ALPACA

Automated Landmarking through Point-cloud Alignment and Correspondence Analysis

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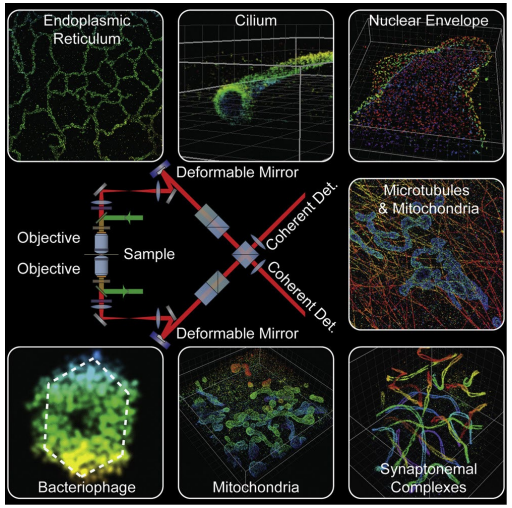
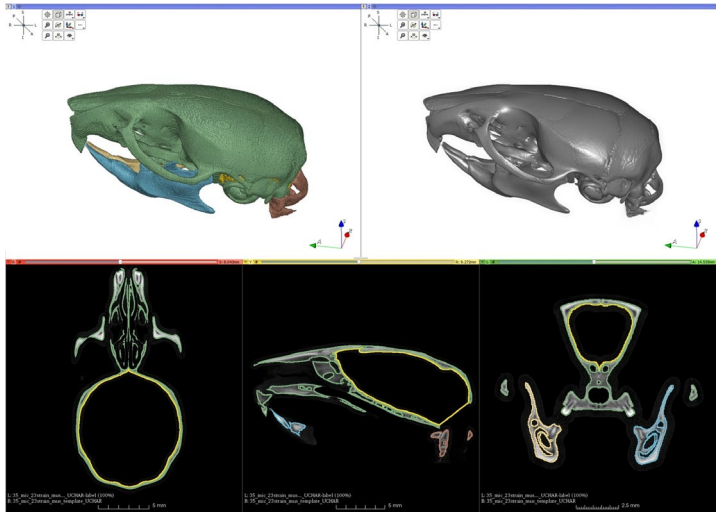
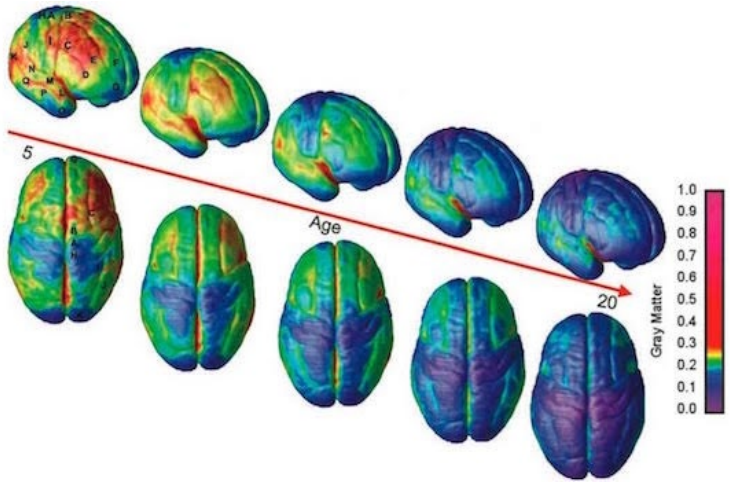
SlicerMorph

Complex shapes

- Quantifying and comparing complex shapes is a key component of fields as diverse as evolutionary morphology, cell biology, computer vision, computational anatomy and paleontology.

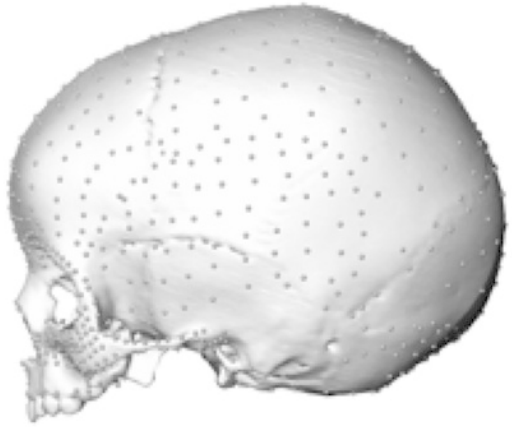




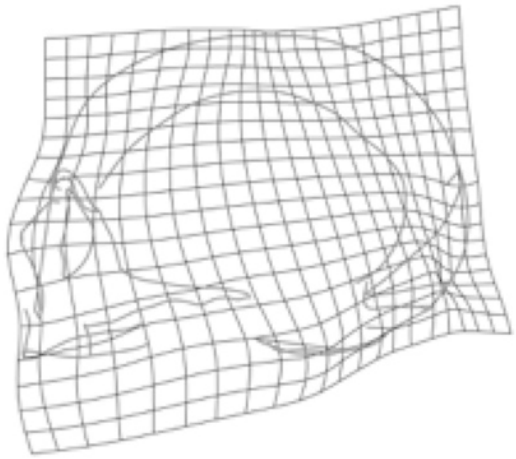


Geometric morphometrics

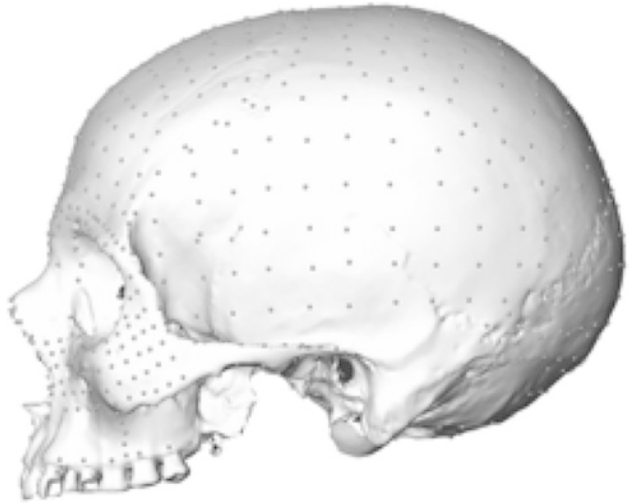
Suite of analytical techniques aimed at studying shape variation through annotation of landmarks corresponding to anatomical structures of interest



Homo sapiens child

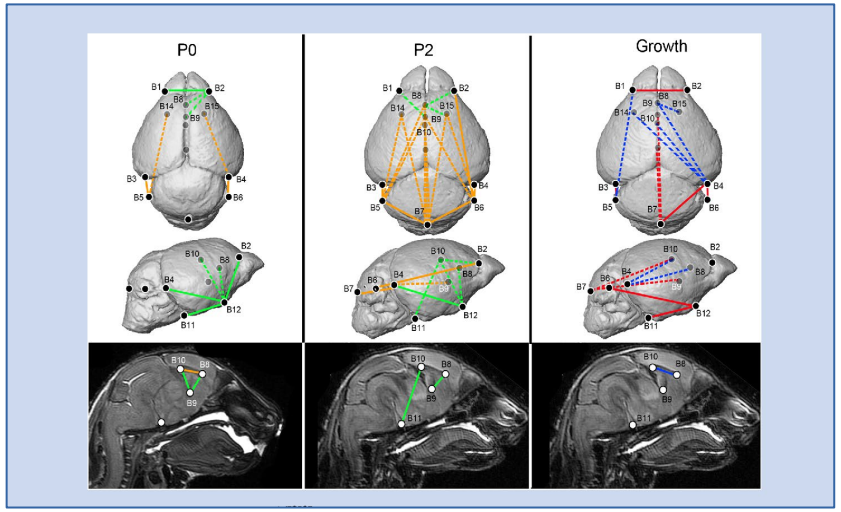


Thin-plate spline deformation grid

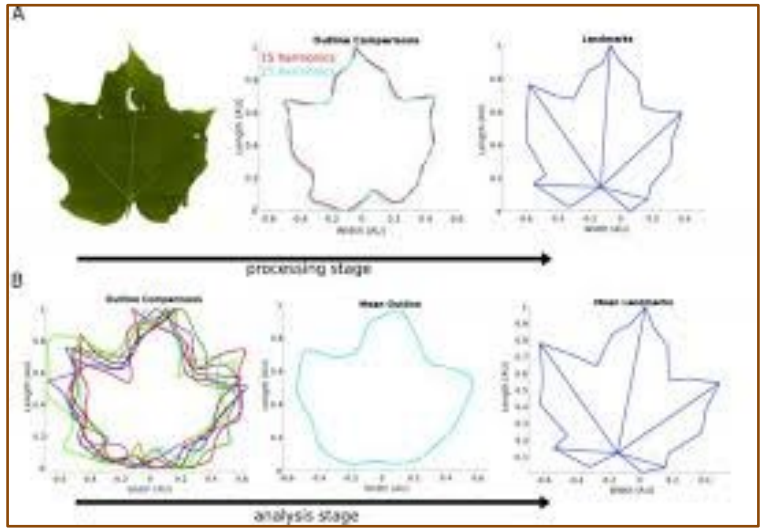


Homo sapiens adult

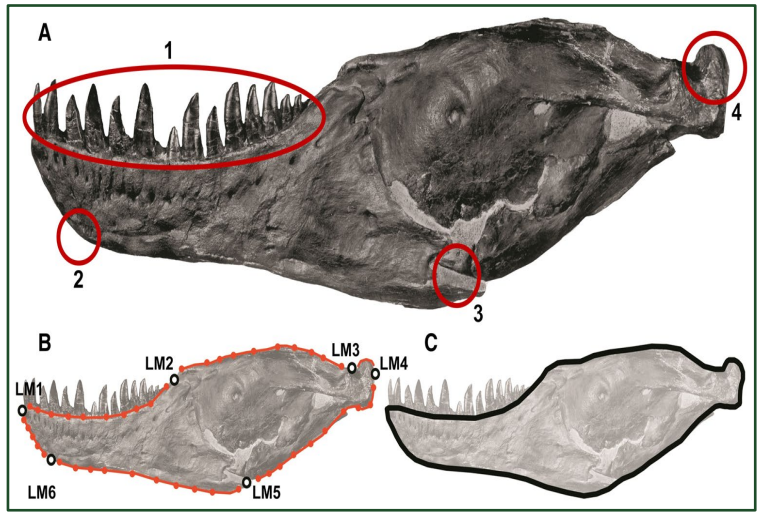
Morphometrics – System agnostic



Genetic contexts
e.g., Apert syndrome

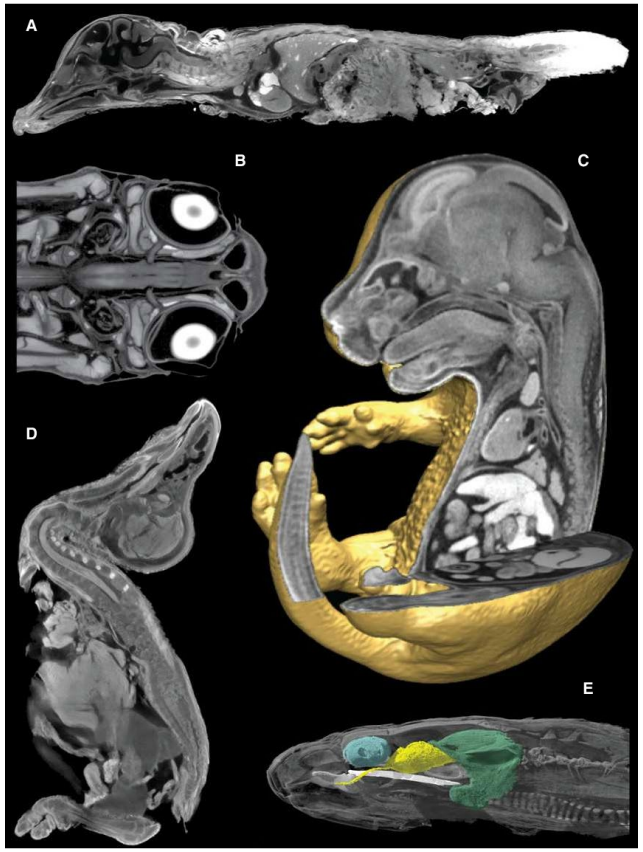


Ecological contexts
e.g., Leaf shape

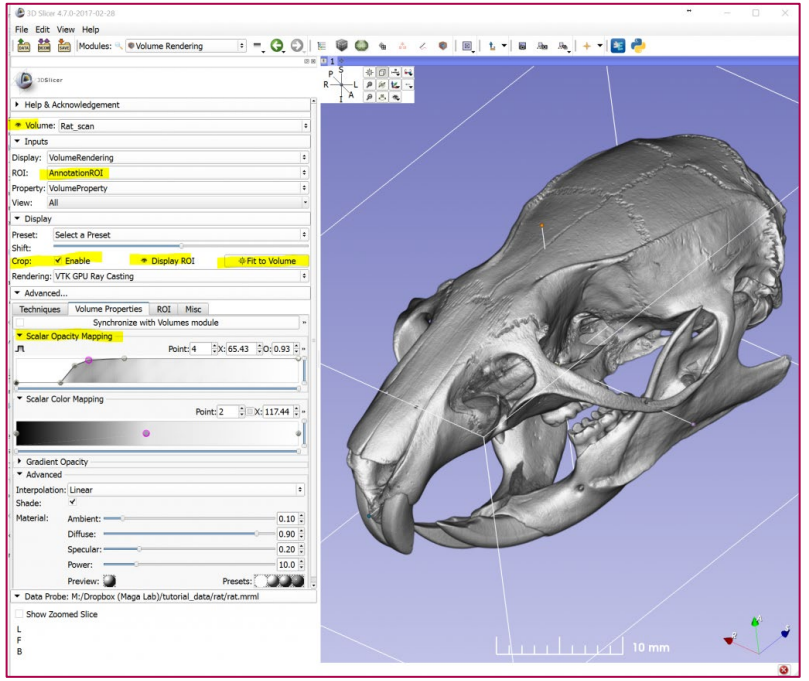


Evolutionary contexts
e.g., Tyrannosaur
Schaeffer et al, 2020

Advances – Image quality and availability



Techniques
e.g., CT



Analytical software
e.g. 3D Slicer

MORPHO SOURCE

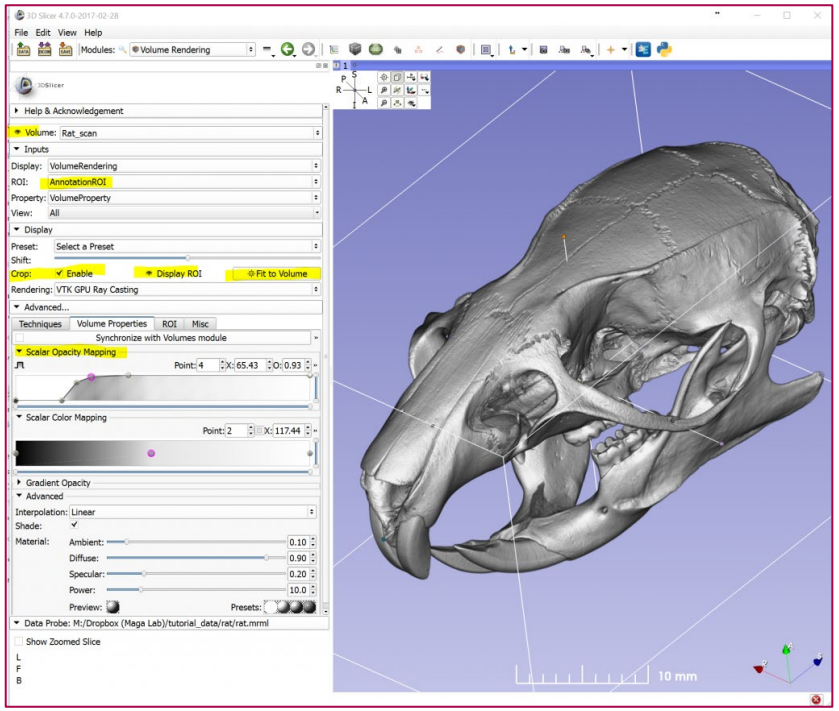
phenome 10k

Public Databases
with High res. images

Challenges of Geometric Morphometrics

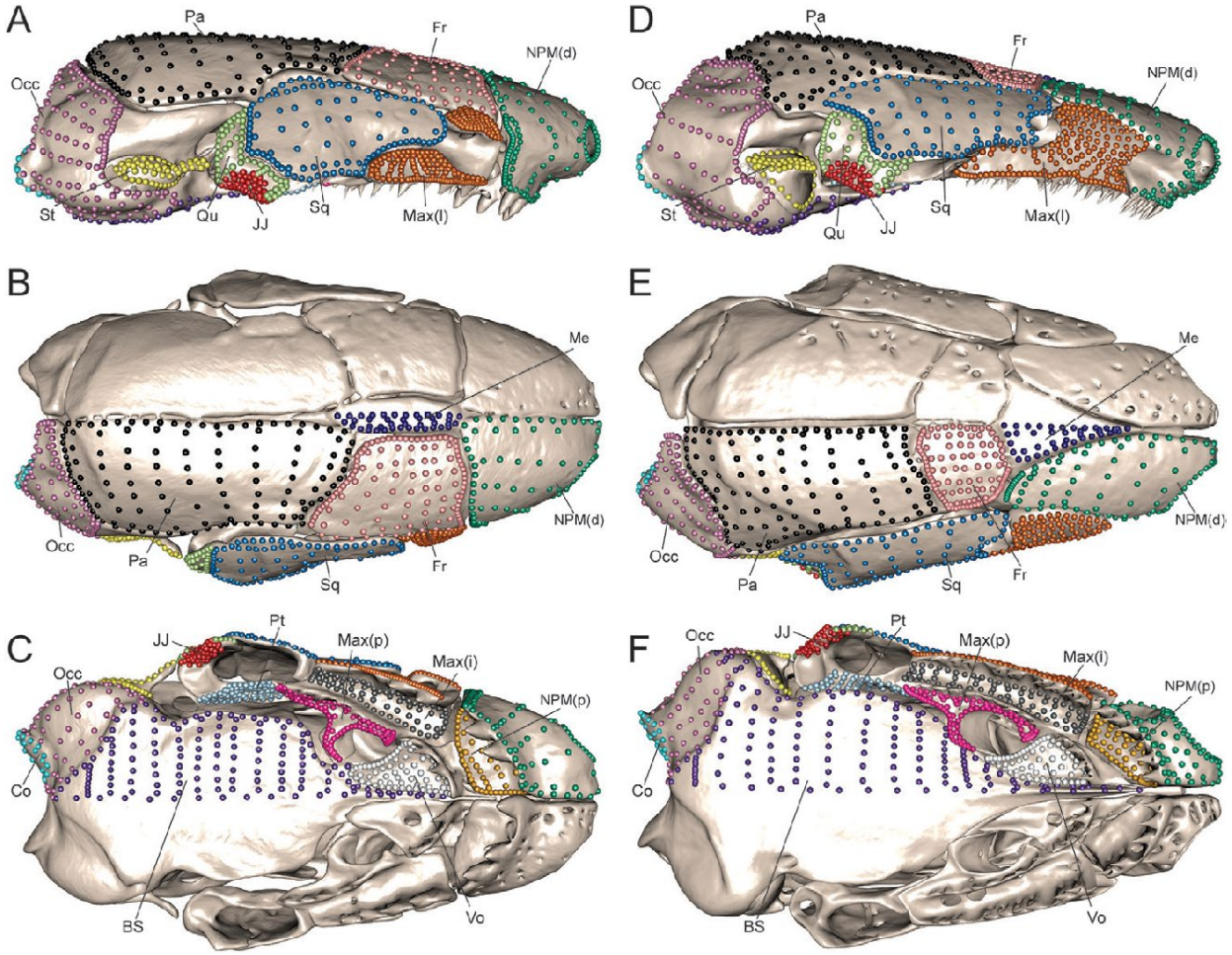
Though popular, geometric morphometrics is nonetheless a labor-intensive process, usually relying on manual annotation of landmarks by a trained expert.

e.g., digitizers



e.g., software

Manual - Time consuming



66 (type 1)
+
336 (sliding)
+
736 (semi)

Marshall et. al., 2019

Manual - Intra- and inter-observer error

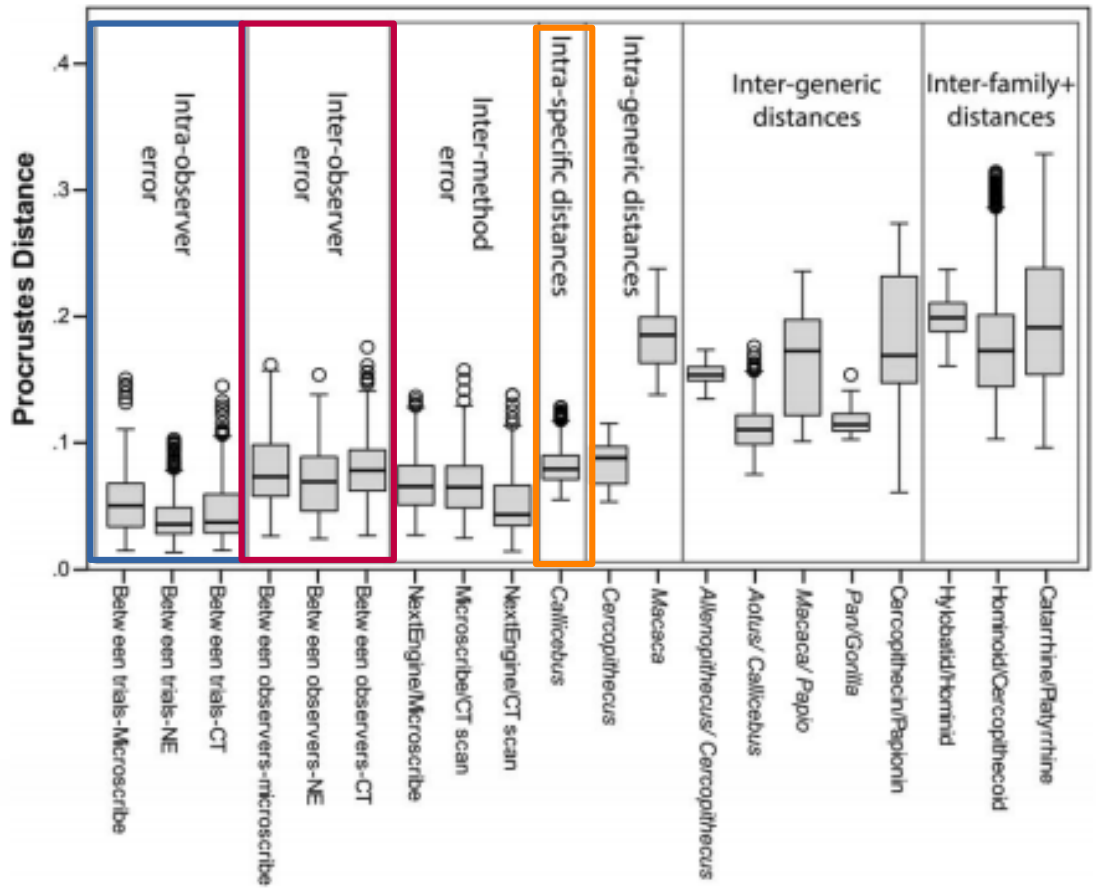


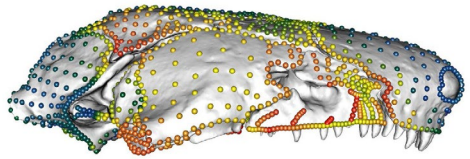
FIGURE 4 Box plot of Procrustes distances within and among observers, methods, and taxa. Darkened bars represent the median value for each group, boxes show the interquartile range (25th to 75th percentile), and the whiskers extend to 1.5 times the interquartile range. Outliers are designated by circles

Robinson and Terhune, 2017

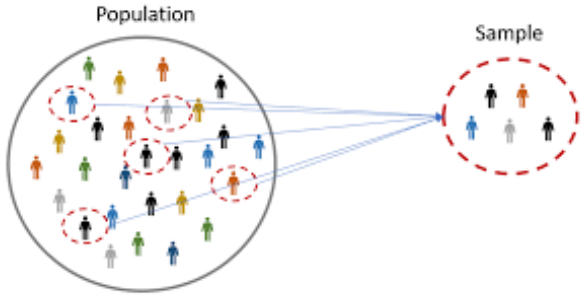
Automated approaches have advantages

Automated methods improve researchers' ability to sample phenotypes in three ways:

* Increase spatial resolution



* Increase sample size



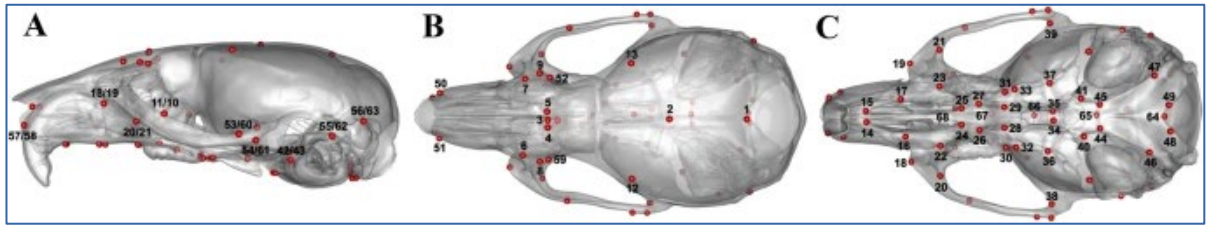
* Reduce subjectivity (reproducible)

Automated approaches face challenges

* Resources

- Personnel: imaging scientist

- Hardware: automation = as much as 10 CPU/hours per specimen



e.g. Devine et al 2020

* System-specificity

- Algorithms: species-specific and hard to generalize

ALPACA

ALPACA

Porto et al, bioRxiv

Intuitive

Users with no prior experience in image analysis could use it

Lightweight

Run in minutes (much less time than manual digitization)

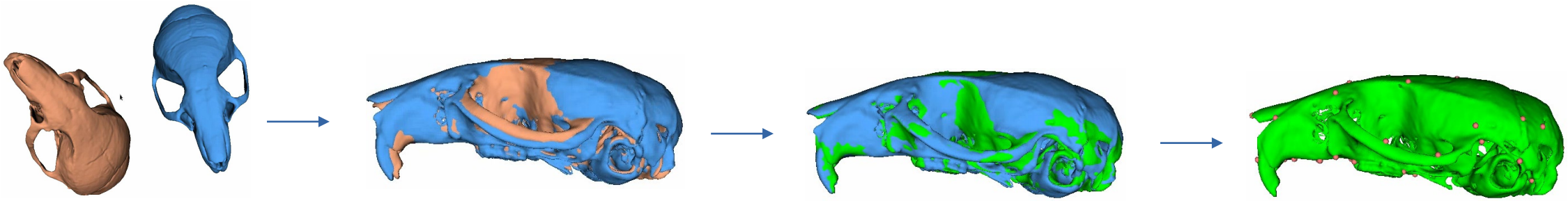
General

Can be applied to any structure of interest, given some limitations in the degree of shape variation

Most automated approaches rely on registration techniques

Registration

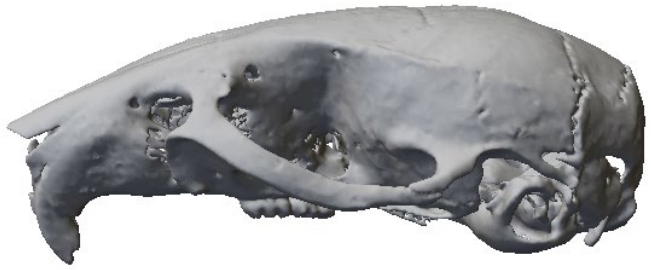
is the process of finding the optimal transformation to maximize correspondence between a template (model) and a specimen



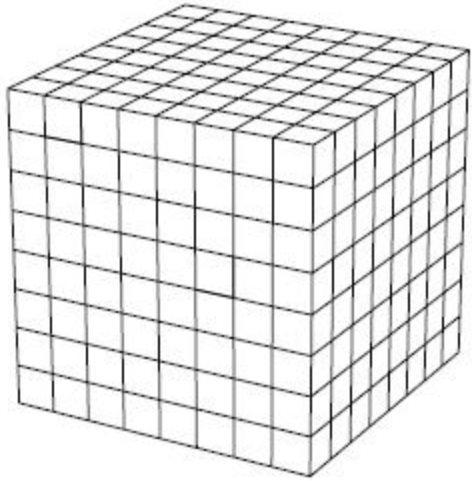
ALPACA is a bit different

Key aspect

Sparse representation can be used to find for alignment

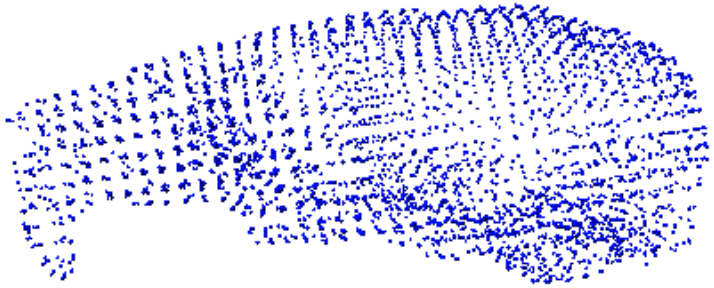


Mesh



Voxel Grid

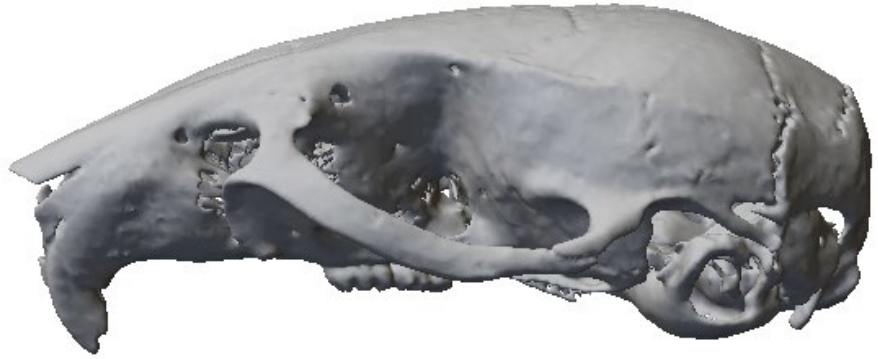
User-specified

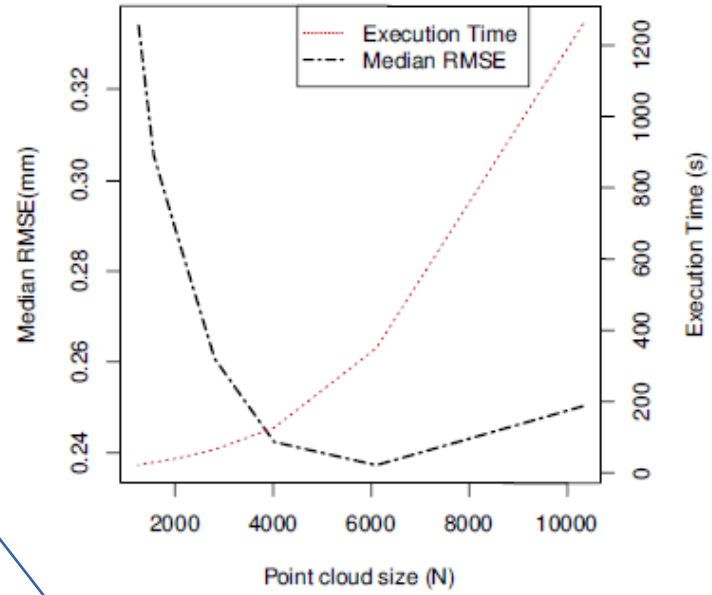


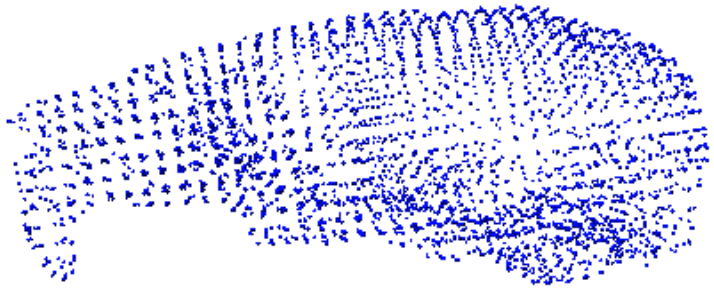
Voxel size = 0.8 mm

Point-cloud

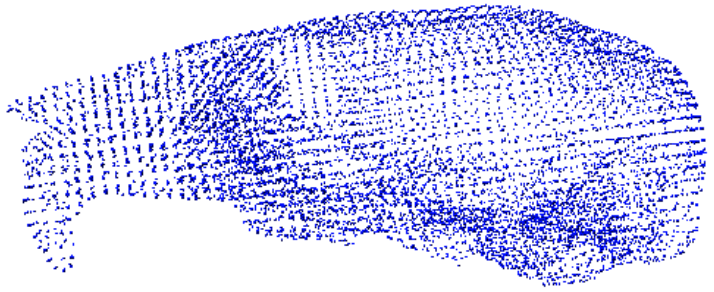
How sparse? User has control over it



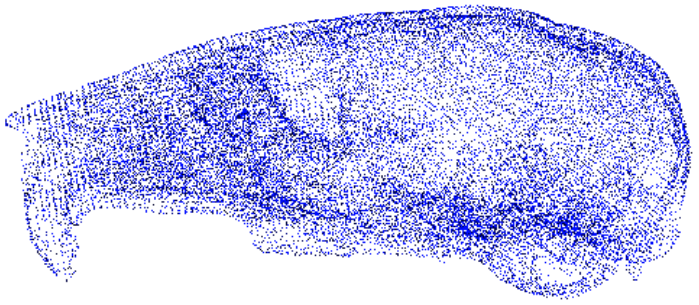




Voxel size = 0.8 mm

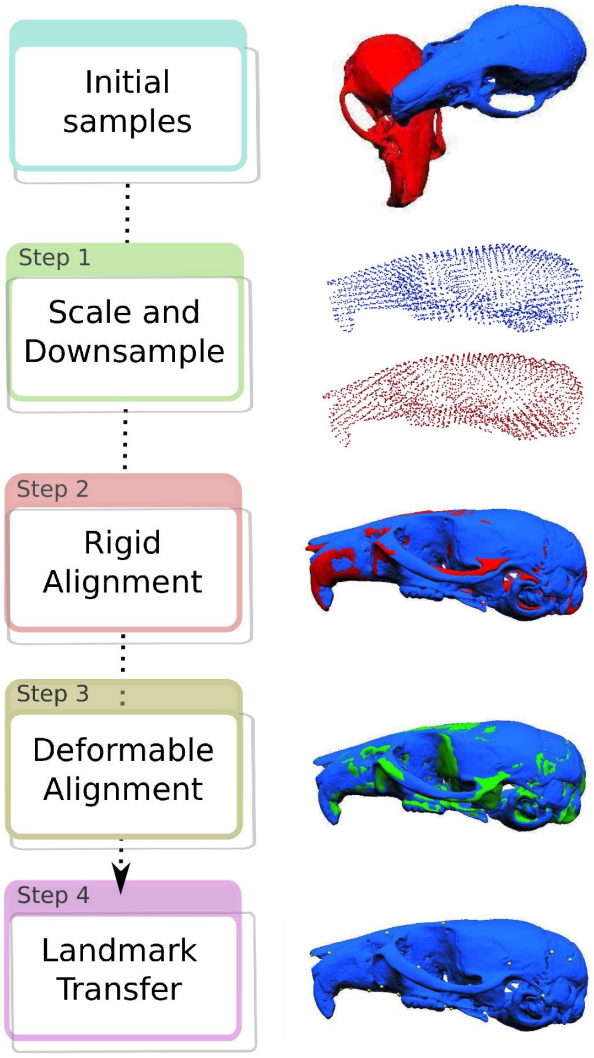


Voxel size = 0.6 mm

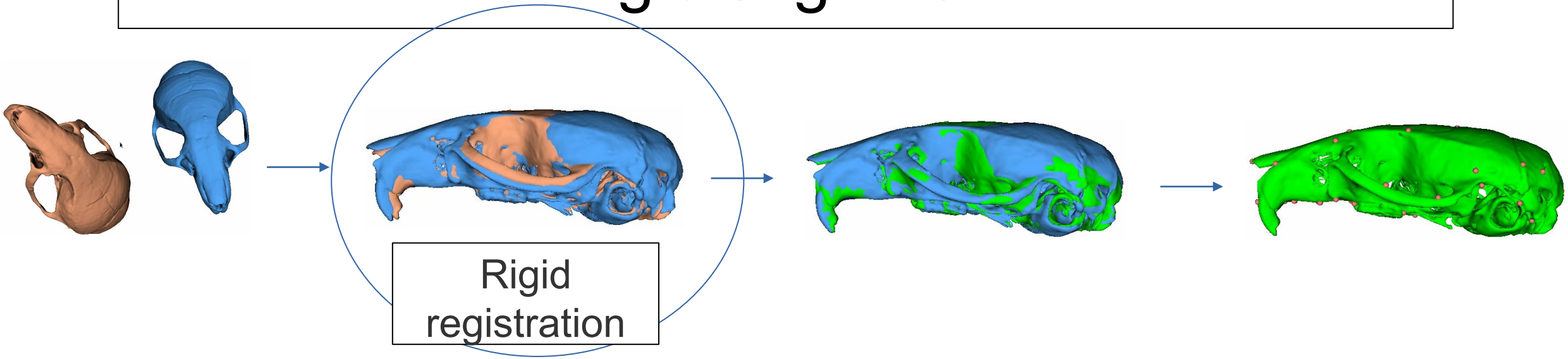


Voxel size = 0.2 mm

ALPACA pipeline overview

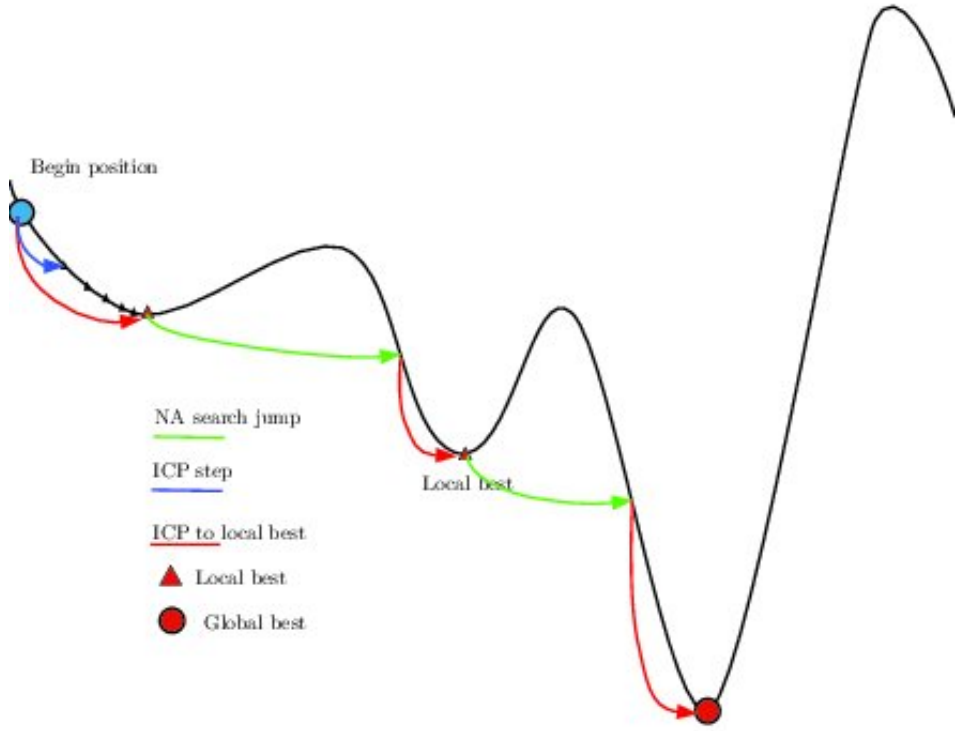


Rigid alignment



Objective: Find the optimal rotation, translation and scaling of the source structure in order to match the target one, starting from arbitrary positions in 3D space

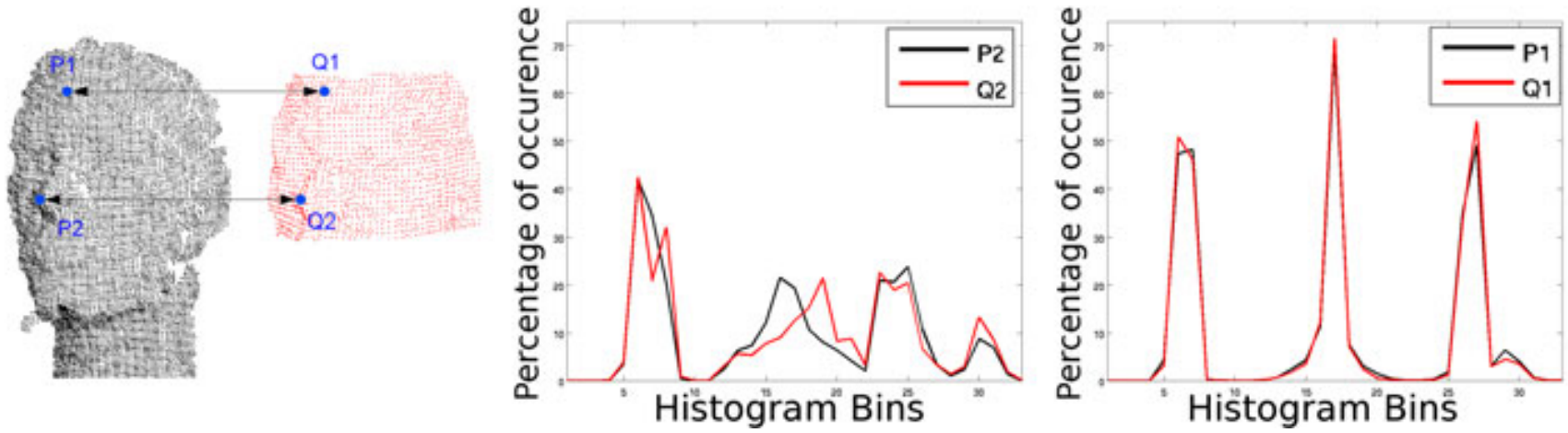
Rigid -Challenges



Main challenge : How to prevent local optima?

Rigid – Our approach

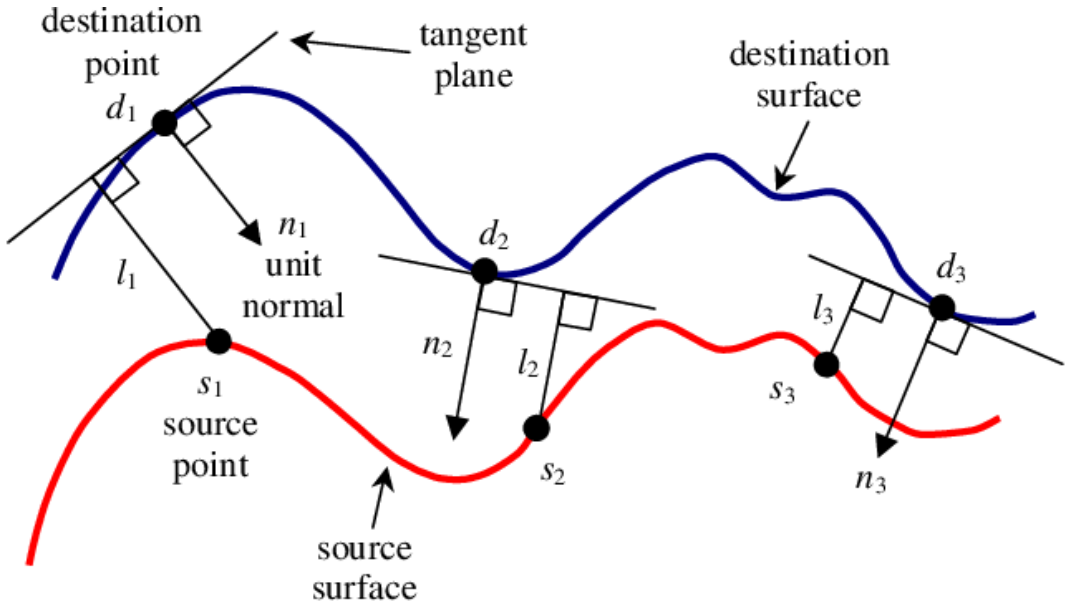
To find the initial rough alignment, ALPACA uses local geometric descriptors (=semantically rich)

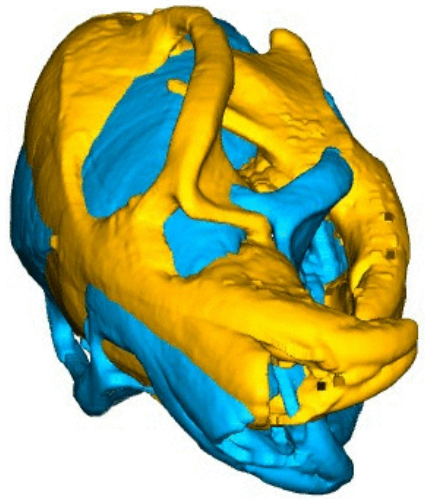


Fast Point Feature Histogram

Rigid – Local registration

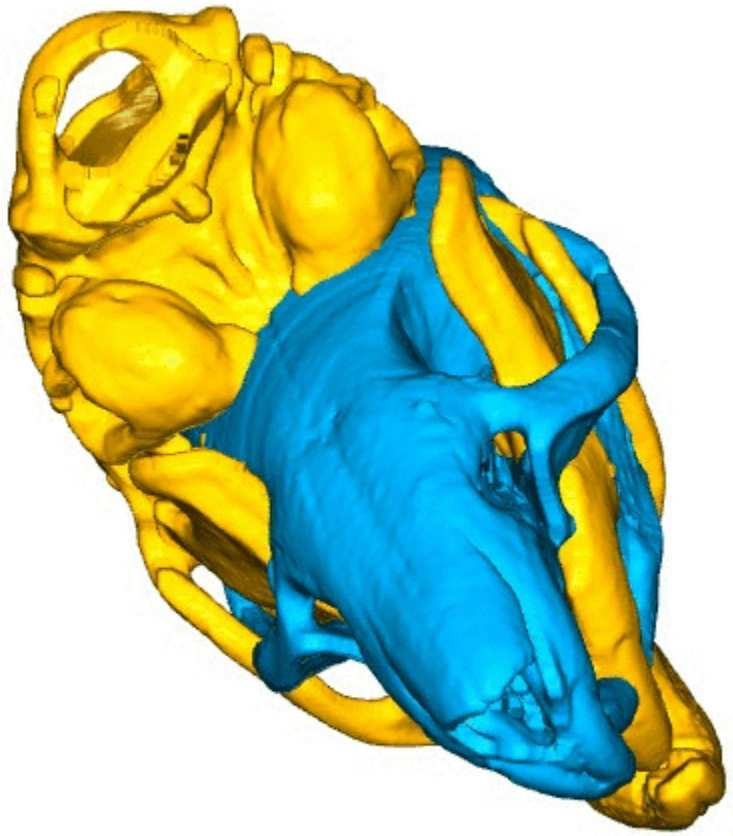
Refine initial alignment using iterative closest point



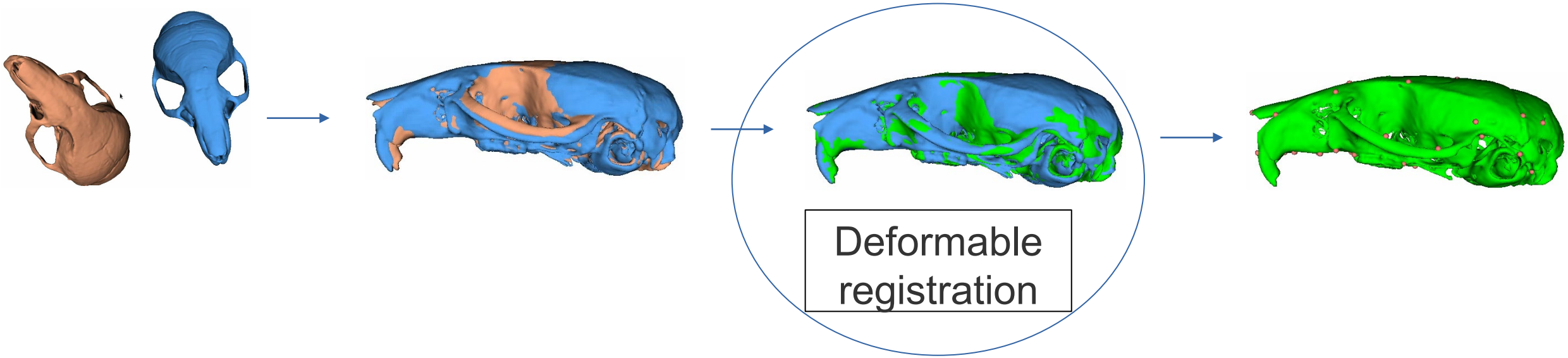


Point-to-plane ICP

Rigid alignment

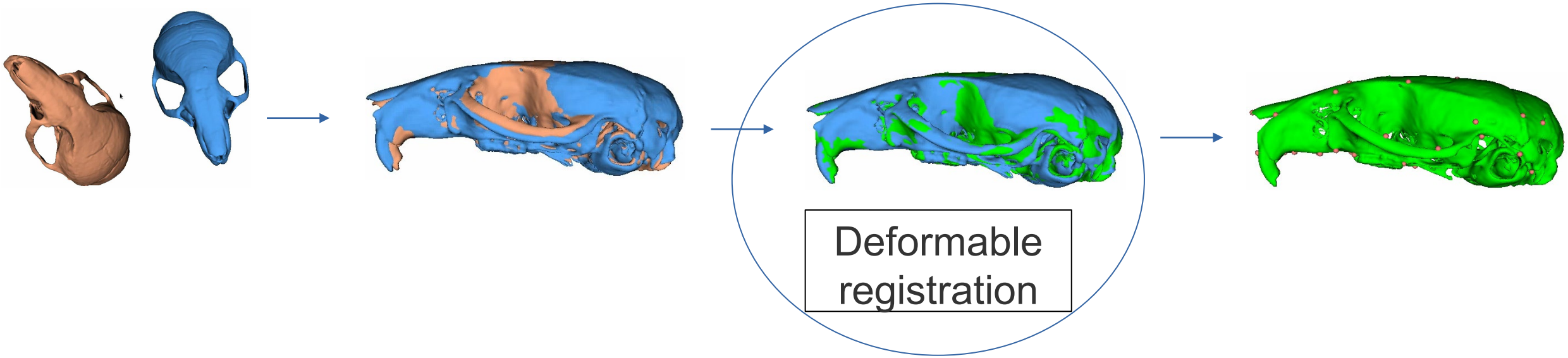


Deformation



Objective : Find the non-linear geometric transformation necessary to map two images onto a common coordinate system.

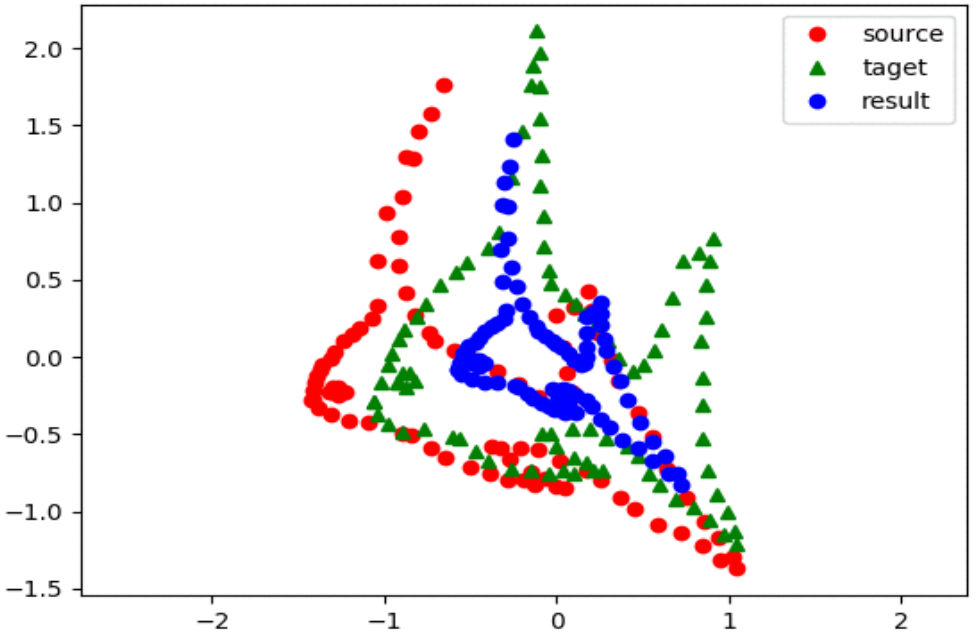
Deformation

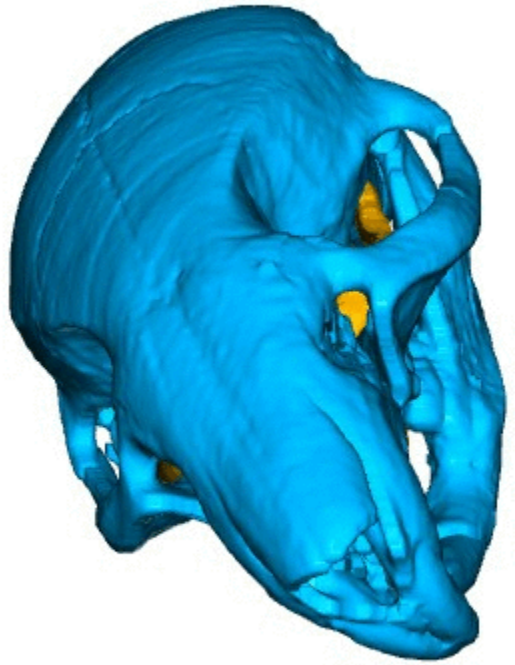


Challenge : Accurately representing biological deformations, and doing so in a reasonable amount of time

Deformable - CPD

Coherent Point Drift – imposes constraints on the deformation in the form of motion coherence among neighbors

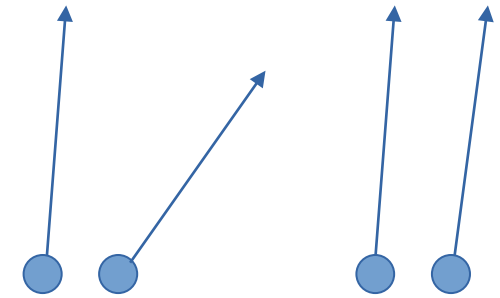




Deformable – Structure specific

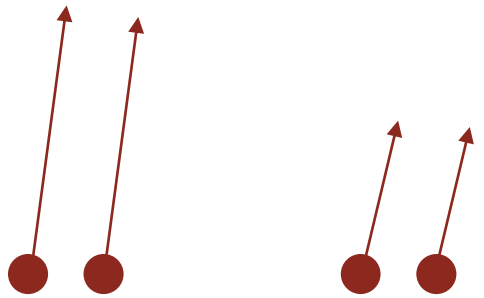
The deformable step has two regularization parameters (α and β) .
These parameters will typically have to be modified to better serve your own needs.

Motion coherence



Small β Large β

Displacement



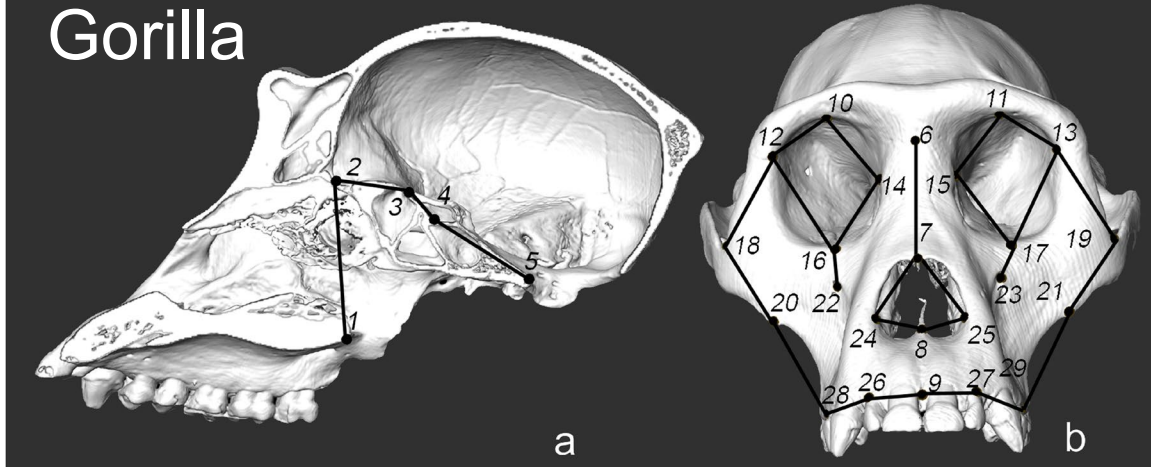
Small α Large α

Testing - Four datasets

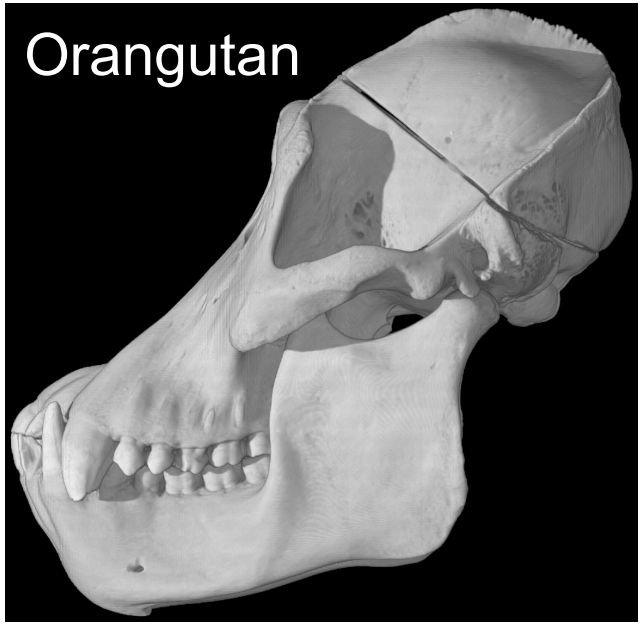
Mouse

Chimps

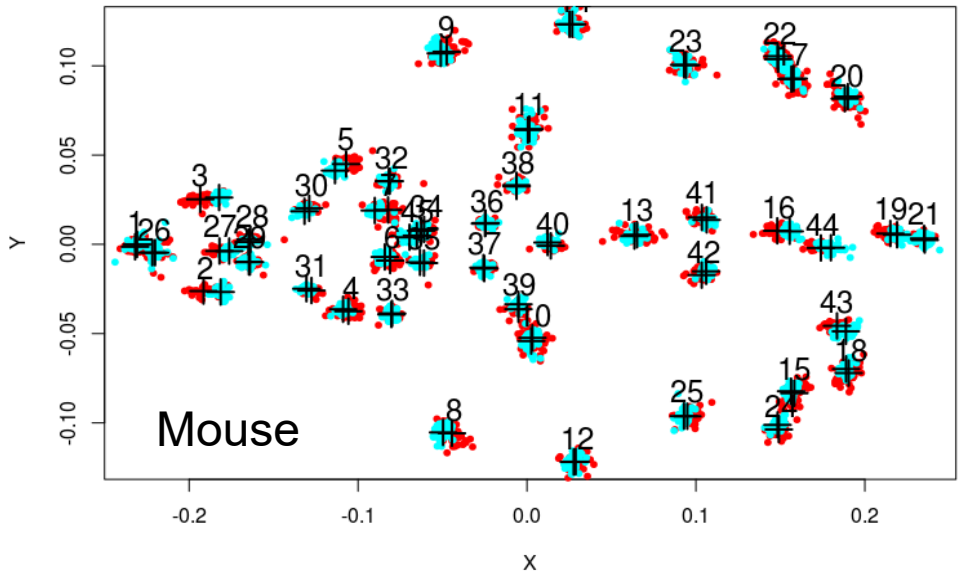
Gorilla

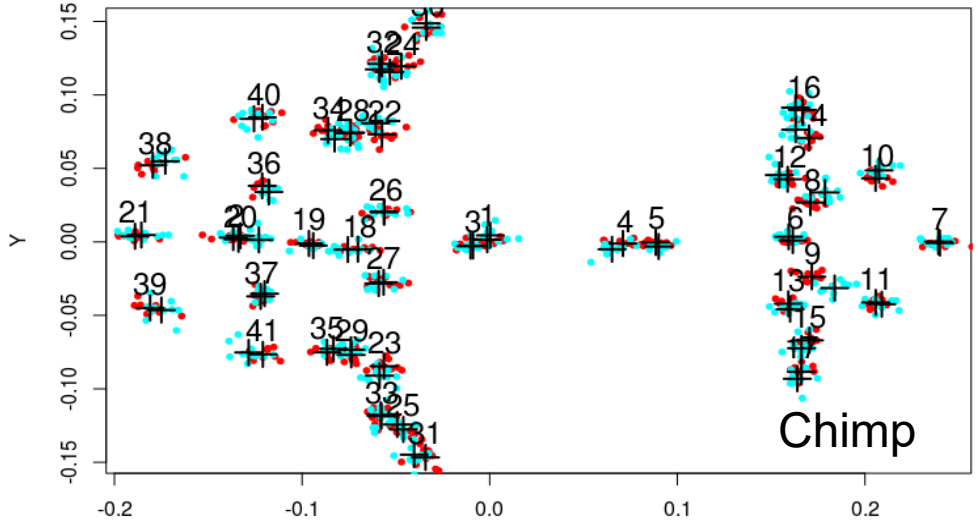


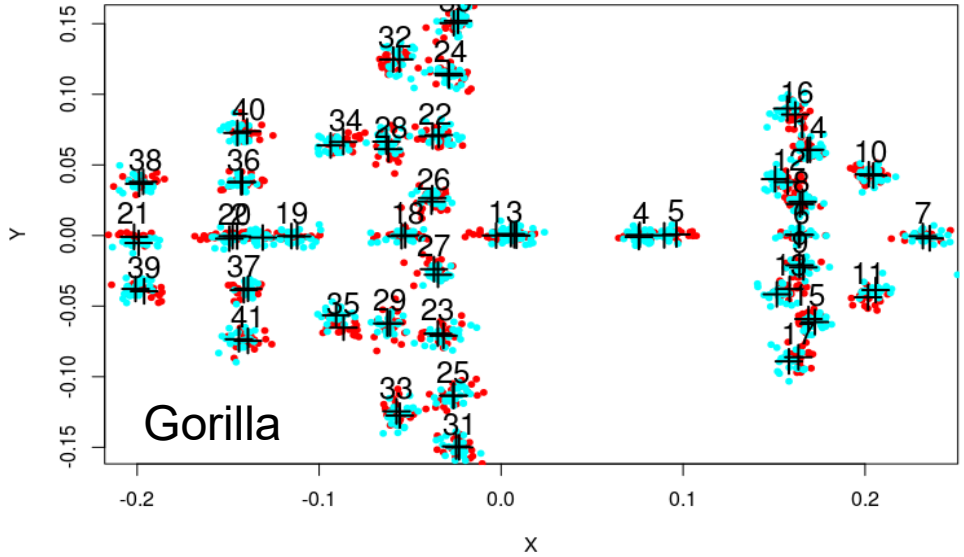
Orangutan

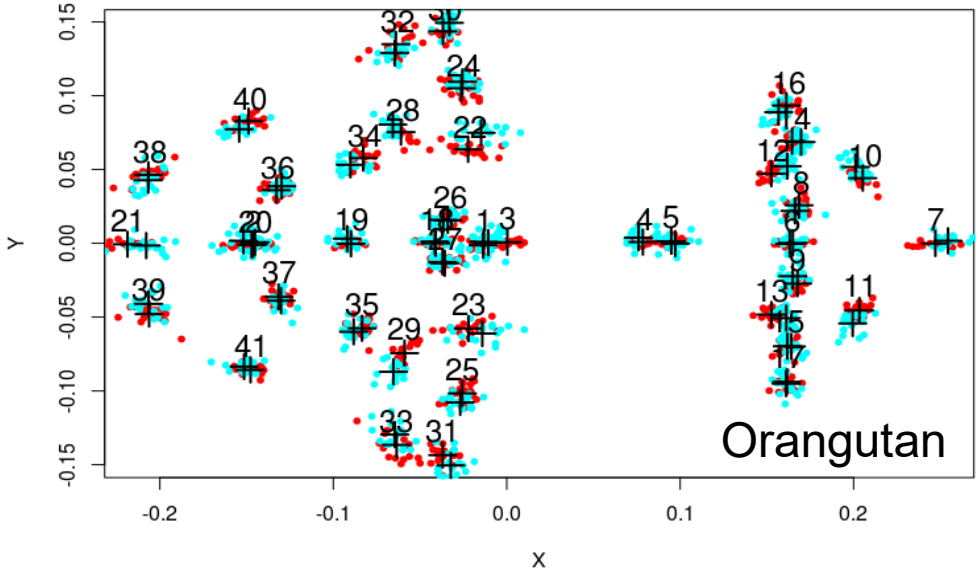


Method comparison – LM configurations

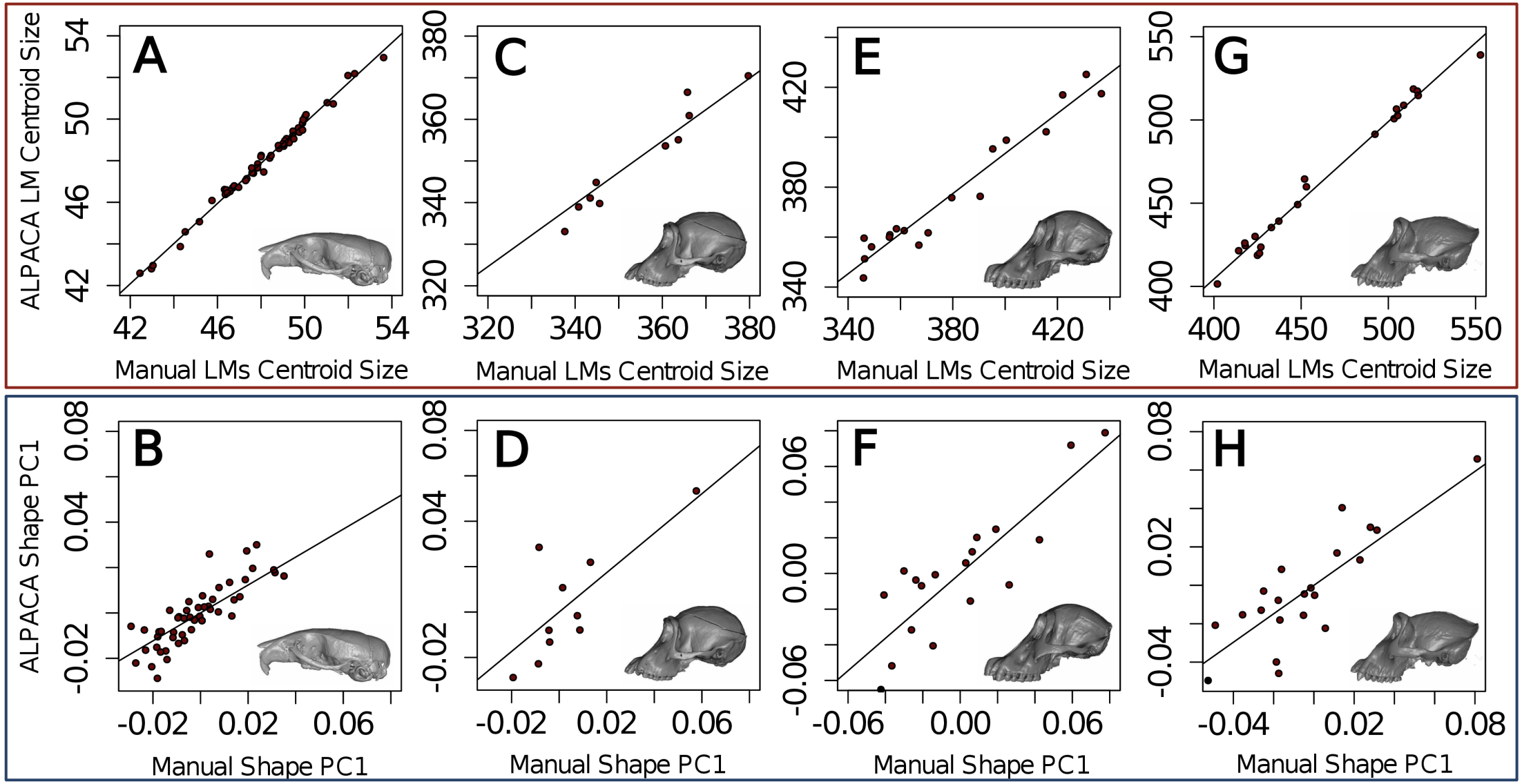








Method comparison - Centroid Size and PC1



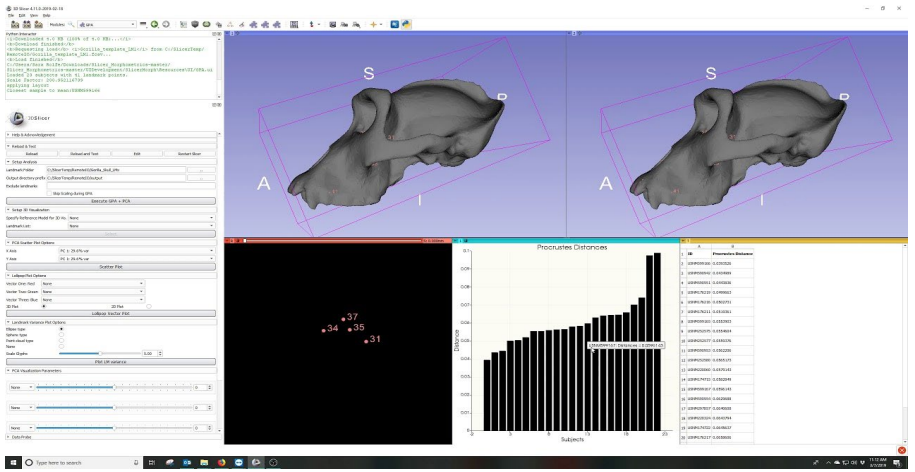
Advantages - ALPACA

Fast – Can process an entire surface in 3 to 4 minutes

High-throughput – Can be run multi-threaded to process hundreds of specimens on a personal computer.

Easily generalizable – Can be used to landmark any 3D structure and has an user interface.

ALPACA



SLICERMORPH

Shortcomings - ALPACA

Mostly intraspecific – Although it can work in certain interspecific contexts (e.g. apes), it is a pipeline that is most useful in intraspecific contexts. (**However, we do have two ALPACA extensions under development, one of which is devoted to interspecific applications**)

Mesh cleaning – It requires more mesh cleaning procedures than one would typically need for manual landmarking (in particular, the two meshes must represent the exact same object).

Conclusion

* Geometric morphometrics provides tools that are useful for shape analysis and that are system-agnostic

* Automation of landmark data collection is now possible given the explosion in computer vision approaches

*Automation can increase the scale and reproducibility of biological research

Thanks!

Sara Rolfe

Murat Maga

Kelly Diamond

Emma Sherratt

Matt Tocheri

SlicerMorph Workshop participants

3D Slicer & Open3D Developers

… and many others

Seattle Children's®
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Join me!

The Porto Lab is looking for PhD students/postdocs

Areas:

- Computer vision / Machine Learning
- Morphometrics
- Evolutionary Morphology

Contact: agporto@gmail.com