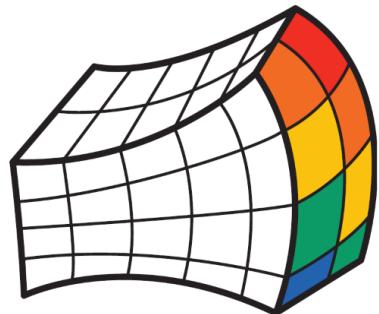


https://github.com/SlicerMorph/Spr_2022

Go to Day 1 for presentation.



SLICERMORPH

3D Visualization and Morphometrics with **SLICERMORPH**

A. Murat Maga

Associate Professor

University of Washington

Department of Pediatrics, Division of Craniofacial Medicine

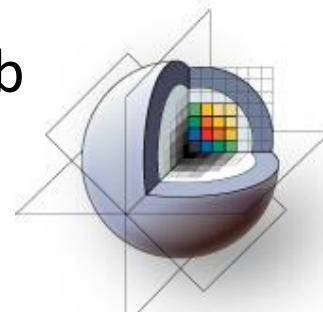
&

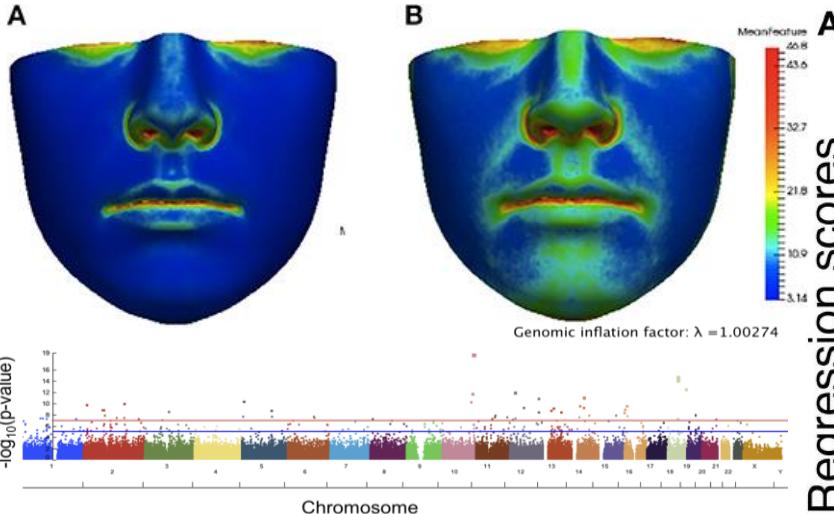
Seattle Children's Research Institute

Center for Developmental Biology

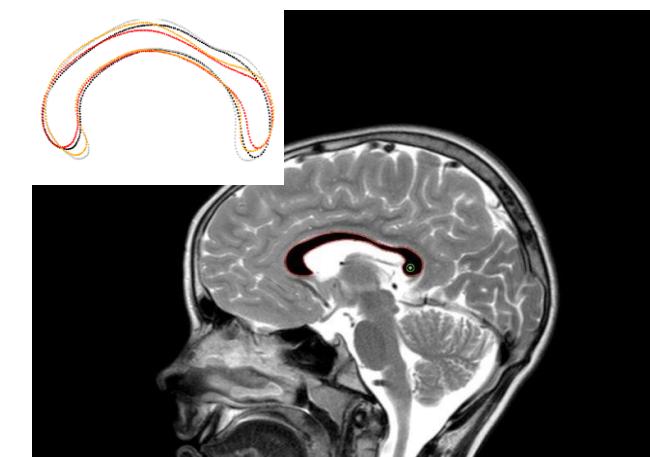
Workshop Co-Instructors:

- **Sara Rolfe, PhD:** Lead Developer for SlicerMorph & Research Scientist at Maga lab
- **Kelly Diamond, PhD:** Post-doc at Maga lab
- **Chi Zhang, PhD:** Post-doc at Maga lab
- **Arthur Porto, PhD:** Assistant Professor of Biology, Louisiana State U.

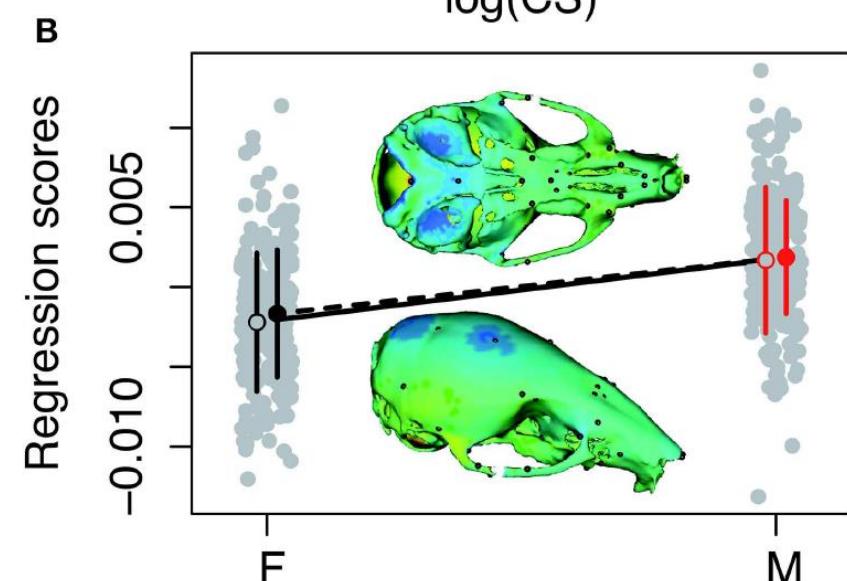
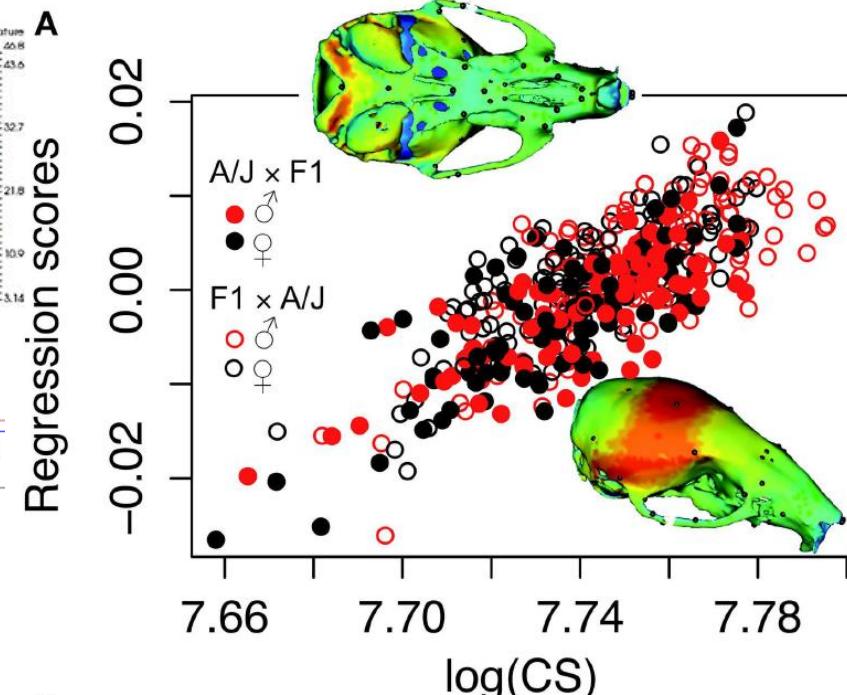




Rolfe et al. 2018. Associations between genetic data and quantitative assessment of normal facial asymmetry. Frontiers in Genetics 9: 659.



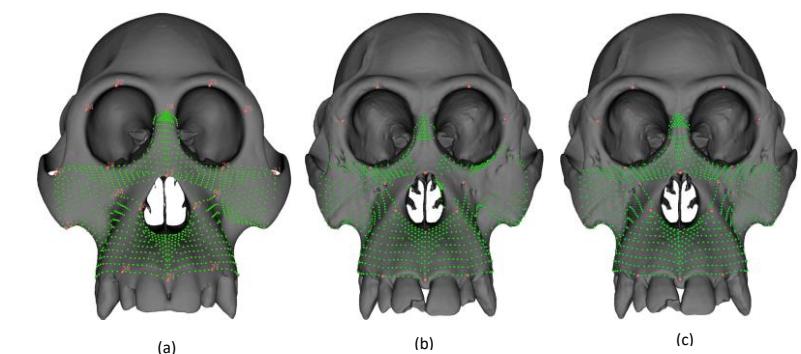
Oesch G, et al. 2018. Geometric morphometrics reveal altered corpus callosum shape in pyridoxine-dependent epilepsy. Neurology. Jul 3;91(1):e78-e86



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.

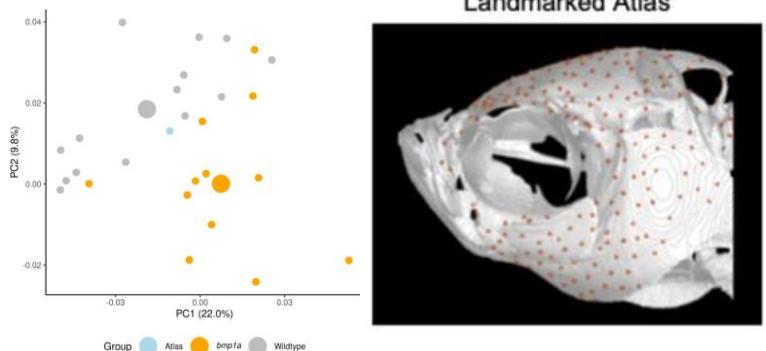
A

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>

Landmarked Atlas



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>

What do we do?

SLICERMORPH

Software Development

3D Geometric Morphometrics and Shape Analysis

Automation

Auto3Dgm: Landmark-free shape correspondence.

ALPACA: automated landmark transfer from a template based on surface registration.

Spherical Sampling: Densely sample semiLMs from a surface model to create a template.

Tools and Utilities

Generalized Procrustes Analysis

Landmark variances
3D PCA visualization
Patch-based semi-Landmarks
Curve-based semi-landmarks
Plotting
Export to R

Extra Modules

SlicerAnimator
ImageStacks
Skyscan µCT import
MorphoSource integration
MarkupsEditor
ExportAs
SplitVolumes

Community Support

Virtual Office Hours
3D Slicer Forum
Documentation
Video Tutorials

Training

Intense Workshops
Short Tutorials
Invited Lectures

Plan for this week

	2/16	2/17	2/18	2/19	2/20	2/21	2/22
7:45-8:15		Breakfast	Breakfast	Breakfast	Breakfast	Breakfast	Breakfast
8:30-10:15		Introduction Maga 3D imaging Summers	Applied Imaging Concepts Rolle	Introduction to Statistical Shape Analysis II: Semi- Landmarks and beyond Rolle	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 Rolle	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 Rolle	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 -	

	Day1	Day2	Day3	Day4
Session #1 9:30-12:00p	Introduction - Maga SlicerMorph and SlicerMorphCloud setup Sample Data Customizations	Imaging Concepts - Rolfe Markups	GMM #1- Maga Markups review Work on your own 10-11 GPA in SlicerMorph Plots & 3D visualization	Getting SlicerMorph data into R ALPACA - Porto K-mean template selection & MALPACA - Zhang
Session #2 12:30-3:00p	ImageStacks DICOM Volumes Models CropVolume Transform Save/Export As Volume Rendering Animations Lighting	Segmentation Concepts Segment Editor Segmentations CropVolume Transform Save/Export As Volume Rendering Animations Lighting	GMM#2 - Rolfe Semi-LMing: Curves Patches PseudoLMGenerator MarkupEditor	Putting it all together - Diamond

What it was like pre-Covid

What it is now

Self-support resources during and after the course

- **Review Course repository:** https://github.com/SlicerMorph/Spr_2022
- **Join Slack Channel (active during course only):** https://join.slack.com/t/slicermorphsp-wzz3095/shared_invite/zt-19j45cx5s-7meqF508UQsH~vT0R5j4sw
- **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
- **Engage with Slicer(Morph) community:** <https://discourse.slicer.org>
- **Follow us on Twitter** <https://twitter.com/SlicerMorph>

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_2022/tree/main/
Evaluations](https://github.com/SlicerMorph/Spr_2022/tree/main/Evaluations)

A final survey for overall course feedback at the end Day 4. Same link as above.

- Critical for our renewal and continuation efforts.

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 Technical Papers

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 Rolfe¹ | Christopher Davis² | A. Murat Maga^{3,4}

¹Friday Harbor Labs, University of Washington, Friday Harbor, Washington, USA

²Department of Anthropology, University of Texas, Austin, Texas, USA

³Department of Pediatrics, University of Washington, Seattle, Washington, USA

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

Correspondence
Sara Rolfe, Friday Harbor Labs, University of Washington, 620 University Rd, Friday Harbor, WA 98280, USA.
Email: smrolfe@uw.edu

Funding information
National Science Foundation, Grant/Award Number: 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

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



WILEY

Received: 15 April 2021 | Accepted: 22 June 2021
DOI: 10.1111/2041-210X.13669

APPLICATION

Methods in Ecology and Evolution

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

Sara Rolfe^{1,2} | Steve Pieper³ | Arthur Porto^{4,5} | Kelly Diamond² | Julie Winchester⁶ | Shan Shan⁷ | Henry Kirveslahti⁸ | Doug Boyer⁴ | Adam Summers¹ | A. Murat Maga^{3,4}

¹Friday Harbor Marine Laboratories, University of Washington, San Juan, WA, USA; ²Seattle Children's Research Institute, Center for Developmental Biology and Regenerative Medicine, Seattle, WA, USA; ³Isomics, Inc., Cambridge, MA, USA; ⁴Department of Biological Sciences, Louisiana State University, Baton Rouge, LA, USA; ⁵Center for Computation and Technology, Louisiana State University, Baton Rouge, LA, USA; ⁶Department of Evolutionary Anthropology, Duke University, Durham, NC, USA; ⁷Department of Mathematics, Mount Holyoke College, South Hadley, MA, USA; ⁸Department of Statistical Science, Duke University, Durham, NC, USA and ⁹Department of Pediatrics, Division of Craniofacial Medicine, University of Washington, Seattle, WA, USA

Correspondence
A. Murat Maga
Email: maga@uw.edu

Funding information
Division of Biological Infrastructure, Grant/Award Number: 1759637, 1759839 and 1759883

Handling Editor: Marta Vidal Garcia

Abstract

1. 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. We anticipate an explosion of quantitative research in organismal biology with the convergence of available data and the methodologies to analyse them.

2. 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, and acquiring measurements and annotations. When scientists use commercial software with proprietary formats, a roadblock for data exchange, collaboration and reproducibility is erected that hurts the efforts of the scientific community to broaden participation in research.

3. We developed SlicerMorph as an extension of 3D Slicer, a biomedical visualization and analysis ecosystem with extensive visualization and segmentation capabilities built on proven python-scriptable open-source libraries such as Visualization Toolkit and Insight Toolkit. In addition to the core functionalities of Slicer, SlicerMorph provides users with modules to conveniently retrieve open-access 3D models or import users own 3D volumes, to annotate 3D curve and patch-based landmarks, generate landmark templates, conduct geometric morphometric analyses of 3D organismal form using both landmark-driven and landmark-free approaches, and create 3D animations from their results. We highlight how these individual modules can be tied together to establish complete workflow(s) from

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1816

wileyonlinelibrary.com/journal/mee3

Methods Ecol Evol. 2021;12:1816–1825.

Accepted: 11 July 2021
DOI: 10.1111/2041-210X.13689

RESEARCH ARTICLE

Check for updates

Methods in Ecology and Evolution

ALPACA: A fast and accurate computer vision approach for automated landmarking of three-dimensional biological structures

Arthur Porto^{1,2} | Sara Rolfe^{3,4} | A. Murat Maga^{4,5}

¹Department of Biological Sciences, Louisiana State University, Baton Rouge, LA, USA

²Center for Computation and Technology, Louisiana State University, Baton Rouge, LA, USA

³Friday Harbor Laboratories, University of Washington, San Juan Island, WA, USA

⁴Center for Developmental Biology and Regenerative Medicine, Seattle Children's Research Institute, Seattle, WA, USA

⁵Division of Craniofacial Medicine, Department of Pediatrics, University of Washington, Seattle, WA, USA

Correspondence
Arthur Porto
Email: aporto3@lsu.edu

Funding information
National Institute of Dental and Craniofacial Research; National Science Foundation

Handling Editor: Natalie Cooper

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 (3D) morphometric data are 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 its wide dissemination.
- Here, we propose and implement a general and lightweight point cloud-based approach to automatically collect high-dimensional 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 can be efficiently run on consumer-grade personal computers. Finally, it is general and can be applied at the intraspecific level to any biological structure of interest, regardless of whether anatomical atlases are available.
- Our validation procedures indicate that the method can recover intraspecific patterns of morphological variation that are largely comparable to those obtained by manual digitization, indicating that the use of an automated landmarking approach should not result in different conclusions regarding the nature of multivariate patterns of morphological variation.
- The proposed point cloud-based approach has the potential to increase the scale and reproducibility of morphometrics research. To allow ALPACA to be used out-of-the-box by users with no prior programming experience, we implemented it as a SlicerMorph module. SlicerMorph is an extension that enables geometric

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Methods Ecol Evol. 2021;12:2129–2144.

wileyonlinelibrary.com/journal/mee3 | 2129

- 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, S., Pieper, S., Porto, A., Diamond, K., Winchester, J., Shan, S., ... Maga, A. M. (2021). SlicerMorph: An open and extensible platform to retrieve, visualize and analyse 3D morphology. *Methods in Ecology and Evolution*, 12(10), 1816–1825. <https://doi.org/10.1111/2041-210X.13669>
- Porto, A., Rolfe, S., & Maga, A. M. (2021). ALPACA: A fast and accurate computer vision approach for automated landmarking of three-dimensional biological structures. *Methods in Ecology and Evolution*, 12(11), 2129–2144. <https://doi.org/10.1111/2041-210X.13689>

SlicerMorph Papers Cont'd (and forthcoming)

© 2022. Published by The Company of Biologists Ltd | *Biology Open* (2022) 11, bio058948. doi:10.1242/bio.058948



METHODS & TECHNIQUES

Computational anatomy and geometric shape analysis enables analysis of complex craniofacial phenotypes in zebrafish

Kelly M. Diamond^{1,*}, Sara M. Rolfe^{1,2}, Ronald Y. Kwon^{3,4} and A. Murat Maga^{1,5}

ABSTRACT

Due to the complexity of fish skulls, previous attempts to classify craniofacial phenotypes have relied on qualitative features or space 2D landmarks. In this work we aim to identify previously unknown 3D craniofacial phenotypes with a semi-automated pipeline in adult zebrafish mutants. We first estimate a synthetic ‘normative’ zebrafish template using MicroCT scans from a sample pool of wild-type animals using the Advanced Normalization Tools (ANTs). We apply a computational anatomy (CA) approach to quantify the phenotype of zebrafish with disruptions in *bmp1a*, a gene implicated in later skeletal development and whose human ortholog when disrupted is associated with Osteogenesis Imperfecta. Compared to controls, the *bmp1a* fish have larger otoliths, larger normalized centroid sizes, and exhibit shape differences concentrated around the opercular, anterior frontal, and posterior parietal bones. Moreover, *bmp1a* fish differ in the degree of asymmetry. Our CA approach offers a potential pipeline for high-throughput screening of complex fish craniofacial shape to discover novel phenotypes for which traditional landmarks are too sparse to detect. The current pipeline successfully identifies areas of variation in zebrafish mutants, which are an important model system for testing genome to phenotype relationships in the study of development, evolution, and human diseases.

This article has an associated First Person interview with the first author of the paper.

KEY WORDS: Cranial morphology, Osteogenesis imperfecta, Geometric morphometrics, Computational anatomy

INTRODUCTION

The fish craniofacial skeleton is a useful system for elucidating genetic and environmental contribution to phenotype in vertebrates. In the context of development, studies have focused on the genetic mechanisms that shape the cranial skeleton (Kimmel et al., 2020; Miller et al., 2007). Craniofacial analyses have been used to understand the pathways that have enabled morphological evolution

¹Center for Developmental Biology and Regenerative Medicine, Seattle Children's Research Institute, Seattle, WA 98101, USA. ²Pediatric Endocrinology Laboratories, University of Washington, Seattle, WA 98195, USA. ³Institute of Orthopaedics and Sports Medicine, University of Washington, Seattle, WA 98195, USA. ⁴Institute for Stem Cell and Regenerative Medicine, University of Washington, Seattle, WA 98109, USA. ⁵Division of Craniofacial Medicine, Department of Pediatrics, University of Washington, Seattle, WA 98105, USA.

*Author for correspondence (KellyMDiamond@gmail.com)

✉ K.M.D., 0000-0001-8639-6795; S.M.R., 0000-0001-9514-7774; A.M.M., 0000-0002-7921-9018

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Diamond, K. M., Rolfe, S. M., Kwon, R. Y., & Maga, A. M. (2022). Computational anatomy and geometric shape analysis enables analysis of complex craniofacial phenotypes in zebrafish. *Biology Open*, 11(2), bio058948. <https://doi.org/10.1242/bio.058948>

bioRxiv posts many COVID19-related papers. A reminder: they have not been formally peer-reviewed and should not guide health-related behavior or be reported in the press as conclusive.

New Results

Follow this preprint

Automated Landmarking via Multiple Templates

Chi Zhang, Arthur Porto, Sara Rolfe, Altan Kocatulum, A. Murat Maga

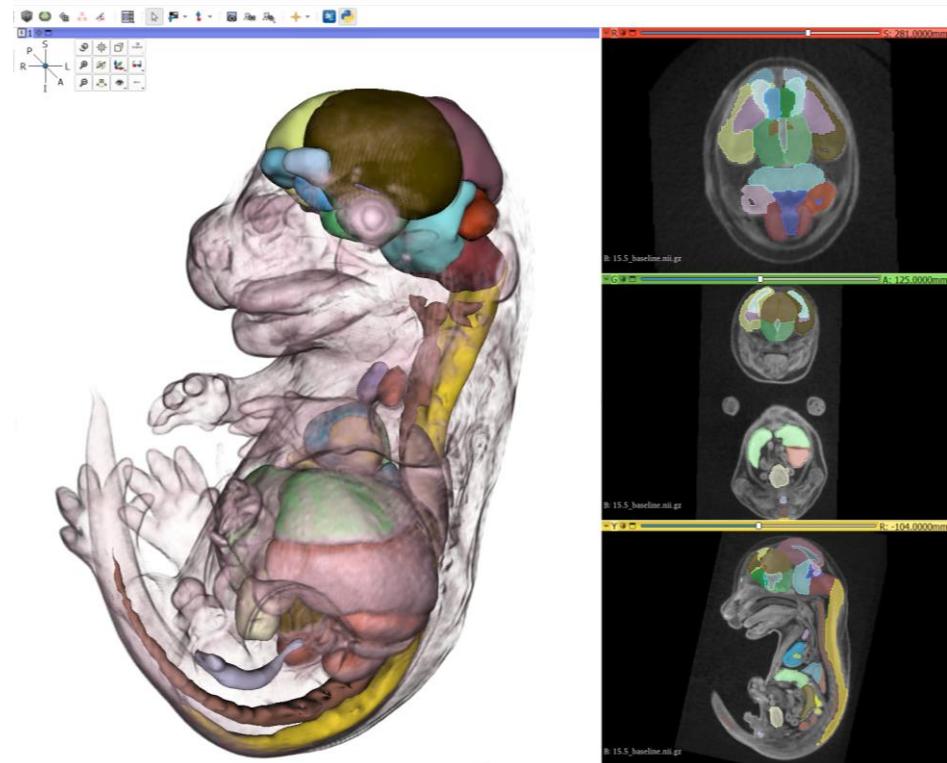
doi: <https://doi.org/10.1101/2022.01.04.474967>

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



Abstract

Geometric morphometrics based on landmark data has been increasingly used in biomedical and biological research for quantifying complex phenotypes. However, manual landmarking can be laborious and subject to intra and interobserver errors. This has motivated the development of automated landmarking methods. We have recently introduced ALPACA (Automated Landmarking through Point Cloud Alignment and Correspondence), a fast method to automatically annotate landmarks via the use of a landmark template as a part of the SlicerMorph toolkit. Yet, using a single template may not consistently perform well for large study samples, especially when the sample consists of specimens with highly variable morphology, as it is common in evolutionary studies. In this study, we introduce a variation on our ALPACA pipeline that supports multiple specimen templates, which we call MALPACA. We show that MALPACA outperforms ALPACA consistently by testing on two different datasets. We also introduce a method of choosing the templates that can be used in conjunction with MALPACA, when no prior information is available. This K-means method uses an approximation of the total morphological variation in the dataset to suggest samples within the population to be used as landmark templates. While we advise investigators to pay careful attention to the template selection process in any of the template-based automated landmarking approaches, our analyses show that the introduced K-means based method of templates selection is better than randomly choosing the templates. In summary, MALPACA can accommodate larger morphological disparity commonly found in evolutionary studies with performance comparable to human observer.



Rolfe S., and Maga AM. Deep Learning Based Fetal Mouse Segmentation. (Work in Progress)

Zhang, C., Porto, A., Rolfe, S., Kocatulum, A., & Maga, A. M. (2022, January 25). *Automated Landmarking via Multiple Templates* (p. 2022.01.04.474967). p. 2022.01.04.474967. bioRxiv. <https://doi.org/10.1101/2022.01.04.474967> (in review at Plos One)

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



...to grow the ecosystem!

How to use

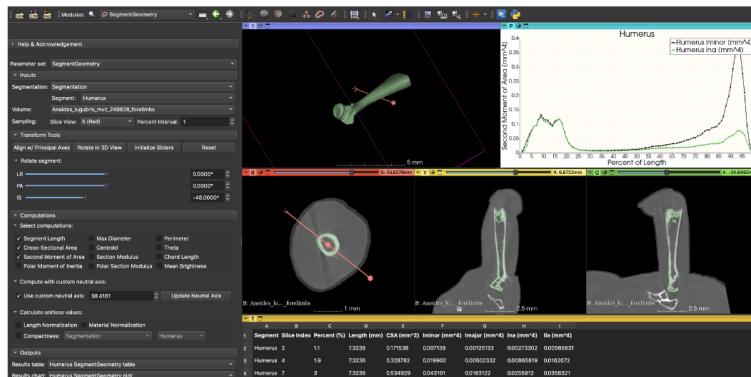
SegmentGeometry	bug	11 days ago
.gitignore	small bugs	2 months ago
CMakeLists.txt	Update CMakeLists.txt	2 months ago
LICENSE.md	add license	9 months ago
README.md	small bugs	2 months ago
SegmentGeometry.png	add white background	8 months ago
SegmentGeometry.s4ext	master to main	8 months ago

README.md

SegmentGeometry

This is the repository for SegmentGeometry, an extension for [3D Slicer](#).

SegmentGeometry iterates slice-by-slice through a segment to calculate the second moment of area and other cross-sectional properties. Results are exported to a table and plotted for quick visualizations.



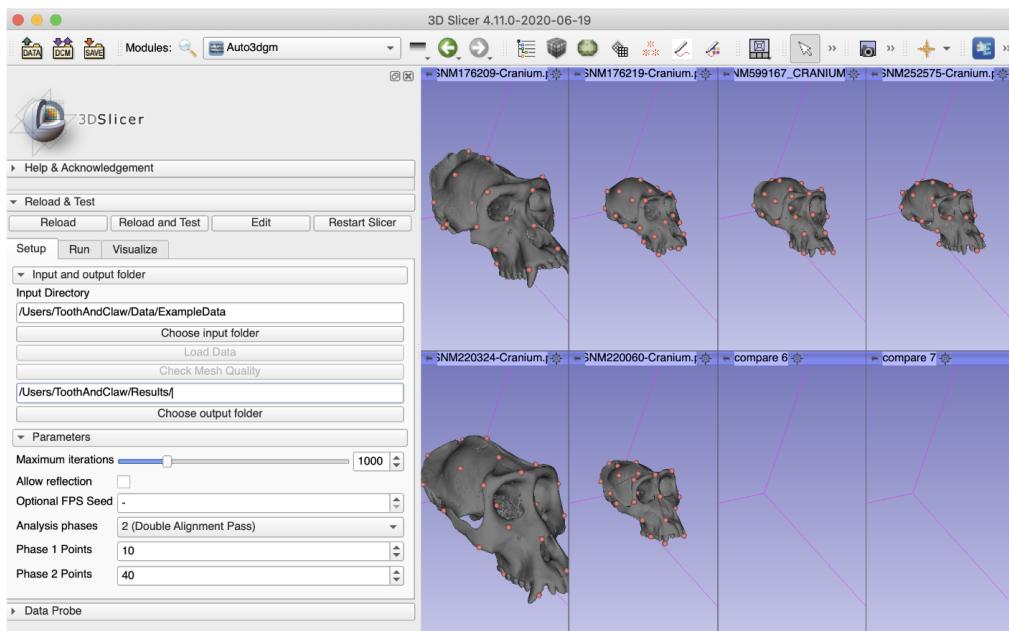
Huie, J. M., Summers, A. P., & Kawano, S. M. (2022). **SegmentGeometry: A Tool for Measuring Second Moment of Area in 3D Slicer**. *Integrative Organismal Biology*, 4(1), obac009. <https://doi.org/10.1093/iob/obac009>

<https://github.com/jmhuie/Slicer-SegmentGeometry>

1. Auto3dgm UI in Slicer

The auto3dgm UI consists of three components:

- **setup**: load data and specify parameters used in the auto3dgm algorithm
- **run**: subsample and align the data
- **visualize**: the aligned data in a pop-up window



Gao, T., et al . (2018). **Development and Assessment of Fully Automated and Globally Transitive Geometric Morphometric Methods, With Application to a Biological Comparative Dataset With High Interspecific Variation**. *The Anatomical Record*, 301(4), 636–658.

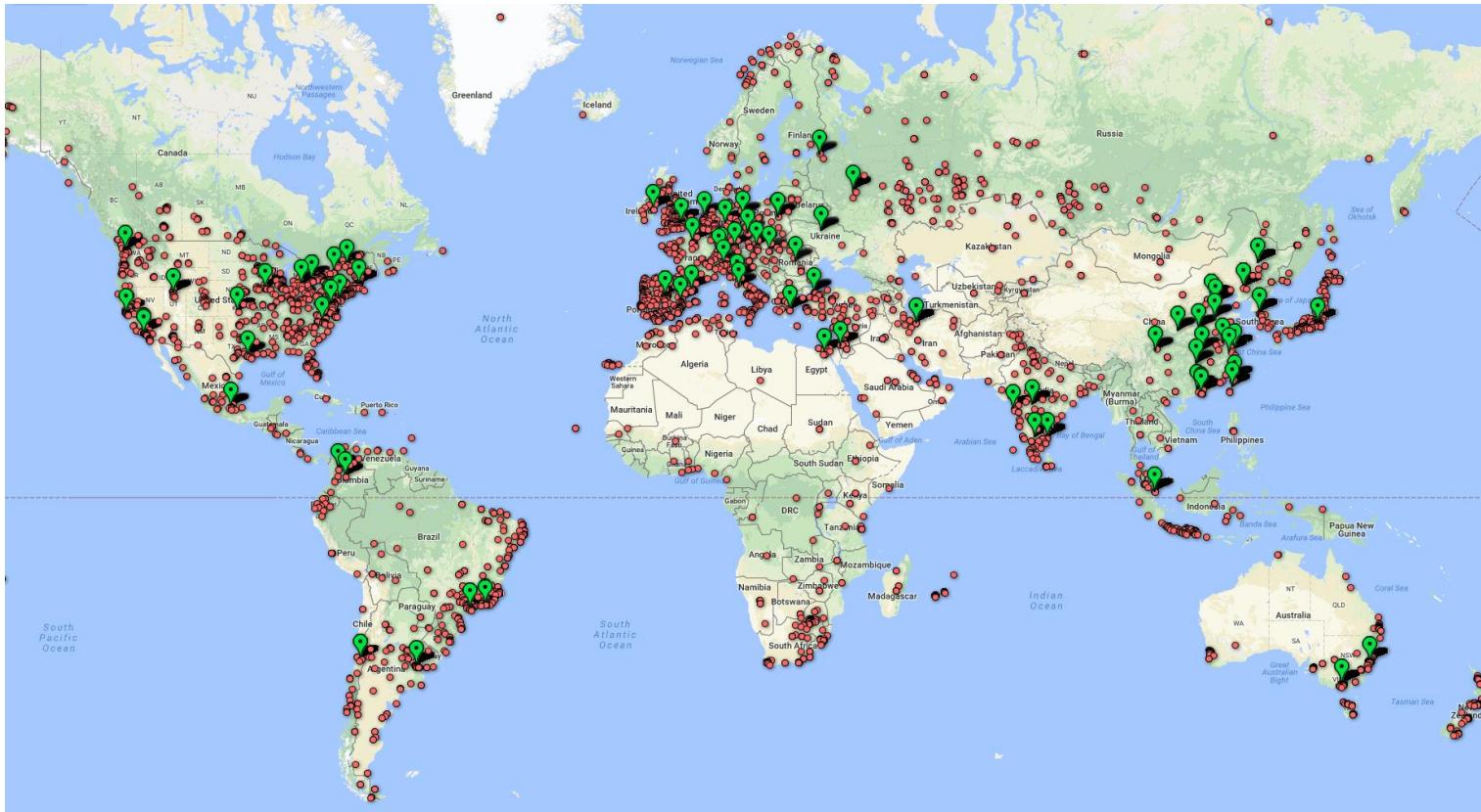
<https://github.com/ToothAndClaw/SlicerAuto3dgm>

Why 3D Slicer? Large existing user community

500 downloads per week in 2012

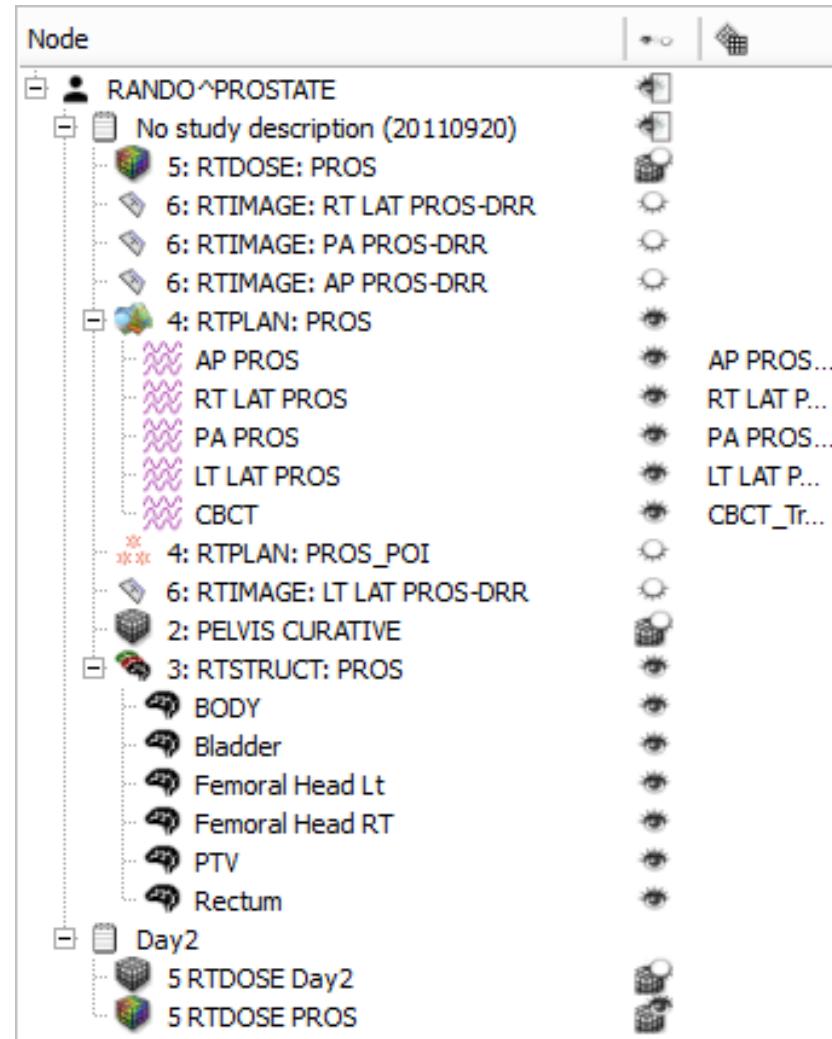
2800 downloads per week in 2018

330 000+ downloads over the past 5 years:



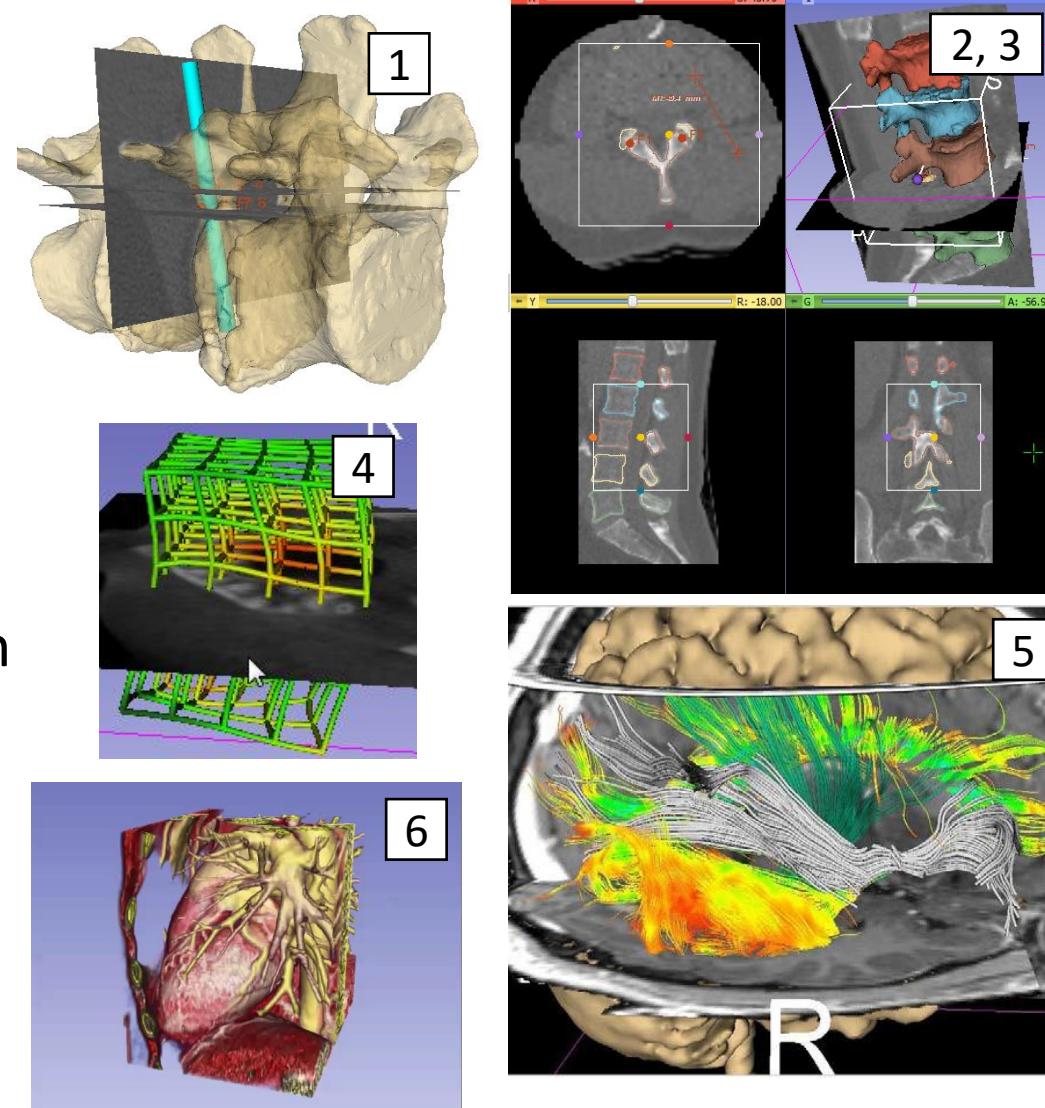
Data import/export

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



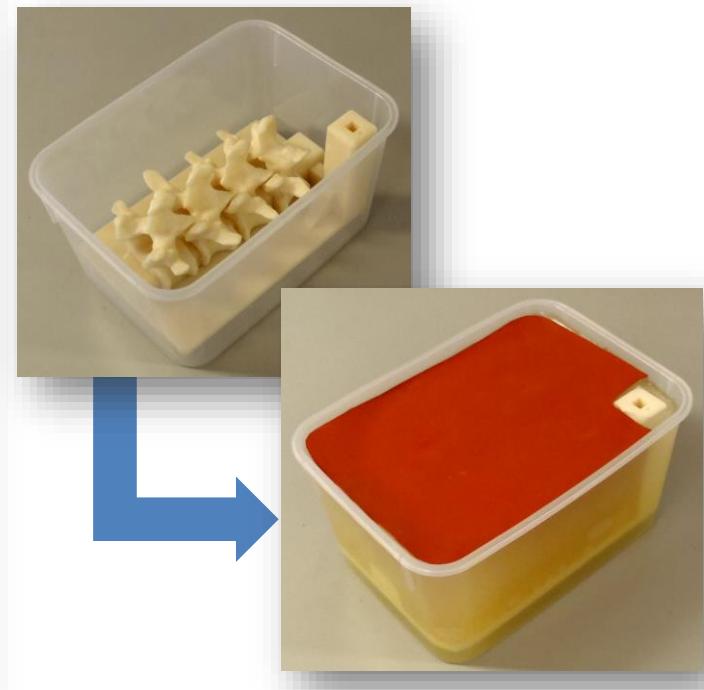
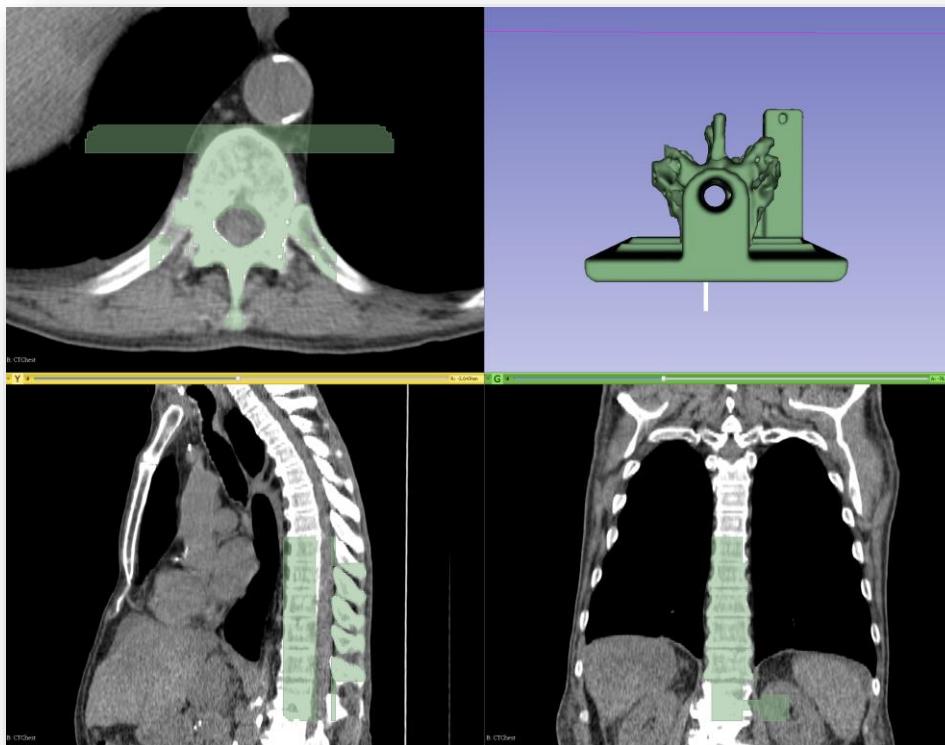
Extensive Visualization Capabilities

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

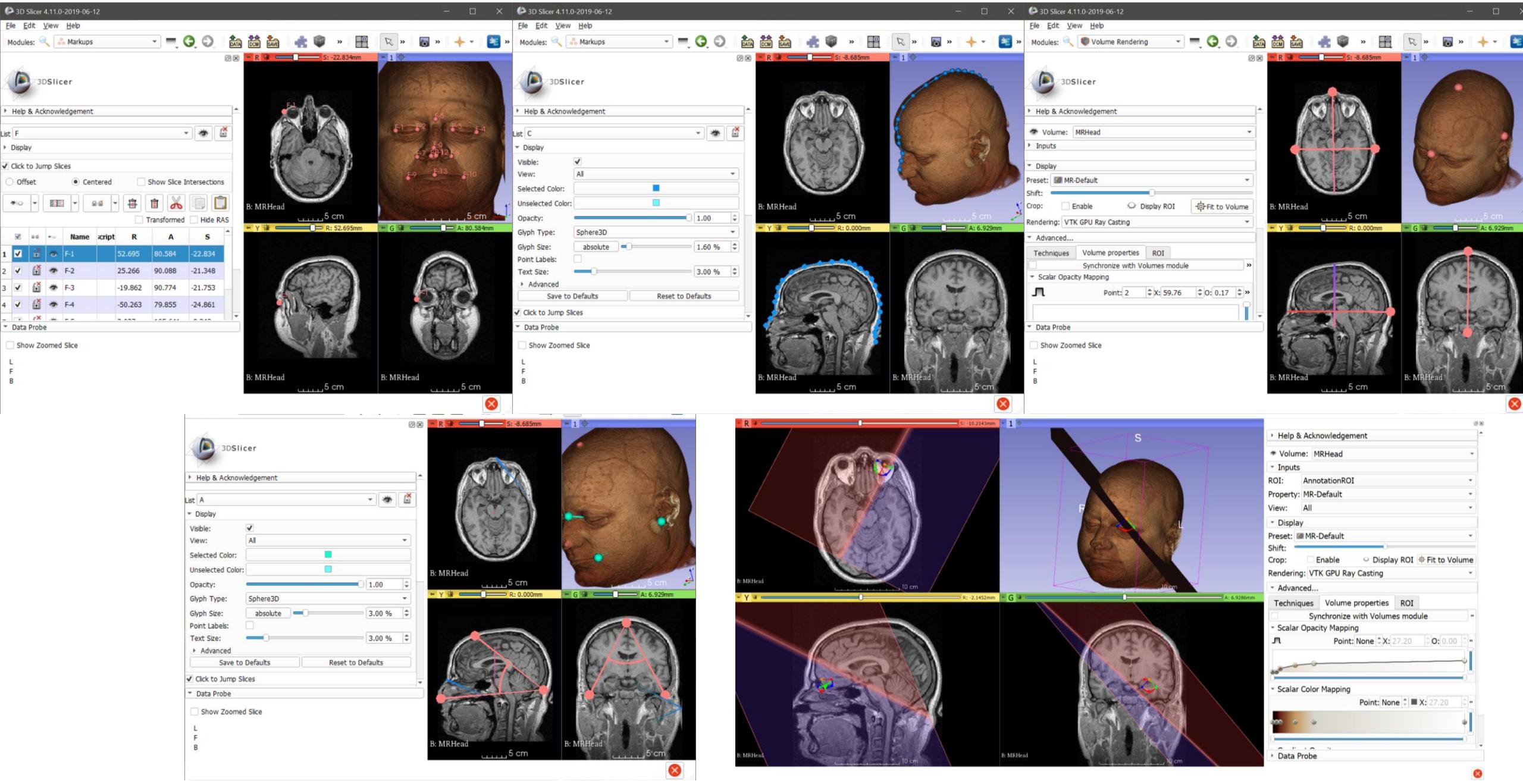


Segmentation

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



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



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

3D Slicer 4.11.0-2019-06-12

File Edit View Help

Modules: Tables

Python Interactor

```
>>> import numpy as np
>>> np.random.seed(12345678)
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> rvs2 = stats.norm.rvs(loc=50,scale=10,size=500)
>>> stats.ttest_ind(rvs1,rvs2)
Ttest_indResult(statistic=-70.40786227894476, pvalue=0.0)
```

3DSlicer

Help & Acknowledgement

pcScores

Edit

A	B	C	D	E	F	G	
1	ID	PC1	PC2	PC3	Group	Age	Sex
2	A20	0.017188	-0.00738102	-0.00408433	Sufficient	60	M
3	A24	0.0244969	0.00919364	-0.0171897	Sufficient	60	M
4	A26	0.0138739	-0.0223299	-0.00882724	Sufficient	60	M
5	A30	0.0189455	-0.00480663	-0.0120918	Sufficient	60	M
6	A33	0.00837771	-0.0139178	0.00668173	Sufficient	60	F
7	A35	0.0239435	-0.0135404	-0.0223772	Sufficient	60	M
8	A47	-0.0064179	-0.0223071	-0.0191055	Sufficient	60	F

Column properties

Name: PC1, PC2

Data type: double

Null value:

Long name:

Description:

Unit label:

New column defaults

Data Probe

Red (L 269.3, A 288.8, S 0.0) Axial Sp: 1.0

L None
F None
B None

10 cm

3D Slicer 4.11.0-2020-06-12

File Edit View Help

Modules: MorphoSourceImport

Help & Acknowledgement

Reload & Test

Reload Reload and Test Edit Restart Slicer

MorphSource Username: SlicerMorph@gmail.com

MorphSource Password:

Log in

Query parameters

Query order: Carnivora

Query element: skull

Submit query

Query results:

order	genus	species	filetype	filesize	element	ownload_linnidia_file_ispecie
Carnivora	Hesperocyon	gregarius	stl	92.42MiB	skull	http://... 5827 2002
Carnivora	Hesperocyon	gregarius	stl	92.42MiB	skull	http://... 5827 2002
Carnivora	Dinictis	squalidens	stl	32.08MiB	skull	http://... 5829 2004
Carnivora	Hesperocyon	gregarius	stl	92.42MiB	skull	http://... 5827 2002

Open specimen page
Load selected models

Data Probe

Search here

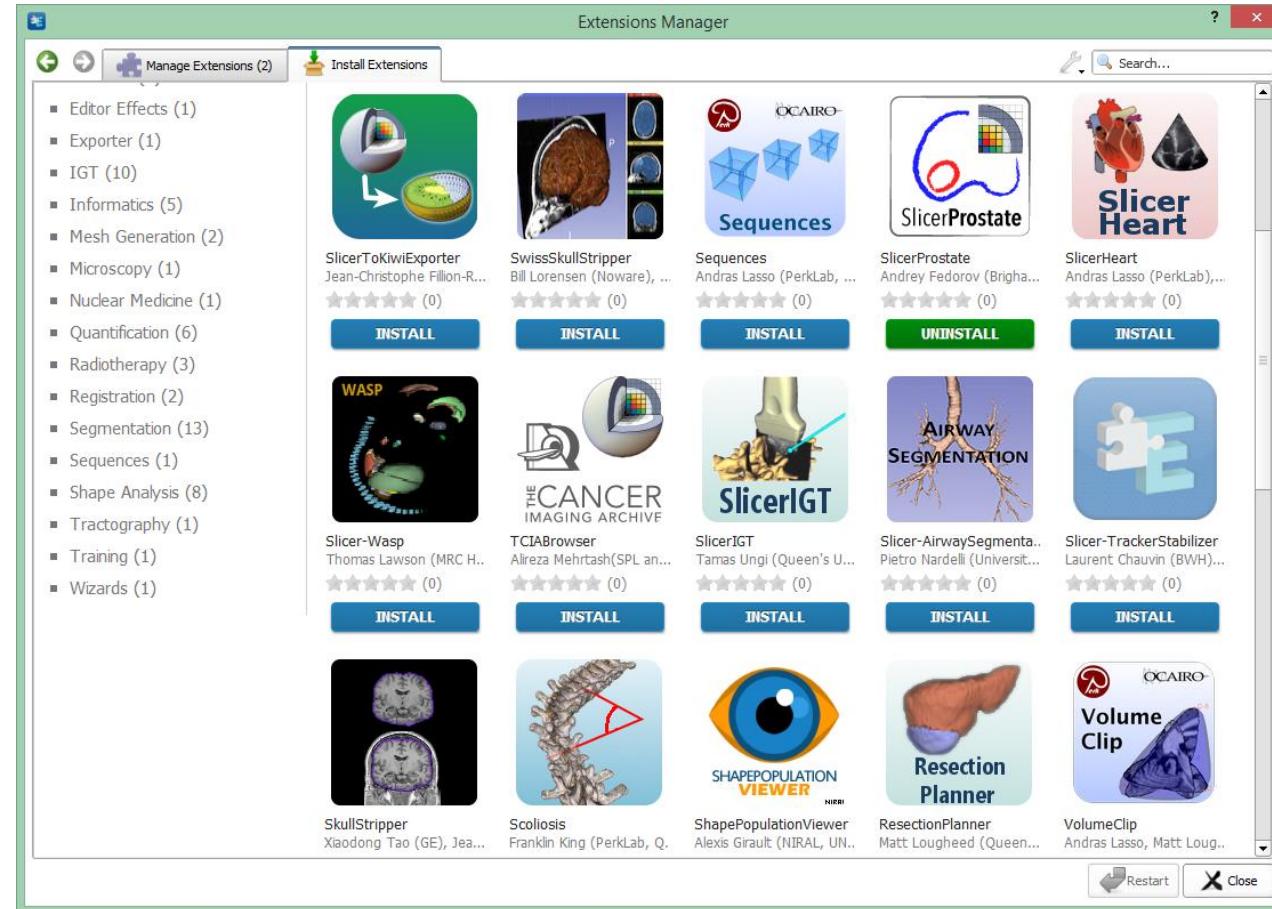
10 cm

5 cm

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

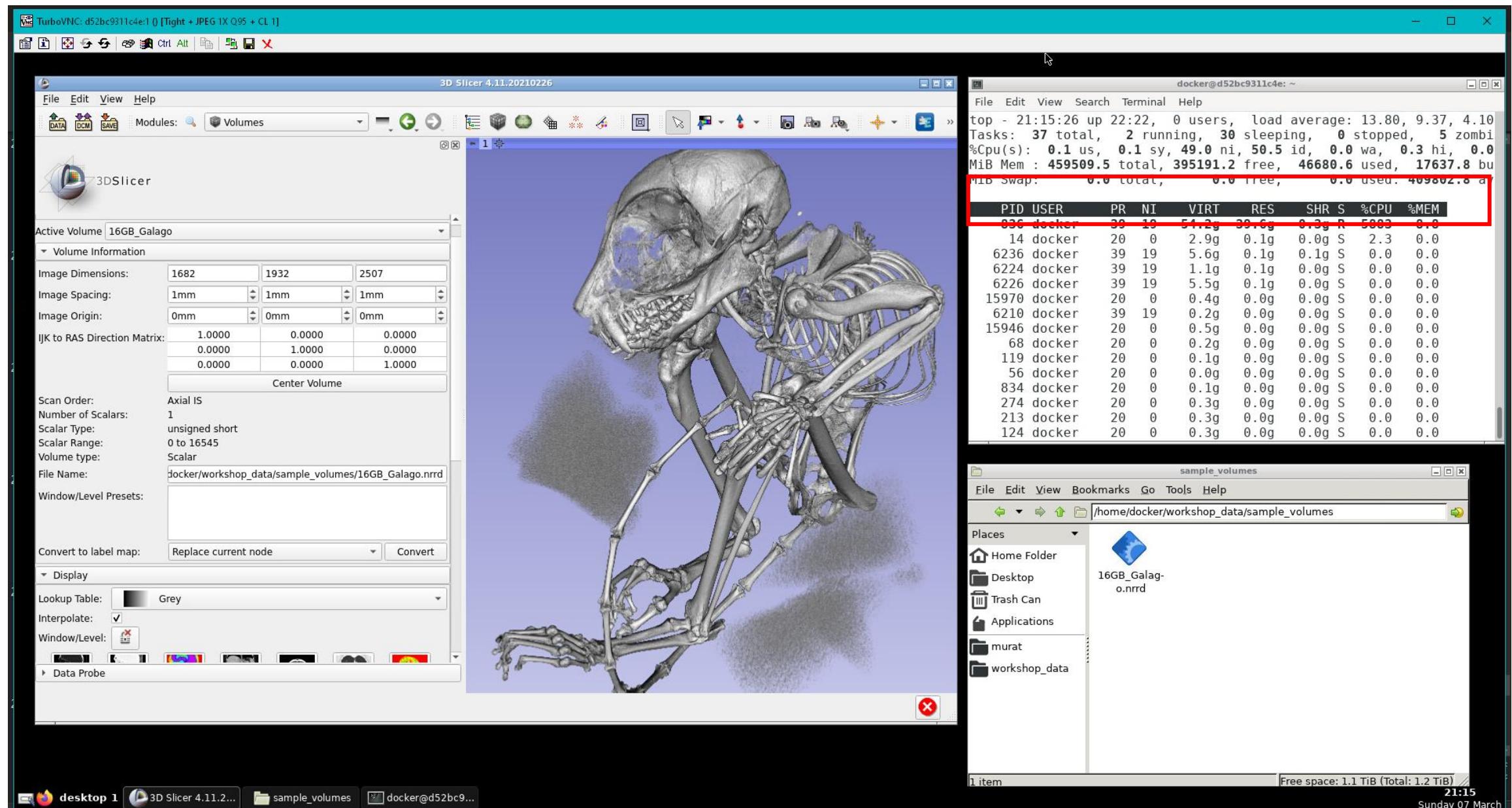


The Slicer Extension Manager offers the possibility to the user to download and install additional Slicer modules

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 how we managed to build SlicerMorph so quickly. If you need something additional, consider [hiring an independent developer](#), then share the result with the community. **PIs: This may cost less than single academic license of VG Studio Max, Avizo or Analyze.**

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



Each SlicerMorphCloud instance has 500GB of RAM, and 64 cores and supports 10-12 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

Core SlicerMorph Team

Sara Rolfe (UW/SCRI, Lead Developer)

Steve Pieper (Chief Software Architect of 3D Slicer)

Kelly Diamond (SCRI, Postdoc)

Chi Zhang (SCRI, Postdoc)

Arthur Porto (now LSU, former post-doc)

SlicerMorph Contributors

Andras Lasso (Queens U, Core Slicer Developer)

Slicer Developer Community

Doug Boyer (Duke University)

Adam Summers (UW FHL)

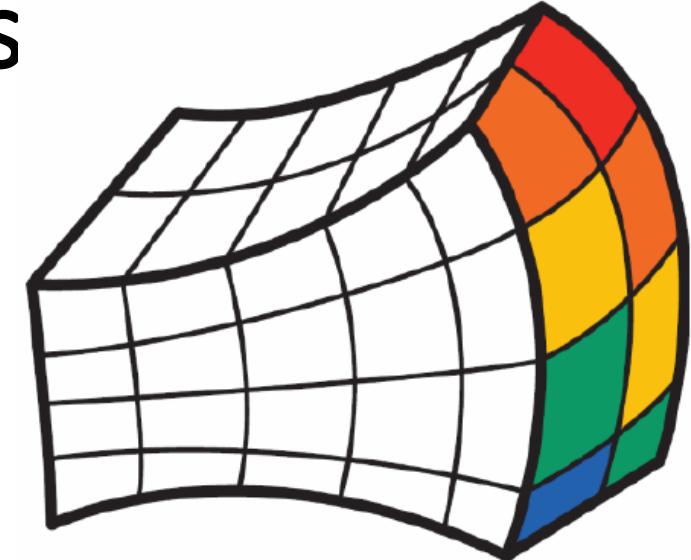
SlicerMorph Advisory Board

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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