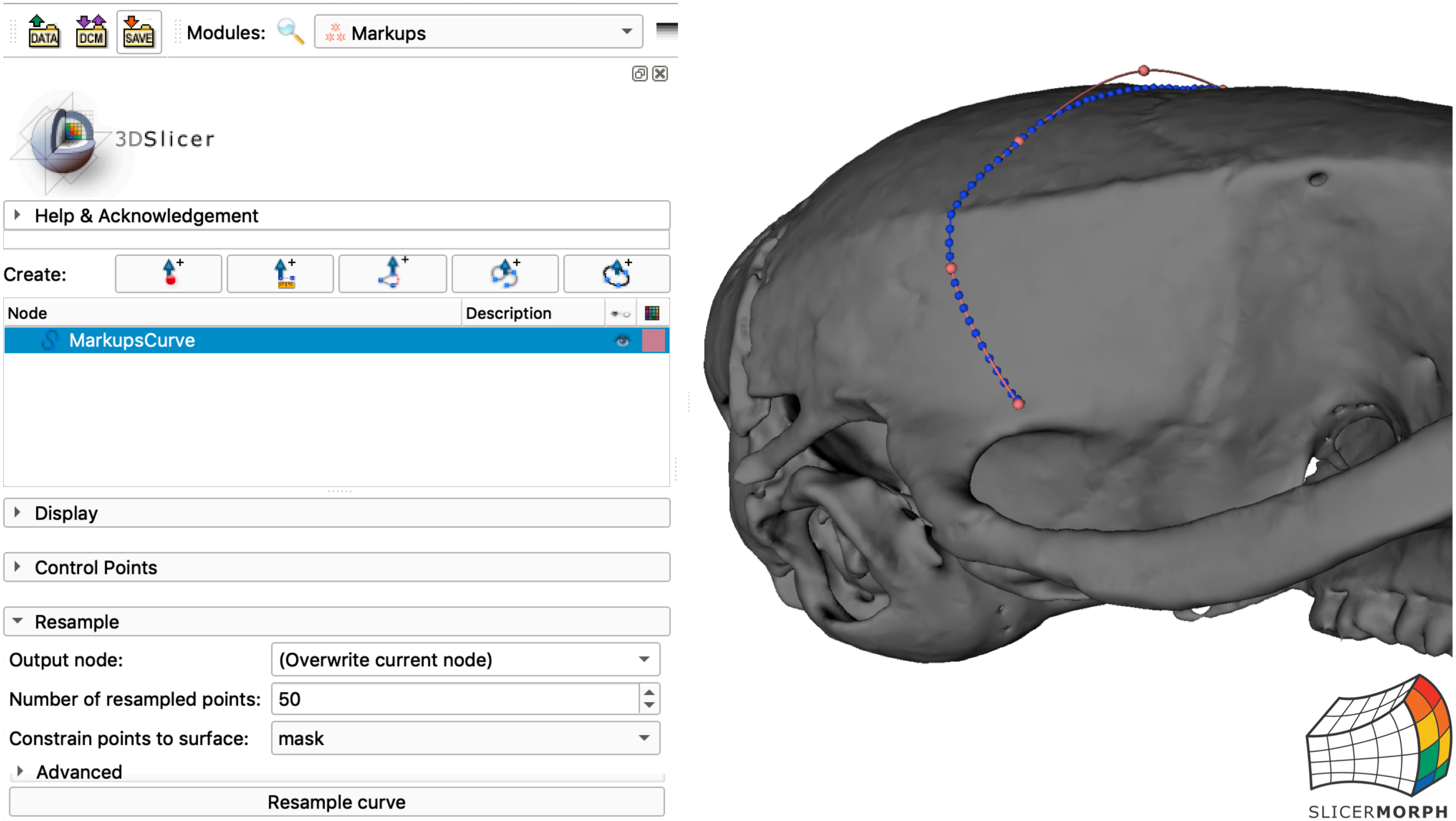
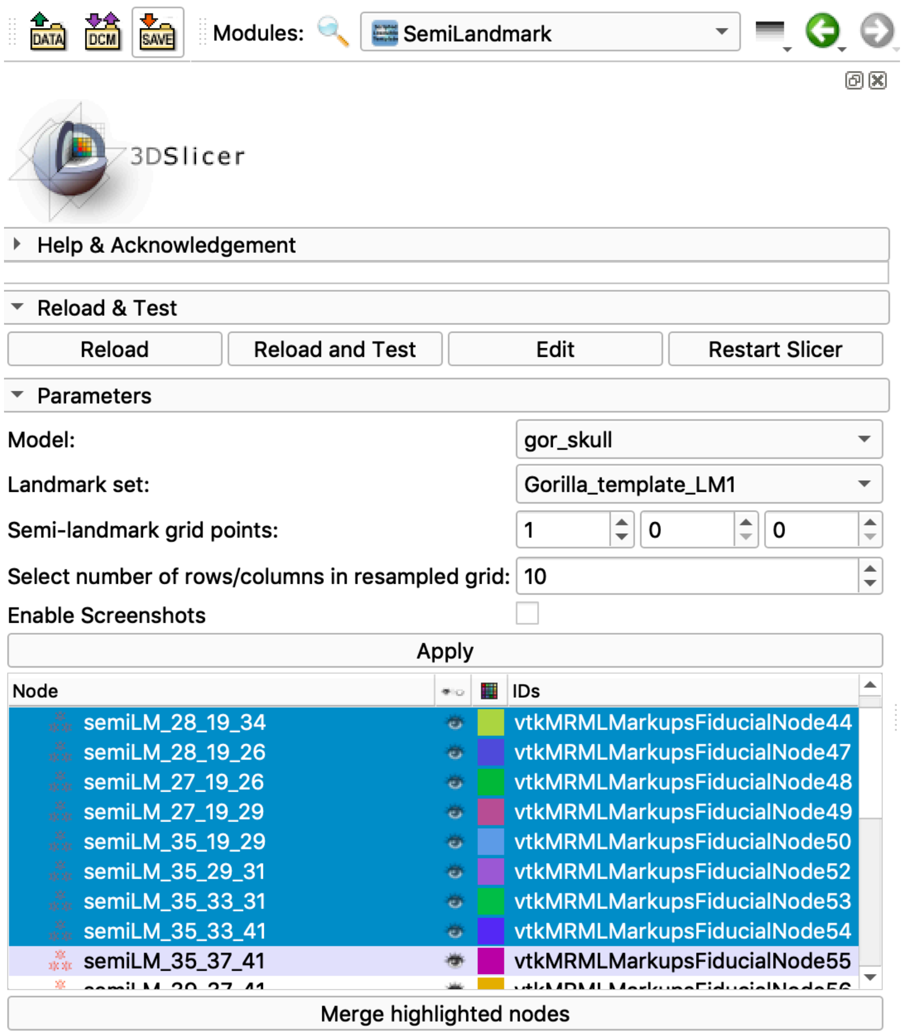
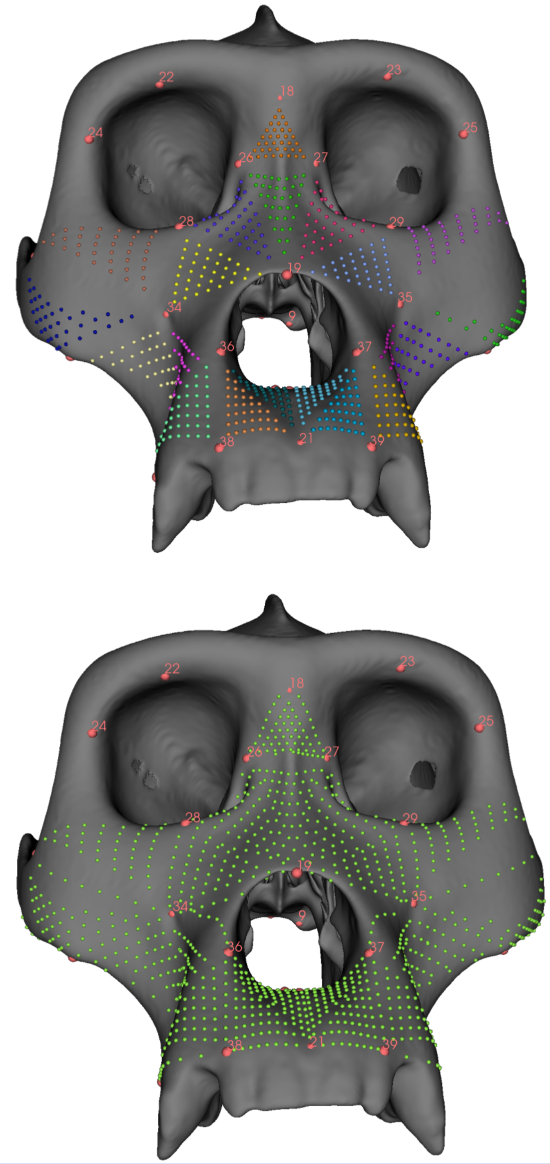
New Support in SlicerMorph for Semi-landmarking: Curves

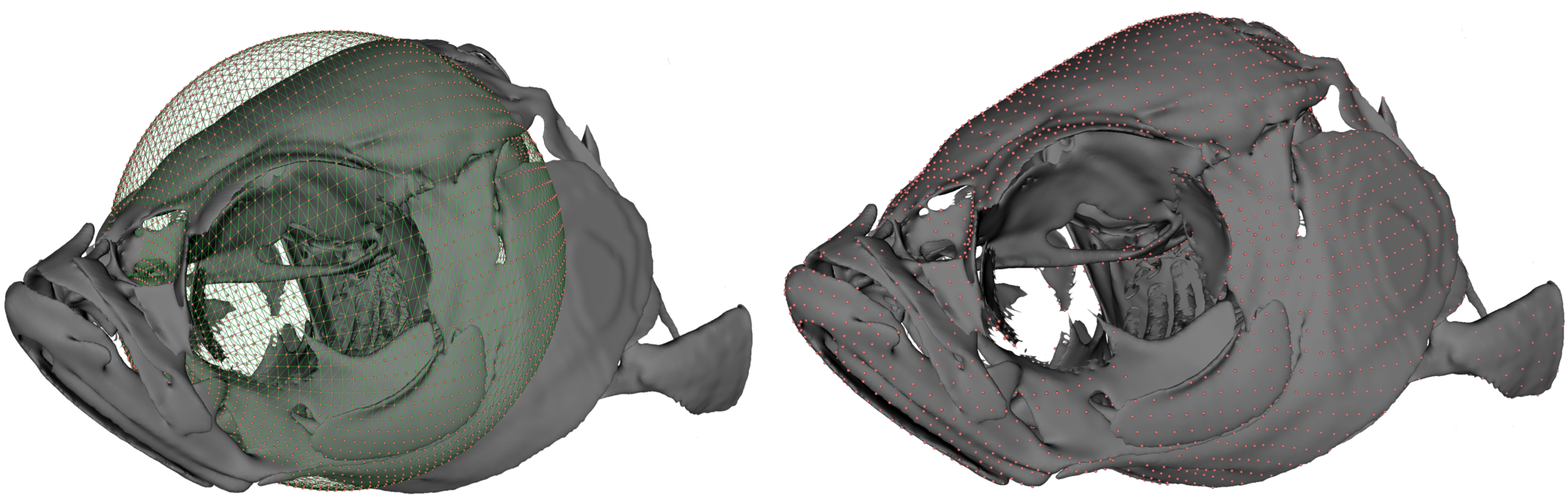


Patch-based placement of semi-landmarks





Coming soon: Spherical sampling



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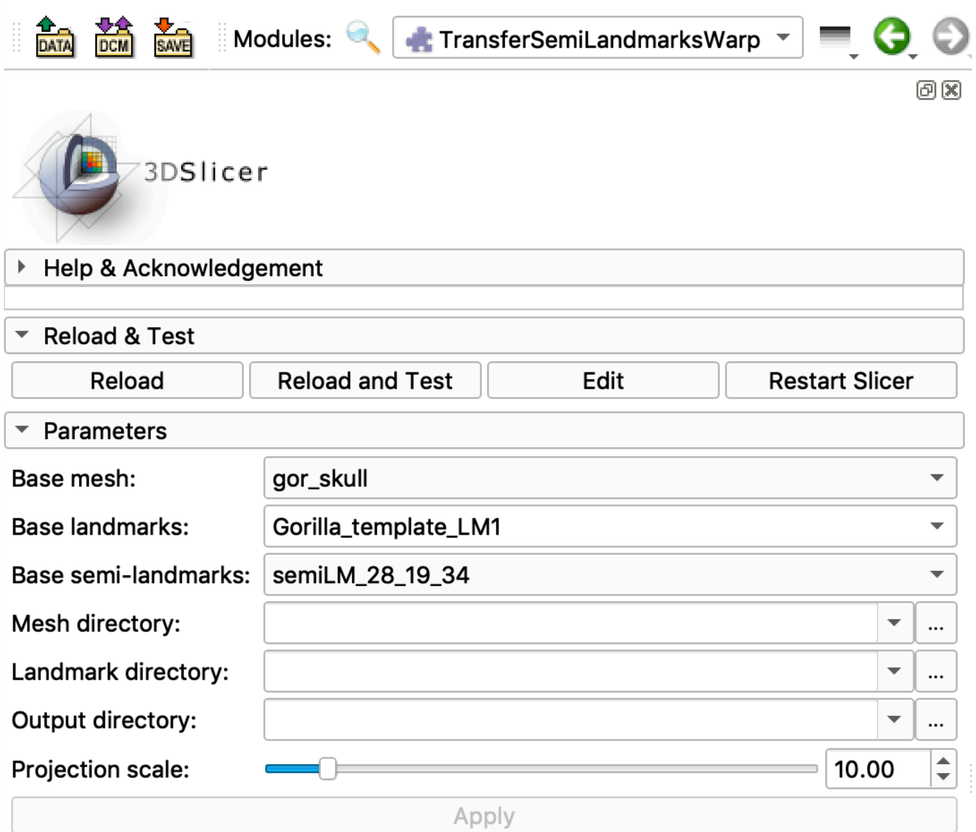
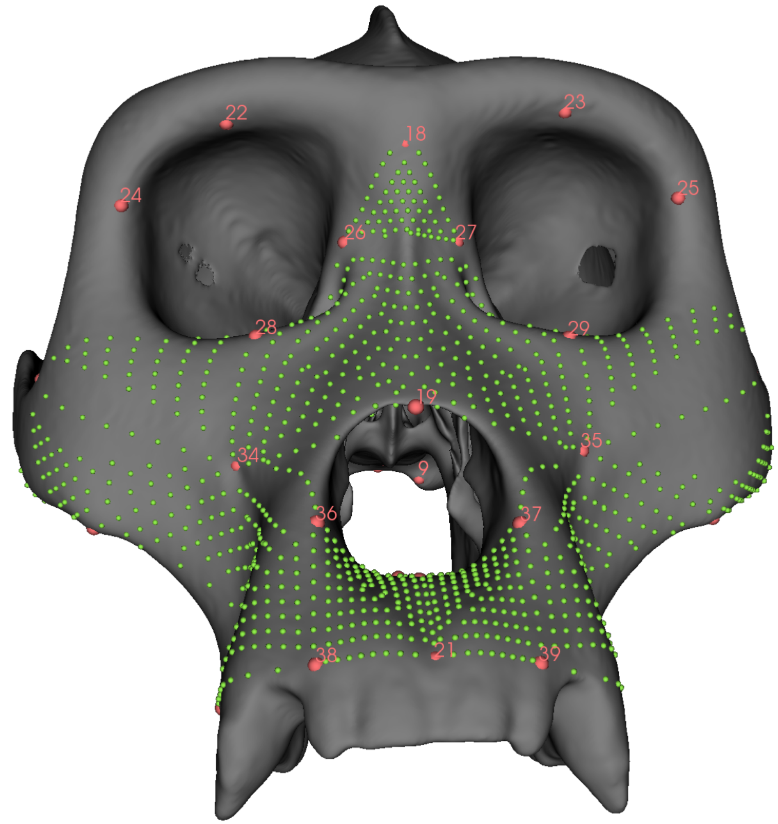
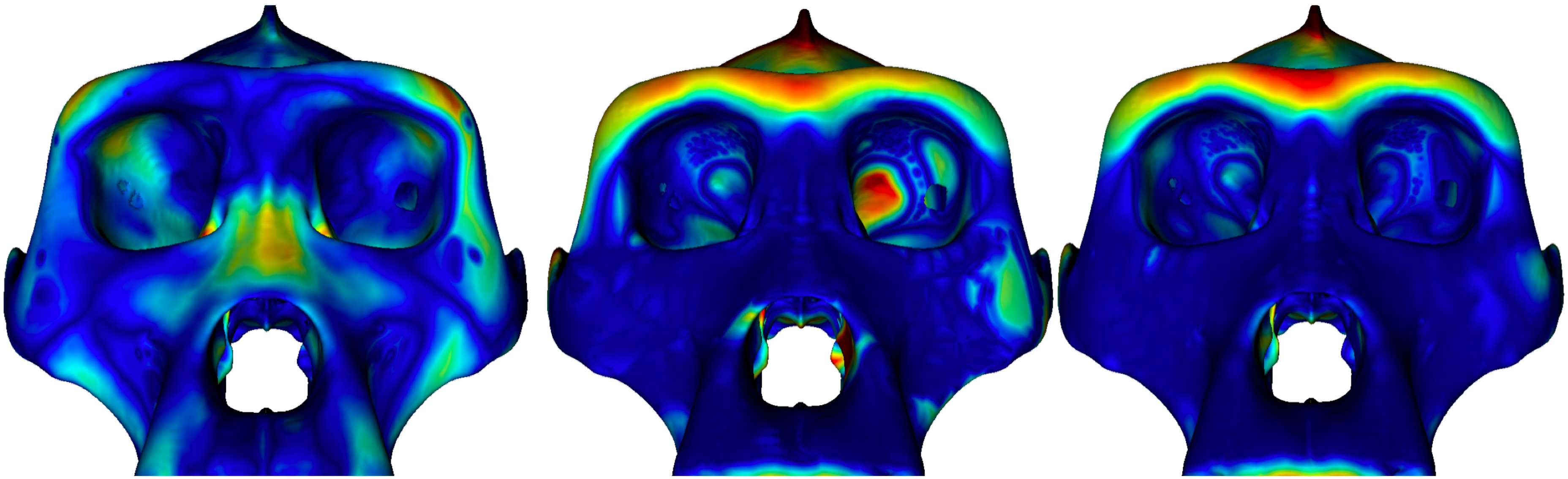
Transferring Semi-landmarks





Comparing Semi-landmark methods – warp to mean shape



	Original	Patch-placed	Warp-placed
Average RMSE	1.27	1.18	1.08

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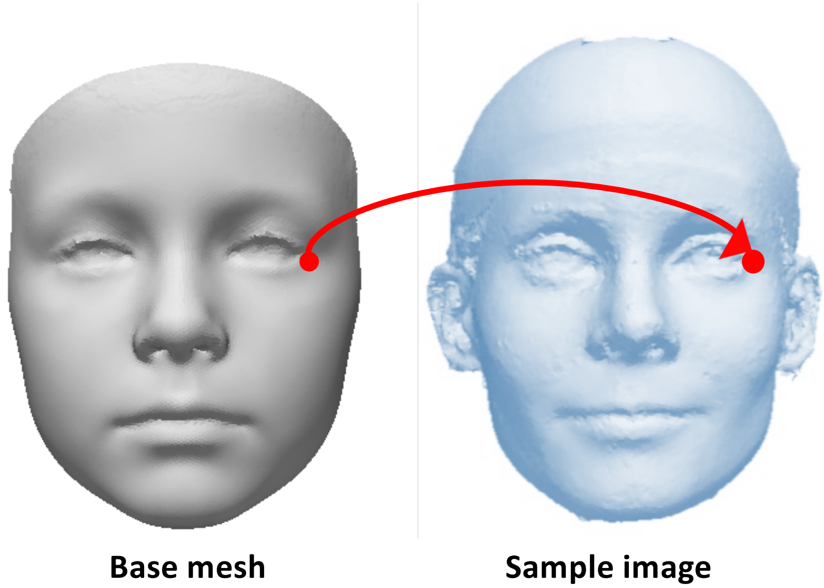
Deformation-based morphology (DBM)

- Calculate or select a base mesh
- Establish point correspondences between the base mesh and all meshes in data set
- Vertices of the base mesh define a new set of dense surface landmarks



Hutton, T. J., Buxton, B. F., Hammond, P. (2001). "Dense surface point distribution models of the human face," in Proceedings IEEE Workshop on Mathematical Methods in Biomedical Image Analysis (MMBIA 2001) (Kauai, HI).

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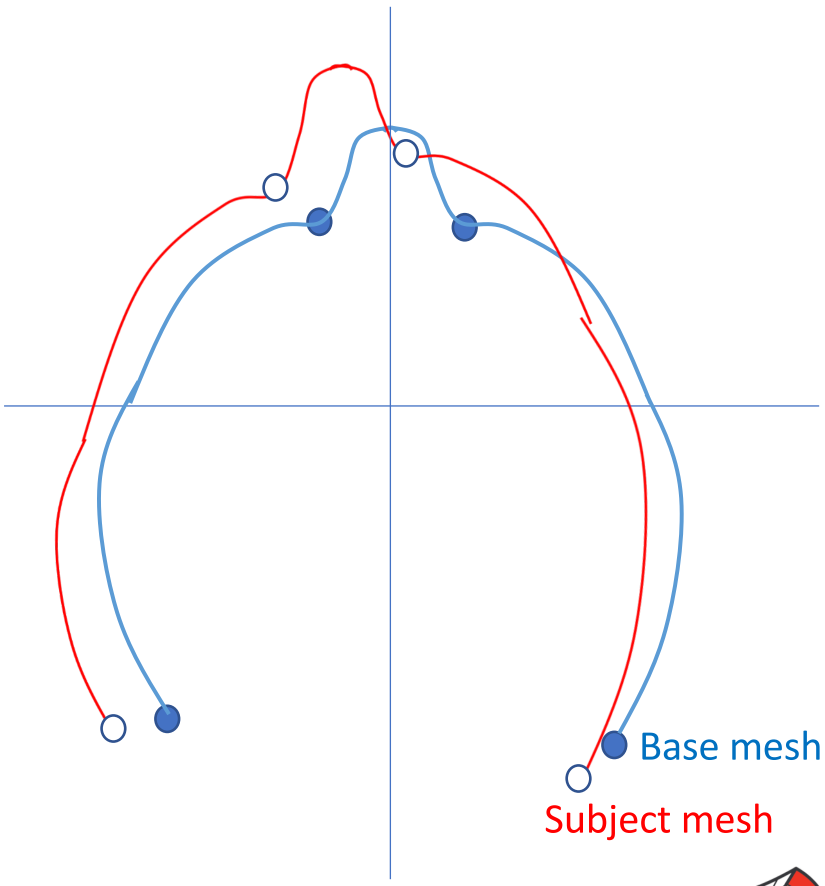
Steps to find point correspondence



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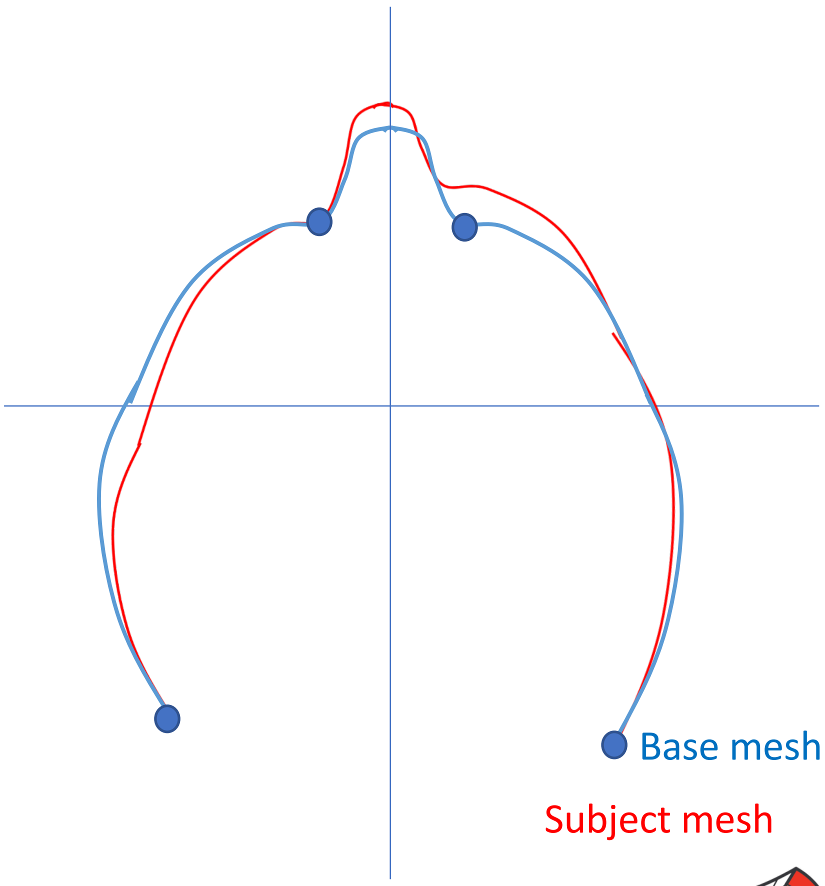
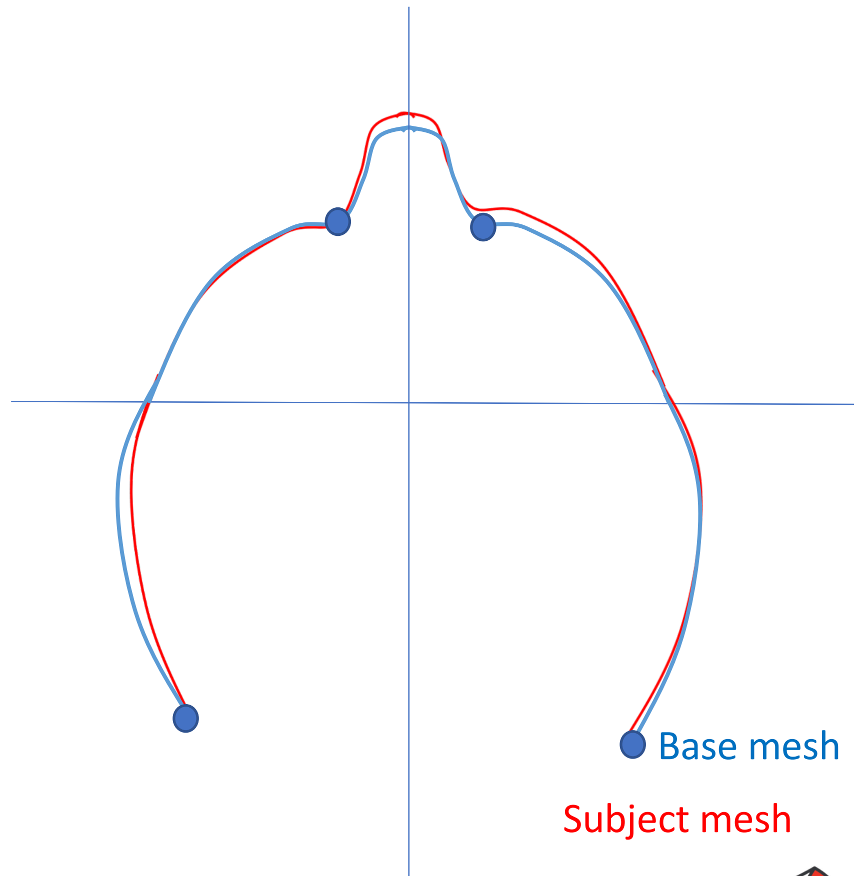
Steps to find point correspondence

1. Align anatomical landmarks with Generalized Procrustes Analysis (GPA)



Steps to find point correspondence

1. Align anatomical landmarks with Generalized Procrustes Analysis (GPA)
2. Warp the meshes to a base mesh with a thin-plate spline (TPS) transformation



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Steps to find point correspondence

1. Align anatomical landmarks with Generalized Procrustes Analysis (GPA)
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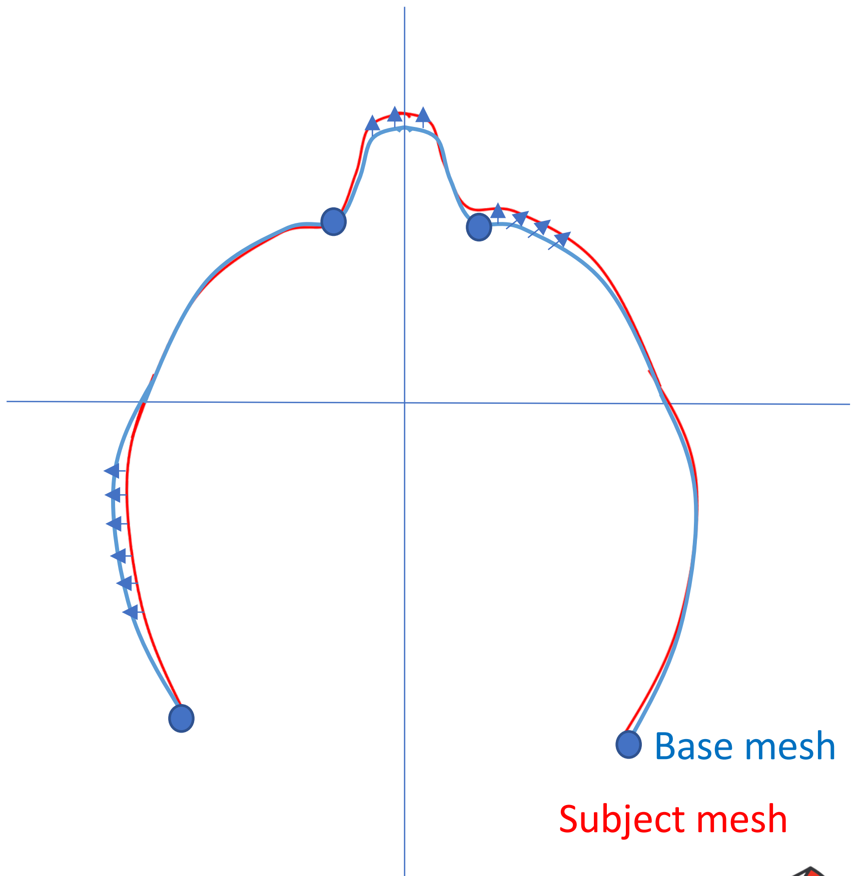
3. Determine point correspondences for each vertex the iterative closest point (ICC) algorithm



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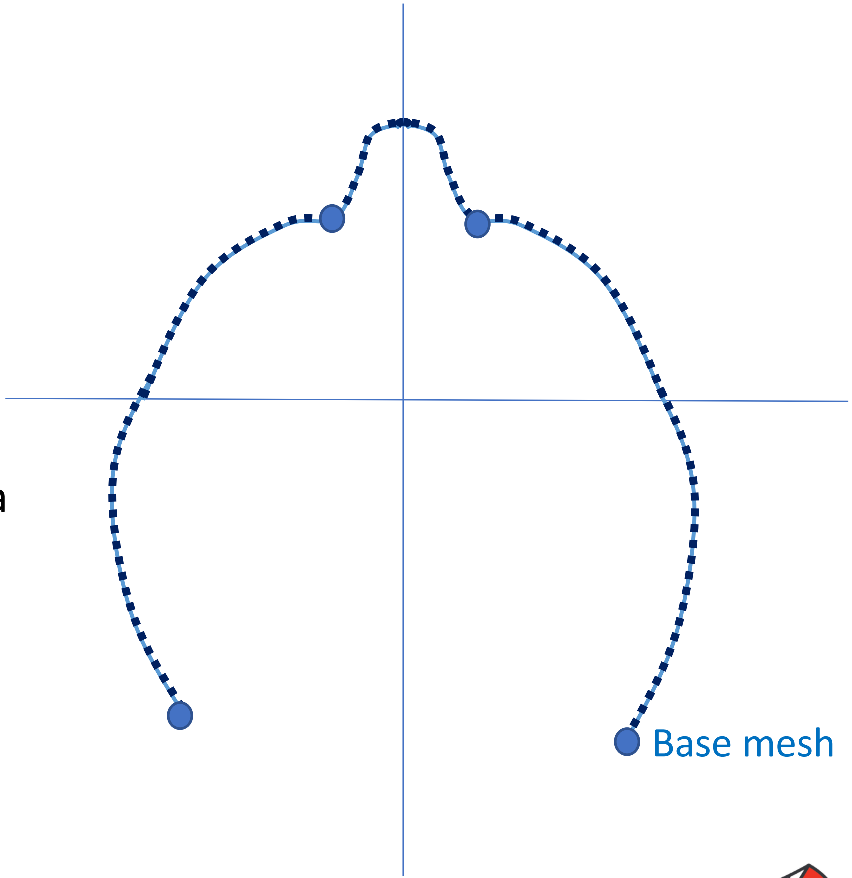
4. Each vertices of the base mesh represents a landmark point with a known correspondences for each subject



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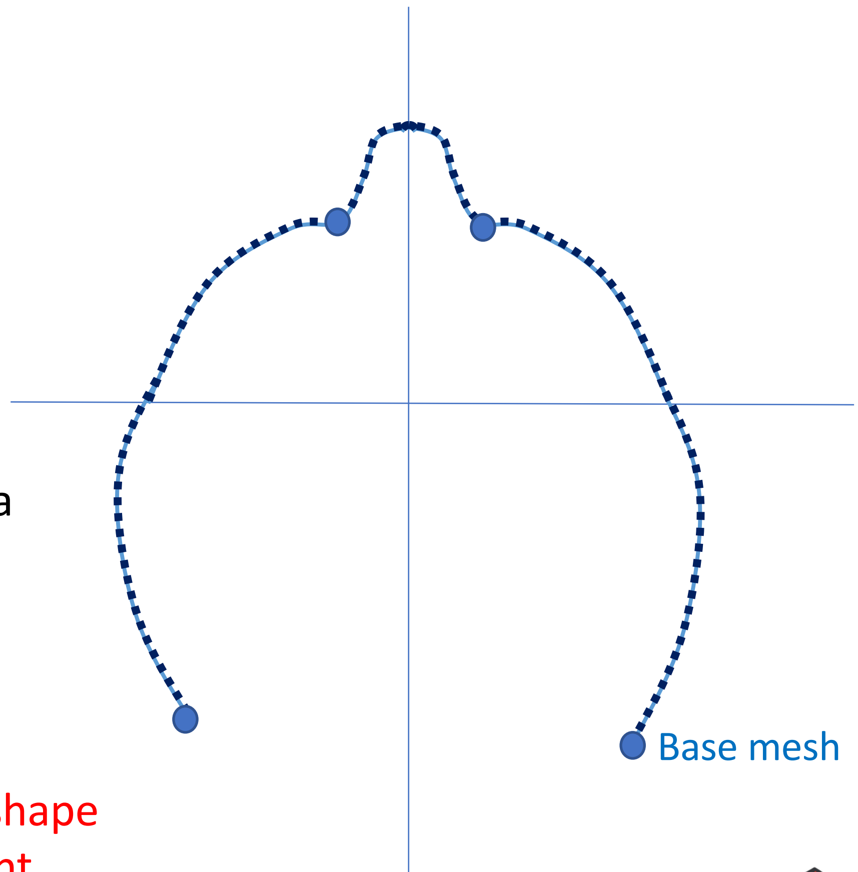
- The TPS warped subjects need to be a reasonable approximation of the mean shape
- This depends on the number of alignment landmarks and the variation in the data set



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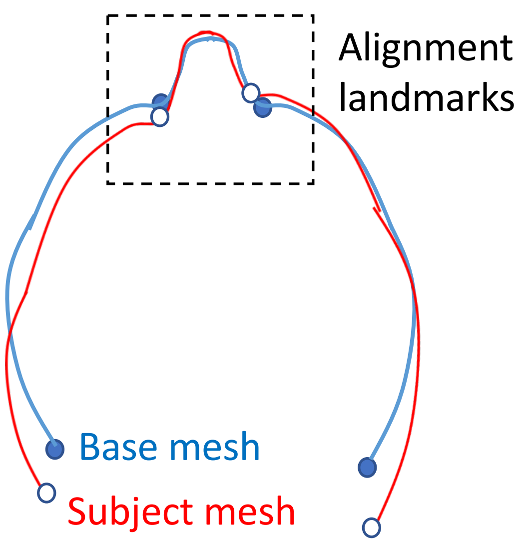
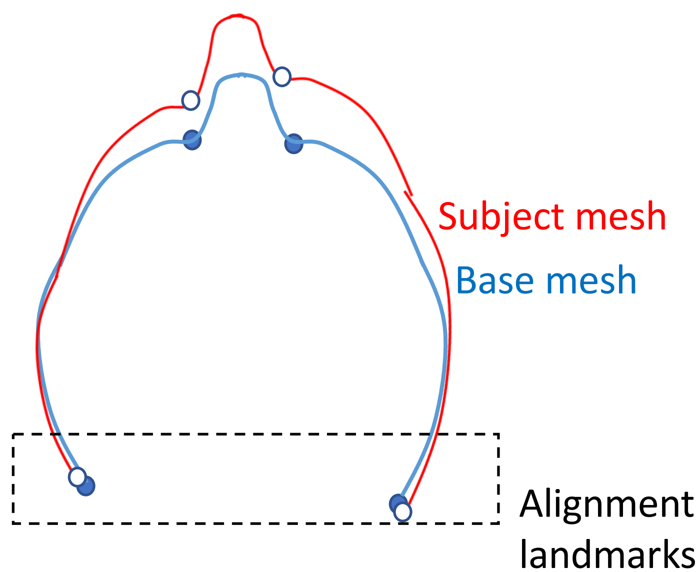
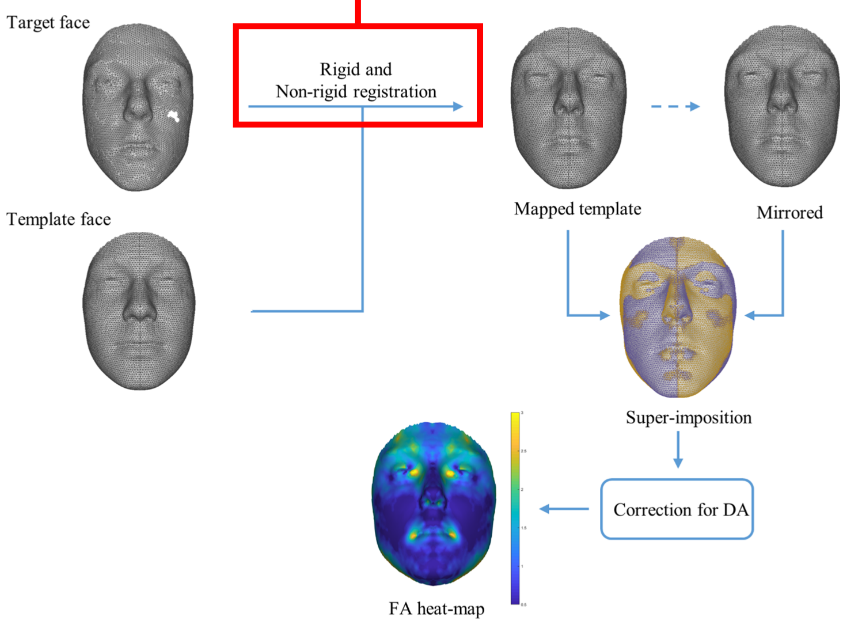
DBM is not “landmark-free”

- Initial alignment defines the frame of reference
- Choice of landmarks for alignment will impact the interpretation of the results
- Alignment landmarks with known homology will provide an interpretable framework for shape change measured





Initial alignment in DBM



Step 1- Rough alignment: We start by using 5 roughly indicated landmarks on *M* and *T* (the outer corners of the eyes, the tip of the nose and the corners of the mouth) to crudely align the surfaces using a superimposition of the points (scaling, rotation, and translation). This superimposition is done by finding the transformation matrix using a least-squares fitting of the two sets of landmarks [32] and applying the transformation to the whole face.

Step 2- Rigid ICP: In this step, we rigidly align the two surfaces as closely as possible. The ICP method introduced by Besl & McKay (1992) is probably the most widely used algorithm for rigid registration of point-clouds. Different survey studies on rigid registration methods show

- Approximate landmarks followed by automated alignment result in a reference frame that’s challenging to interpret
- Method and choice of landmarks should be carefully evaluated

Ekrami, Omid, et al. "Measuring asymmetry from high-density 3D surface scans: An application to human faces." *PloS one* 13.12 (2018): e0207895.

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Quantifying facial shape with Dense Surface Models

3D surface images

Calculate corresponding points
GPA,TPS, ICP

Feature extraction

Feature heat maps

Summarize local features

Score

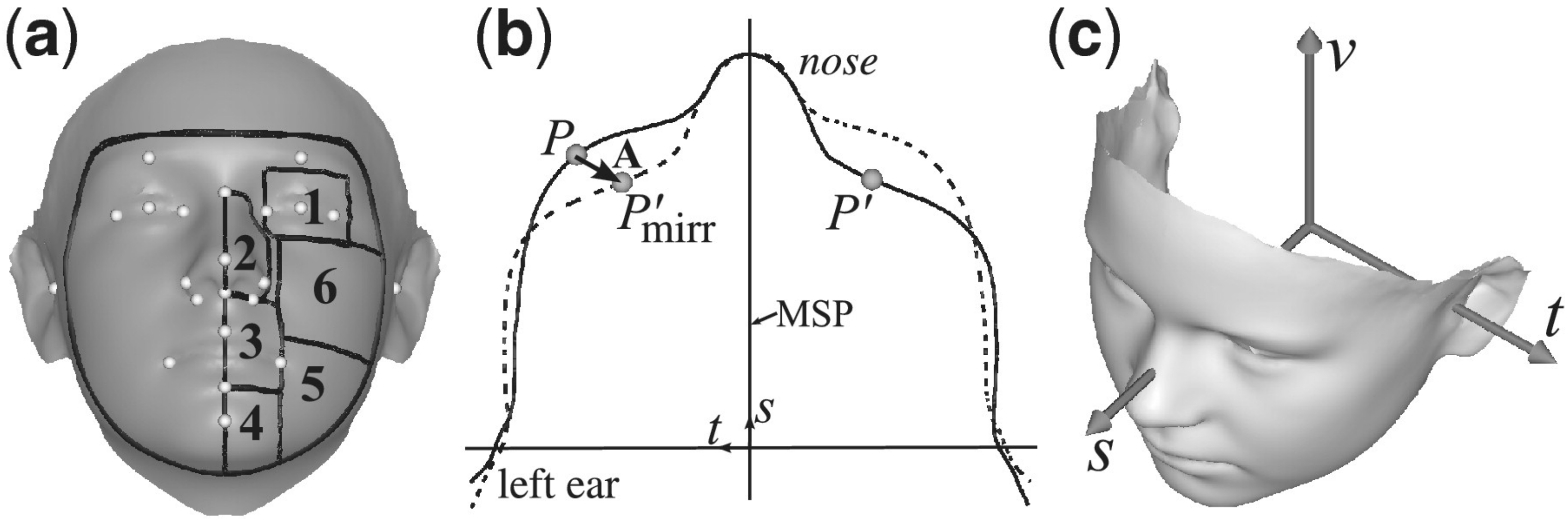
Feature extraction

Magnitude of flow vectors

Summarize local features

Average transform magnitude or RMS error
Principal modes of variation
Facial signatures (Hammond et al., 2012)
BRIM method (Claes et al., 2014)

Automated Quantification of facial asymmetry



Darvann, Tron A., et al. "Automated quantification and analysis of facial asymmetry in children with arthritis in the temporomandibular joint." *2011 IEEE International Symposium on Biomedical Imaging: From Nano to Macro*. IEEE, 2011.

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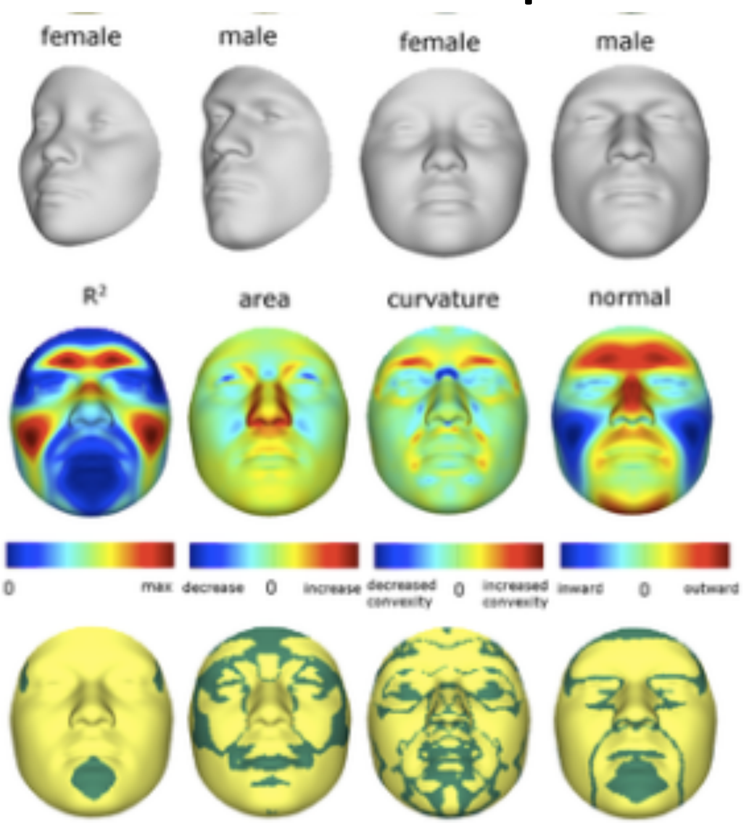
BRIM: bootstrapped response-based imputation modeling



- Technique to investigate the genetic basis for variation in the shape of the human face
- Estimation of a single quantitative axis of variation correspond to effects of single genes, ancestry, or sex

Claes, Peter, et al. "Modeling 3D facial shape from DNA." *PLoS genetics* 10.3 (2014): e1004224.

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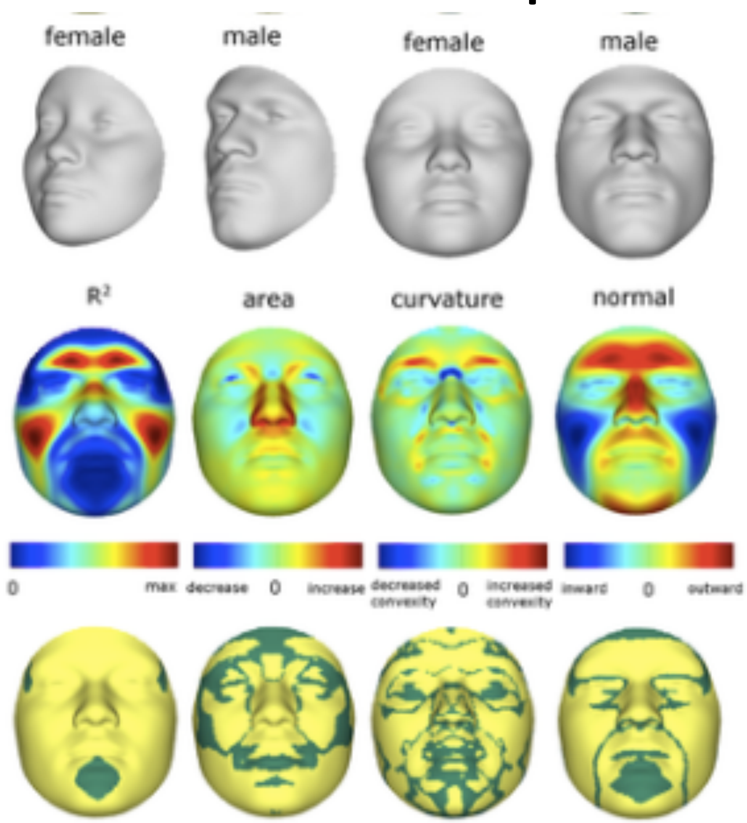

- Technique to investigate the genetic basis for variation in the shape of the human face
- Estimation of a single quantitative axis of variation correspond to effects of single genes, ancestry, or sex

"…our methods provide the means of identifying the genes that affect facial shape and for modeling the effects of these genes to generate a predicted face."

Claes, Peter, et al. "Modeling 3D facial shape from DNA." *PLoS genetics* 10.3 (2014): e1004224.
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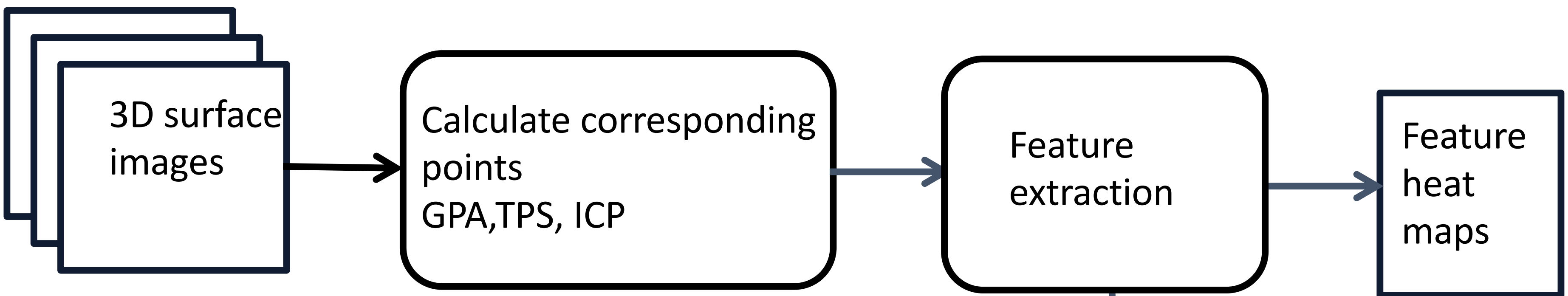
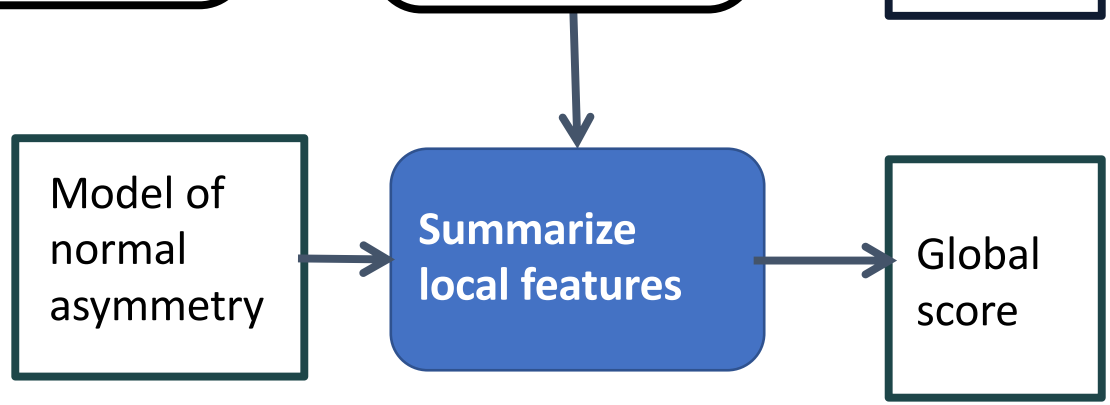
Summarizing local features





Feature extraction
Magnitude of flow vectors
Angle of flow vectors
Local shape descriptors

Summarize local features
Global-plus-local similarity metric

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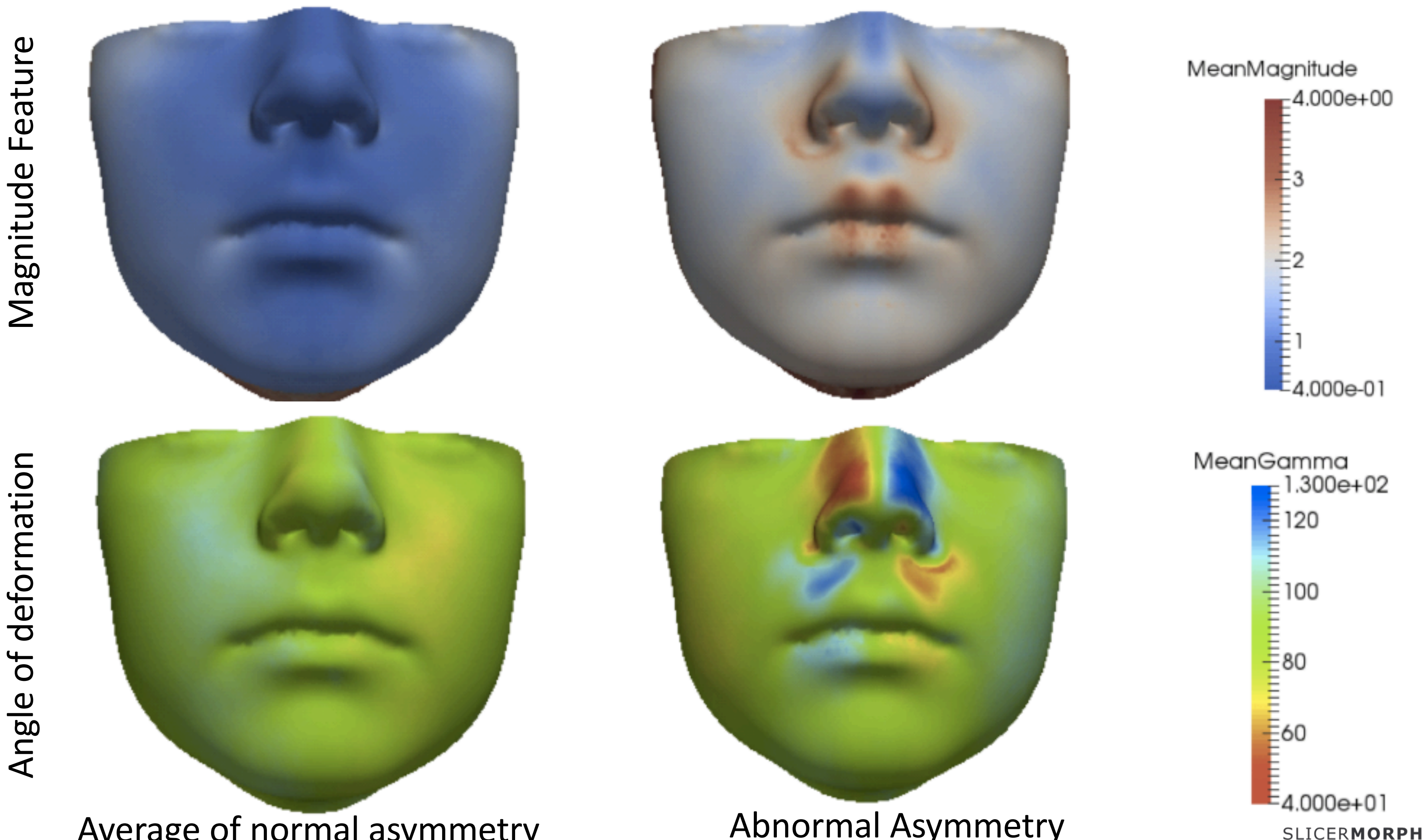
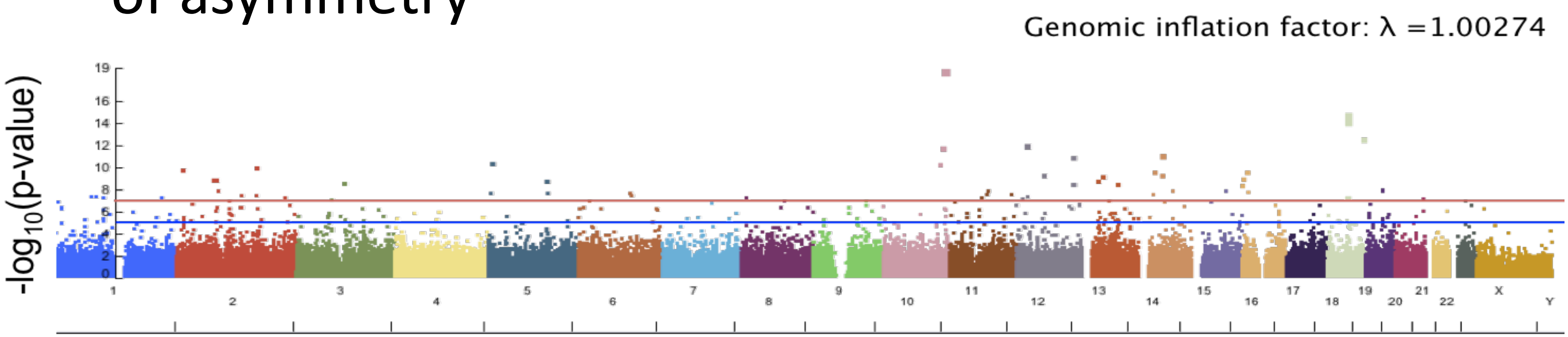
Quantification of abnormal asymmetry



Genetic basis of facial asymmetry

- Aim to use automated phenotyping to produce a score of facial asymmetry that can summarize local deviations from normal asymmetry
- Correlate with SNP data to investigate genetic basis of asymmetry



Normal angle difference

Chromosome

Rolfe, Sara, Su-In Lee, and Linda Shapiro. "Associations between genetic data and quantitative assessment of normal facial asymmetry." Frontiers in genetics 9 (2018): 659.

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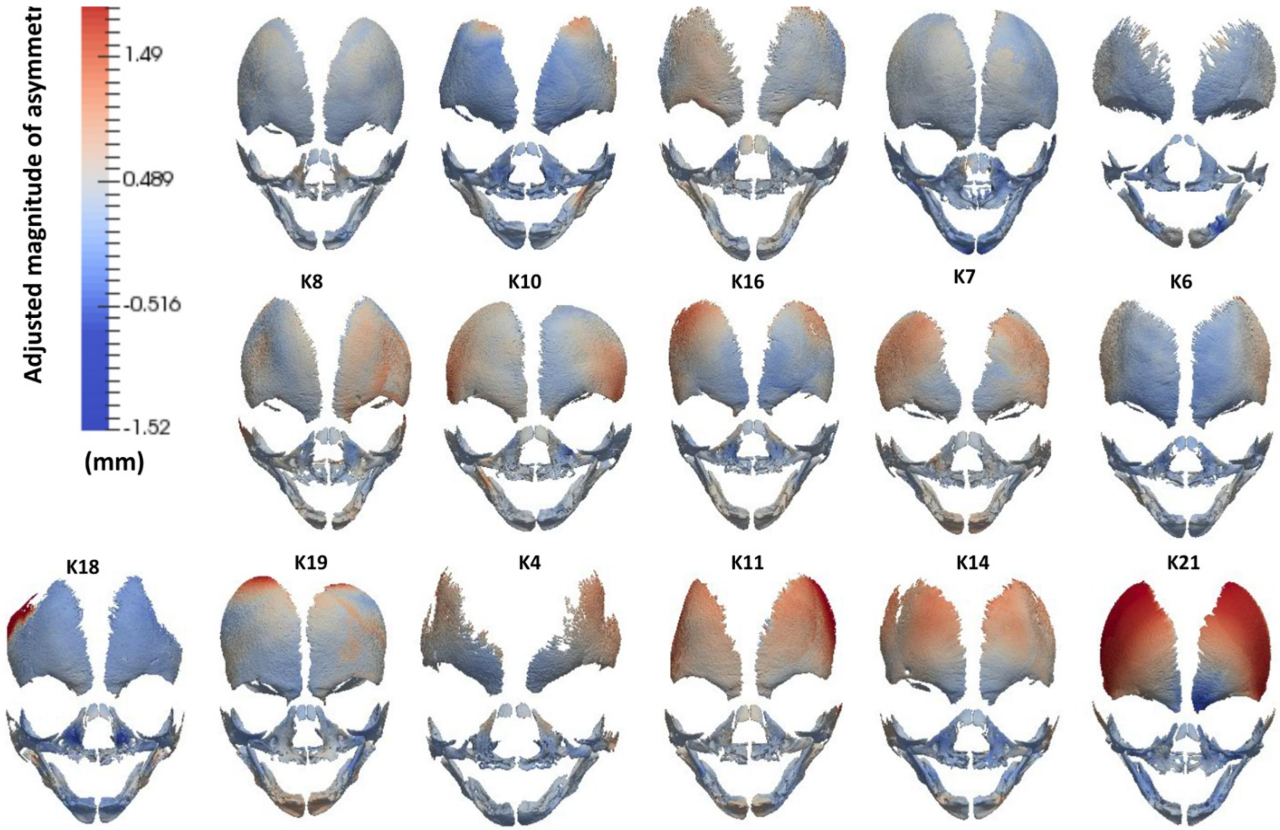
Analysis of asymmetry in developing facial bones



Katsube, M., Rolfe, S.M., Bortolussi, S.R., Yamaguchi, Y., Richman, J.M., Yamada, S. and Vora, S.R., 2019. Analysis of facial skeletal asymmetry during foetal development using µCT imaging. Orthodontics & craniofacial research, 22, pp.199-206.

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Limitations of DBM

- No guarantee of homology
- Results need to be interpreted with respect to initial alignment
- High dimensional data output
- Computationally intensive for large datasets

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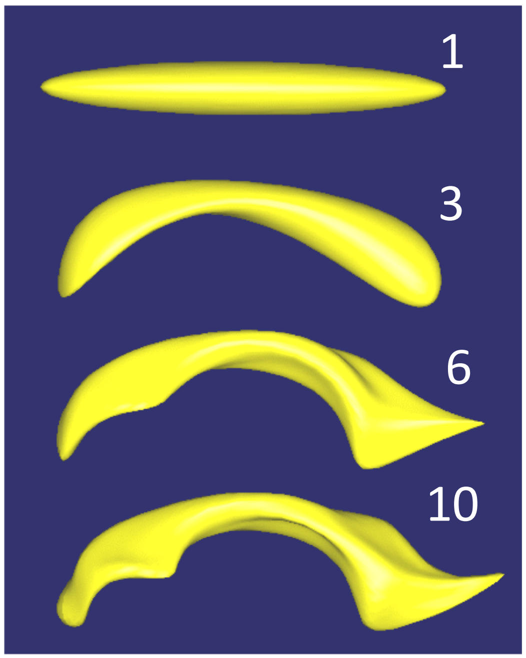
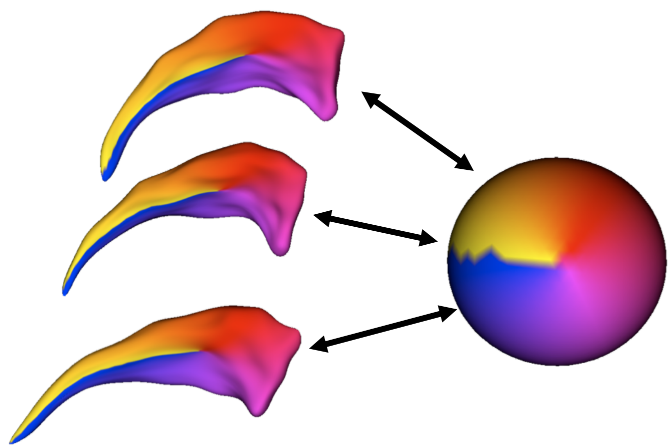
Spherical harmonic representation and point distributed models (SPHARM-PDM)





SPHARM description is computed from the mesh and its spherical parameterization

Styner, Lieberman, Pantazis, Gerig: Boundary and Medial Shape Analysis of the Hippocampus in Schizophrenia, Medical Image Analysis, 2004, pp 197-203

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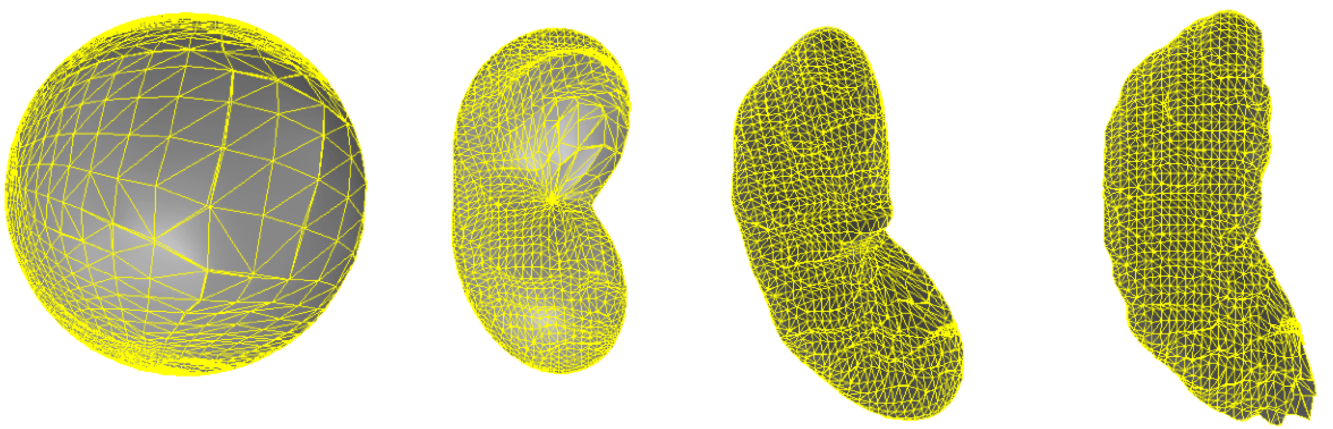
SPHARM modeling

Overfitting



degree 1 degree 5 degree 10 degree 50

- The SPHARM description is then sampled into a triangulated surface
- Triangulated surfaces with correspondences are computed via icosahedron of the spherical parameterization

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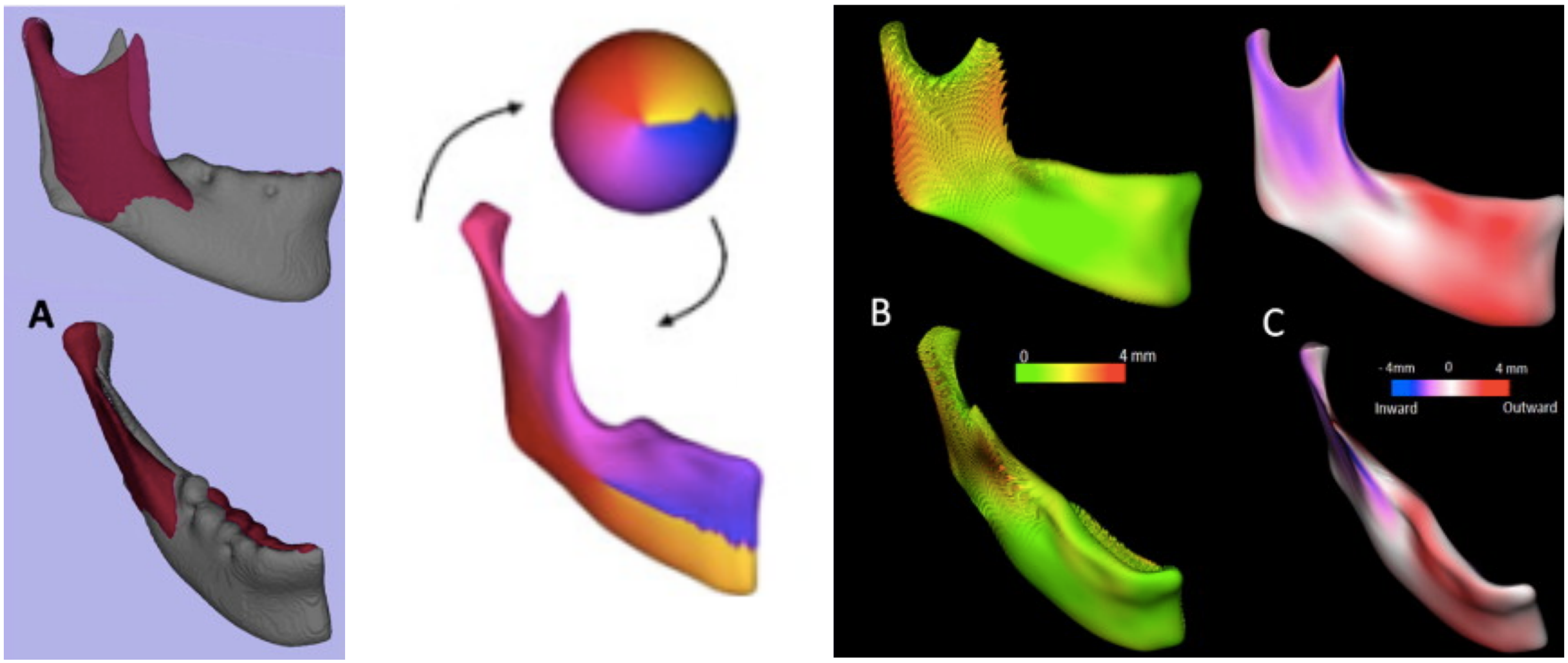
SPHARM analysis of mandibular asymmetry



Cevidanes, Lucia HS, et al. "Three-dimensional quantification of mandibular asymmetry through cone-beam computerized tomography." Oral Surgery, Oral Medicine, Oral Pathology, Oral Radiology, and Endodontology 111.6 (2011): 757-770.

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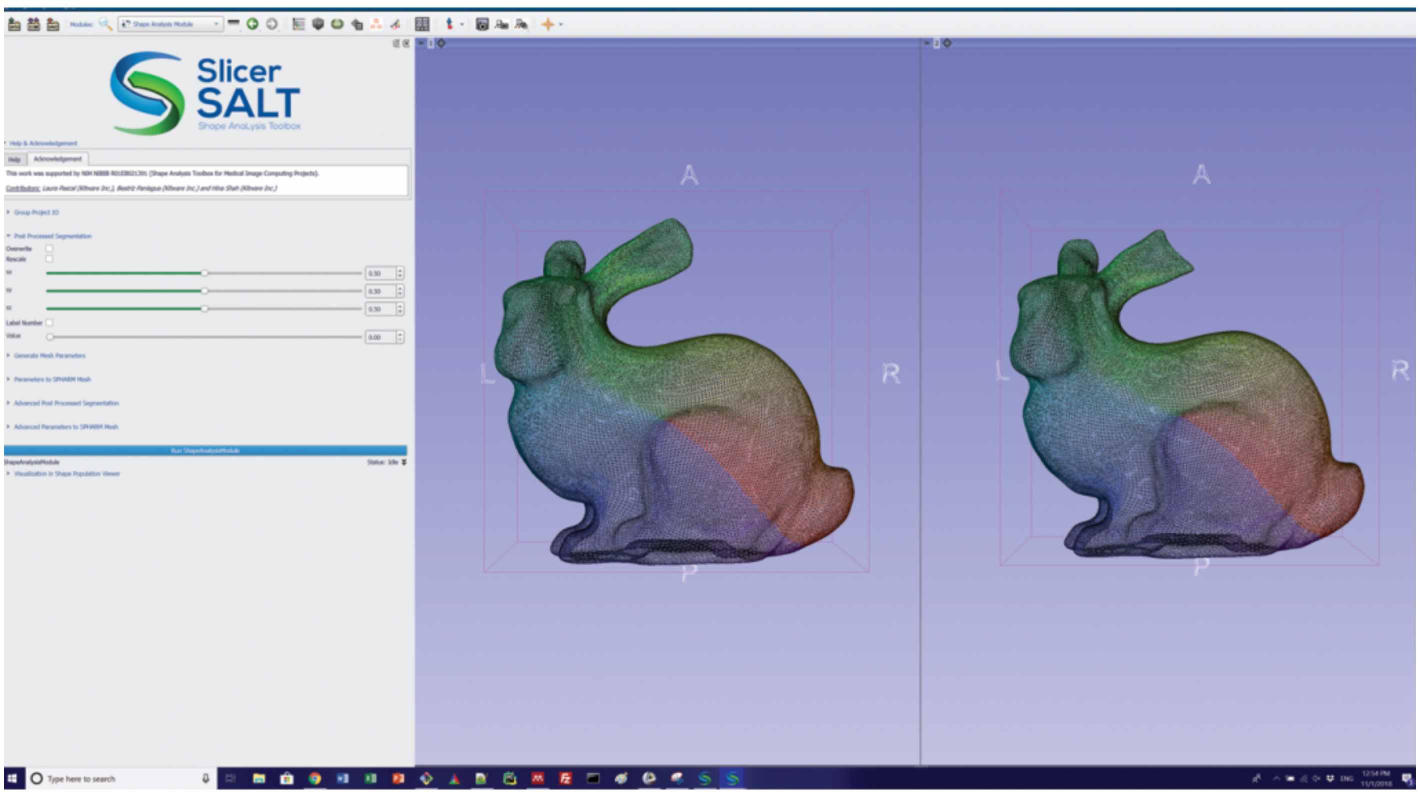
Limitations of SPHARM methods

- Requirement for spherical topology of meshes
- Challenging for complicated or noisy data sets
- Developed for high N of shapes with similar morphology – should preform a quality assessment to check for correspondence issues

Slicer SALT: Shape AnaLysis Toolbox



Compute point distributed models (pdm) using spherical harmonic representation (SPHARM-PDM)

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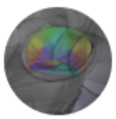
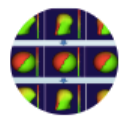
Coming soon

With SlicerSALT you can...

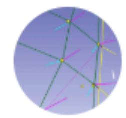


Compute Point Distributed Models (PDM) using Spherical Harmonic Representation (SPHARM-PDM)

Run 4D regression in a collection of 3D PDMs associated to a linear variable (i.e. age)



Perform correspondence optimization using study-wise shape analysis



Fit skeletal representations (s-reps) to a collection of binary volumes

Compute image-based correspondence in binary volumes of non-spherical and complex topologies

Use advanced shape statistics for scientific hypothesis testing

Access all functionality through the graphical user interface

Perform command line batch processing

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Questions?

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Resources

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