

SLICERMORPH

Introduction to 3D imaging and Morphometrics

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&

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Center for Developmental Biology and Regenerative Medicine

SlicerMorph Core Team:

Co-PI: **Adam Summers** (UW FHL)

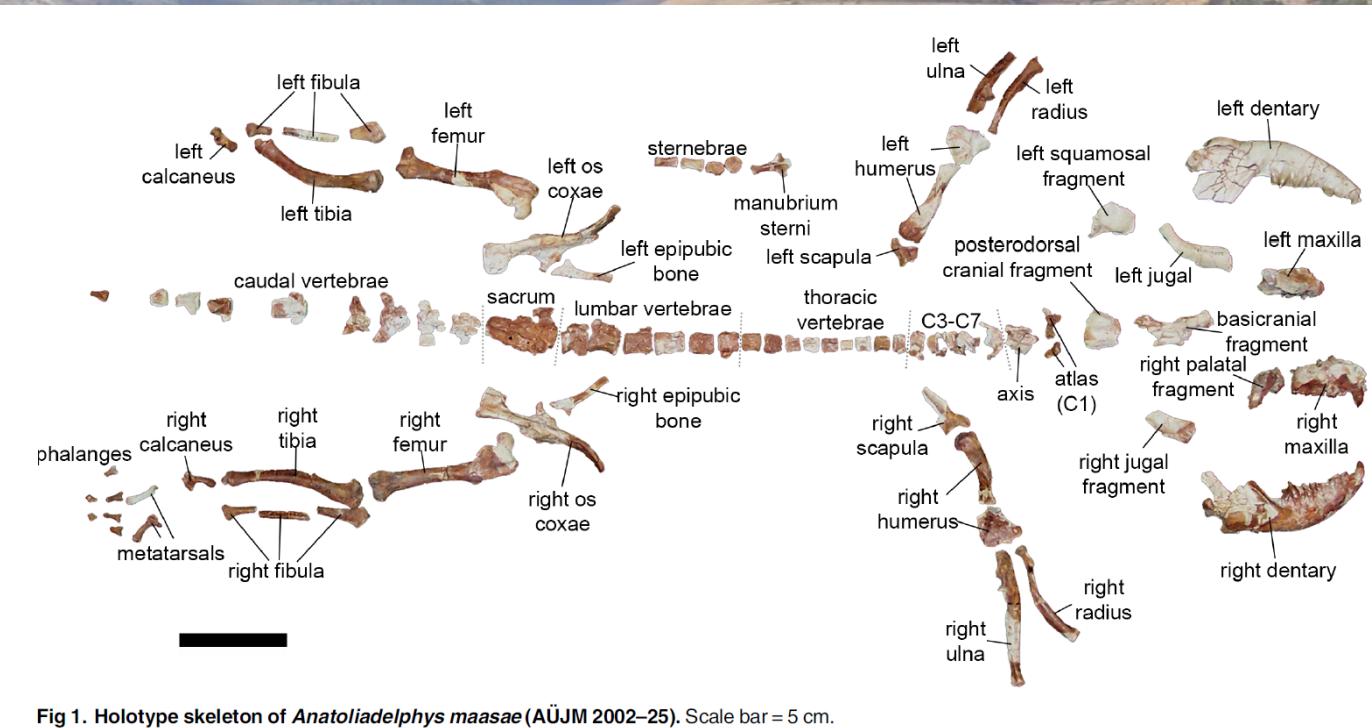
Co-PI: **Doug Boyer** (Duke Evol. Anthropology & Director of MorphoSource.org)

Consultant: **Steve Pieper** (Isomics Co., Chief Software Architect of 3D Slicer)

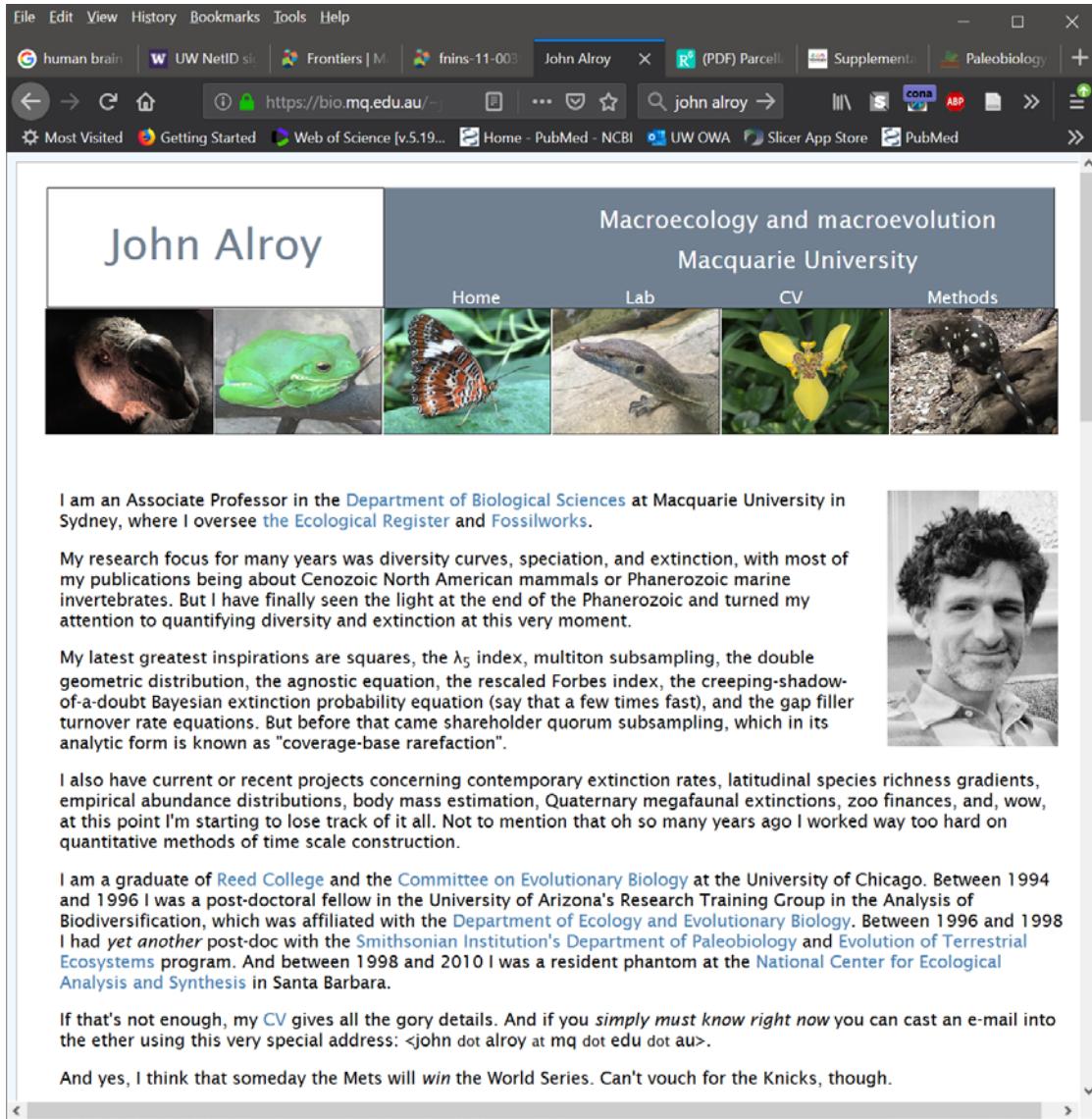
Lead Developer: **Sara Rolfe** (UW FHL & SCRI)



A marsupial in Turkey



Workshops can be transformational!



The screenshot shows a web browser window with multiple tabs open. The active tab displays John Alroy's homepage from Macquarie University. The page features a header with "Macroecology and macroevolution" and "Macquarie University". Below the header is a navigation menu with links to "Home", "Lab", "CV", and "Methods". A grid of six images shows various organisms: a bird, a green frog, a butterfly, a lizard, a flower, and a beetle. The main content area includes a bio section, a research focus section, a writing section, and a sidebar with a photo of John Alroy.

John Alroy

Macroecology and macroevolution
Macquarie University

Home Lab CV Methods

I am an Associate Professor in the Department of Biological Sciences at Macquarie University in Sydney, where I oversee the Ecological Register and Fossilworks.

My research focus for many years was diversity curves, speciation, and extinction, with most of my publications being about Cenozoic North American mammals or Phanerozoic marine invertebrates. But I have finally seen the light at the end of the Phanerozoic and turned my attention to quantifying diversity and extinction at this very moment.

My latest greatest inspirations are squares, the λ_5 index, multiton subsampling, the double geometric distribution, the agnostic equation, the rescaled Forbes index, the creeping-shadow-of-a-doubt Bayesian extinction probability equation (say that a few times fast), and the gap filler turnover rate equations. But before that came shareholder quorum subsampling, which in its analytic form is known as "coverage-base rarefaction".

I also have current or recent projects concerning contemporary extinction rates, latitudinal species richness gradients, empirical abundance distributions, body mass estimation, Quaternary megafaunal extinctions, zoo finances, and, wow, at this point I'm starting to lose track of it all. Not to mention that oh so many years ago I worked way too hard on quantitative methods of time scale construction.

I am a graduate of Reed College and the Committee on Evolutionary Biology at the University of Chicago. Between 1994 and 1996 I was a post-doctoral fellow in the University of Arizona's Research Training Group in the Analysis of Biodiversification, which was affiliated with the Department of Ecology and Evolutionary Biology. Between 1996 and 1998 I had yet another post-doc with the Smithsonian Institution's Department of Paleobiology and Evolution of Terrestrial Ecosystems program. And between 1998 and 2010 I was a resident phantom at the National Center for Ecological Analysis and Synthesis in Santa Barbara.

If that's not enough, my CV gives all the gory details. And if you *simply must know right now* you can cast an e-mail into the ether using this very special address: <john dot alroy at mq dot edu dot au>.

And yes, I think that someday the Mets will *win* the World Series. Can't vouch for the Knicks, though.

The Ten Statistical Commandments of Chairman Alroy

1. **Thou shalt log thy data!** We live in a multiplicative world, which means our data live in a log world. Always log any data with a lower zero bound, unless there's also an upper bound, in which case thou shalt perform a logit transformation. *Log until proven linear, and be holy.*
2. **Thou shalt run non-parametric tests!** If the parametric and non-parametric tests come out the same, thou hast lost nothing. If they don't, the data are non-normal, the parametric test is wrong, and thou shalt use the non-parametric result. Spearman, Mann-Whitney, and Kolmogorov-Smirnov are the Holy Trinity (or Quintinity, or whatever). Worship them!
3. **Thou shalt disdain p-values!** $p = 0.05$ is a heathen idol, and ANOVAs are for those who have not yet seen the light, still dwelling in the darkness of obsessive frequentist hypothesis testing. Remember, *if thou hast enough data anything will turn significant, no matter how small the difference*. And the "significance level" is whatever thou choosest it to be, not what someone tells thee it should be. So, *describe* data, don't just *test* data. Don't merely ask *whether* there's a significant difference, ask *what* is the difference, *why* is there a difference, and *have I confidence* in that difference?
4. **Thou shalt worship the almighty power!** Despite the preceding commandment, accepting the null hypothesis is a vile, ungodly thing. Always make sure thou hast the statistical power and *a small enough difference relative to what thou carest about* to argue that a difference doesn't matter (not just that it isn't "significant"). When in doubt, find a power calculator on the web and do a proper power analysis.
5. **Thou shalt abhor tiny little time series!** All too often people are seduced by "trends" of two or three data points, damning themselves to eternal hellfire. The two-tailed probability of a flawless "trend" with six points is 0.0625 (!). "Before" and "after" comparisons are no better than a single coin flip, unless the points in each category have significantly different averages. Coincidences are often coincidences: if (say) the biggest extinction happened in the same interval as the biggest climate change, and there are ten intervals, well, $p = 0.10$. So, demand that a time series analysis include a healthy number of data points, at least a dozen or a score or a cubit.
6. **Thou shalt difference thy data!** Time series data are almost always autocorrelated (and thou shalt test for that). Still, people insist on interpreting "trends" shared by pairs of time series as meaningful cross-correlations, even though autocorrelation makes finding these demonic things *the null hypothesis!* Even random walks produce such patterns! FEAR YE SINNERS! The easiest and most powerful way to remove the autocorrelation is to take first differences. So, the next time thou wantest to correlate population growth with the rate of sea-floor spreading - and people will - *difference thy !@#\$% data.*
7. **Thou shalt not play with PCA!** Principal components analysis assumes linear responses of observed variables to underlying variables, but most ecological data show modal responses. Vain mortal, what power grants thee the right to assume linearity? Correspondence analysis can handle both kinds of responses and works wonderfully on modal data (we won't mention that nasty little arch effect...).
8. **Thou shalt not cluster shamelessly!** The world is full of fuzziness and apostasy, not cool, clean Platonic categories. But cluster analysis imposes categories on data regardless of whether they're gradational. If the clusters are really there, thou shalt see them as a ray of divine light in the shadowy purgatory of a multivariate ordination space. So why bother?
9. **Thou shalt stand awe-struck before the shining brilliance of the G-test!** Chi-square this, chi-square that. The G is easier to compute, it doesn't blow up as easily because of small values, it depends on the awesome power of the log transform, it stands for "GOD," and most importantly it's a maximum likelihood ratio...
10. **Thou shalt sing the praises of likelihood, not "fit"!** Anyone can design another fit statistic. Why minimize the

https://www.nceas.ucsb.edu/~alroy/JA_commandments.html

Anatoliadelphys maasae

RESEARCH ARTICLE

Skeleton of an unusual, cat-sized marsupial relative (Metatheria: Marsupialiformes) from the middle Eocene (Lutetian: 44–43 million years ago) of Turkey

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OPEN ACCESS

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Data Availability Statement: All relevant data are within the paper and its Supporting Information files.

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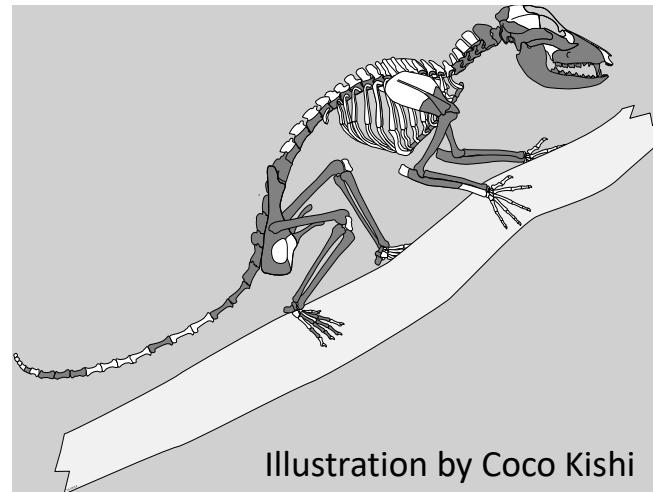
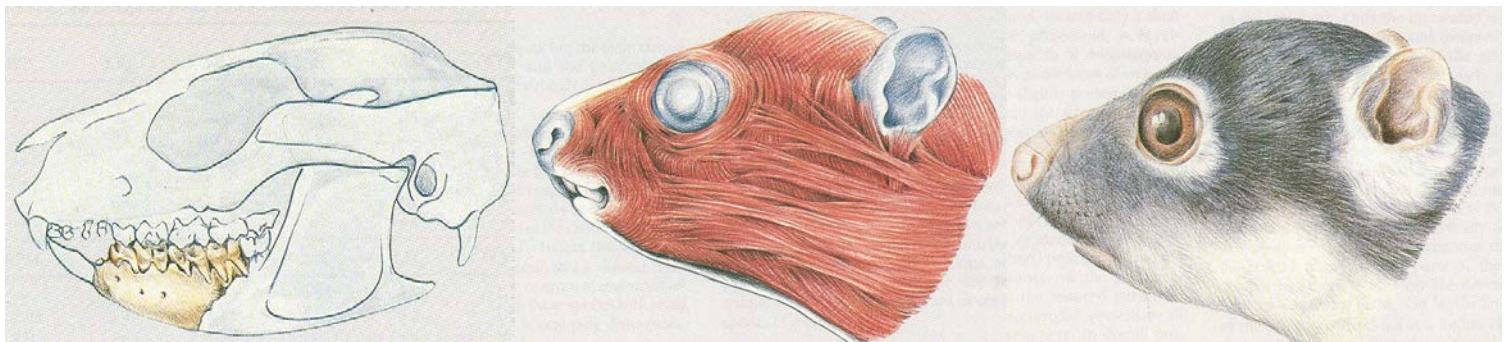


Illustration by Coco Kishi

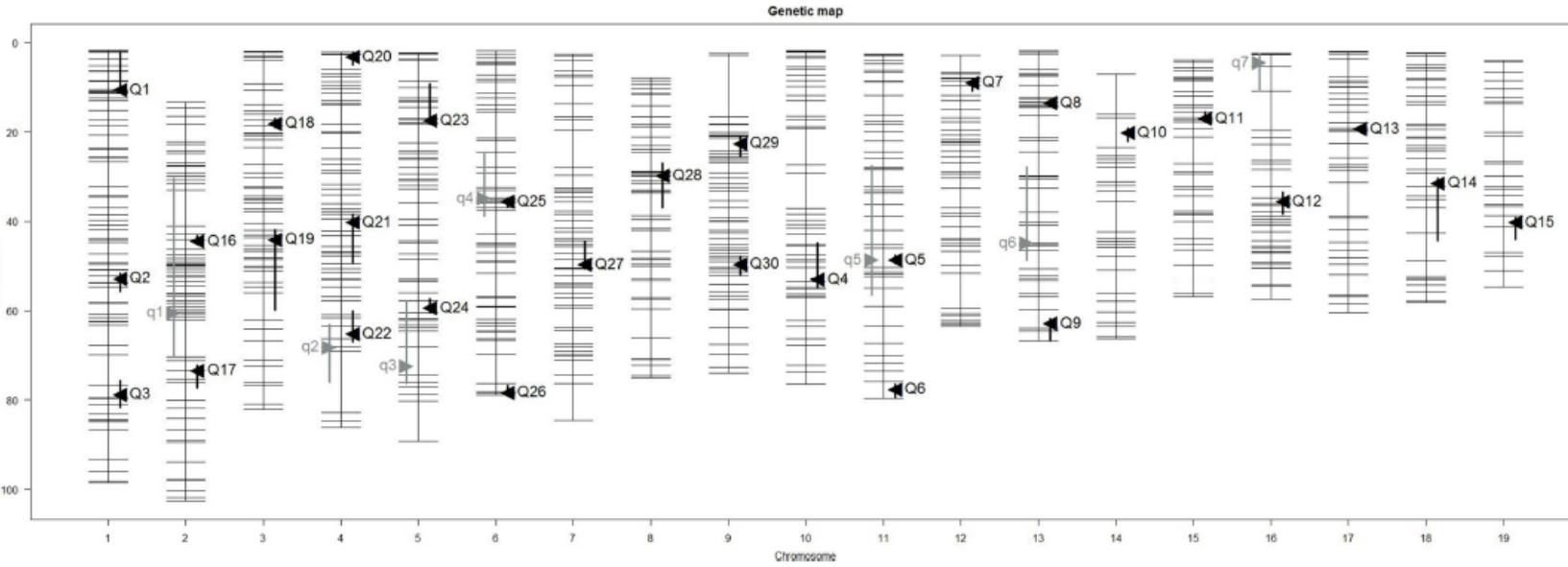
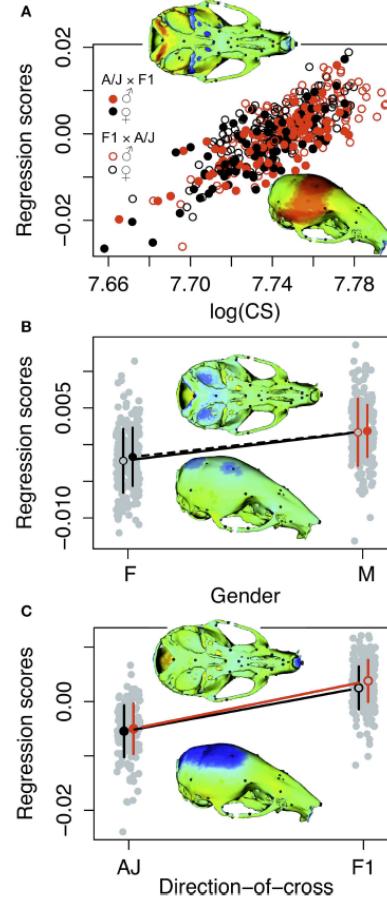
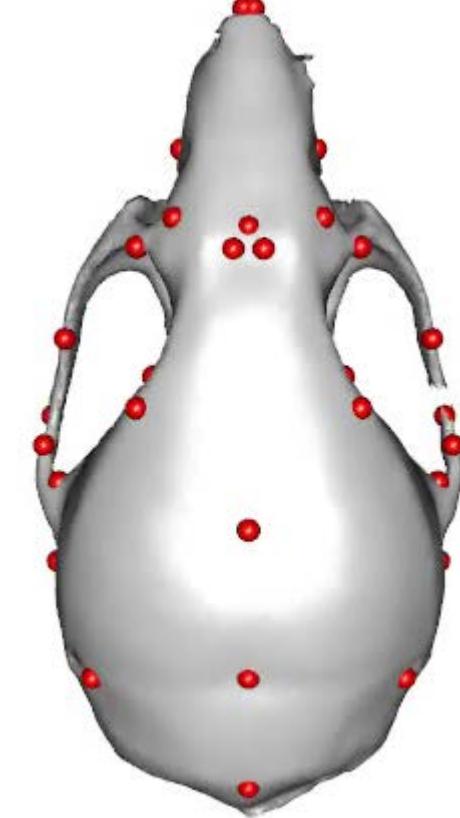


Illustration by Peter Schouten



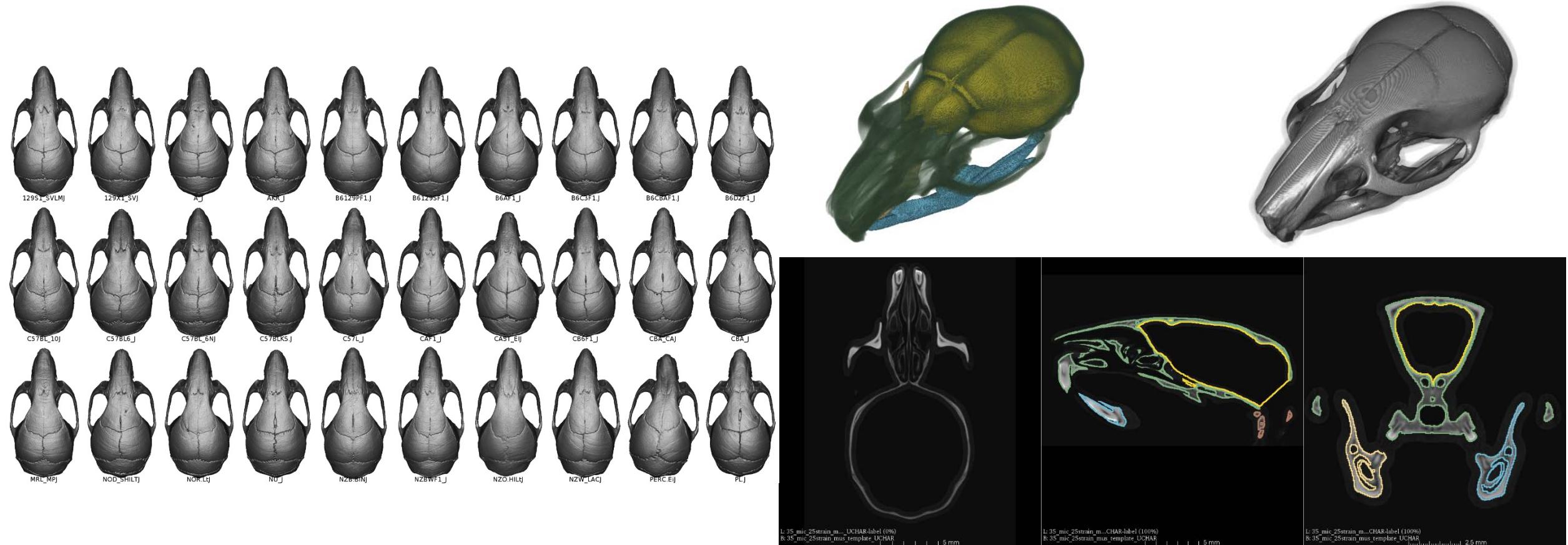
Woodburne et al. 1987. New Miocene ringtail possums from South Australia

Unfolding the genotype/phenotype map in craniofacial system



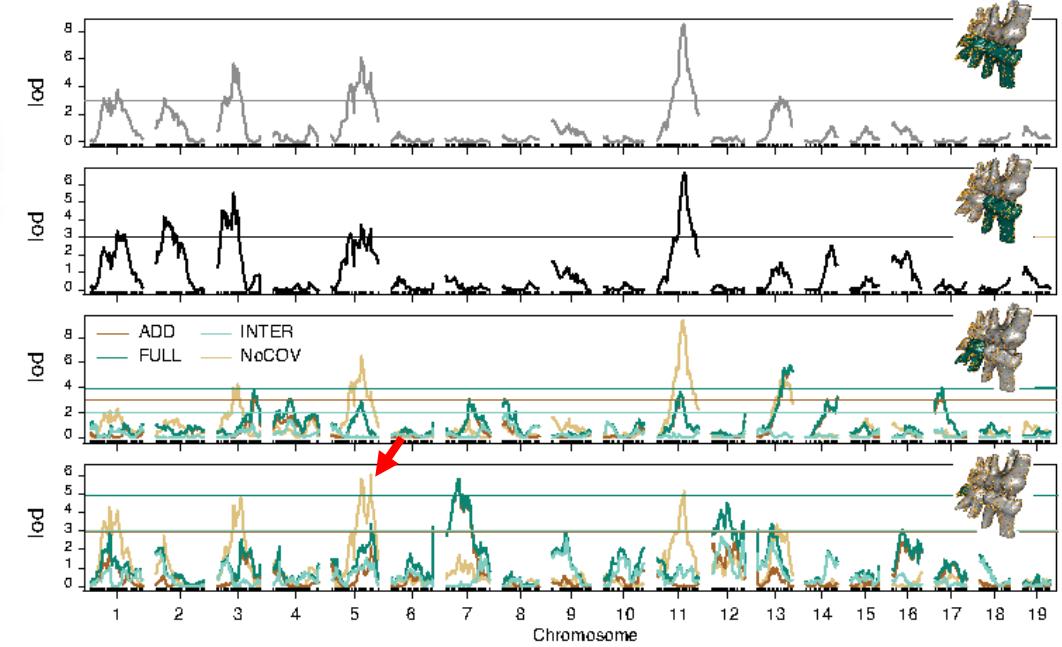
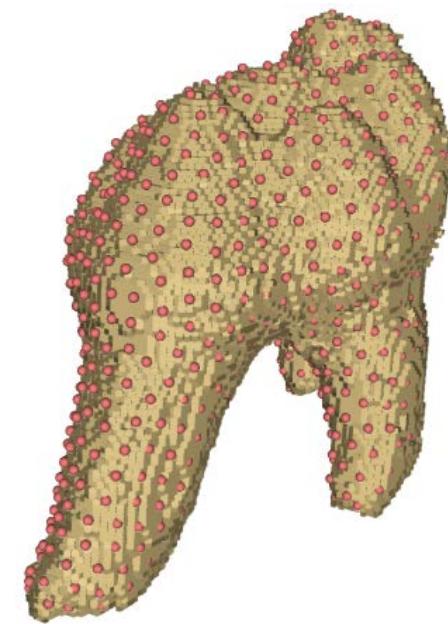
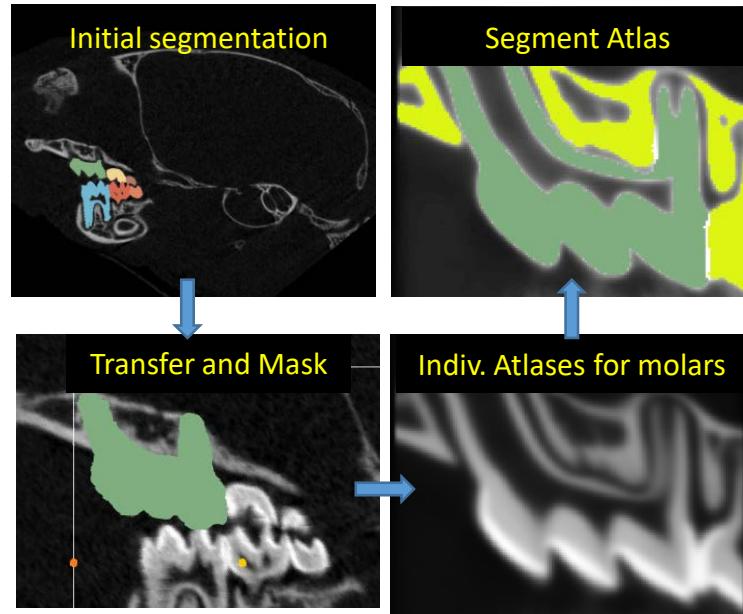
- Maga AM, et al. 2015. Quantitative trait loci affecting the 3D skull shape and size in mouse and prioritization of candidate genes in-silico. *Frontiers in Physiology / Craniofacial Biology* 6:92.
- Navarro N, Maga AM. 2016. Does 3D Phenotyping Yield Substantial Insights in the Genetics of the Mouse Mandible Shape? *G3: Genes, Genomes, Genetics* 6:1153–1163.
- Navarro N, Maga AM. 2018. Genetic mapping of molar size relations identifies inhibitory locus for third molars in mice. *Heredity* 121:1–11.

Image-based analysis (registration & segmentation)

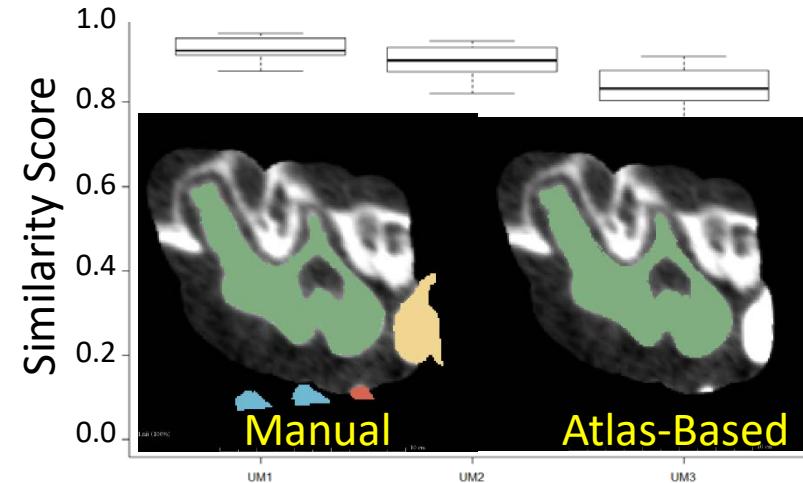


- Young R, Maga AM. 2015. Performance of single and multi-atlas based automated landmarking methods compared to expert annotations in volumetric microCT datasets of mouse mandibles. *Frontiers in Zoology* 12:33.
- Maga AM, Tustison NJ, Avants BB. 2017. A population level atlas of *Mus musculus* craniofacial skeleton and automated image-based shape analysis. *Journal of Anatomy* 231:433–443.

Genetic control of 3D molar size



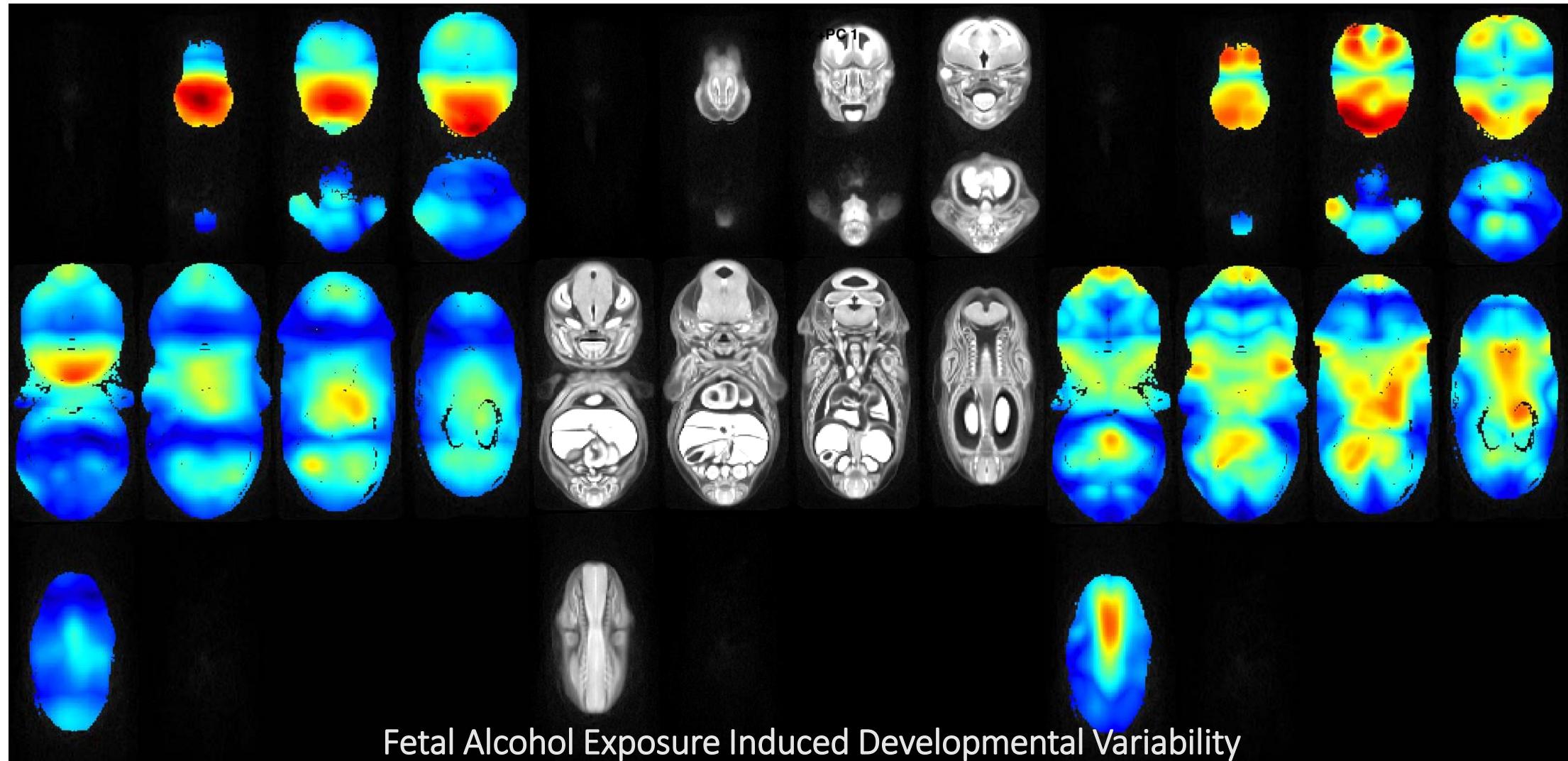
Atlas Validation



Pipeline for automated segmentation of 2,500 molars from more than 400 mouse scans

- Navarro N, Maga AM. 2018. Genetic mapping of molar size relations identifies inhibitory locus for third molars in mice. *Heredity* 121:1–11.

PCA as a tool for exploratory analysis in mouse screens



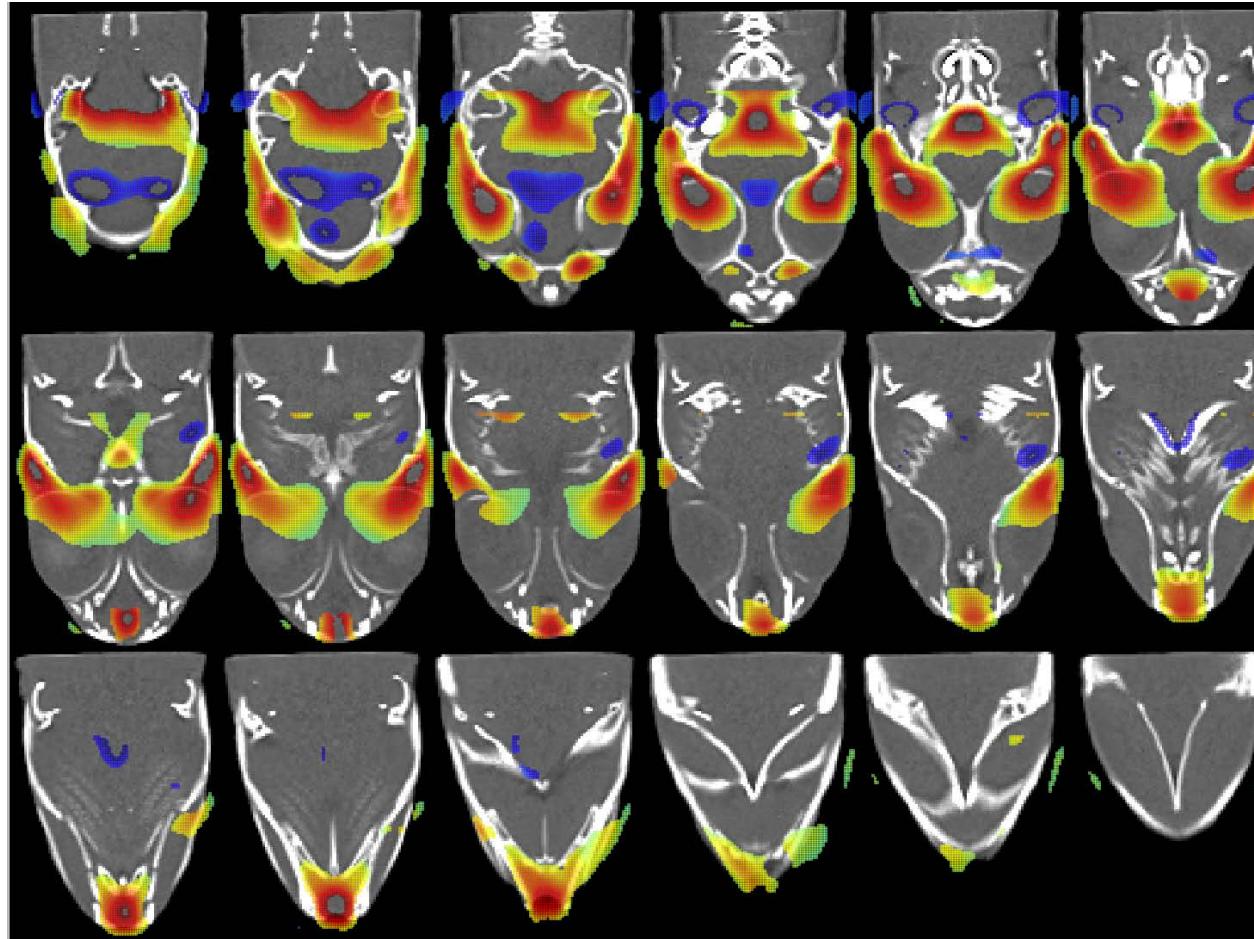
Control mice fetuses at E15

Maga lab unpublished data (undergrad project)

Study template
(Population average)

E15 fetuses from dams consumed
10% v/v EtOH *ad-libidum* during the
first 8 days of pregnancy (E0-E8)

Littermates vs bmp1a mutants growth differences



Warmer colors, regions significantly **shrunk** in mutants compared to littermates
Colder colors, regions significantly **enlarged** in mutants compared to littermates

- Bhimani RM, Watson CJ, Maga AM, Kwon RY. 2019. FishCuTv2: An Extensible Software for microCT-Based Whole-Body Skeletal Phenomics in Zebrafish. Annual Meeting of Orthopaedic Research Society. Austin, TX

Maga Lab is hiring! Two open post-doc positions

- Postdoc in Genetics of Craniofacial Shape and Form

This NIH funded project is aimed at using computational anatomy and 3D morphometrics to understand the [genetic structure of craniofacial shape and form using inbred strains of mice](#).

Qualified candidates are expected to have a strong background in **craniofacial biology and development, or in quantitative genetics and bioinformatics**.

Preference will be given to candidates with experience conducting genome-wide efficient mixed-model association studies.

Proficiency with R or python is mandatory. This is a one-year position, with an option to renew for one more year based on performance and available funding.

Expected start date is October 1st 2019 (or sooner).

<http://faculty.washington.edu/maga/post-docs/>

Or email maga@uw.edu

- Postdoc in Machine Learning in 3D Image Analysis

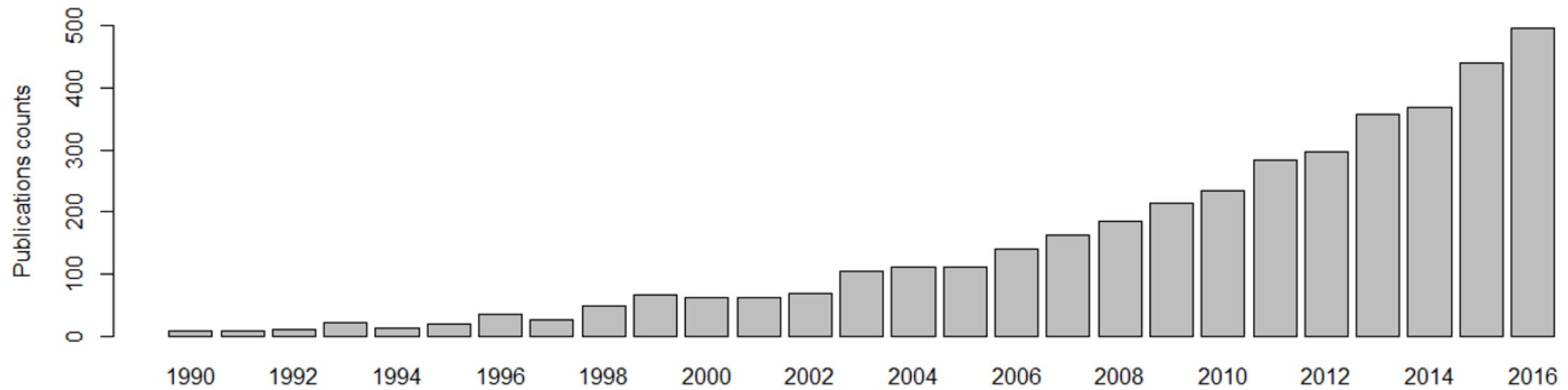
This NSF funded position is a collaborative project between five institutions (University of South Dakota, Seattle Children's, Virginia Tech, Drexel, and Tulane) to develop biology-guided convolution neural nets to enable machine discovery of organismal traits using existing 2D and 3D annotated imagery from aggregate specimen archives, as well as existing information from developmental and anatomical ontologies and phylogenies.

Post-docs in the project will have a chance to cross-train in different fields of phylogenetics, vertebrate morphology (ichthyology in particular), data-science and machine learning through rotations in participating sites.

For the project at Magalab, we are seeking trainees that either have PhDs in computer vision (or related) research and interested in applying their research in organismal biology context, or **biologists with a strong computational background interested in learning image analysis**. This is a two-year position, with an option to renew based on performance and pending project renewal.

Expected start date is December 1st 2019 (or sooner).

Quantitative Analysis of organismal form via geometric morphometrics is booming.



Data from Web of Science. Topic keywords: 'geometric morphometrics' OR procrustes

Moving beyond state-of-art and why now?

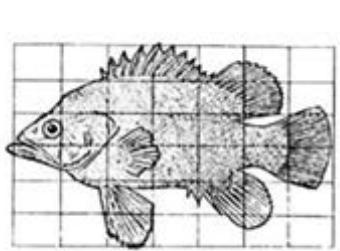


Fig. 150. *Polyprion*.

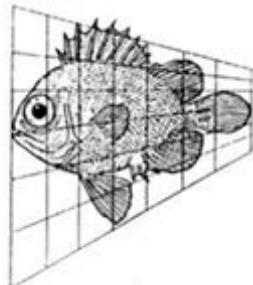


Fig. 151. *Pseudopriacanthus altus*.

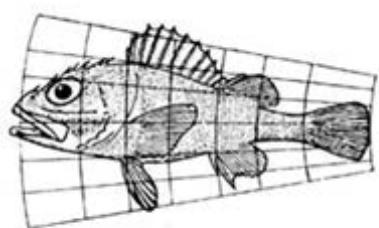


Fig. 152. *Scorpaena* sp.

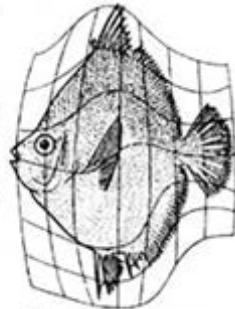
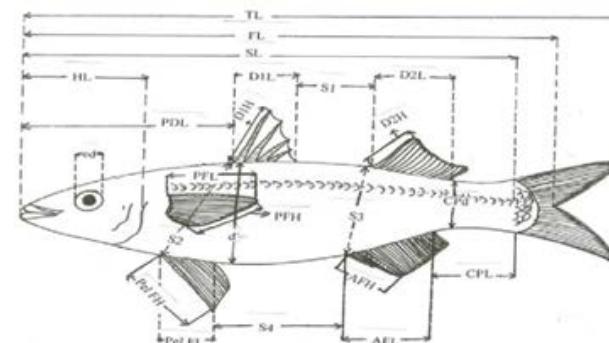
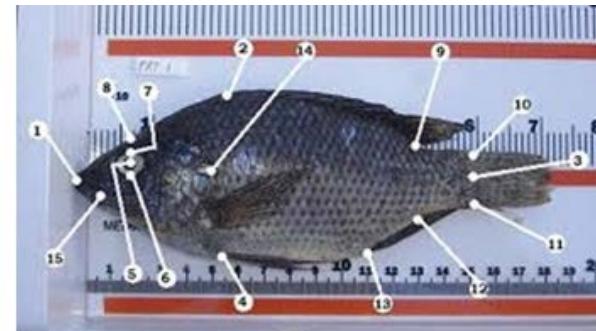
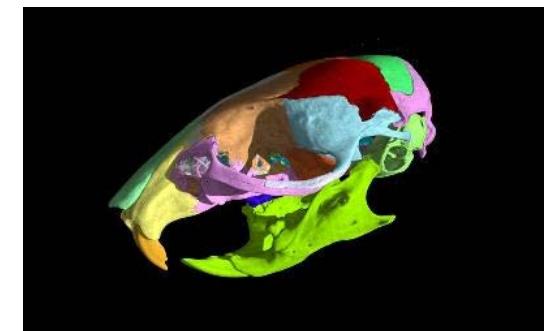
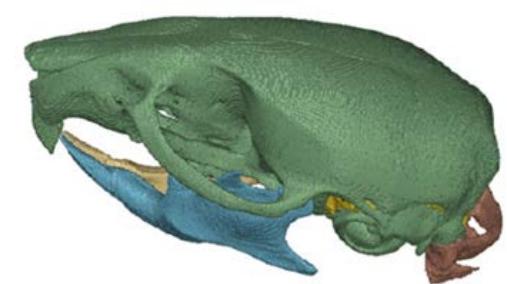
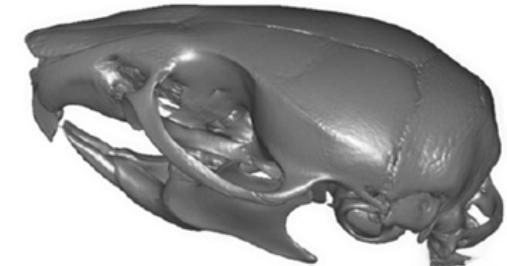


Fig. 153. *Antigonia capros*.

1900s



1990s-2010s



2010s-

The final frontier



#ScanAllFish

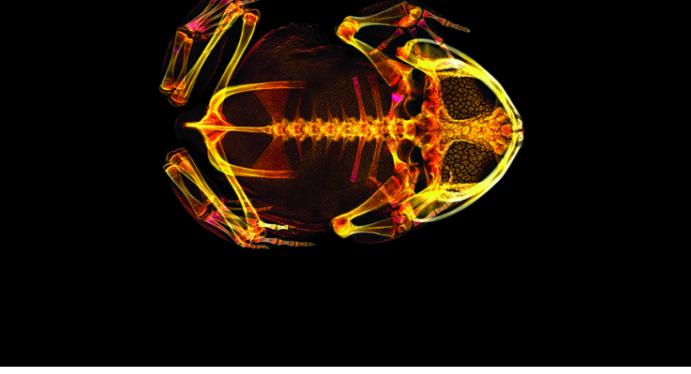
I am on a mission to scan all the ray-finned fishes in the world. And it's not just me! I am working with collaborators from around the world to create detailed CT scans of fish from museum specimens. One of the very, very useful things is to understand exactly what the skeleton looks like. It is shockingly complex. For comparison, your skull is just a few bones, but fish skulls are dozens and dozens of bones. In the first three months of the project, we were able to scan more than 500 species!

An important part of this project is getting all our results up on the web for anyone to access for any purpose. To allow the general public and every scientist out there to just download these data is fabulous. It also eliminates the needs for multiple teams to scan the same species of fish and using valuable resources for overlapping work.

these scans & data are available to anyone who wants to use them, for research or otherwise.

ct scanner scans available 3-d printing

#ScanAllFishes



Research News

What is oVert?

oVert, short for openVertebrate, is a new initiative to provide free, digital 3-D vertebrate anatomy models and data to researchers, educators, students and the public. Over the next four years, the oVert team will CT scan 20,000 fluid-preserved specimens from U.S. museum collections, producing high-resolution

Open Vertebrate



MORPHO SOURCE
BY DUKE UNIVERSITY

Getting Started

Find & Download Datasets Useful Info

BROWSE enter search terms

• About MorphoSource
• Information for Users
• Information for Contributors
• Terms
• User Guide

LOGIN OR REGISTER

Recently Published

The Arene Candide 3D database - Upper Paleolithic funerary behavior in Liguria (Italy)

See all project specimens
Read the published article

Welcome

MorphoSource is a project-based data archive that allows researchers to store and organize, share, and distribute their own 3d data. Furthermore any registered user can immediately search for and download 3d morphological data sets that have been made accessible through the consent of data authors.

The goal of MorphoSource is to provide rapid access to as many researchers as possible, large numbers of raw microCt data and surface meshes representing vouchered specimens.

File formats include tiff, dicom, stanford ply, and stl. The website is designed to be self explanatory and to assist you through the process of uploading media and associating it with meta data. If you are interested in using the site for your own data but have questions

MorphoSource.org

Morphometrics discussion list

<https://groups.google.com/forum/#!forum/morphmet2>

- ~1000 members from a global pool of scientists interested in using quantitative methods to analyze organismal shape and form.
- Diverse body of interests: Ecologists, evo/devo biologists, systematists, paleontologists, anthropologists and biomedical researchers.
- Motivating question: **“I want to analyze shape variation patterns in XYZ species... I found datasets in MorphoSource / DigiMorph etc....., but don’t know what to do”.**

Survey of 3D morphometrics

- A survey for people who are working (or planning to work) with volumetric datasets (CT, MR, and likes).
- Challenges identified were:
 1. Data wrangling (converting formats)
 2. Annotation (measurements)
 3. Analysis and visualization

2. What organism are you working on? (choose multiple if need)

Other	26
Human (including archaeologic)	22
Non-human primates	14
Mouse	6



5. What are your challenges working with these data? (choose multiple if need)

Processing (e.g. format conversion)	35
Annotation (landmarking)	32
Analysis and visualization of results	29
Throughput	12
Reproducibility	12



3. What is your main research focus ? (choose multiple if need)

Ecology and Evolution	34
Biomedical (including development)	14
Systematics	11



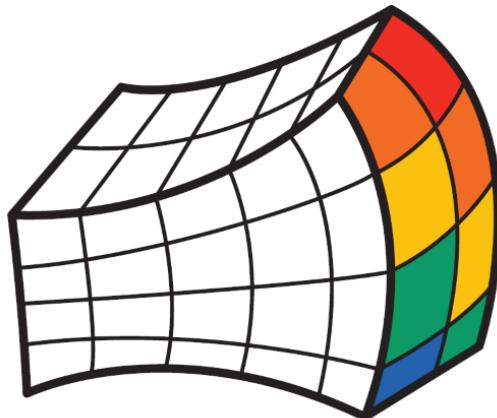
A typical workflow:

1. Download data from one or more of the repositories in different formats and/or modalities.
2. Find a software that will enable 3D visualization/segmentation and conversion to mesh, then landmark digitization (commercial software like Aviso, Mimics, Geomagics, Analyze, or free ImageJ, 3D Slicer, ITK-Snap)
3. Export landmark data into a format that can be understood by the analysis software.
4. Analyze using R (or MorphoJ)
5. Export results back to the digitization software to visualize (may not be necessary for everyone).

SlicerMorph Project Organization

- **SlicerMorph Core Team:**

- Lead-PI: **Murat Maga** (UW / Seattle Children's)
- Co-PI: **Adam Summers** (UW FHL)
- Co-PI: **Doug Boyer** (Duke Evol. Anthropology & Director of MorphoSource.org)
- Consultant: **Steve Pieper** (Isomics Co., Chief Software Architect of 3D Slicer)
- Lead Developer: **Sara Rolfe** (UW FHL & SCRI)



SLICERMORPH

- **SlicerMorph Advisory Committee:**

- James Rohlf (Stony Brook U)
- Dean Adams (Iowa State U)
- David Polly (Indiana U)
- Anjali Goswami (Natural History Museum, London)

Collaborative Proposal: ABI Development: An Integrated Platform for Retrieval, Visualization and Analysis of 3D Morphology From Digital Biological Collections (ABI 1759883, 1759637, 1759839) 08/01/2018-07/31/2021
https://nsf.gov/awardsearch/showAward?AWD_ID=1759883&HistoricalAwards=false

SlicerMorph Road Map

- We just finished year 1. Current grant ends in 08/2021:
 - Implement Generalized Procrustes Analysis (GPA) and PCA visualization of shapes
 - Data import tools (IDAV Landmark, morphologika, Bruker/Skyscan)
 - Documentation, virtual office hours, and community forming
- WIP for the on-going grant
 - 5 intense workshops, one symposium, and bunch of half-day tutorials organized around major professional meetings (UW FHL)
 - Implement deformable grids/meshes for semi-landmarking
 - Implement landmark-free correspondence (auto3Dgm) between shapes (Duke)
 - *Better integration with MorphoSource*
 - *Minor support tools*
 - *Optimize the GPA UI*

We are essentially a bridge between the core Slicer Developers and biosciences community.

SlicerMorph Road Map

- **Pending grant with Kitware to Chan-Zuckerberg Initiative:**
 - Lots of software re-engineering for working with large datasets (>10 Gigavoxels)
 - Better H/W capability detection and user guidance
 - Complex animations based on keyframes (more on this later in the labs)
 - Easier deployment of Slicer on cloud platforms or virtualized environments.
(you get to have a test of it during the workshop, if you like)
- **For SlicerMorph2:**
 - Seamless integration with R (geomorph specifically) for modeling and domain specific analyses (i.e., phylogenetics, quantitative genetics etc)
 - Cloud-based platform for data analysis, visualization and collaboration

But future is dependent on the community input and engagement.

Workshop Resources

- **SlicerMorph website:** <https://SlicerMorph.github.io>
- **Sign up for announcements' and updates:** <http://bit.ly/SM-listserv>
- **Course lectures and labs:** https://github.com/SlicerMorph/S_2019
- **Data upload link:** https://faculty.washington.edu/maga/data_dropbox/
(provide a short description of what you uploaded and your email)
- **Download sample data** (same set as the one in your usb drives):
<https://seattlechildrens1.box.com/v/S-2019-DataSets>

Overview of the week

	8/25	8/26	8/27	8/28	8/29	8/30	8/31	9/1
7:45-8:15		Breakfast	Breakfast	Breakfast	Breakfast	Breakfast	Breakfast	
8:30-10:15		Introduction / 3D Morphometrics and Imaging Maga	Introduction to Statistical Shape Analysis I: Landmark-based methods Maga	Template-based analysis and computational anatomy Maga	Auto3Dgm and landmark-free correspondence of biological form Boyer/Shan	Machine Learning and classification Mercan	Data processing in R: import/export data; intro to geomorph Rolfe	
10:15-10:30		Coffee Break	Coffee Break	Coffee Break	Coffee Break	Coffee Break	Coffee Break	
10:30-12:00		Applied Imaging Concepts Rolfe	Introduction to Statistical Shape Analysis II: Semi-Landmarks and beyond Rolfe	Application of SSA: Modeling growth Mercan	Applications of SSA: Phylogenetics Shan	Biomechanics and 3D imaging Summers	Data processing in R: Plotting, modeling Maga	Brunch / Checkout
12:15-12:45		Lunch	Lunch	Lunch	Lunch	Lunch	Lunch	
1:00-2:30		Attendee project Presentations - Initial	Slicer #1: UI, overview of functionality, extensions, finding help Mercan	Slicer #3: Measurements (angles, lines, 3D curves, landmarks) and Visualization Rolfe	SlicerMorph # 1: Statistical Shape Analysis: Work with sample data Maga	iPython Notebook for Slicer: Generating movies Rolfe	Attendee project Presentations - Final	
2:30-2:45		Coffee Break	Coffee Break	Coffee Break	Coffee Break	Coffee Break	Coffee Break	
2:45-4:45	Course Check-in Pre-course survey	Tools for reproducible research: git/github, Rstudio Shan	Slicer #2: Data formats, getting data from M/S, saving Maga	Slicer #4: Segmentation, mesh conversion, 3D printing Mercan	SlicerMorph #2: Statistical Shape Analysis: Work with your own data	Auto3Dgm: Establishing Landmark-free correspondence Shan	Concluding remarks SlicerMorph team	
4:45-5:30		Debrief	Debrief	Debrief	Debrief	Debrief	Post-course survey	
6:00-6:30		Dinner	Dinner	Dinner	Dinner	Dinner	Dinner	
7:00-8:00		Study Hall	Study Hall		Study Hall	Study Hall		

Upcoming Geometric morphometrics specific short courses

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Geometric morphometrics us... +
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+44 (0) 7966500340 oliver.hocker@prstatistics.com

PR STATISTICS

« All Events

Geometric morphometrics using (Geomorph) R (GMMR02)

14 October 2019 - 18 October 2019

£275.00 - £500

Course overview:

The field of geometric morphometrics (GM) is concerned with the quantification and analysis of patterns of shape variation, and its covariation with other variables. Over the past several decades these approaches have become a mainstay in the field of ecology, evolutionary biology, and anthropology, and a panoply of analytical tools for addressing specific biological questions have been developed. The goal of this course is to provide an introduction to the basic concepts and methods of GM, and to demonstrate how they can be applied to a variety of biological problems.

<https://www.prstatistics.com/course/geometric-morphometrics-using-r-gmmr02/> (Dean Adams)

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Analysis of Organismal Form +
https://mophometrics.uk/MorphoCourse/
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MANCHESTER 1824
The University of Manchester

Analysis of Organismal Form

An introduction to morphometrics, delivered as a Web-based course

4 November – 13 December 2019

Instructor: Chris Klingenberg

Morphometrics is a rapidly growing field. Quantitative analyses of the size and shape of organisms or their parts are more and more widely used in biological and medical research. Applications of morphometrics address diverse questions in many areas such as evolutionary and developmental biology, ecology, palaeontology, and systematics. Morphometric studies have been conducted in animals, including humans, plants and protists.

<https://mophometrics.uk/MorphoCourse/> (Chris Klingenberg)

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transmitting science

Advanced Courses in Life Sciences

Home / Courses / Geometric Morphometrics / Geometric Morphometrics and Phylogeny

Menu: Instructor Requirements Program Fees & Accommodation Schedule Funding

9th Edition

GEOMETRIC MORPHOMETRICS AND PHYLOGENY

September 9th-13th, 2019, Barcelona (Spain)

Geometric Morphometrics

<https://www.transmittingscience.org/courses/geometric-morphometrics/geometric-morphometrics-phylogeny/>

Course package:

- **Evaluation forms:** We need your feedback both right at the end of each lecture and lab. Please return them to the collection box right after the lecture/lab. There will be a survey for overall feedback at the end of the course (Saturday PM).
 - **Follow up survey:** We will contact you in 3-4 months for a brief survey.
- **Username and password:** If you need/want to connect to the remote server from your lab. (instructions at:
https://github.com/SlicerMorph/S_2019/blob/master/remote.md)

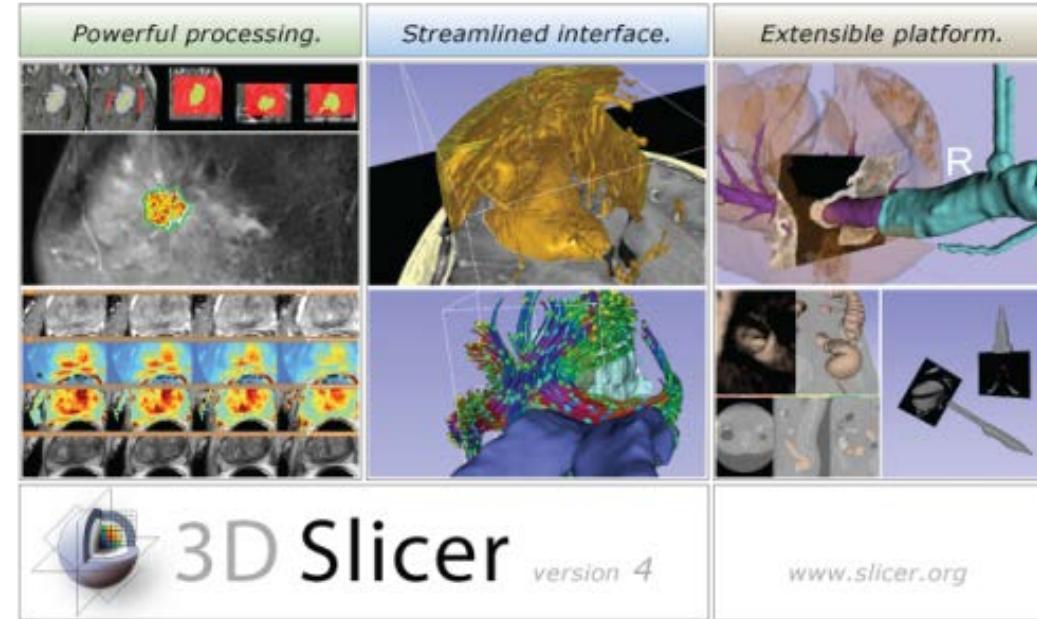
Slicer/SlicerMorph Champions

- “Volunteer” someone from your lab to be the resident-expert.
- Write and share SOPs on the SlicerMorph website (it is a git repository)
- Develop tutorials/use cases



Background for 3D Slicer

- Software application for medical image computing: data import/export, visualization, segmentation, registration, quantification, real-time guidance
- Application framework: customizable, extensible custom modules
- Completely free (BSD)
- Multi-platform



- User and developer support
- Training courses, documentation, tutorials

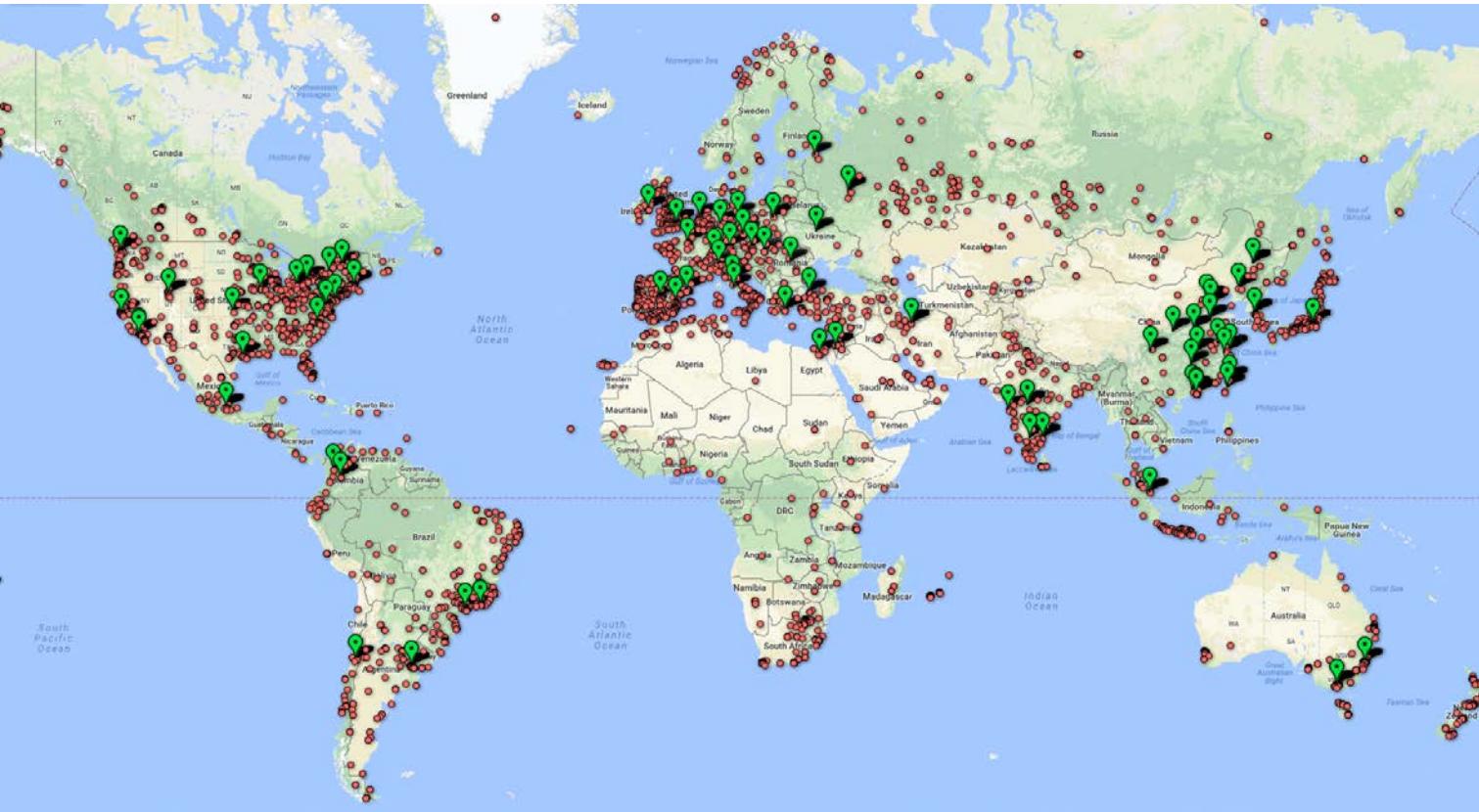
Fedorov, et al. "3D Slicer as an image computing platform for the Quantitative Imaging Network." Magnetic resonance imaging 30.9 (2012): 1323-1341.

Large user community

500 downloads per week in 2012

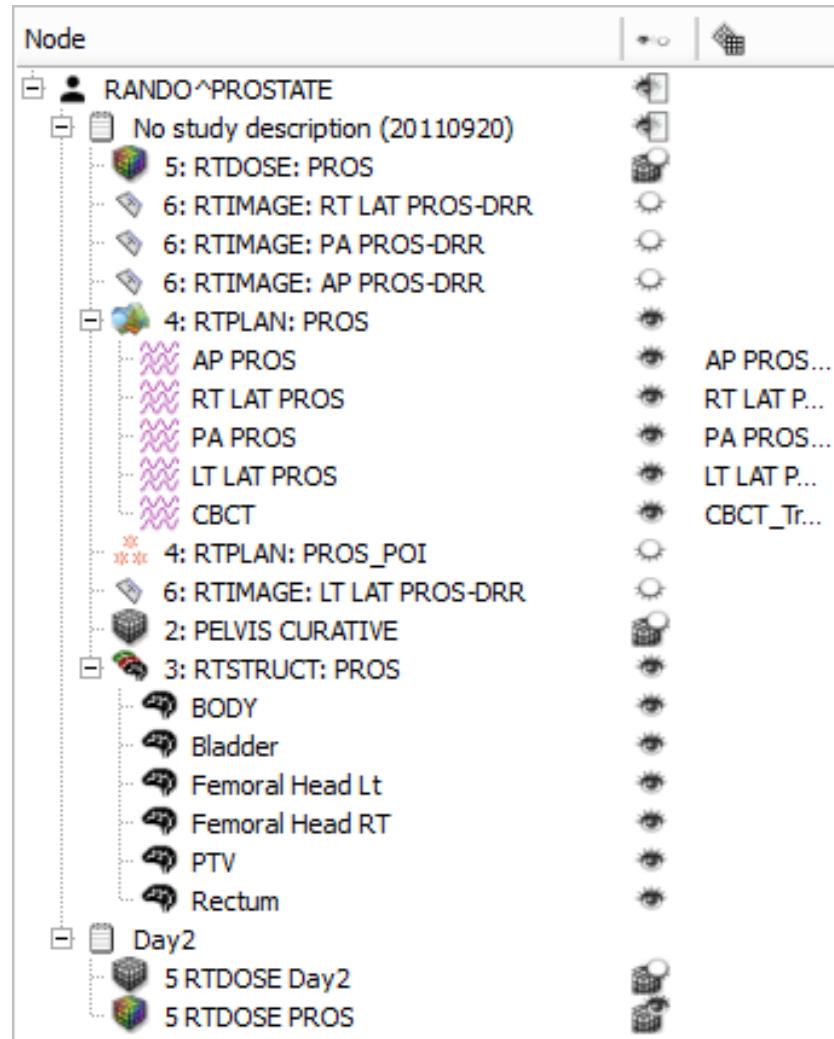
2800 downloads per week in 2018

330 000+ downloads over the past 5 years:



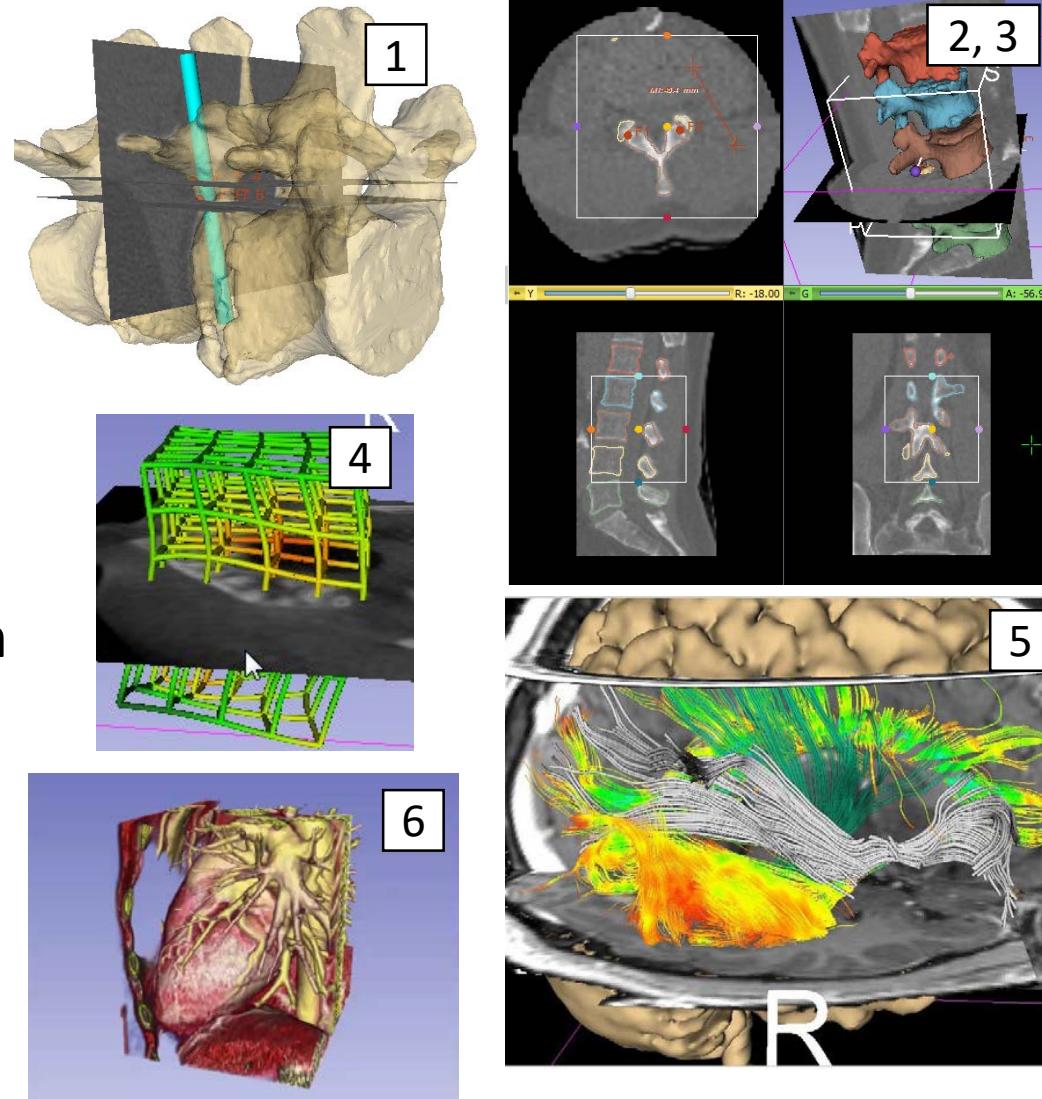
Data import/export

- DICOM: 2D/3D/4D volumes, structure sets, dose volumes, etc. (extensible without Slicer core changes)
- Research data formats for volumes, meshes, transforms (NRRD, MetalIO, VTK, HDF, etc.)
- Common non-medical data formats (JPEG, TIFF, etc.)
- Save and complete restore of application state



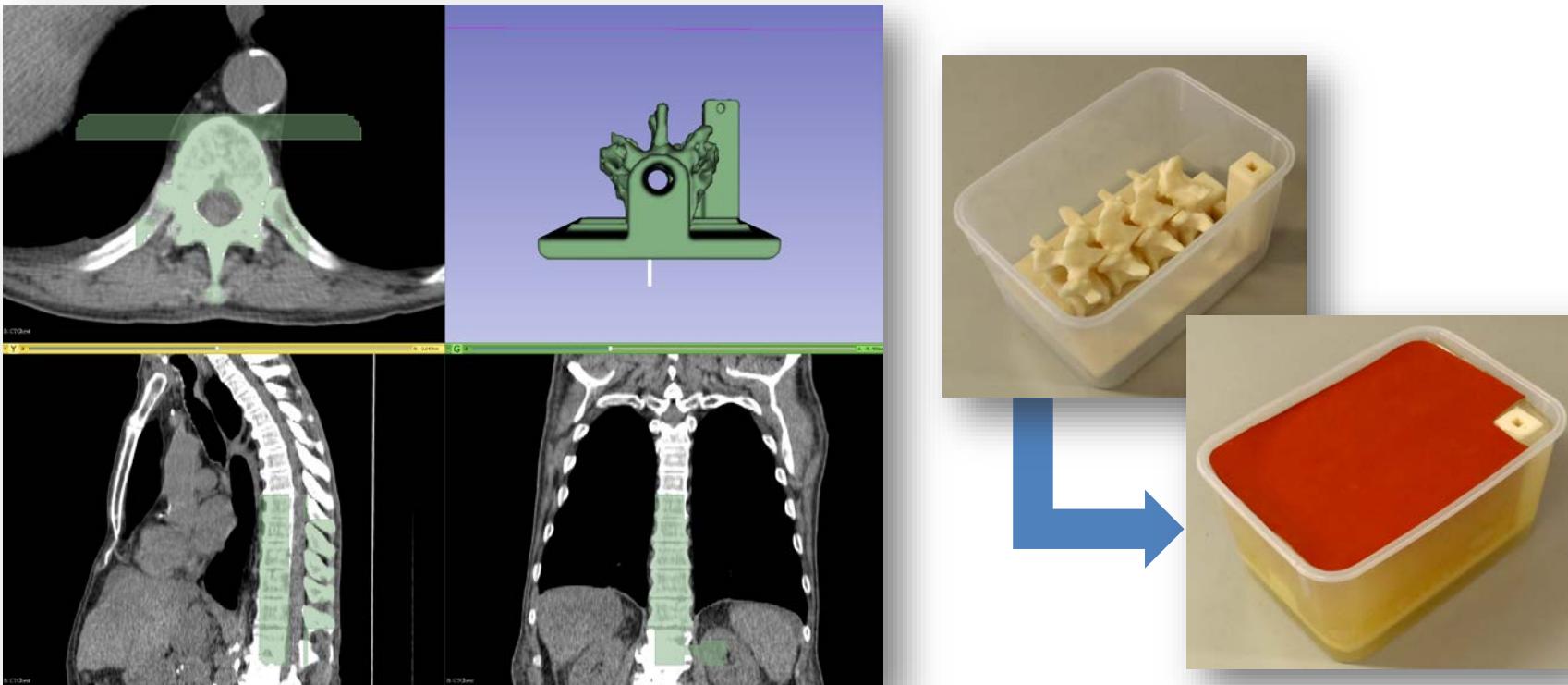
Extensive Visualization Capabilities

1. 2D (slice) and 3D views, chart views
2. Configurable layout
3. Multi-modality image fusion (foreground, background, label map)
4. Transforms, vector and tensor field visualization
5. Surface and volume rendering
6. Time sequence data

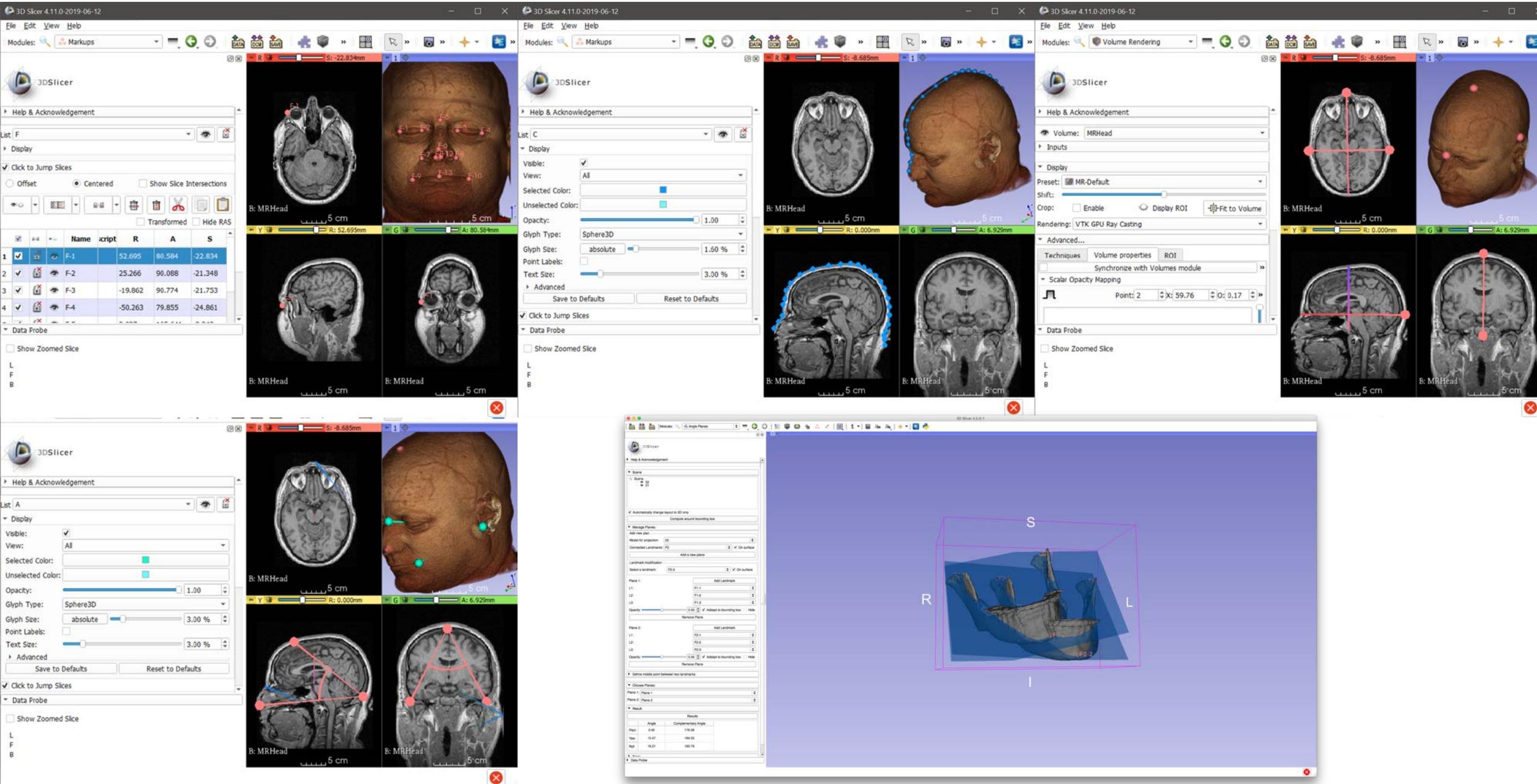


Segmentation

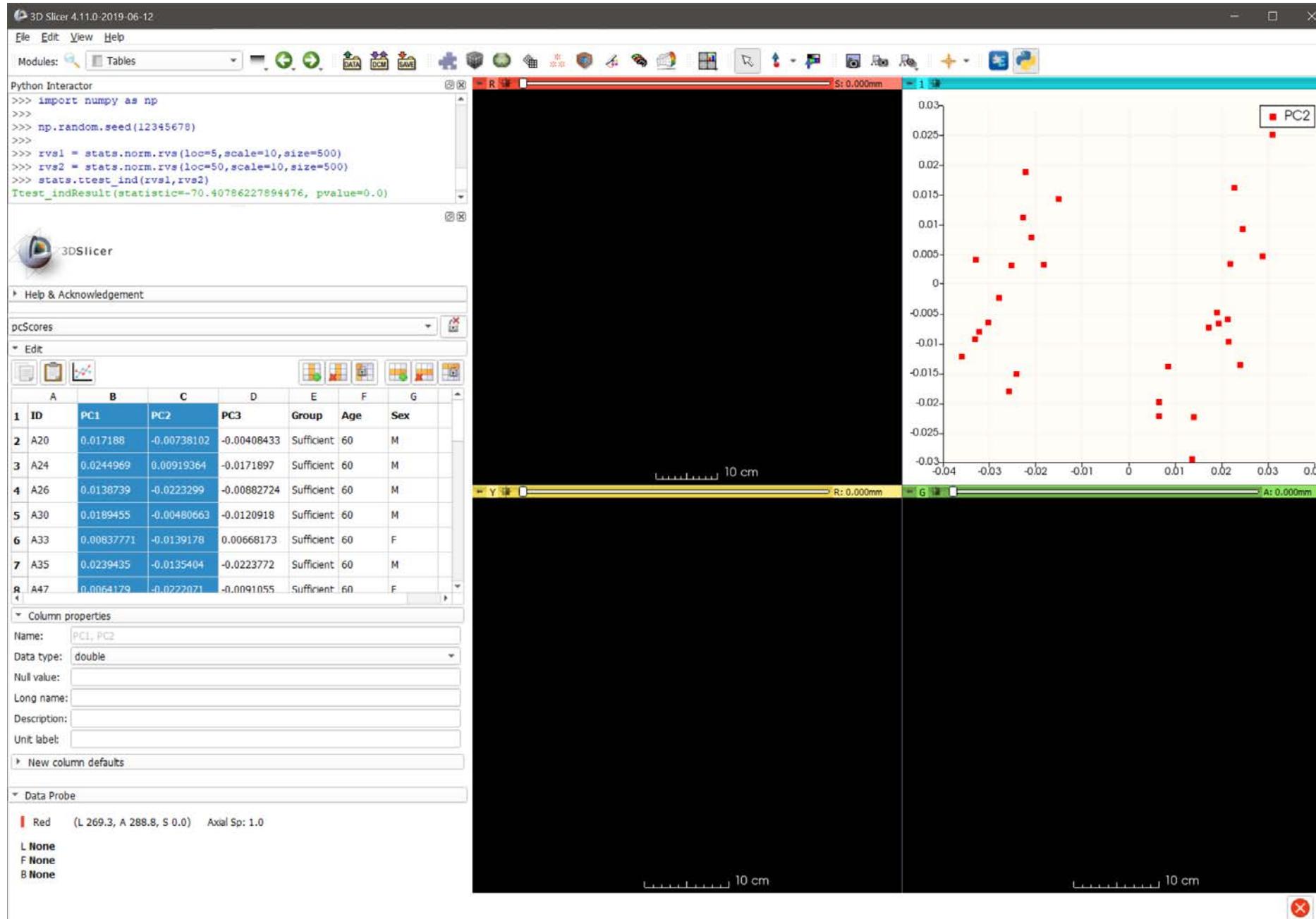
- Manual (paint, draw, scissor, threshold, etc.)
- Semi-automatic (region-growing, fill between slices, etc.)
- Automatic (atlas-based, robust statistics, etc.)



Annotations (Landmarks, Lines, Angles, Curves, Planes)

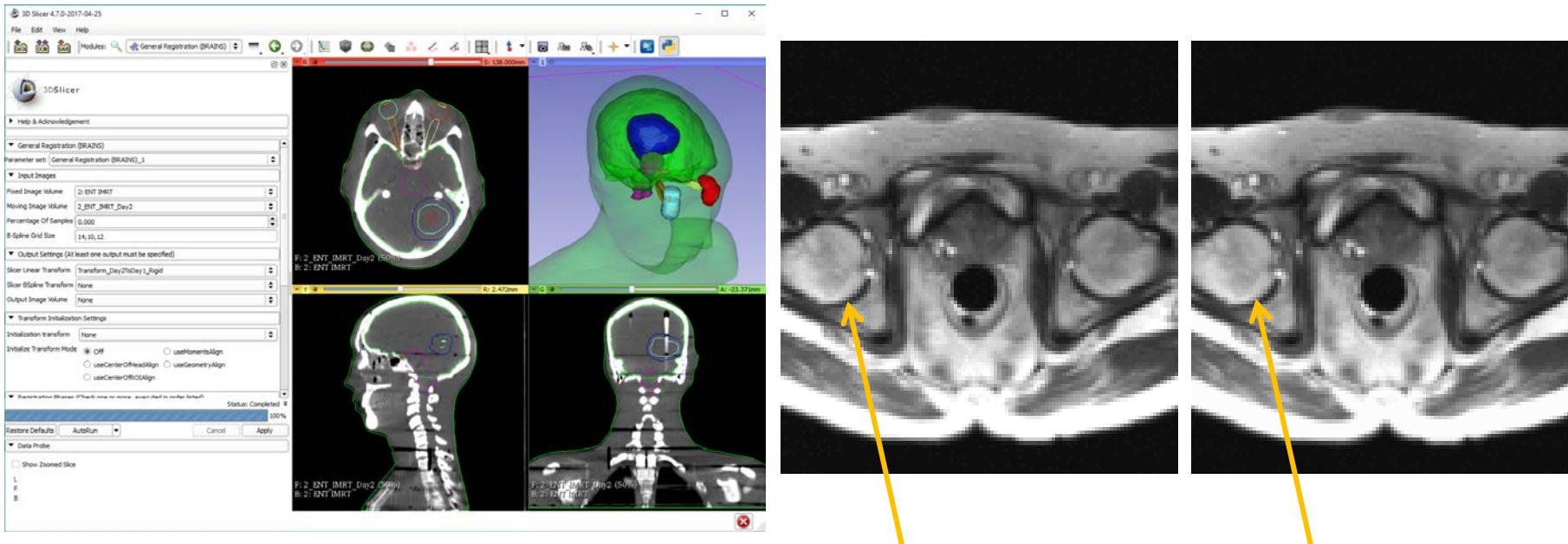


Data Tables, Plots, and statistics (w/ Python)



Registration

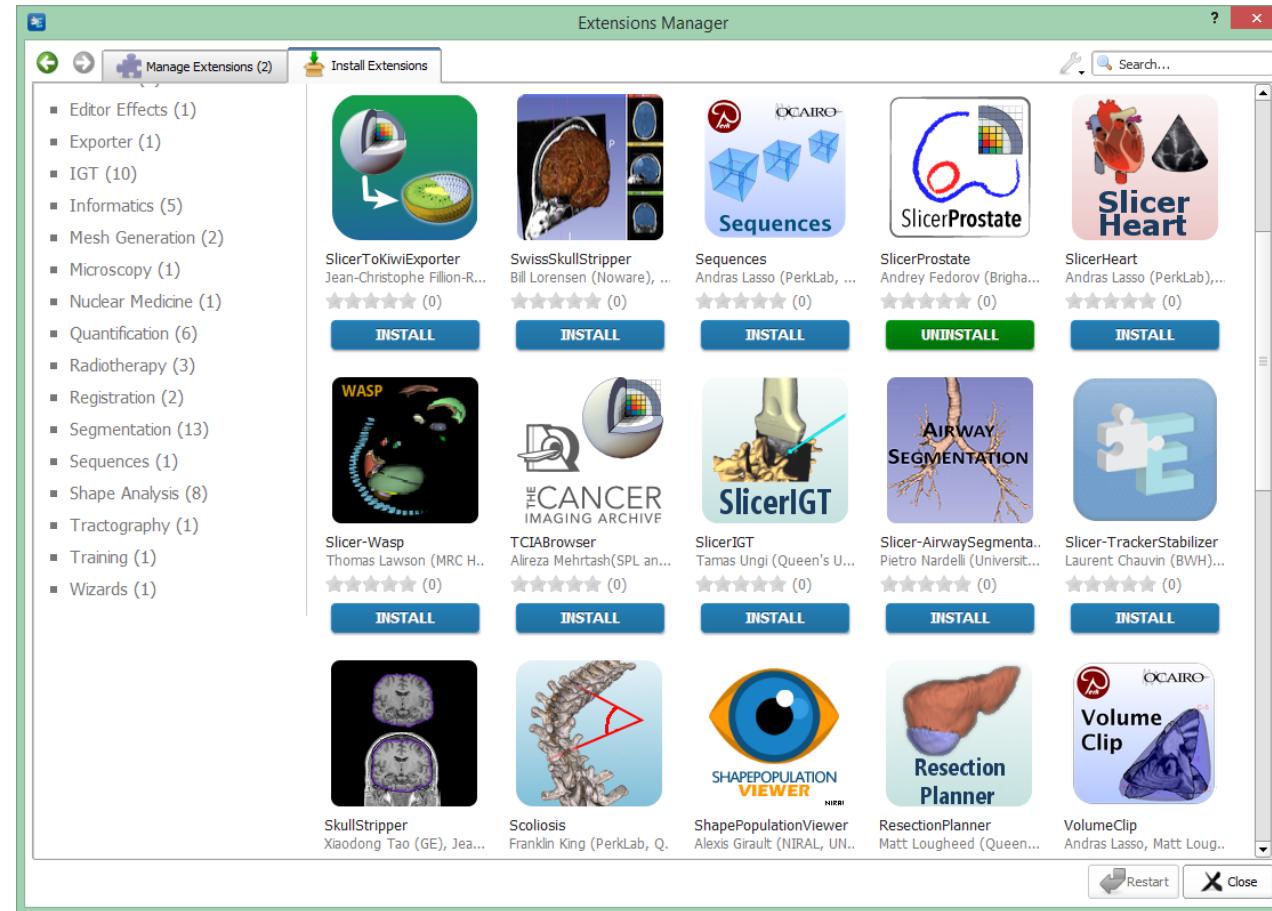
- Manual: translation, rotation in 3D
- Automatic: rigid, deformable, with various similarity metrics, initialization methods, optimizers, masking, etc.
- Extensions: structure-based registration, Elastix, etc.



What's inside Slicer?

- **Slicer core:** Slicer GUI, I/O, visualization and developer interfaces
- **Slicer modules:** internal plugins that depend on the slicer core
- **Slicer extensions:** external plugins installed on demand by the user

Slicer is extensible



The Slicer Extension Manager offers the possibility to the user to download and install additional Slicer modules

Data handling: the MRML scene

- **MRML:** Medical Reality Modeling Language
- All objects (volumetric images, surface models, transforms, etc.) are stored in a hierarchical structure of MRML nodes
- Each MRML node has its own list of custom attributes that can be used to specify additional characteristics for the data object
- Enables the modules to have access to the MRML tree, allowing new extensions to leverage existing processing and visualization functions without directly interfering with other modules

Python in Slicer

The Python console of Slicer gives access to

- Scene objects (MRML)
- Data arrays (volumes, models)
- GUI elements (Qt) that can be encapsulated in a module
- Processing Libraries (more can be installed)
 - numpy
 - VTK
 - ITK
 - CTK

Without an application platform

- Each application is developed from ground up
- Completely new software is developed for each problem/procedure/device
- Significant work is needed to integrate new, advanced algorithms



Quick start.



Huge waste of time, money, and effort overall.

Building on an application platform

- Core functionalities are already implemented
- New software modules can be developed for specific needs
- Many new, advanced algorithms are available
- Well-supported with a large user and developer community



Investment at the beginning: learning.



Minimal wasted efforts.

Benefit of open-source development

- In the event of loss of funding, or the developer losing interest (or the ability) in maintaining the software, there is nothing for community to keep the software up-to-date (or even available as-is because of technology changes).
- In open-source model, even if the core development group loose funding, disband or change focus, the community have access the full source code and any one else can pick up the development or maintain as it is in perpetuity.
- It is particularly appealing for publicly funded projects.

Challenges of open-source development

- Usually not as ‘finessed’ as the commercial software.
- **Users have to engage with developers. There is usually no phone number to call, but a community support system***
- Priorities of multiple and geographically separated developer groups may clash and create conflict**
- Open source licenses can be incompatible (e.g., bioformats in Slicer)
- Up until now development of Slicer has been mostly through research being conducted on clinical datasets. MicroCT, CryoEM, 3D light-sheet microscopy have the potential to change that.

... In the end, to help yourselves you do need to know some basic concepts of open-source software development (this afternoon's lab)

The screenshot shows a GitHub repository page for 'SlicerAnimator'. The repository has 9 commits, 1 branch, 0 releases, and 1 contributor. The branch is 'master'. A pull request button is visible. The commit history includes:

- pieper Add demo link
- Animator Create default actions so interface is usable
- .gitignore Add .gitignore
- Animator.png Initial commit of extension
- CMakeLists.txt Basic animation framework and test
- README.md Add demo link

The latest commit was 12 days ago. Below the commit history, there is a section titled 'SlicerAnimator' with the following text:
A high-level animation interface that operates on top of the Sequences and Screen Capture interfaces.
Steve Pieper (Isomics, Inc.) Murat Maga (UW)
Inspired by [discussions at Project Week in June 2019](#) about Keyframing.
Example animation demo here: <https://youtu.be/9GBekYcJR4E>



<https://www.youtube.com/watch?v=9GBekYcJR4E>

But Slicer doesn't work with my datasets!!!

- On 64-bit Oses, Slicer is **only limited by the hardware capabilities of your system**:
However:
 - All operations in Slicer are done **in-memory**. I.e., you need to have more quite a bit more memory than your dataset (more on this later). You can address this in two ways:
 1. Buy as much memory as your H/W will support (typically 64-128GB for i7 processors)
 2. Increase the virtual memory on your computer (everything will work but will be quite slow).
 - **For 3D rendering**, you need to have GPU that's capable of displaying large 3D texture dimensions and have lots of GPU memory (e.g., TITAN RTX will load datasets up to 24GB). A **2080TI** (about 1/3rd of price of TITAN) is more than sufficient for most datasets.
 - **Datasets are sacrosanct**, Slicer will NOT do anything to your data until you tell it to do explicitly

But I can't get my data into Slicer!!!

- Slicer uses open volume formats by default. (We will see more in detail in Lab4).
 - Have your imaging center provide the original scan in DICOM or TIFF stacks.
 - If you have already done work in a software with proprietary software, see if you can export it into one of the common formats.
 - If not, see the company provide documentation on their format (especially problematic for microscope data). You can then describe the data to Slicer using NHDR format or Nearly Raw Raster Data format. Or we/developer community can possibly develop an import plugin that other can benefit too.
 - Try the rawImageGuess extension
(<https://github.com/lassoan/SlicerRawImageGuess>)
 - Try the Bioformats plugin from Open Microscopy (available in Fiji).

How big of a dataset I can work on with Slicer?

- Depends on what you want to do:
- Rule of thumb 6-10X more RAM than your dataset size.
 - E.g. 1024x1024x1024 scan with intensity ranges from 0-4096 would be 2GB when loaded
 - Depending on the type of the action, RAM requirement would be 4-20GB.
 - Most filters and tasks Slicer is multi-threaded, thus would benefit from multi-core computer architecture
 - If you do registration, requirements would approximately double.
- 3D Volume Rendering (Raycasting) needs a high-end GPU with more memory than your largest dataset.
 - So, example above would work on a GPU with 3GB GPU RAM.
 - It also depends on your GPUs OpenGL hardware capabilities (check <https://opengl.gpuinfo.org/>)
 - CPU rendering always works, but usually slow (unless you have dozens of cores).
- You can use downsample or crop your volume to match it to your hardware.
- Keep your data as a 3D volume. Reading one large files is faster compared to reading thousands of small files.
- NVME SSDs are very good investments.

3D scans to 3D meshes

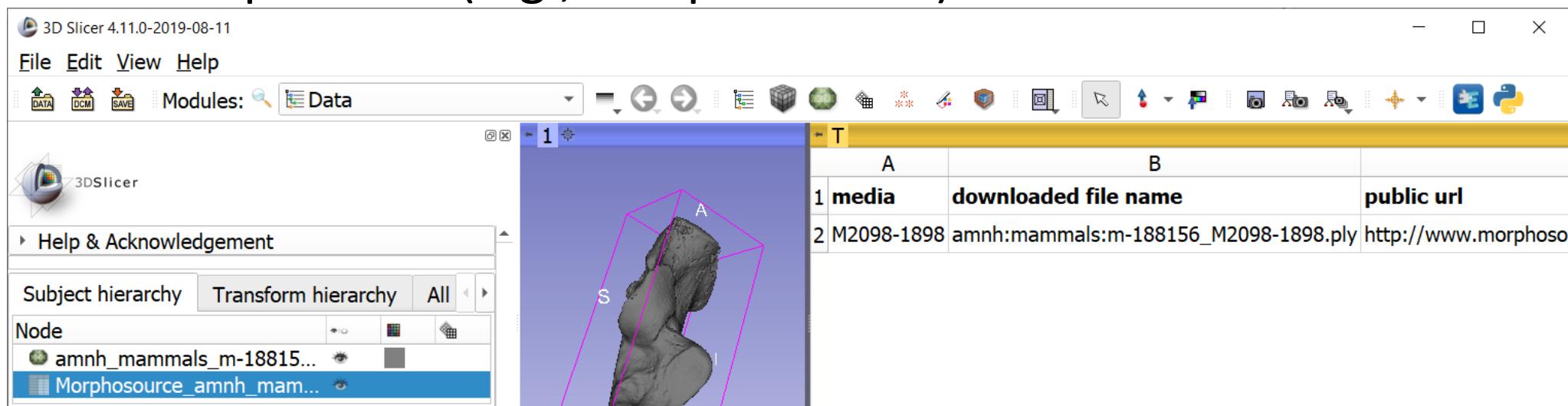
- In general avoid **mCT-> polygon mesh conversion**, unless your analytical software calls specifically for geometry (e.g., auto3Dgm). Because:
 - Image intensity information is useful and necessary for certain tasks (e.g., registration, segmentation)
 - Volume rendering of a volumetric scan is typically superior to the 3D rendering of meshes derived from the same scans.
 - Most importantly for landmarking you do **NOT** need meshes (unless your data comes from surface scanners). In fact, one of the benefits of volumetric scan is to be able to look at cross-sections (e.g., endocranial landmarks), which would be difficult with meshes.
- **If you do need meshes, do the conversion yourself by knowing each of the steps involved and what it does to the data.**

Don't believe everything you see.

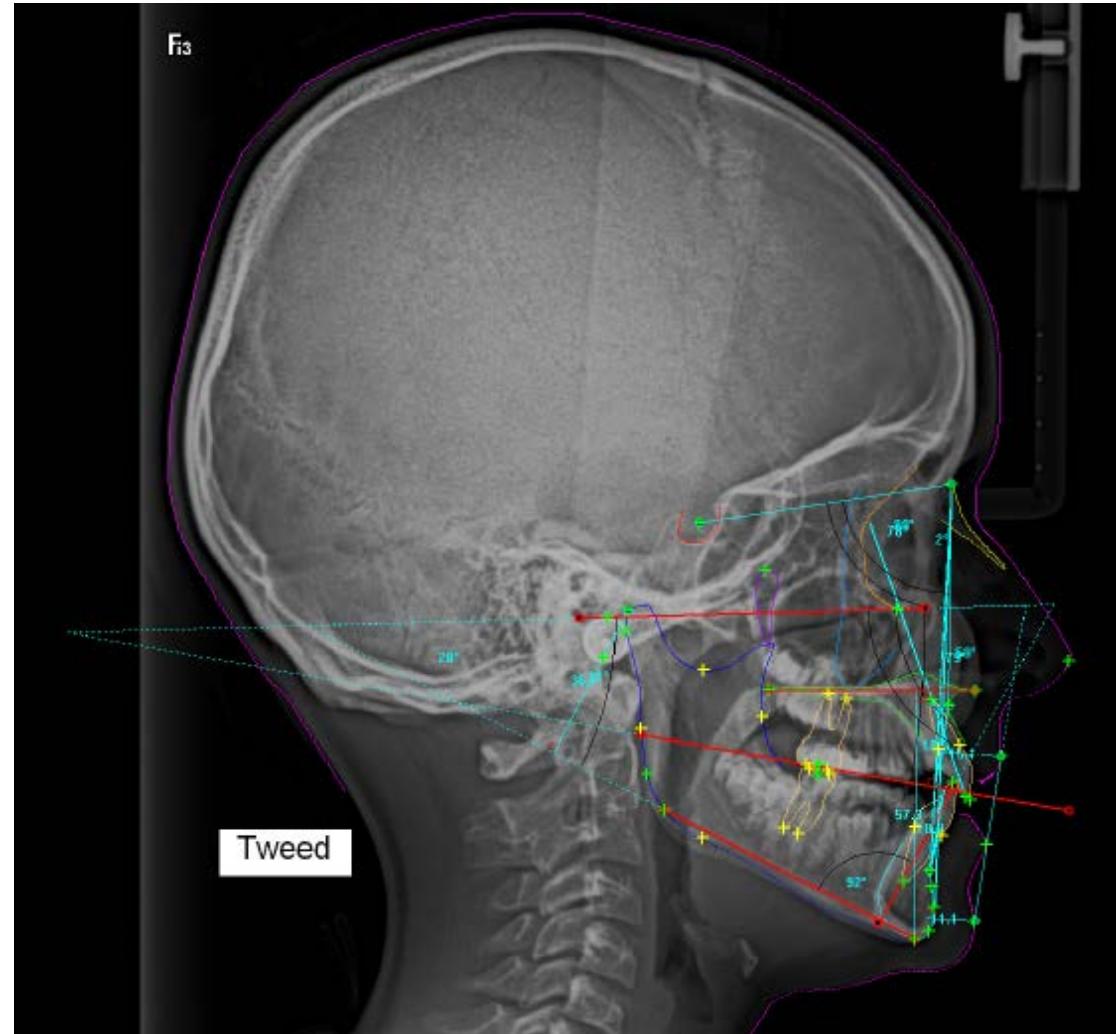
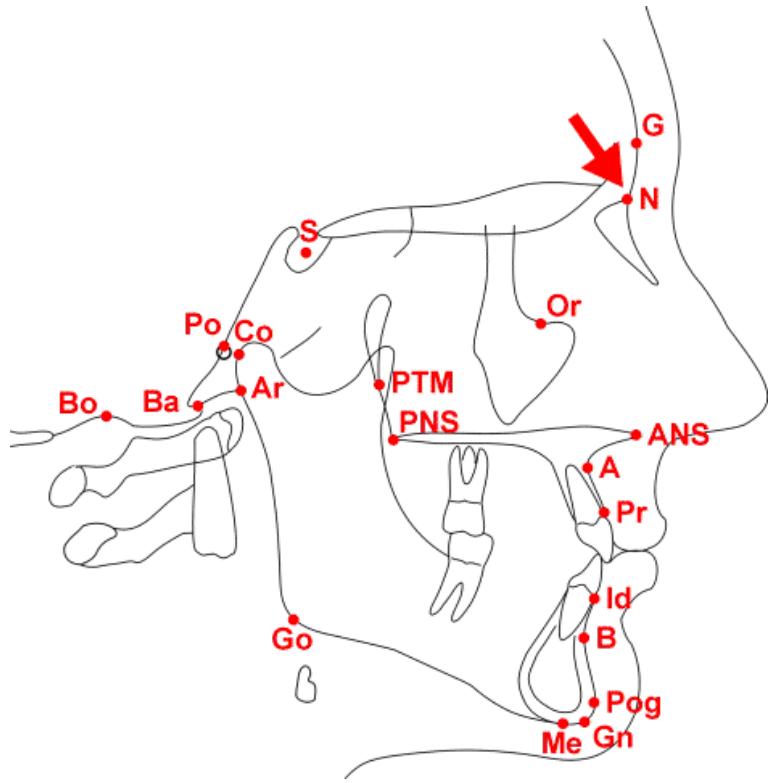
The image shows a screenshot of the FaceBase website running in a Firefox browser. The main content area displays a 3D grayscale rendering of a mouse embryo's head and brain. On the left, a 2D histological section of the embryo is shown with various anatomical regions labeled: Forebrain (green), Midbrain (blue), Nose (orange), Maxillary Region (cyan), Mandibular Region (magenta), Eye (purple), Hair Follicle Placodes (white), and Otic Placode (yellow). A scale bar indicates 1 mm. The top navigation bar includes links for 'About' and 'Help'. Below the navigation, there is a search bar and a 'SEARCH' button. The main menu features four categories: 'Genetics', 'Anatomy', 'Species', and 'Development'. Under 'Development', there is a timeline from E12.5 to E14.5. Under 'Species', there are links for Human, Mouse, Zebrafish, and Jackson Laboratory M. Under '3D Images', there are links for '3D Facial Normative' and 'Mouse Image Search'.

3D specimens are same thing as museum specimens

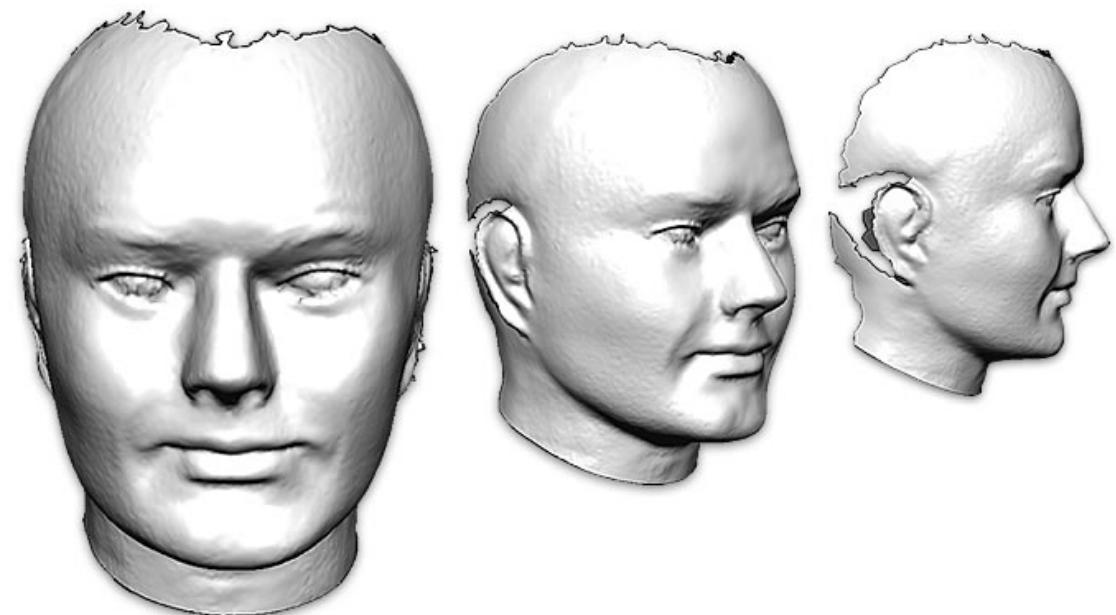
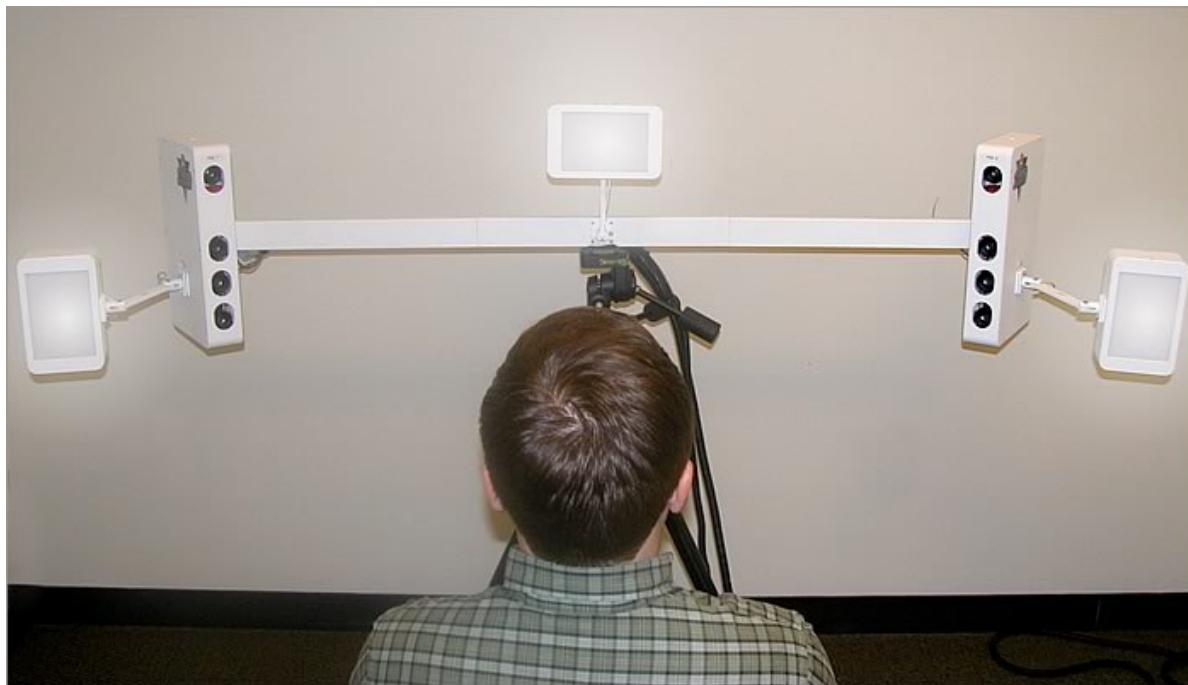
- You wouldn't work on random specimens without provenance information
- Why would you work with random 3D meshes on internet?
(metrological quality, what was the segmentation pipeline, etc)
- Our goal is to teach you the basic concepts of image manipulation so that you can do all necessary steps on your own using Slicer (or other software of your choice).
- When you publish results/scans, consider making the raw image (scan) data available as part of it (e.g., MorphoSource).



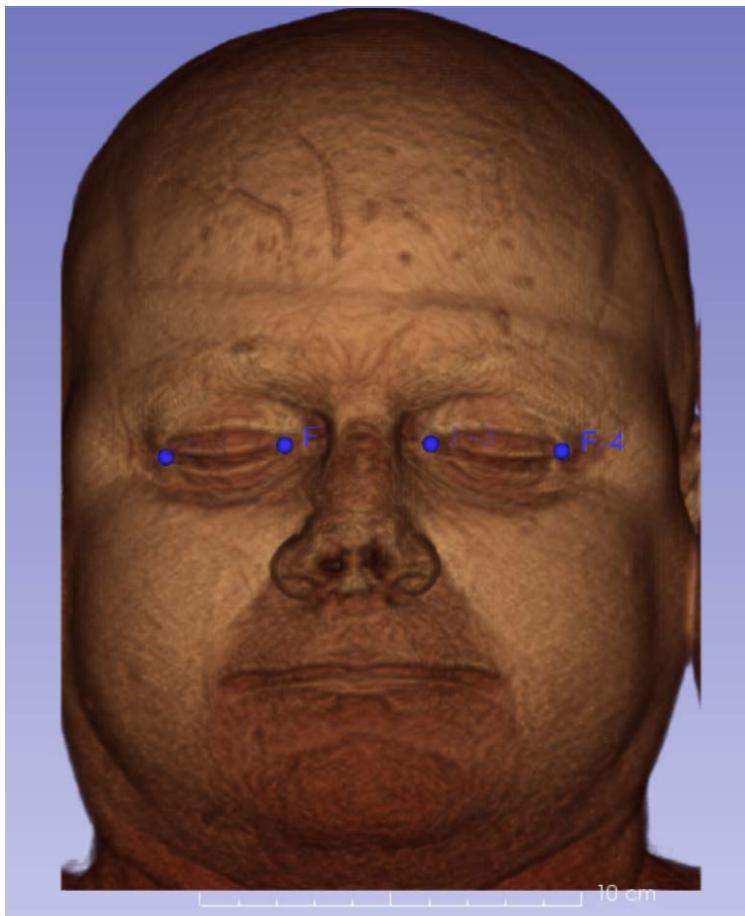
Data acquisition: 2D, Cephalometry



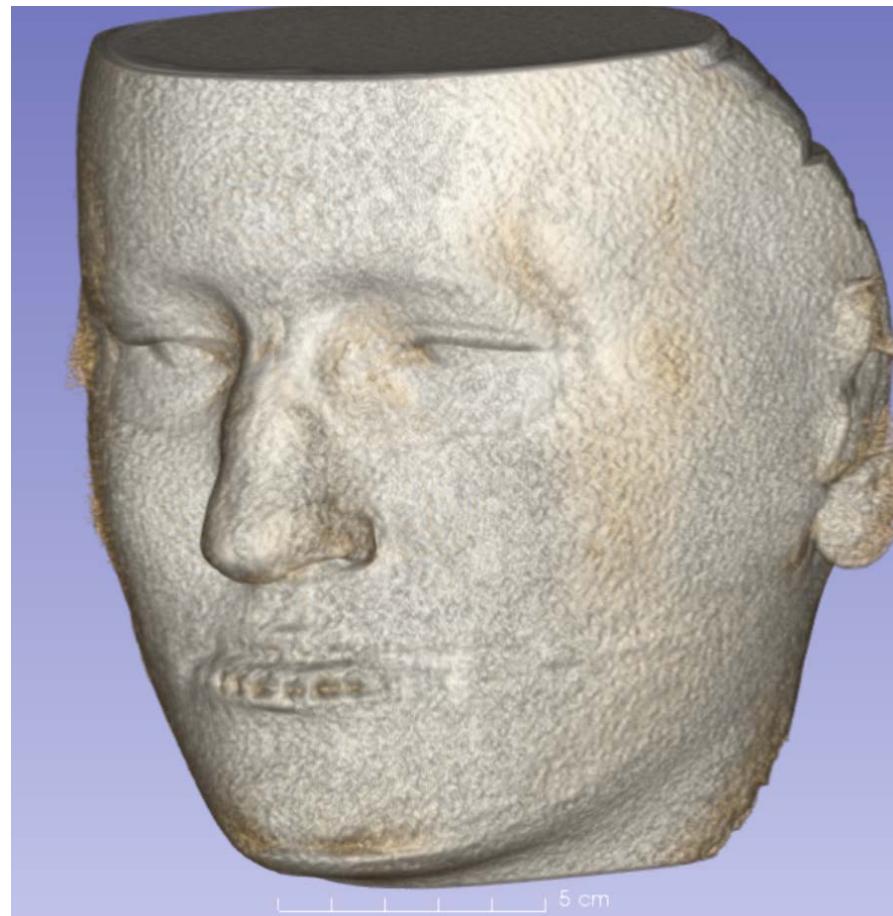
Data acquisition: 3D Photo-stereogrammetry



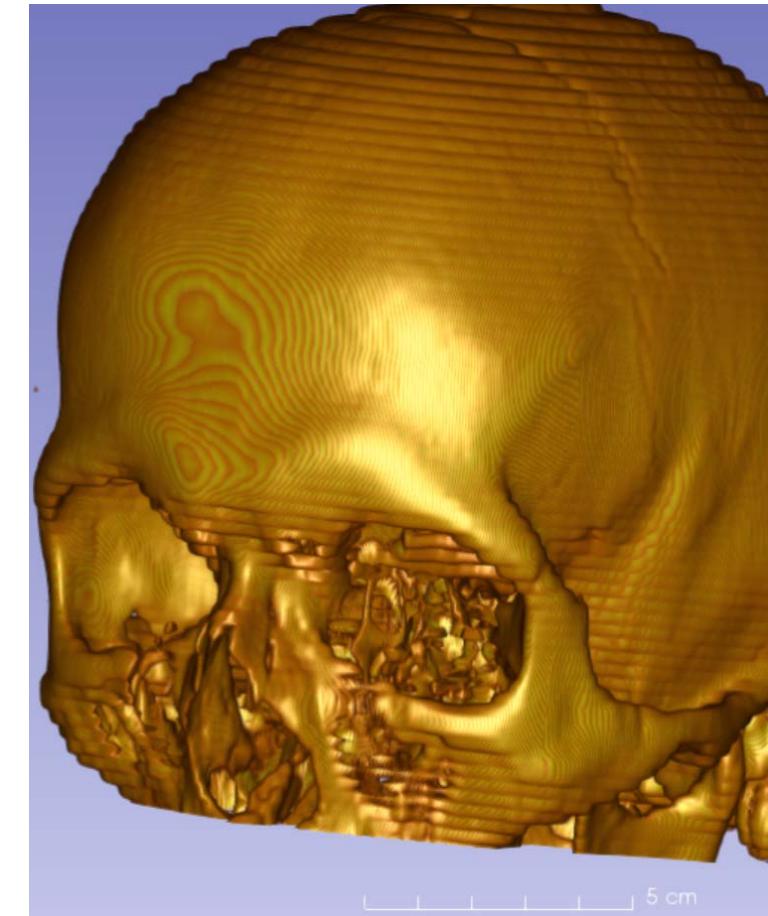
Data acquisition: Volumetric scans (MR, CT, CBCT)



MRI

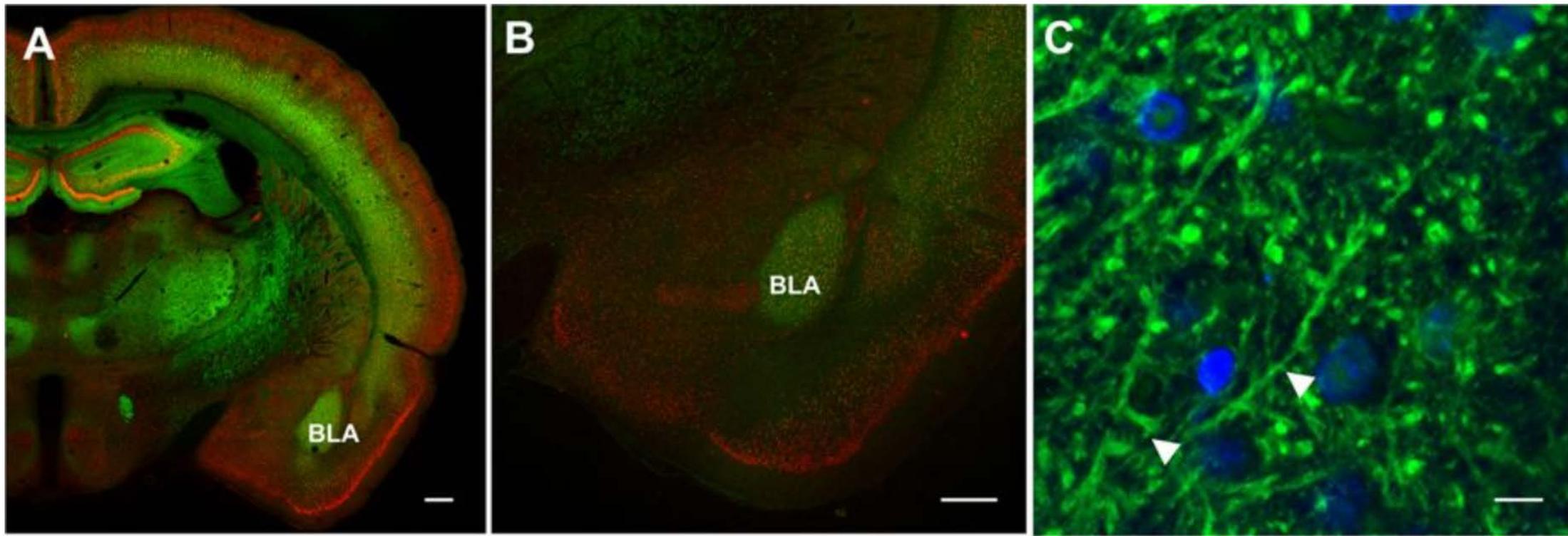


CBCT



CT

3D Fluorescent Microscopy Revolution



Key Point

SlicerMorph is not a regular research project, but a chance to build a community for people working on 3D Morphometrics around Slicer.

https://faculty.washington.edu/maga/data_dropbox/

Acknowledgements

Extended SlicerMorph Team

Sara Rolfe (UW/SCRI, Lead Developer)

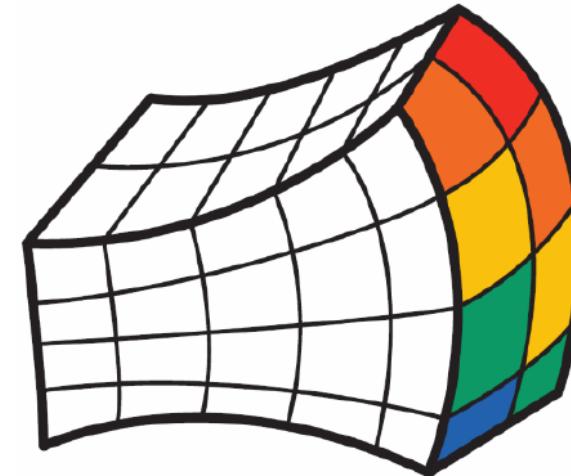
Doug Boyer (Duke, SlicerMorph Co-PI)

Julie Winchester (Duke, MorphoSource)

Adam Summers (UW, SlicerMorph Co-PI)

Steve Pieper (Chief Software Architect of 3D-Slicer)

Slicer Developer Community



SLICERMORPH

SlicerMorph Advisory Board

James Rohlf (Stony Brook University)

Dean Adams (Iowa State University)

David Polly (Indiana University)

Anjali Goswami (Natural History Museum, London)

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NSF-Advances in Biological Informatics

Murat Maga (Seattle Children's): Award #1759883

Adam Summer (UW): Award #1759637

Doug Boyer (Duke University): Award #1759839