

[https://github.com/SlicerMorph/Spr\\_2021](https://github.com/SlicerMorph/Spr_2021)

Go to Day 1 for presentation.



# 3D Visualization and Morphometrics with **SLICERMORPH**

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Associate Professor

University of Washington

Department of Pediatrics, Division of Craniofacial Medicine

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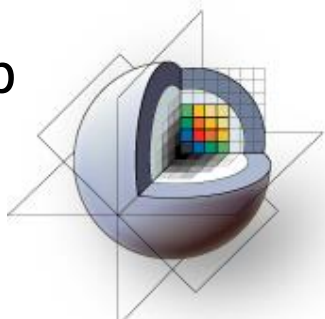
Seattle Children's Research Institute

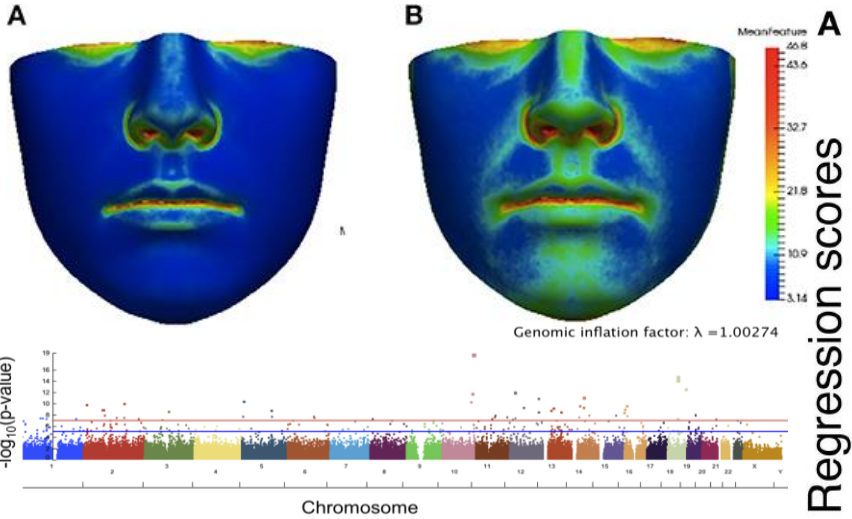
Center for Developmental Biology

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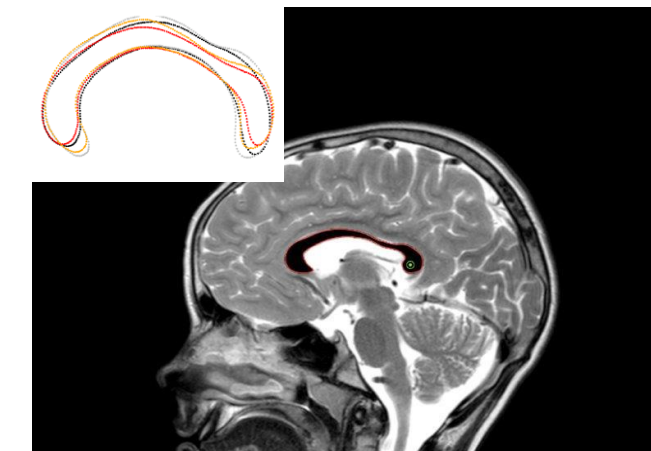
## Workshop Instructors:

- **Sara Rolfe, PhD:** Lead Developer for SlicerMorph & Research Scientist at Maga lab
- **Kelly Diamond, PhD:** Post-doc at Maga lab
- **Ezgi Mercan, PhD:** Research Scientist at Children's Craniofacial Center

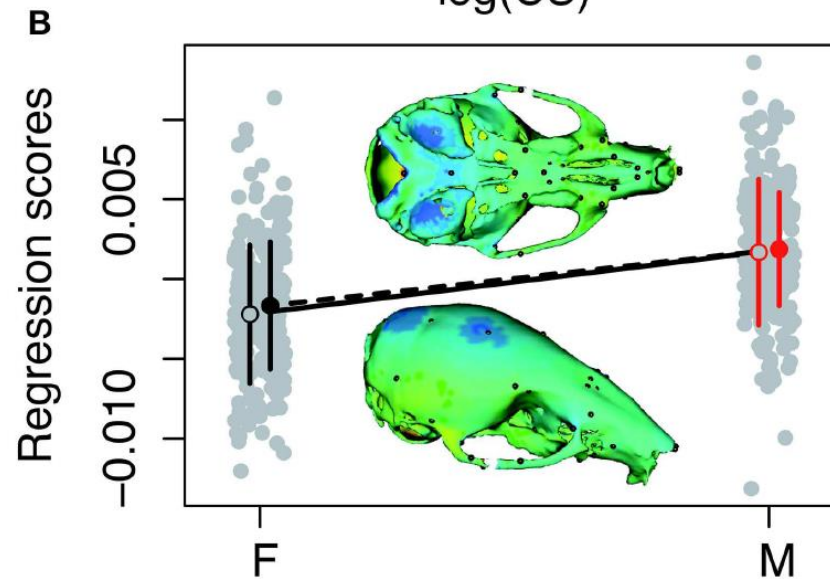
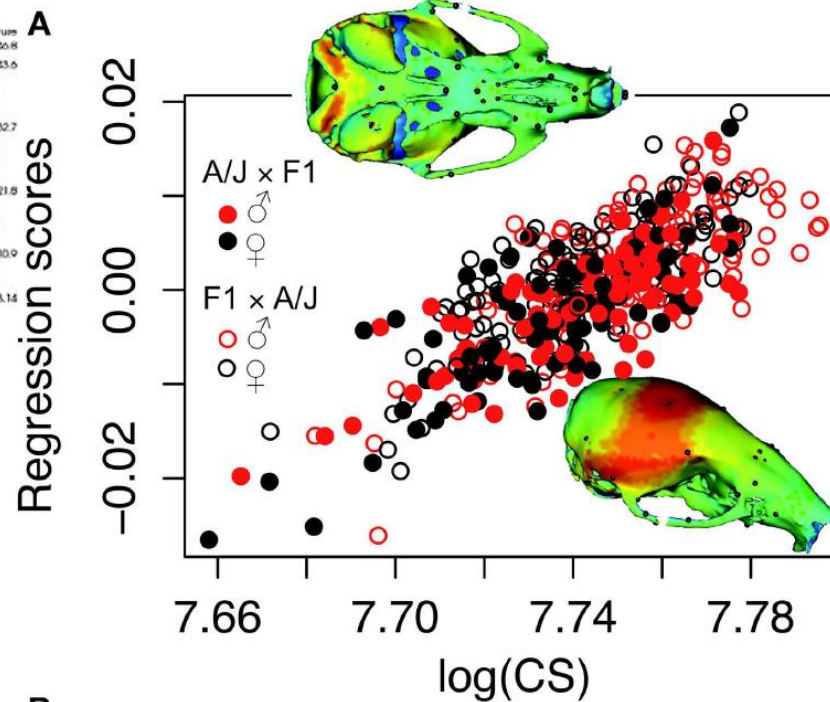




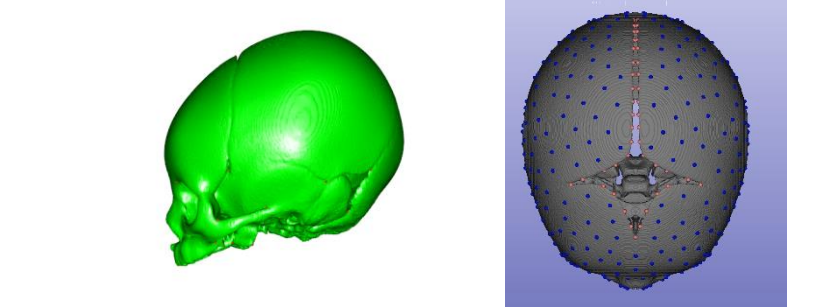
Rolfe et al. 2018. **Associations between genetic data and quantitative assessment of normal facial asymmetry.** *Frontiers in Genetics* 9: 659.



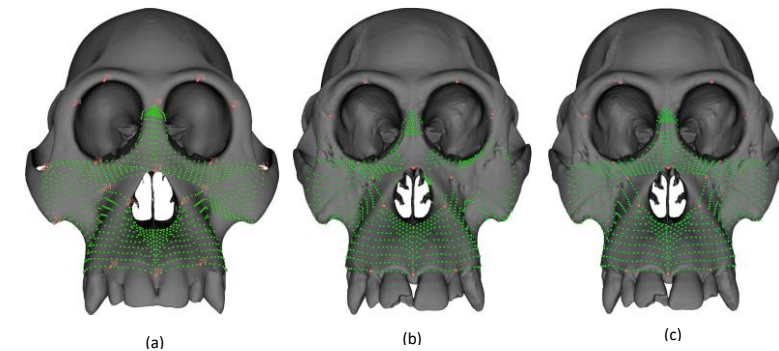
Oesch G, et al. 2018. **Geometric morphometrics reveal altered corpus callosum shape in pyridoxine-dependent epilepsy.** *Neurology*. Jul 3;91(1):e78-e86



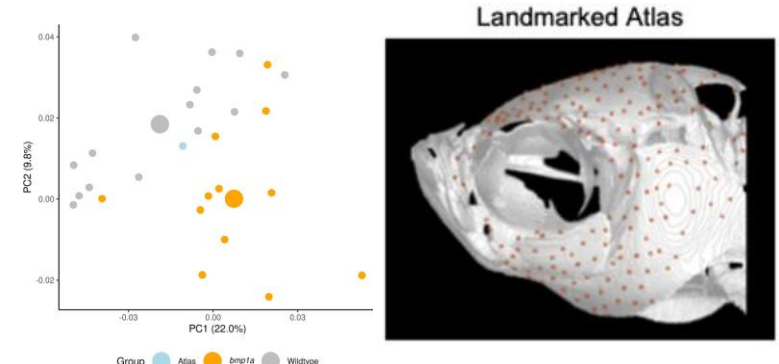
Maga AM, et al. 2015. **Quantitative trait loci affecting the 3D skull shape and size in mouse and prioritization of candidate genes in-silico.** *Frontiers in Physiology | Craniofacial Biology* 6:92.



Mercan, et al . 2020. **Cranial Growth in Isolated Sagittal Craniosynostosis Compared with Normal Growth in the First Months of Age.** *Journal of Anatomy* 236:105--116.



Rolfe, SM, Davis, C, Murat, AM. 2020. **Comparing semi-landmarking approaches for analyzing 3D cranial morphology.** *AJPA*. <https://doi.org/10.1002/ajpa.24214>



Diamond, K. M., et al (2021). **Computational anatomy and geometric shape analysis enables analysis of complex craniofacial phenotypes in zebrafish mutants.** *BioRxiv*, 2021.02.12.431035. <https://doi.org/10.1101/2021.02.12.431035>

# A typical 3D morphometrics workflow:

1. Find your data (e.g., MorphoSource, DigiMorph, your lab etc).
2. Find a software that will enable 3D visualization/segmentation and conversion to mesh, then landmark digitization (commercial software like Aviso, Mimics, Geomagic, Analyze, or free ones like ImageJ, 3D Slicer, ITK-Snap)
3. Export landmarks/measurements data into a format that can be understood by the analysis software.
4. Analyze using R (or MorphoJ)
5. Go back and forth steps #2 and #4 until you clean up all your data for final analysis.

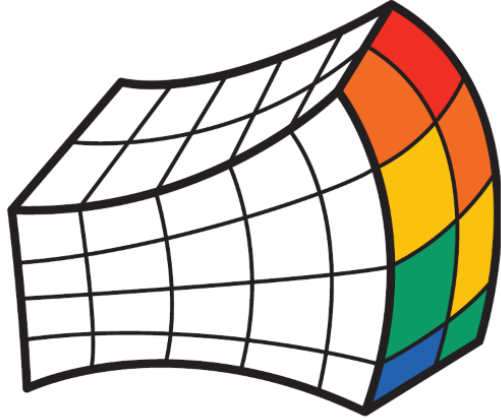
# Let's fix that! (Thank you NSF!)

1. Find your data, download, visualize, segment, animate, measure, annotate, vet your landmarks, and construct your basic morphospace in **SlicerMorph**. Then, export result for:
2. Domain-specific analysis (symmetry decomposition, phylogenetic PCA, linear models based on Procrustes Anova, covariation) in R (geomorph, Morpho, momocs etc).

# SlicerMorph Project Organization

- **SlicerMorph Core Team:**

- Lead-PI: **Murat Maga** (UW / Seattle Children's Research Institute)
- 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 & Seattle Children's Research Institute)



**SLICERMORPH**

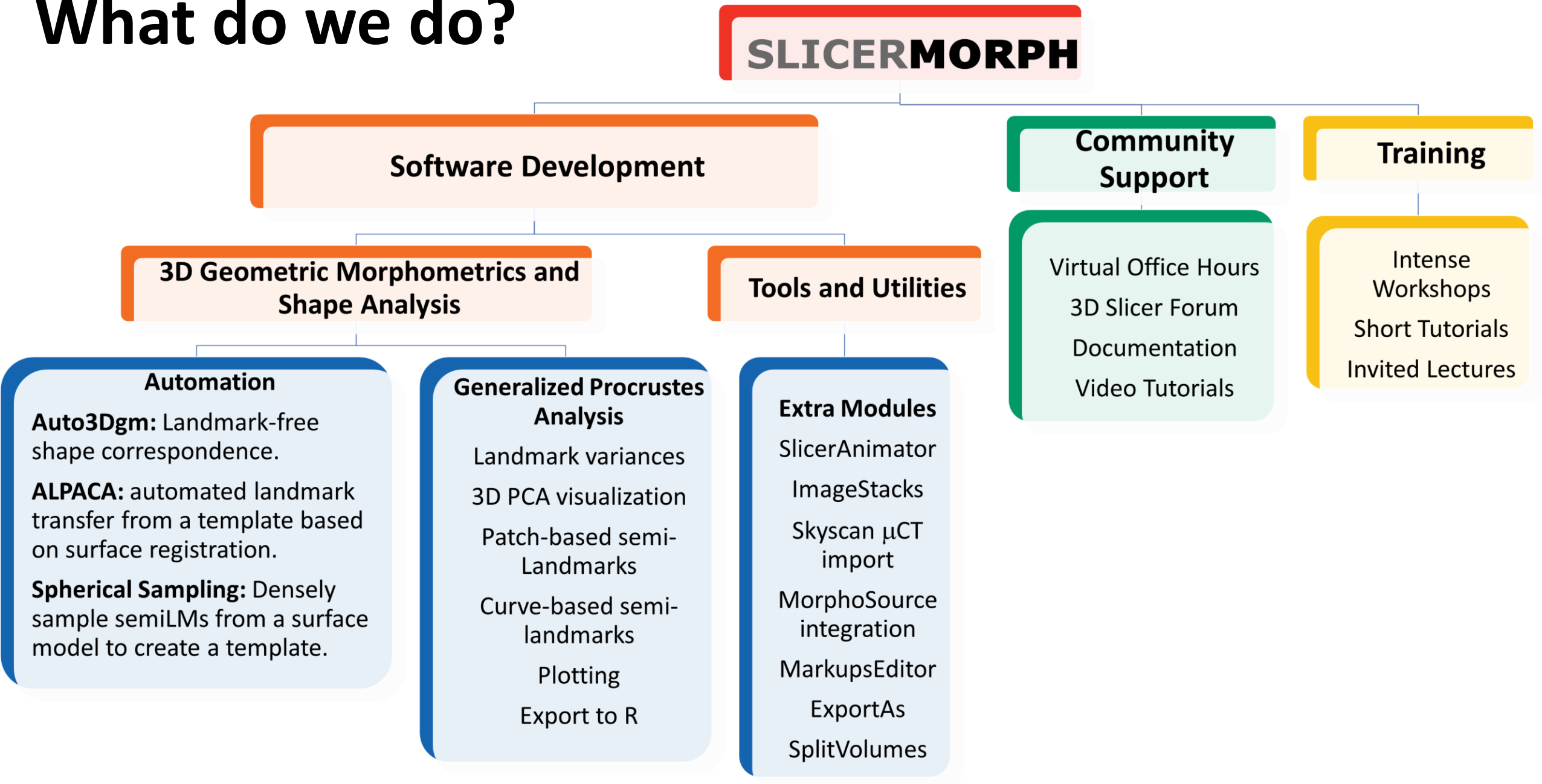
- **SlicerMorph Advisory Committee:**

- 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

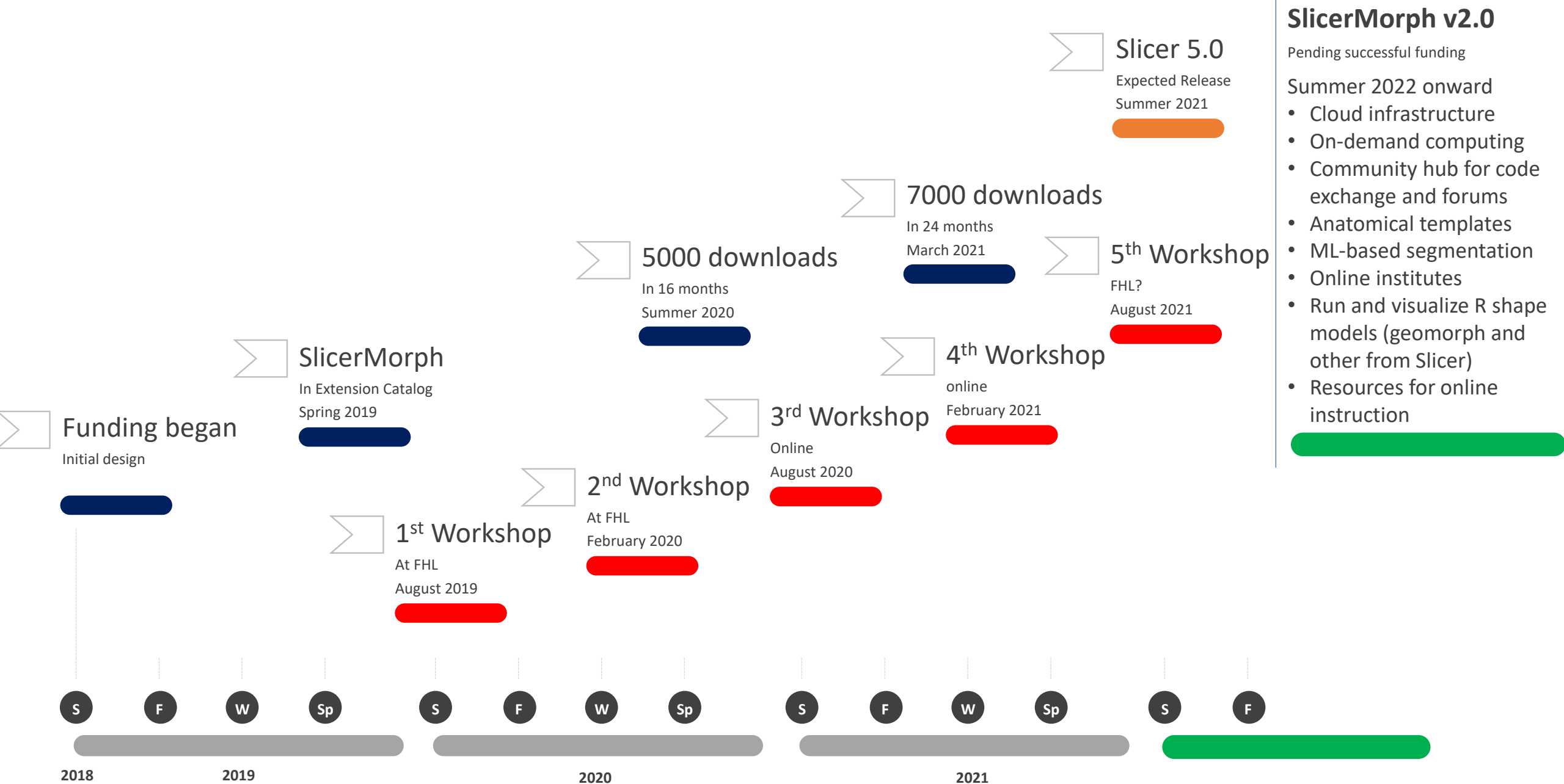
[https://nsf.gov/awardsearch/showAward?AWD\\_ID=1759883&HistoricalAwards=false](https://nsf.gov/awardsearch/showAward?AWD_ID=1759883&HistoricalAwards=false)

# What do we do?





# Road Map since Summer 2018





# Plan for the week normally

	2/16	2/17	2/18	2/19	2/20	2/21	2/22	2/23
7:45-8:15		Breakfast	Breakfast	Breakfast	Breakfast	Breakfast	Breakfast	Brunch / Checkout
8:30-10:15		Introduction Maga 3D imaging Summers	Applied Imaging Concepts Rolfe	Introduction to Statistical Shape Analysis II: Semi- Landmarks and beyond Rolfe	Auto3Dgm and landmark-free correspondence of biological form Boyer	Applications of SSA: Phylogenetics Shan	Work on your on data / TBD	
10:15-10:30		Coffee Break	Coffee Break	Coffee Break	Coffee Break	Coffee Break	Coffee Break	
10:30-12:15		Attendee project Presentations - Initial	Slicer #3: Segmentation, mesh conversion Maga	SlicerMorph # 1: Statistical Shape Analysis: Work with sample data Maga	Auto3Dgm: Establishing Landmark-free correspondence Shan	Repetitive tasks, Scripting in Slicer Rolfe	Work on your on data / TBD	
12:15-12:45		Lunch	Lunch	Lunch	Lunch	Lunch	Lunch	
1:00-3:00	Course check- in & Self- Paced Pre Course Lab (Dining Hall)	Slicer #1: UI, overview of functionality, extensions, finding help Mercan	Introduction to Statistical Shape Analysis I: Landmark-based methods Maga	Template-based analysis and computational anatomy Maga	Application of SSA: Modeling growth Mercan	Building Statistical Shape Models in R Schlager	Setting your own lab / Concluding remarks SlicerMorph team	
3:00-3:15		Coffee Break	Coffee Break	Coffee Break	Coffee Break	Coffee Break	Coffee Break	
3:15-5.15		Slicer #2: Data formats, getting data from M/S, saving Maga	Slicer #4: Measurements and Visualization Rolfe	SlicerMorph # 2: Statistical Shape Analysis: Work on your data	Integrating SlicerMorph with R Mercan	Data processing in R: Plotting, modeling Schlager	Visualization Competition and Social	
6:00-6:30	Dinner	Dinner	Dinner	Dinner	Dinner	Dinner	Dinner	
7:00-8:00		Smores on beach	Study Hall @Dining Hall -	Study Hall @Dining Hall -	Study Hall @Dining Hall -	Study Hall @Dining Hall -		

# Plan for this week

	Day1	Day2	Day3	Day4	Day5
Session 1 9.30-11.30	<b>Introduction - Maga</b>  SlicerMorph and SlicerMorphCloud setup Sample Data Customizations	<b>Imaging Concepts - Rolfe</b>  Volume Rendering Animations Lighting Markups	<b>GMM #1- Maga</b>  Markups review SampleData review GPA in SlicerMorph Plots & 3D visualization	Semi-LMing * Curves * Patches PseudoLMGenerator MarkupEditor  <b>ALPACA - Rolfe</b>	<b>Meet a Slicer Developer</b> Andras Lasso  Q&A: Bring your questions * How can I do X in Slicer? * Segmentation Challenges * Your question here....
Session 2 12:00-2:00p	ImageStacks DICOM Volumes Models CropVolume Transform Save/Export Data	Segmentation Concepts Segment Editor Segmentations Segmentation vs Labelmap importing/Exporting Segmentations Segment Statistics Surface Toolbox Dynamic Modeler	<b>GMM#2 - Rolfe</b>  GPA cont'ed Continuing analysis in R	<b>Putting it all together - Diamond</b>  ALPACA Tutorial	<b>Setting up a lab - Maga</b>  Auto3Dgm tutorial Odds and Ends Evaluations

# EVALUTIONS

- **Evaluation forms:** We need your feedback both right at the end of each day. Please find the online surveys at:

[https://github.com/SlicerMorph/Spr\\_2021/blob/main/Evaluations/README.md](https://github.com/SlicerMorph/Spr_2021/blob/main/Evaluations/README.md)

- A final survey for overall course feedback at the end Day 5. Same link as above.
- Critical for our renewal and continuation efforts.

# Self-support resources during and after the course

- **Review Course repository:** [https://github.com/SlicerMorph/Spr\\_2021](https://github.com/SlicerMorph/Spr_2021)
- **Slack Channel (active during course only):** [https://join.slack.com/t/slicermorph21/shared\\_invite/zt-mqey0gkz-qRcilex8OZdvoicex3BPFQ](https://join.slack.com/t/slicermorph21/shared_invite/zt-mqey0gkz-qRcilex8OZdvoicex3BPFQ)
- **SlicerMorph Project website:** <http://SlicerMorph.org> (links to tutorials, data etc)
- **Official SlicerMorph Modules Documentation:** <https://github.com/SlicerMorph/SlicerMorph#module-descriptions>
- **Sign up for announcements and updates:** <http://bit.ly/SM-listserv>
- **SlicerMorph video tutorials:** [http://bit.ly/SM\\_youtube](http://bit.ly/SM_youtube)
- **Engage with Slicer(Morph) community:** <https://discourse.slicer.org>
- **Monthly zoom meetings (Pending):** 4<sup>th</sup> Wednesday of each month @11 (PDT)
- **Follow us on Twitter** <https://twitter.com/SlicerMorph>

# SlicerMorph Publications

Received: 10 June 2020 | Revised: 13 November 2020 | Accepted: 8 December 2020  
DOI: 10.1002/ajpa.24214

## RESEARCH ARTICLE

## Comparing semi-landmarking approaches for analyzing three-dimensional cranial morphology

Sara Rolfe<sup>1</sup> | Christopher Davis<sup>2</sup> | A. Murat Maga<sup>3,4</sup>

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<sup>2</sup>Department of Anthropology, University of Texas, Austin, Texas, USA

<sup>3</sup>Department of Pediatrics, University of Washington, Seattle, Washington, USA

<sup>4</sup>Center for Developmental Biology and Regenerative Medicine, Seattle Children's Research Institute, Seattle, Washington, USA

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**Funding information:**  
National Science Foundation, Grant/Award Numbers: 1759637, 1759883

### Abstract

**Objectives:** Increased use of three-dimensional (3D) imaging data has led to a need for methods capable of capturing rich shape descriptions. Semi-landmarks have been demonstrated to increase shape information but placement in 3D can be time-consuming, computationally expensive, or may introduce artifacts. This study implements and compares three strategies to more densely sample a 3D image surface.

**Materials and methods:** Three dense sampling strategies: patch, patch-thin-plate spline (TPS), and pseudo-landmark sampling, are implemented to analyze skulls from three species of great apes. To evaluate the shape information added by each strategy, the semi or pseudo-landmarks are used to estimate a transform between an individual and the population average template. The average mean root squared error between the transformed mesh and the template is used to quantify the success of the transform.

**Results:** The landmark sets generated by each method result in estimates of the template that on average were comparable or exceeded the accuracy of using manual landmarks alone. The patch method demonstrates the most sensitivity to noise and missing data, resulting in outliers with large deviations in the mean shape estimates. Patch-TPS and pseudo-landmarking provide more robust performance in the presence of noise and variability in the dataset.

**Conclusions:** Each landmarking strategy was capable of producing shape estimations of the population average templates that were generally comparable to manual landmarks alone while greatly increasing the density of the shape information. This study highlights the potential trade-offs between correspondence of the semi-landmark points, consistent point spacing, sample coverage, repeatability, and computational time.

### KEYWORDS

3D morphometrics, cranial morphology, geometric morphometrics, great apes, landmarks

## 1 | INTRODUCTION

Quantitative assessment of morphological variation using landmark coordinates placed on three-dimensional (3D) images requires the ability to locate homologous points across images. Gold-standard methods generally rely on an expert to manually place landmarks at

locations that are considered "biologically homologous" (Adams et al., 2013; Bookstein, 1997b). The shape information captured using these anatomical landmarks is limited by the number of these landmark points available, often resulting in a sparse representation of the anatomy. Regions that pose challenges to reliable landmark identification, such as smooth surfaces, poorly defined boundaries between

Am J Phys Anthropol. 2021;1–11.

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bioRxiv is receiving many new papers on coronavirus SARS-CoV-2. A reminder: these are preliminary reports that have not been peer-reviewed. They should not be regarded as conclusive, guide clinical practice/health-related behavior, or be reported in news media as established information.

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New Results

Comment on this paper

Previous

Next

### SlicerMorph: An open and extensible platform to retrieve, visualize and analyze 3D morphology

Sara Rolfe, Steve Pieper, Arthur Porto, Kelly Diamond, Julie Winchester, Shan Shan, Henry Kirveslahti, Doug Boyer, Adam Summers, A. Murat Maga

doi: <https://doi.org/10.1101/2020.11.09.374926>

This article is a preprint and has not been certified by peer review [what does this mean?]

Abstract Full Text Info/History Metrics Preview PDF

### ABSTRACT

Large scale digitization projects such as *#ScanAllFishes* and *oVert* are generating high-resolution microCT scans of vertebrates by the thousands. Data from these projects are shared with the community using aggregate 3D specimen repositories like MorphoSource through various open licenses. MorphoSource currently hosts tens of thousands of 3D scans of eukaryotes. Along with the data from similarly scoped projects such as 10kPhenomes, DigiMorph and many others, soon hundreds of thousands of specimens that represent biodiversity of extinct and extant organisms will be conveniently available to researchers. We anticipate an explosion of quantitative research in organismal biology with the convergence of available data and the methodologies to analyze them.

Though the data are available, the road from a series of images to analysis is fraught with challenges for most biologists. It involves tedious tasks of data format conversions, preserving spatial scale of the data accurately, 3D visualization and segmentations, acquiring measurements and annotations. When scientists use commercial software with proprietary formats, a roadblock for data exchange, collaboration, and reproducibility

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Posted November 09, 2020.

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Clinical Trials\*  
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Ecology  
Epidemiology\*  
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Genomics

New Results

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### ALPACA: a fast and accurate approach for automated landmarking of three-dimensional biological structures

Arthur Porto, Sara M. Rolfe, A. Murat Maga

doi: <https://doi.org/10.1101/2020.09.18.303891>

This article is a preprint and has not been certified by peer review [what does this mean?]

Abstract Full Text Info/History Metrics Preview PDF

### Abstract

Landmark-based geometric morphometrics has emerged as an essential discipline for the quantitative analysis of size and shape in ecology and evolution. With the ever-increasing density of digitized landmarks, the possible development of a fully automated method of landmark placement has attracted considerable attention. Despite the recent progress in image registration techniques, which could provide a pathway to automation, three-dimensional morphometric data is still mainly gathered by trained experts. For the most part, the large infrastructure requirements necessary to perform image-based registration, together with its system-specificity and its overall speed have prevented wide dissemination.

Here, we propose and implement a general and lightweight point cloud-based approach to automatically collect highdimensional landmark data in 3D surfaces (Automated Landmarking through Point cloud Alignment and Correspondence Analysis). Our framework possesses several advantages compared with image-based approaches. First, it presents comparable landmarking accuracy, despite relying on a single, random reference specimen and much sparser sampling of the structure's surface. Second, it is performant such that it can be efficiently run on consumer-

Posted September 19, 2020.

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Genetics  
Genomics

Rolfe, SM, Davis, C, Murat, AM. 2020. **Comparing semi-landmarking approaches for analyzing 3D cranial morphology.** AJPA. <https://doi.org/10.1002/ajpa.24214>

Rolfe et al. (2020). **SlicerMorph: An open and extensible platform to retrieve, visualize and analyze 3D morphology.** *BioRxiv*, 2020.11.09.374926. <https://doi.org/10.1101/2020.11.09.374926>  
(User Manual of SlicerMorph and Digital Morphology)

Porto, A., Rolfe, S. M., & Maga, A. M. (2020). **ALPACA: A fast and accurate approach for automated landmarking of three-dimensional biological structures.** *BioRxiv*, 2020.09.18.303891. <https://doi.org/10.1101/2020.09.18.303891>

# We need SlicerMorph champions

- “Volunteer” for your lab to be the resident-expert.
- Write and share SOPs on the SlicerMorph website (it is a git repository, we welcome ‘contributions’)
- Develop tutorials/use cases
- File bugs / report issues



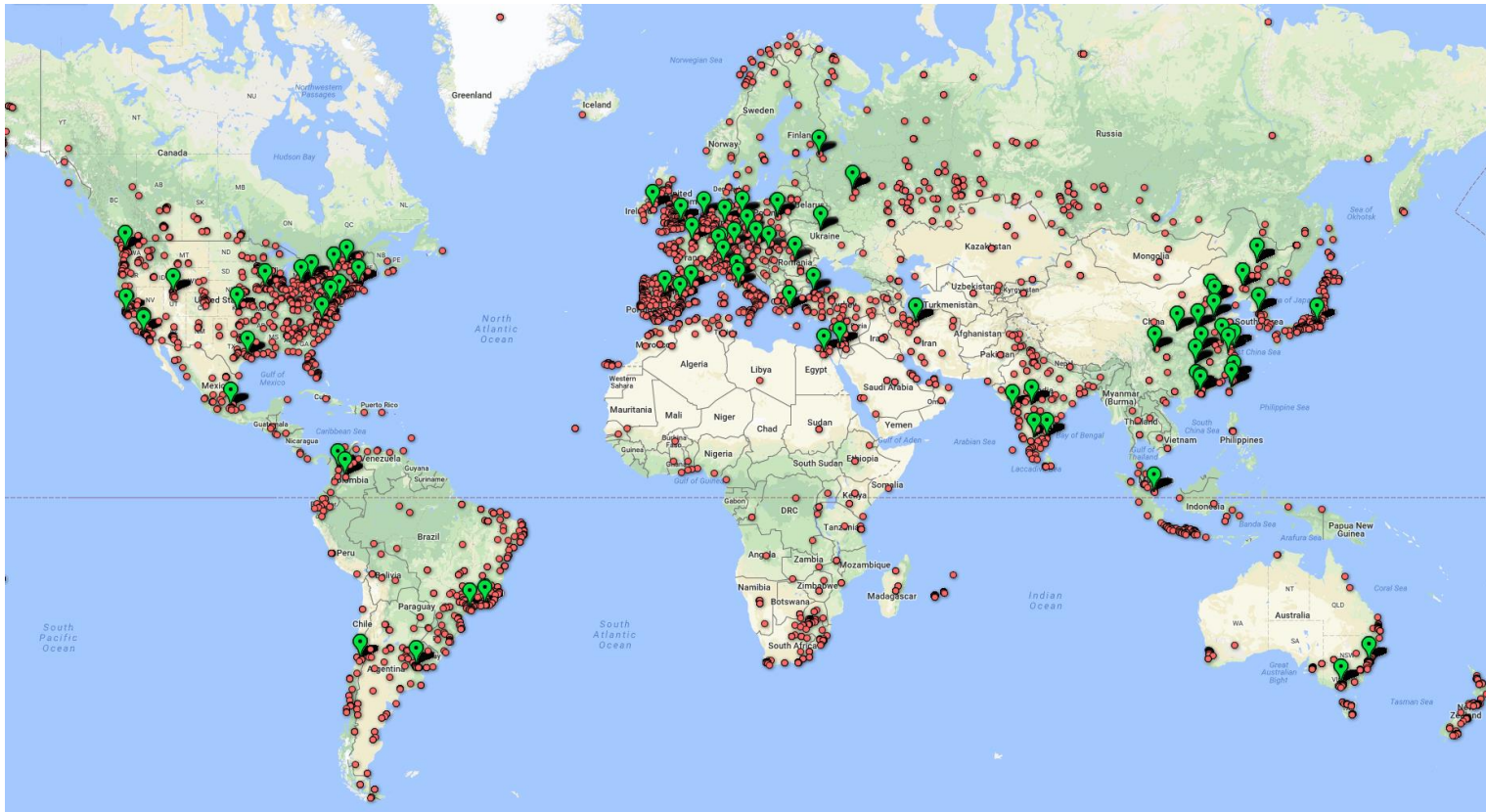


# Why 3D Slicer? Large existing user community

500 downloads per week in 2012

2800 downloads per week in 2018

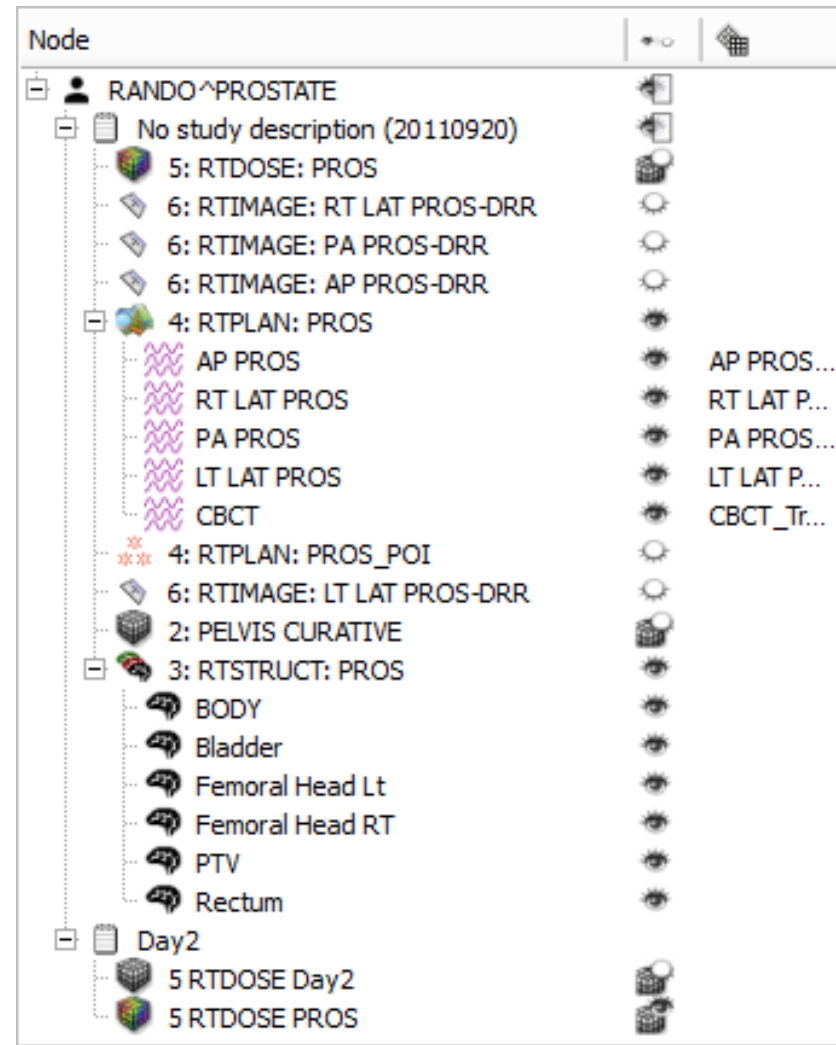
330 000+ downloads over the past 5 years:





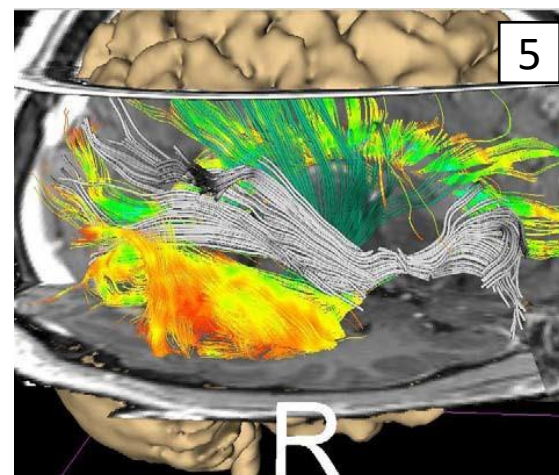
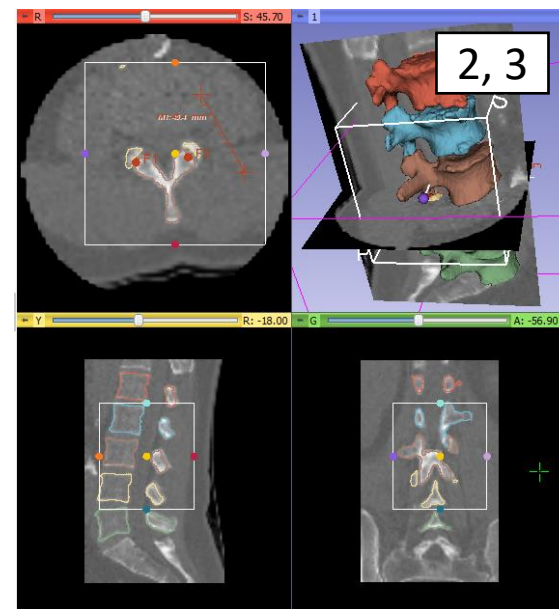
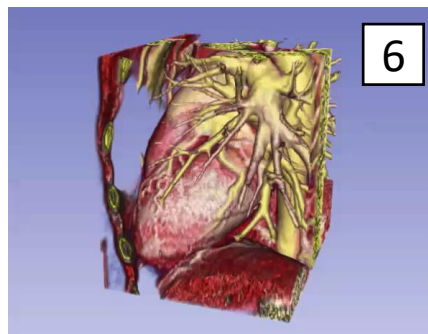
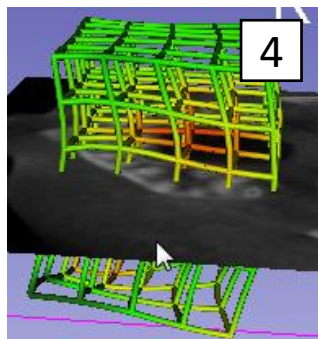
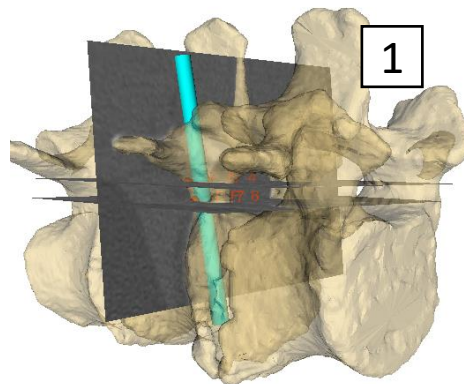
# Data import/export

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



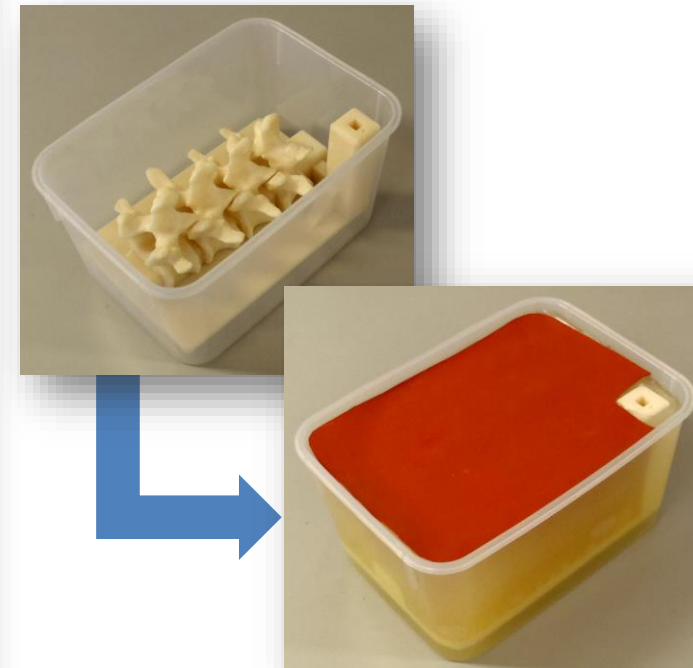
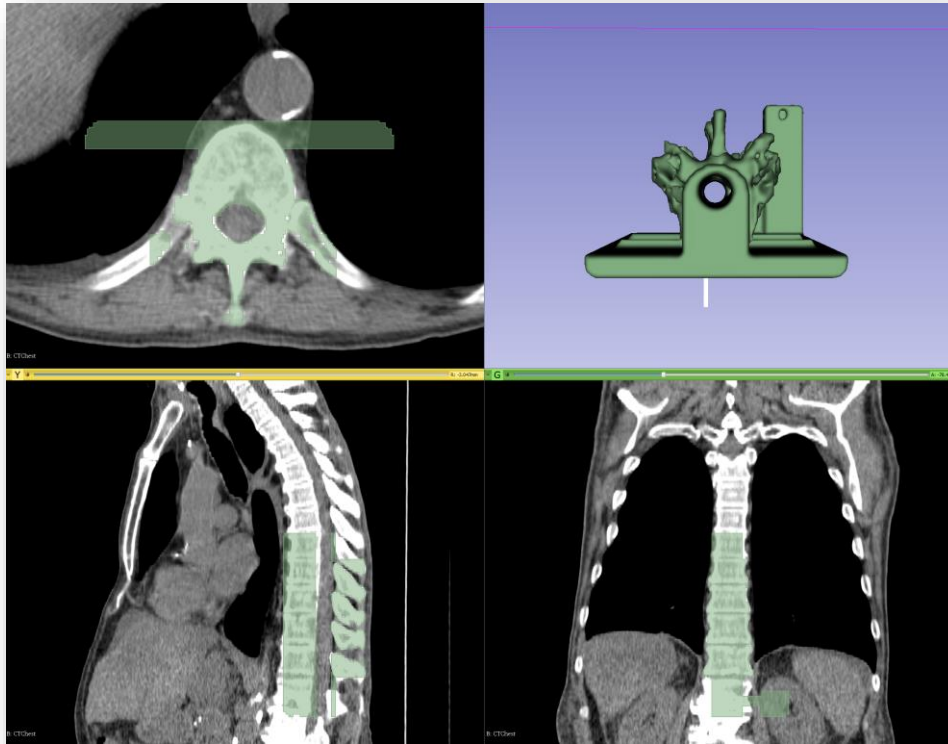
# Extensive Visualization Capabilities

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



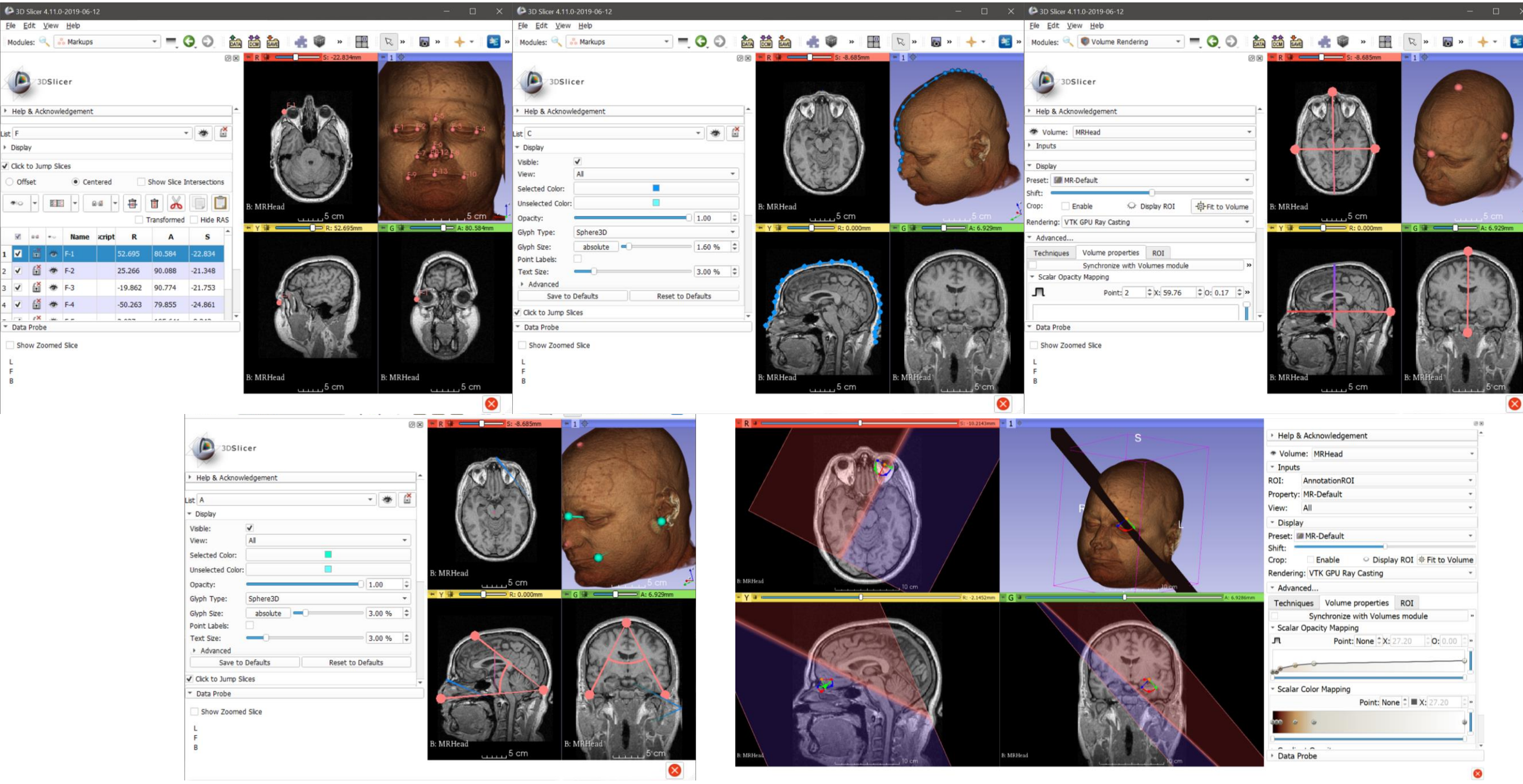
# Segmentation

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

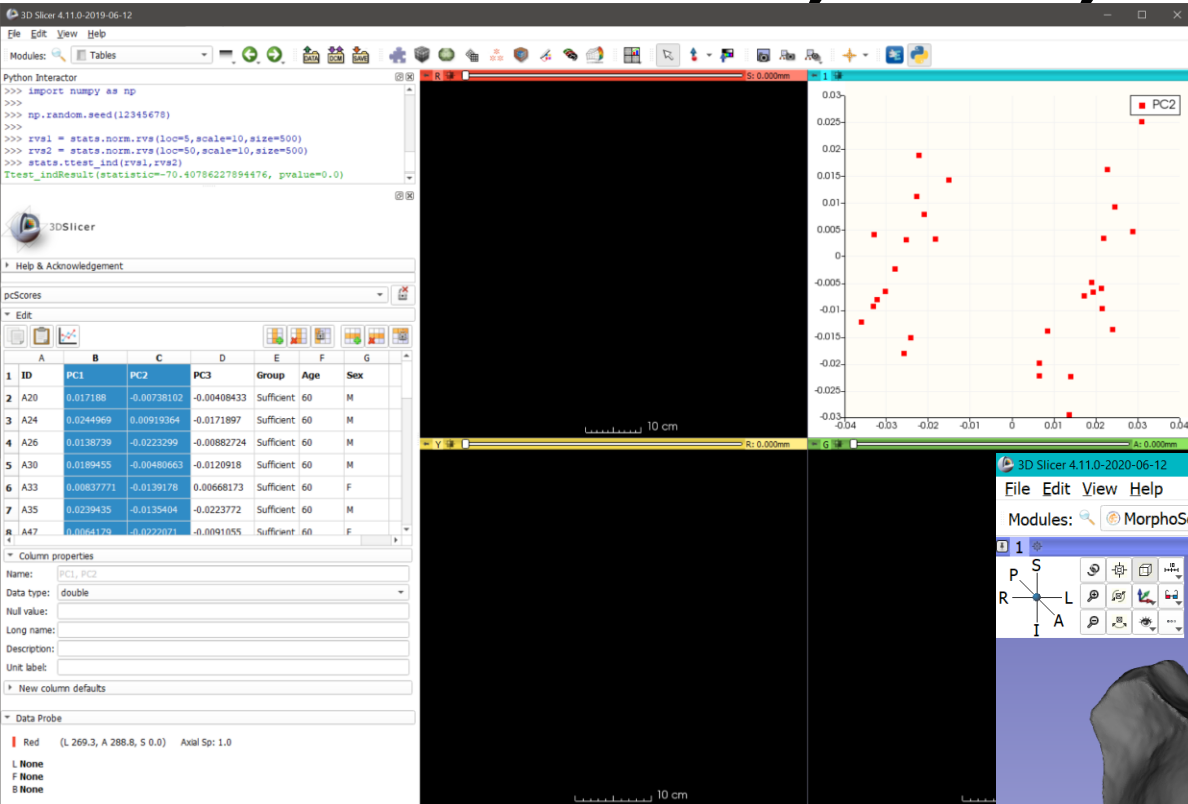




# Markups (Landmarks, Lines, Angles, Curves, Planes)



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



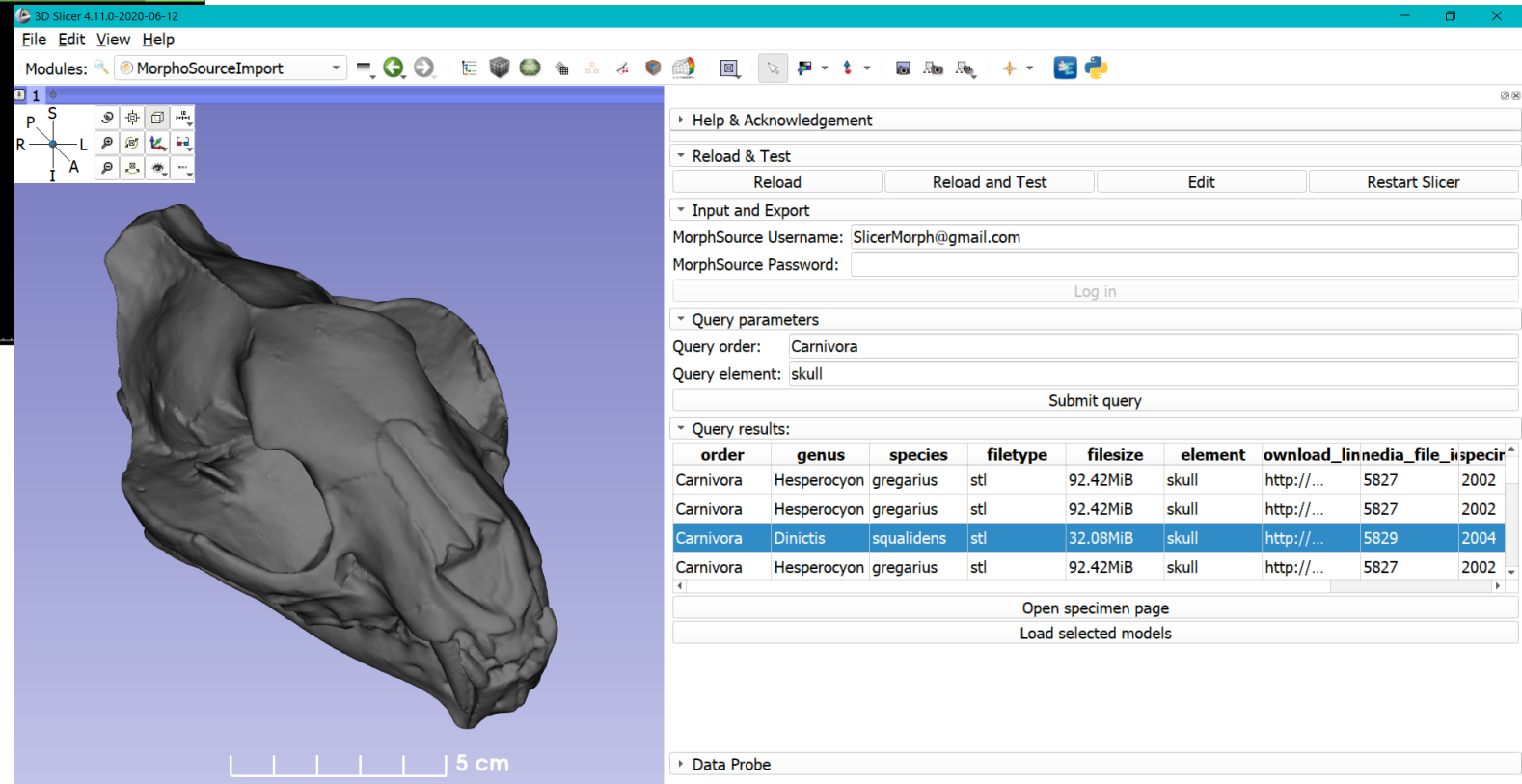
3D Slicer 4.11.0-2020-06-12

File Edit View Help

Modules: MorphoSourceImport

1

P S  
R L  
I A



The figure shows the 3D Slicer software interface. On the left, a 3D model of a skull is displayed. On the right, the 'MorphoSourceImport' module is active, showing a table of query results. The table lists specimens with columns for order, genus, species, filetype, filesize, element, download link, and specimen ID. The 'Query parameters' section shows 'Carnivora' as the query order and 'skull' as the query element. The 'Query results' table has 9 columns and 5 rows. The 'Data Probe' section is also visible.

order	genus	species	filetype	filesize	element	download link	specimen ID
Carnivora	Hesperocyon	gregarius	stl	92.42MiB	skull	http://...	5827
Carnivora	Hesperocyon	gregarius	stl	92.42MiB	skull	http://...	5827
Carnivora	Dinictis	squalidens	stl	32.08MiB	skull	http://...	5829
Carnivora	Hesperocyon	gregarius	stl	92.42MiB	skull	http://...	5827

Help & Acknowledgement

Reload & Test

Reload Reload and Test Edit Restart Slicer

Input and Export

MorphSource Username: SlicerMorph@gmail.com

MorphSource Password:

Log in

Query parameters

Query order: Carnivora

Query element: skull

Submit query

Query results:

Open specimen page

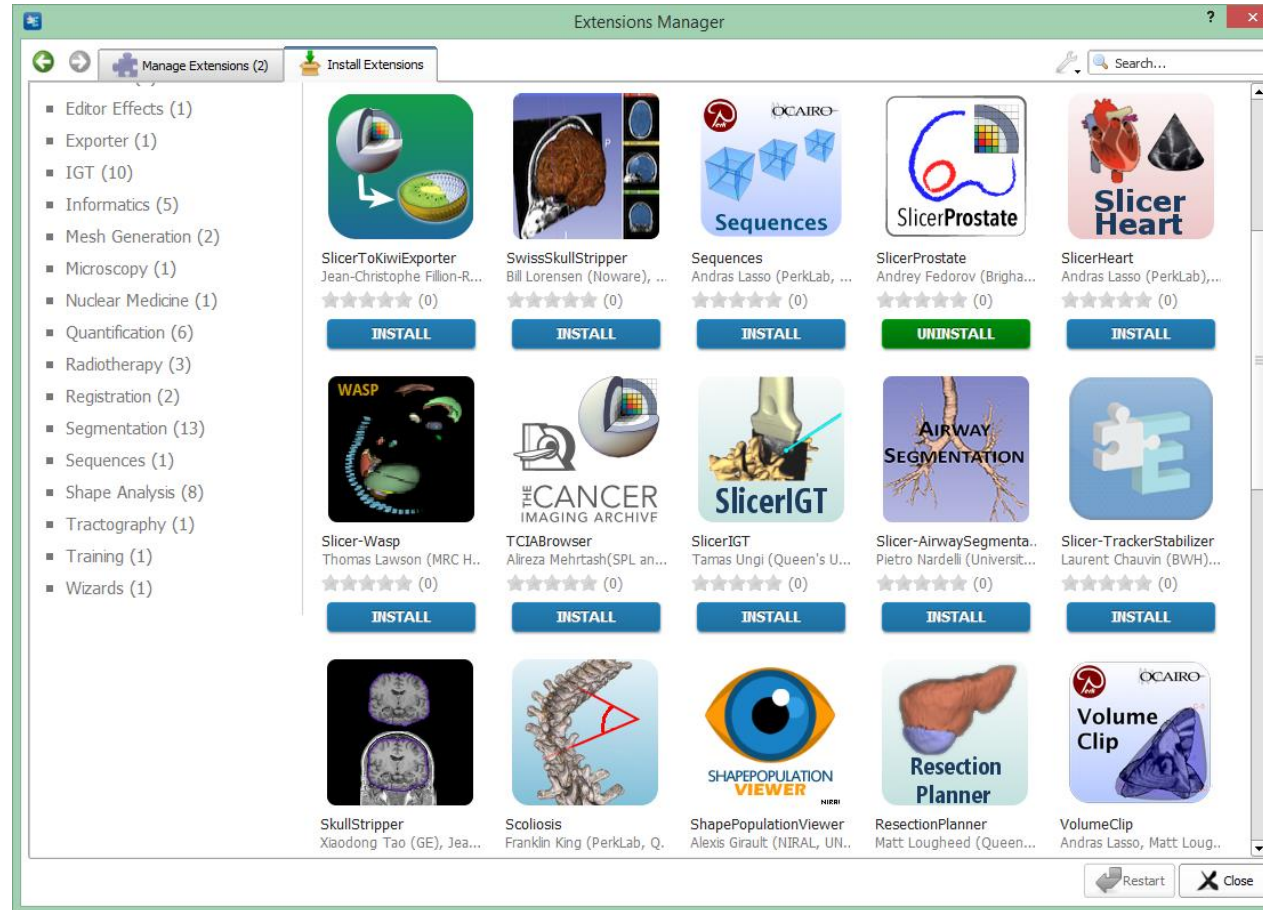
Load selected models

Data Probe

# What's inside Slicer?

- **Slicer core:** Slicer GUI, I/O, visualization and developer interfaces
- **Slicer modules:** internal plugins that depend on the slicer core (e.g., Segmentation, Segment Editor)
- **Slicer extensions:** external plugins installed on-demand by the user (e.g., SlicerMorph, auto3Dgm)

# Slicer is extensible



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



# Benefit of open-source development

- Full access to analytic code enables transparency, and reproducibility
- Enables collaboration by recycling codes across different projects.
- Other can continue or contribute to the development
- It is a **pay-forward model**: i.e., you get free access to all the development that's already paid for over the years. That's why we managed to build SlicerMorph so quickly. If you need something additional, consider [hiring an independent developer](#), then share the result with the community. **Pls: This may cost less than single academic license of VG Studio Max, Avizo or Analyze.**
- It **SHOULD BE** particularly appealing for publicly funded projects.

# Slicer is only limited by the hardware capabilities of your system:

3D Slicer 4.11.20210226

File Edit View Help

Modules: Volumes

Active Volume: 16GB\_Galago

Volume Information

Image Dimensions: 1682 1932 2507

Image Spacing: 1mm 1mm 1mm

Image Origin: 0mm 0mm 0mm

IJK to RAS Direction Matrix:

1.0000	0.0000	0.0000
0.0000	1.0000	0.0000
0.0000	0.0000	1.0000

Center Volume

Scan Order: Axial IS

Number of Scalars: 1

Scalar Type: unsigned short

Scalar Range: 0 to 16545

Volume type: Scalar

File Name: docker/workshop\_data/sample\_volumes/16GB\_Galago.nrrd

Window/Level Presets:

Convert to label map: Replace current node Convert

Display

Lookup Table: Grey

Interpolate: ☒

Window/Level:

Data Probe

docker@d52bc9311c4e: ~

```
top - 21:15:26 up 22:22, 0 users, load average: 13.80, 9.37, 4.10
Tasks: 37 total, 2 running, 30 sleeping, 0 stopped, 5 zombi
%Cpu(s): 0.1 us, 0.1 sy, 49.0 ni, 50.5 id, 0.0 wa, 0.3 hi, 0.0
MiB Mem : 459509.5 total, 395191.2 free, 46680.6 used, 17637.8 bu
MiB Swap: 0.0 total, 0.0 free, 0.0 used, 100002.0 sy
```

PID	USER	PR	NI	VIRT	RES	SHR	S	%CPU	%MEM
836	docker	39	19	54.2g	39.6g	0.3g	R	5883	8.8
14	docker	20	0	2.9g	0.1g	0.0g	S	2.3	0.0
6236	docker	39	19	5.6g	0.1g	0.1g	S	0.0	0.0
6224	docker	39	19	1.1g	0.1g	0.0g	S	0.0	0.0
6226	docker	39	19	5.5g	0.1g	0.0g	S	0.0	0.0
15970	docker	20	0	0.4g	0.0g	0.0g	S	0.0	0.0
6210	docker	39	19	0.2g	0.0g	0.0g	S	0.0	0.0
15946	docker	20	0	0.5g	0.0g	0.0g	S	0.0	0.0
68	docker	20	0	0.2g	0.0g	0.0g	S	0.0	0.0
119	docker	20	0	0.1g	0.0g	0.0g	S	0.0	0.0
56	docker	20	0	0.0g	0.0g	0.0g	S	0.0	0.0
834	docker	20	0	0.1g	0.0g	0.0g	S	0.0	0.0
274	docker	20	0	0.3g	0.0g	0.0g	S	0.0	0.0
213	docker	20	0	0.3g	0.0g	0.0g	S	0.0	0.0
124	docker	20	0	0.3g	0.0g	0.0g	S	0.0	0.0

sample\_volumes

File Edit View Bookmarks Go Tools Help

/home/docker/workshop\_data/sample\_volumes

Places

- Home Folder
- Desktop
- Trash Can
- Applications
- murat
- workshop\_data

16GB\_Galago.nrrd

1 item

Free space: 1.1 TiB (Total: 1.2 TiB)

21:15 Sunday 07 March

Each SlicerMorphCloud instance has 480GB of RAM, and 120 cores and supports 12-15 users

# Take Home Message

**SLICER****MORPH** is not a traditional research project, but a chance to build a digital community of organismal biologists and quantitative morphologists around 3D Slicer that value open science and collaboration. We are looking forward to your engagement.

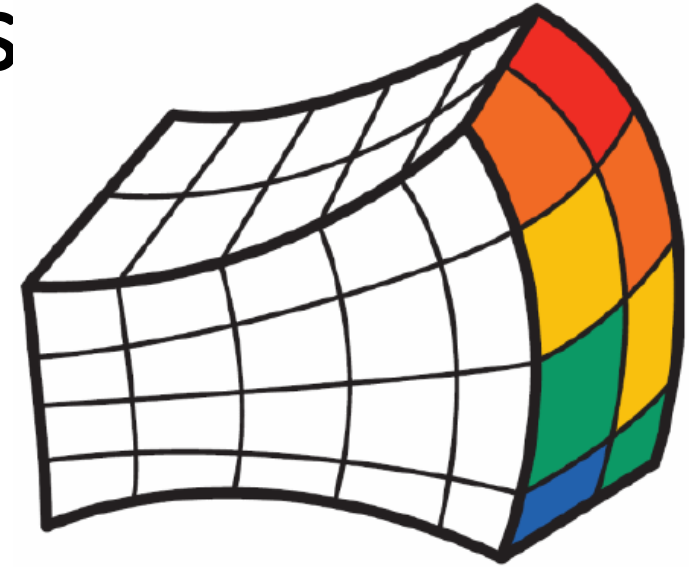
# Acknowledgements

## 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)  
Kelly Diamond (SCRI, Postdoc)  
Arthur Porto (now LSU, former post-doc)  
Andras Lasso (Queens U, Core Slicer Developer)  
Slicer Developer Community

## SlicerMorph Advisory Board

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



**SLICERMORPH**

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