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Review Article / *Derleme Makalesi*

Digital Morphology: The Final Frontier

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ABSTRACT

Morphology is central to biological anthropology and its allied fields of anatomical sciences, forensics, and other related disciplines. Many biological anthropology students have their first real foray into the discipline after completing a course in osteology, craniometry, or vertebrate morphology. Unfortunately, the natural history collections that support this type of research and training have not grown. Many countries have strict rules about natural history specimen collections, and these collections seem to be concentrated in a few developed countries, regardless of where the specimens had been collected. Thus, access to comparative material can be problematic where such collections are not readily available. Even if collections are available, accessing them can be severely restricted due to external circumstances, as the prolonged pandemic has shown. Luckily, digital morphology has emerged over the last decade as a new field that stands to change the landscape of specimen-based research and training. Concerted 2D and 3D digitization efforts, the emergence of online aggregate specimen repositories, and availability of comprehensive open-source software tools (such as 3D Slicer) for utilizing these resources has conveniently transformed the field of quantitative and comparative morphology. In this brief review, I will focus explicitly on the 3D Slicer ecosystem and how it can be leveraged as part of a curriculum or research program on digital morphology. In a nutshell, the primary differentiator of the 3D Slicer is not that it is just free but that it is open-source and extensible, making access to digital data more equitable for everyone. I will particularly focus on the 3D Slicer's SlicerMorph extension, which facilitates 3D geometric morphometric data collection and analysis within the Slicer ecosystem, so all the steps in the digital morphology workflow from import, visualization, and data collection to visualizing the morpho-space can be achieved in a single, well-documented environment.

Keywords: Digital morphology, Quantitative morphology, Geometric morphometrics, 3D imaging, Segmentation, Visualization

Introduction

Morphology is the study of forms, with morphology in life sciences in particular being the study of the form of whole organisms and their components. As a fundamental topic within the life sciences, the goal of morphological studies can range from understanding the functional significance of a structure to quantitatively assessing natural variations in form when comparing species. This latter topic is called quantitative morphology, and its application in organismal biology (including that of humans and their extinct and extant relatives) is the focus of this review.

At the most basic level, quantitative morphology involves length, cross-sectional, surface area, volume, and mass measurements. These measurements can then be used as input for statistically analyzing variances for comparative purposes. Traditionally, these data came from measuring actual specimens of the same (or closely related) species that had been housed and curated in natural history museums. This task itself can be challenging in countries where such collections are limited or even absent, sometimes because a culture of collecting and housing specimens had never existed there. Even when collections are available, access to these specimens may not be possible, as demonstrated recently by the COVID-19 pandemic lockdowns. Even in the best of times, access might be restricted due to how many visiting researchers can be accommodated at the same time or to limits on shipping samples.

Since before the pandemic even, various natural history museums and universities in the USA and EU have been actively working on digitizing their biological collections. Typically, the goals of these projects are to (1) make the biological and paleontological specimen information readily available online and (2) preserve them for perpetuity in digital form through advanced imaging techniques, such as non-invasive 3D scanning techniques including computerized tomography (CT) or other techniques such as stereophotogrammetry (e.g., 3D model reconstruction from a series of 2D pictures taken from different poses or orientations). While the initial results of these digitization efforts have been distributed by the individual institutions, a number of digital specimen repositories have also emerged that aggregate the data from these different museums and collections. At the moment of writing, the largest of these repositories for biological specimens is MorphoSource (Boyer et al., 2016), but a number of other repositories with different specialties also exist. In medical and forensic sciences, similar data collection and aggregation efforts have also occurred, perhaps the most notable of these efforts for biological and forensic anthropologists being the New Mexico Decedent Image Database (USA) that provides whole-body CT scans of over 15,000 New Mexicans who died between 2010-2017 (Berry & Edgar, 2021). Table 1 lists some of these larger biological and medical 3D scan repositories as well as the types of datasets they offer. The Digital Morphology Museum of Kyoto is also noteworthy due to the large number of volumetric scans of non-human primates, mostly from the Kyoto Zoo.

Table 1. Various repositories containing 3D datasets of natural history specimens, including humans and primates

Repository	URL	Available data and types
MorphoSource	https://www.morphosource.org/	MorphoSource is a project-based data archive with over 50,000+ physical objects that allows researchers to store, organize, share, and distribute their own 3D data.
New Mexico Decedent Image Database	https://nmdid.unm.edu/	Provides researchers with access to whole human body computed tomography (CT) scans of cadavers and a wide range of associated metadata.
DigiMorph	http://www.digimorph.org/	High-resolution X-ray computed tomography of (mostly holotype) biological specimens.
FaceBase	https://www.facebase.org/	Comprehensive craniofacial data from model organisms (mouse and zebrafish) and humans (3D facial scans).
Digital Morphology Museum of Kyoto University	http://dmm.ehub.kyoto-u.ac.jp/	DMM provides a large collection of volumetric scans (CT and MRI) of various extant primates.
Phenome10K	http://phenome10k.org/	A free online repository for 3D models of biological and paleontological specimens.
Genetics of craniofacial shape in *Mus*	https://osf.io/w4wvg/	High-resolution 3D micro-CT head scans of a mouse panel between C57BL/6J and A/J mouse strains and associated genotype data. Contains micro-CT scans of ~500 mouse heads and associated cranial landmarks.
The Open Research Scan Archive	https://www.penn.museum/sites/orsa/	Penn Cranial CT Database) contains high resolution (sub-millimeter) scans of human and non-human crania from the University of Pennsylvania Museum of Archeology and Anthropology (Penn Museum) and other institutions.
MorphoMuseuM (M3)	http://morphomuseum.com/	MMM is an online peer-reviewed journal that publishes 3D models of vertebrates, including models of type specimens, anatomy atlases, reconstructions of deformed/damaged specimens, and 3D datasets.
International Mouse Phenotyping Consortium	https://mousephenotype.org	Thousands of contrast-enhanced 3D micro-CT scans of mouse fetuses derived from knockout lines and wildtypes at different developmental stages (E15.5 and E18.5).

Clearly the existence of these resources is extremely beneficial for researchers doing specimen-based research and they are particularly important for researchers who have limited access to comparative materials. But it is also equally important to be able to interact and process these datasets, otherwise their existence is of limited utility to the scientific community.

The Logistics of Using 3D Digital Specimens for Research and Education

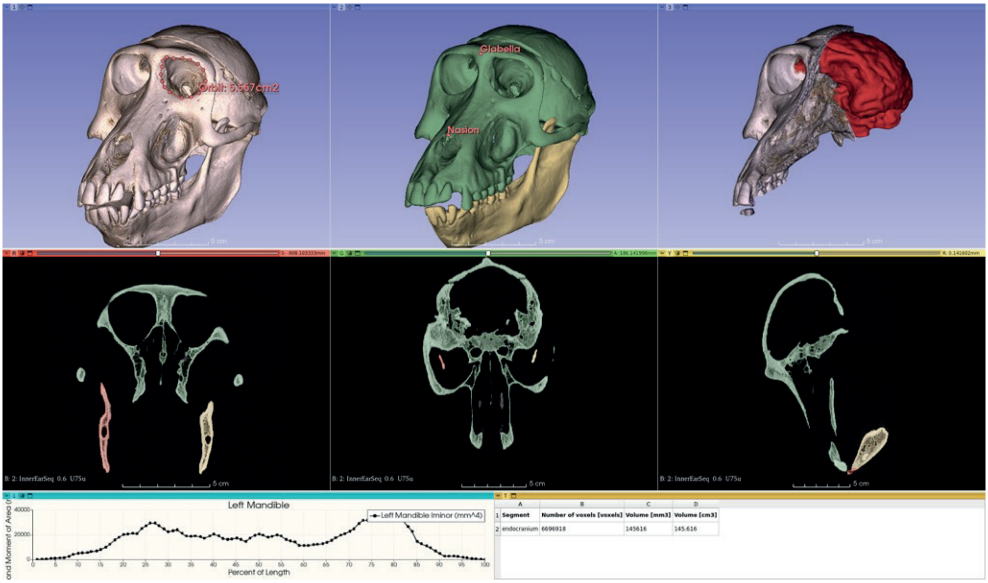
Several commercial 3D biomedical visualization packages are available for biologists and anthropologists to use. While these packages are capable, they are often also very expensive. But perhaps more importantly, they all tend to use proprietary data formats that cannot be opened by other applications, or converting the data for use by other applications for analysis that are not available within that package is not easy because the format is poorly documented. This is a significant concern in situations where a group needs to collaborate, or in cases where an instructor is incorporating digital morphology as part of an academic curriculum where the cost of a large number of required software licenses would be prohibitive.

A number of free open-source 3D visualization and image processing software programs are found, including ImageJ (image processing), Drishti (3D rendering), and ITK-Snap (segmentation). A fourth program, 3D Slicer, is a comprehensive, open-source 3D-image processing and visualization software that has been in development for over 20 years and now offers the functionality of the other three aforementioned programs in addition to others, all within one single application (Fedorov et al., 2012; Kikinis et al., 2014). 3D Slicer will be focus of this review, but first a brief review of the steps involved in working with digital specimens is needed.

In broad terms, digital morphology workflow includes four steps: data import, visualization, segmentation, and quantification (including measurements). Importing raw data tends to involve sequences of 2D images in various file formats such as DICOM, TIFF, or others and correctly defining certain attributes of the dataset such as image resolution, data type, and coordinate system is critical for being able to quantitatively analyze the resultant data (Table 2). Visualization involves converting the discrete pixels stored in the images into continuous 3D surfaces using different visualization algorithms so that the user can interact with the virtual object in 3D. Segmentation involves defining distinct values for structures of interest (e.g., individual ribs, vertebrae, sternum, and other structures constituting the thorax) within the dataset so that these can be visually distinguished from one another, often by assigning different colors to different indices. Segmentation also allows distinct structures to be extracted as independent objects, from which either physical 3D models can be printed, or quantitative data such as physical volumes, surface areas, or cross-sectional properties can also be extracted. Additionally, this step can be supplemented by collecting measurements such as lengths, angles, and 3D coordinates of specific anatomical structures, sometimes referred to as landmarks. Importance is also had in noting that 3D Slicer is a comprehensive software program that allows all these steps to be completed within a single platform (Figure 1).

Table 2. Some common data formats and descriptions associated with 3D digital specimens

Format	Description
DICOM	Digital Imaging and Communications in Medicine is the standard for the communication and management of medical imaging information and related data. It is the standard output from commercial medical scanners. As a metadata rich format, it provides all image spacing and coordinate system information necessary to correctly construct virtual anatomical representations. Some research scanners do not necessarily comply with the standard and may produce invalid DICOM sequences that may require further tweaking.
TIFF PNG JPG BMP	These 2D image formats are used to save to individual slices of a volumetric image sequence similar to DICOM sequences. While they can comprise the common output from some research micro-CT scanners and 3D microscopes, they lack the standard DICOM metadata tags for describing important aspects of the imaging data to correctly construct the virtual representation. Therefore, such image metadata should be retained external to the imaging data (e.g., text file), thus making data management more difficult. These formats should not be used to represent volumetric 3D imaging data or should be immediately exported as NRRD.
NRRD	Nearly Raw Raster Data is a library and file format for the representation and processing of n-dimensional raster (bitmap) data. It is a flexible and open data format that supports multiple data types and data encodings. It contains a human readable header that contains image metadata, with users able to add their own tags to the header. NRRD is the default format for 3D Slicer and can be read by many other open-source imaging software such as ImageJ, ITK-Snap, Drishti, and others.
NIFTI	The Neuroimaging Informatics Technology Initiative (NIfTI) is an open file format commonly used to store brain imaging data obtained using magnetic resonance imaging (MRI) methods. NIFTI has limited applications beyond neuroimaging.
STL	Stereolithography is a file format commonly used for 3D printing and computer-aided design (CAD). While common for 3D printing, the format has certain deficiencies such as lack of explicit unit description, making it ill-suited or problematic for representing anatomy. PLY or OBJ are more suitable alternatives.
OBJ	OBJ is a geometry definition file format. The file format is open-sourced and has been adopted by other 3D graphics application vendors, including 3D Slicer.
PLY	Polygon File Format was principally designed to store three-dimensional data from 3D surface scanners. The data storage format supports a relatively simple description of a single object as a list of nominally flat polygons. A variety of properties such as surface normals and texture coordinates containing color and transparency values can be stored.



	A	B	C	D
1	Segment	Number of voxels [voxels]	Volume [mm3]	Volume [cm3]
2	endocranium	6696918	145616	145.616

Figure 1. A Slicer scene showing the functionalities of the application. **(A)** Volume rendering (ray casting) of a baboon [*Papio anubis*] skull CT. The area of the orbital aperture is calculated by drawing a closed curve markup. **(B)** Result of the segmentation of the same dataset in a cranium and two hemi-mandibles (the right hemi-mandible is hidden). **(C)** Same volume rendering of the cranium as in A, only with a clipped volume rendering that shows the endocranial space and nasal passages. The endocast is automatically generated using the **Segment Endocranium** module of SlicerMorph. Cross sectional views of the baboon scan in **(D)** frontal, **(E)** transverse, and **(F)** sagittal planes, with the segments in **B** overlaid in color. Users can navigate through the slices of each plane using the slider above the slice views. **(G)** Second moment of area (moment of inertia) of the left hemi-mandible is plotted as a function of the mandible's length. Cross-sections are calculated in the **SegmentGeometry** extension using the orientation in **D**. **(H)** The volume of the endocast **C** is reported in terms of number of voxels as well as mm^3 or cm^3 units using the **Segment Statistics** module. The baboon dataset was obtained from the publicly available DICOM dataset found in the MorphoSource repository available from: https://www.morphosource.org/concern/parent/000S11331/media/000045065. This specimen is part of a larger collection of baboons housed at the Southwest National Primate Research Center (Texas, USA). The digital collection features 933 scans and is an excellent resource for studying the genetics of skull shape because the pedigrees of all specimens are known.

3D Slicer (hereafter referred to as Slicer) is an open-source biomedical visualization and image analysis software initially developed by members of neuroimaging and surgical planning communities with the goal of facilitating collaboration (Fedorov et al., 2012; Kikinis et al., 2014) and has been in continuous development for over 20 years. The initial goal was to offer a free, feature-rich, open, and expandable program for visualizing data across projects consisting of multiple investigator teams and a mix of operating systems. Throughout the years though, Slicer has grown into a mature ecosystem of tools, plugins, and custom software (e.g., SlicerSALT) that are able to handle all the tasks associated with 3D image analysis as well as support a large number of 3D data formats (Table 2). Slicer's core functionality provides a complete solution for 3D visualization, linear and nonlinear spatial transforms (registration), manual and semi-automatic segmentation tools, 3D landmark (point lists) and other measurement digitization, multiple image processing and enhancement filters that are specifically 3D in nature, data-type conversion (e.g., from 3D models to segmentations), plotting, and tabular data representation (Figure 1). A built-in Python3 environment provides access to common analysis libraries used in scientific computing such as NumPy and SciPy. Functionality that is unavailable in the core application can be developed through an extension mechanism. Additionally, most Python3 libraries from the PyPi repository can be installed into the integrated Python environment using the standard pip utility. As of this writing, the combined downloads of the previous and current stable versions since November 2018 have exceeded 1,112,000 worldwide, and over 10,000 publications are indexed in Google scholar that cite 3D Slicer. Slicer has also been adapted to a wide range of use cases, such as the substantial SlicerAstro effort (Punzo et al., 2017). Thus, Slicer has a vibrant ecosystem, thanks in particular to its extensible code base and its reliance on proven open-source libraries such as Visualization Toolkit (VTK) and Insight Toolkit (ITK), an active global developer community. The Slicer community of users are supported through an active forum that includes over 4,500 subscribers averaging 275 posts a week. These community activities are further supplemented by semi-annual Project Weeks that have been running for over 15 years. Project weeks are hackathons aimed at bringing the Slicer community together to develop new functionalities that will benefit everyone (Kapur et al., 2016).

The Slicer community maintains an app store for Slicer extensions and currently has over 150. These extensions provide domain-specific functionality so that users can customize Slicer to their needs without introducing a special case code into the core of Slicer that would complicate it for other users. The integrated Extension Manager provides a convenient search tool for finding extensions with relevant functionality for new use cases. Our group recently introduced the SlicerMorph extension to Slicer, which allows the retrieval, visualization, measurement, and annotation of high-resolution 3D specimen images both from volumetric scans (CTs and MRIs) as well as from surface scanners to be more effective within 3D Slicer(S. Rolfe, et al., 2021).

The Impact of Geometric Morphometric Methods on Digital Morphology

The last several decades have witnessed the application of quantitative approaches to characterizing form and shape that have also been integrated with the methods from evolutionary biology, genetics, and developmental biology. This approach has led to a flexible set of analytical tools for addressing a broad range of questions, whether the data be from experiments in model organisms or from natural populations of major taxonomic groups (Adams et al., 2013; Bookstein, 1997; Goodall, 1991; Kent & Mardia, 1997; Klingenberg, 2010; Mitteroecker & Gunz, 2009; Richtsmeier et al., 2002; Rohlf, 2000b; Rohlf & Slice, 1990). These analytical tools have been broadly classified as geometric morphometric methods (GMM) in which the shape of a structure is represented using the Euclidean coordinates of anatomical landmarks. To extract the shape information from the coordinates of these landmarks, the variations in size, position, and orientation are removed through a procedure called Procrustes superimposition (Figure 2). All the possible shapes for any given number of landmarks define the shape space: a multidimensional, nonlinear space in which each point represents a different shape, and from which the Procrustes-aligned shapes in a sample provide a local approximation (Kendall, 1984; Rohlf, 2000a).

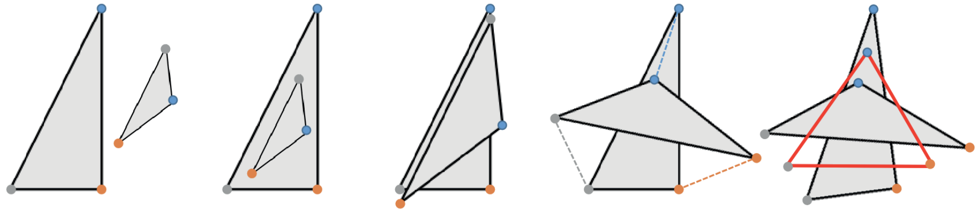
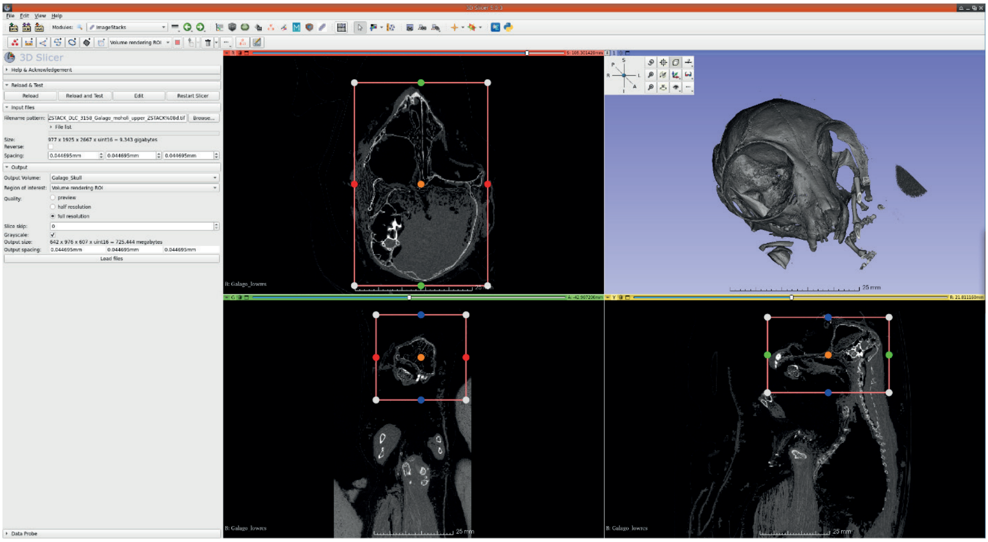


Figure 2. (A) Visualization of the steps in the Procrustes superimposition in 2D using two triangles. The color-coded vertices of the triangles represent corresponding structures. **(B)** Shape configurations are superimposed by aligning the centroid (average of coordinates). **(C)** Configurations are scaled to the same size (typically unit size). **(D)** One configuration is rotated to minimize the distance between the corresponding sets of landmarks. **(E)** A mean shape is estimated by averaging the rotated landmarks. Steps **D** and **E** are iterated until the final estimated mean shape does not appreciably change from the previous iteration.

Morphometric studies address specific biological questions by examining the variations in this shape space using the methods of multivariate statistical analysis, typically either through multivariate regression of the Procrustes coordinates onto explanatory variables (e.g., size, sex, age, and genotype) or by ordinating them in a multi-dimensional space using principal component analysis (PCA; Bookstein, 1989) These latent variables (e.g., principal component [PC] scores) provide convenient proxies for the underlying multi-dimensional morphological data and can be used to test questions regarding ecology (e.g., Do the trophic levels of the sample correspond to any axis of their morphological variation?), evolution (e.g., What are the patterns of variation in the cranial forms of the hominid lineage?), or developmental biology (e.g., Are there any correlations between the localized shape difference and the corresponding source of embryonic progenitors cells or morphogen gradients?). For readers who are new to the field of geometric morphometrics and would like to start learning, I would suggest *Geometric Morphometrics for Biologists: A Primer* by Zelditch (2012), an excellent introductory text with just enough mathematics to explain the concepts and theory behind statistical shape analysis that comes with a good workbook with examples of R computer code. A more mathematical treatment of the topic can be found in Dryden & Mardia's (2008) work. A number of reviews are also available on key concepts such as performing asymmetry analysis (Klingenberg, 2015), allometry (Klingenberg, 2016), modularity and integration using the GMM framework (Adams, 2016). Since being introduced in the 1980s, GMM has become widely adopted in morphology-driven studies, as shown by the consistent increase in the number of publications, from a handful of studies in the early 1990s to more than 2,500 studies in 2022, all largely thanks to the availability of free high-quality analysis software such as MorphoJ or the various R packages regarding statistical shape analyses (Adams & Otarola-Castillo, 2013; Klingenberg, 2011), as well as to the ease of collecting data from 2D digital pictures.

3D data pose their own unique set of challenges in collecting morphometric data. Unlike digital pictures that can be displayed in many applications, 3D datasets need to be processed similar to the workflow presented above so that a virtual 3D reconstruction of the sample can be constituted on the computer screen, after which the coordinates of the landmarks (or any other measurement) can then be collected. Historically, each of these steps had been completed using different programs. Because it is open-source and extensible, we have developed the SlicerMorph extension to fill the gaps in the Slicer ecosystem in order to have a complete workflow for digital morphology, from importing data to analysis. SlicerMorph provides functionality for importing non-DICOM image sequences (ImageStacks) while allowing it to downsample, change its ordering, or import only a section of the sequence (Figure 3).



Filename pattern: ZSTACK_DLC_3158_Galago_moholi_upper_ZSTACK%08d.tif

Size: 977 x 1925 x 2667 x uint16 = 9.343 gigabytes

Reverse: ☐

Spacing: 0.044695mm 0.044695mm 0.044695mm

Output Volume: Galago_Skull

Region of interest: Volume rendering ROI

Quality: ○ preview ○ half resolution ● full resolution

Slice skip: 0

Grayscale: ☑

Output size: 642 x 976 x 607 x uint16 = 725.444 megabytes

Output spacing: 0.044695mm 0.044695mm 0.044695mm

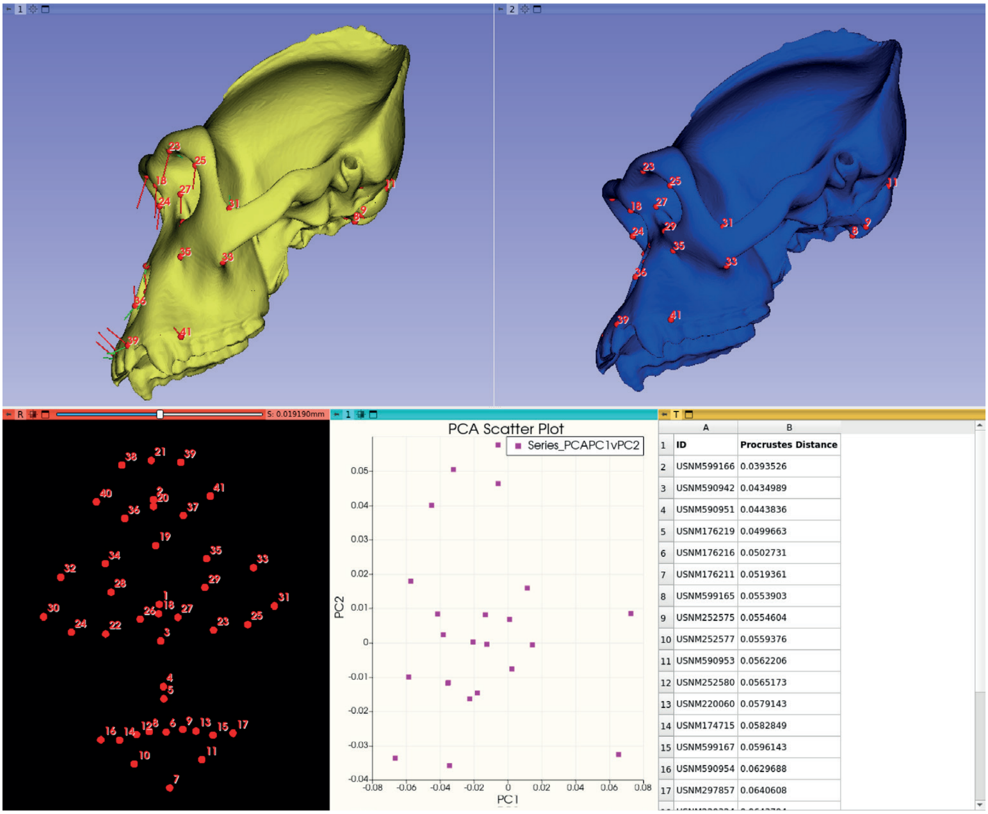
Figure 3. Screen capture of the SlicerMorph's ImageStacks module, which facilitates operations on non-DICOM image sequences. The sample data is a whole-body scan of the African strepsirrhini *Galago moholi* from the MorphoSource repository (https://www.morphosource.org/concern/biological_specimens/0000S4230). The **ImageStacks** module reports expected memory usage by the whole sequence at full resolution. Using this information, the user can decide whether to use the downsample (quality) setting or to import a section of the image (in this case, the cranium). In this case, the whole dataset at full resolution will be 9.34 GB in size. The screenshot shows a preview version of the dataset that was loaded into Slicer, which was only 150MB. A region of interest regarding the specimen's cranium is specified and then re-imported into Slicer at full resolution (only 725MB). Users are expected to save the imported data as a Nearly Raw Raster Data (NRRD) volume to avoid having to import the dataset multiple times.

In Slicer's most-recent stable version (5.0.3), the SlicerMorph team reworked the Markups functionality (Slicer's measurement tools) to allow for generating landmark templates (e.g., standard sets of craniometric landmarks for human skulls) to facilitate data collection with less room for error in the data collection process. In addition to standard landmarks (i.e., point lists), length, and angle measurements, SlicerMorph also allows for many other common morphometric digitization techniques such as generating curve-based semi-landmarks, patch-based surface landmarks, and dense pseudo-landmarks. Table 3 provides a summary of the current modules within the SlicerMorph extension.

Table 3. Description of some of the variables and procedures associated with shape analysis

Variable	Procedure
Procrustes superimposition	The procedure through which variations in size, position, and orientation in landmark configurations are removed (Figure 2). It is an iterative procedure in which the difference between configurations is minimized using the least-squares optimization technique.
Procrustes Coordinates	New sets of coordinates obtained after landmark configurations are then subjected to Procrustes superimposition.
Mean shape	The average of the individual landmarks in landmark configurations after superimposition
Procrustes Residuals	Description of how each individual landmark configuration is different from the mean shape. Calculated by subtracting the mean shape's coordinates from a landmark configuration's Procrustes coordinates.
Procrustes Distance	The squared sum of the Procrustes residuals (i.e., measure of how far an individual landmark configuration is from the mean shape).
Eigenvectors	The new linear combinations of Procrustes coordinates obtained after PCA decomposition.
Eigenvalues	The factor by which the corresponding eigenvector is scaled. When sorted by descending eigenvalues, the first eigenvector is the linear combination of variables that has the greatest variance.

Whether anatomical landmarks generated using the Markup tools or semi/pseudo-landmarks generated by SlicerMorph's modules, the outputs of these digitization tools are all saved using the industry-standard JSON format. JSON is an open standard file format and data interchange format that uses human-readable text to store and transmit data objects consisting of attribute–value pairs and arrays. The generalized Procrustes analysis (GPA) module reads these JSON files (along with the older comma-separated .fcsv format) to initialize the analytical pipeline. Optionally, samples can be left out of the analysis during the file selection process, with landmarks also able to be dropped out of the analysis by entering their indices. In addition to the Procrustes superimposition, the GPA module also performs the principal component analysis (PCA) decomposition of the variance and reports the PC scores for each sample data, which then can in turn be plotted within Slicer. Finally, the constructed morphospace can be investigated either by using the mean shape landmarks or more completely by specifying a reference model, which on return warps to the mean shape (Figure 4). As of this writing, SlicerMorph does not offer inferential statistics on the coordinate but is instead aimed at data exploration. For hypothesis testing, users can utilize the SlicerMorphR package to import the SlicerMorph's GPA output into the R statistical environment and benefit from the excellent statistical shape analysis packages such as Geomorph or Morpho. For more detailed instructions on the SlicerMorph module and its capabilities, readers can refer to the online tutorials at https://github.com/SlicerMorph/Tutorials), as well as the open-access publications that illustrate SlicerMorph's functionalities in more detail (Porto et al., 2021; Rolfe, Davis, & Maga, 2021; Rolfe, Pieper, et al., 2021; Zhang et al.R, 2022).



	A	B
1	**ID**	**Procrustes Distance**
2	USNM599166	0.0393526
3	USNM590942	0.0434989
4	USNM590951	0.0443836
5	USNM176219	0.0499663
6	USNM176216	0.0502731
7	USNM176211	0.0519361
8	USNM599165	0.0553903
9	USNM252575	0.0554604
10	USNM252577	0.0559376
11	USNM590953	0.0562206
12	USNM252580	0.0565173
13	USNM220060	0.0579143
14	USNM174715	0.0582849
15	USNM599167	0.0596143
16	USNM590954	0.0629688
17	USNM297857	0.0640608

Figure 4. Visualization features of the generalized Procrustes analysis (GPA) module of the SlicerMorph extension. **(A)** The mean shape of the sample can be visualized as a 3D model (yellow gorilla [*Gorilla gorilla*] cranium). **(C)** The magnitude of the landmark deformations associated with principal components PC1 (red) and PC2 (green) can be visualized as vectors starting from the mean shape landmarks. **(B)** Alternatively, a new 3D model (blue cranium) is generated on the fly as the user explores the morphospace interactively by sliding the PC values in negative and positive directions in selected PCs. Note the increased facial angle in blue (the deformed skull) is due to the large deformation associated with landmarks around the orbital region and the maxilla. The mean landmark configuration can be projected in 2D slice views (lower row, left). **(D)** Bivariate plots display where each specimen is in the PCA space (lower row, middle). Each sample is sorted by increasing the Procrustes distance from the mean shape (lower row, right). **(E)** By convention, the sample that is closest to the mean shape is commonly used as the reference model for 3D visualizations.

Table 4. Description of some SlicerMorph modules and their functionality.

Module	Functionality
ImageStacks	A general-purpose tool for importing non-DICOM image sequences into Slicer. Provides options for specifying voxel size, selecting image quality (preview, half, full), defining an ROI for import, loading of every *n*th slice (skip slice), or reverse stack order (to deal with mirroring of the specimen)
SkyscanReconImport	Imports an image stack from the Bruker/Skyscan reconstruction software (Nrecon) with correct voxel spacing and orientation as a 3D volume.
ImportFromURL	A utility for downloading data from a provided URL into the current Slicer scene. Data format must be supported by Slicer.
CreateSemiLMPatches	Provides triangular patches of semi-landmarks that are constrained by three fixed anatomical landmarks. The input into the module is a 3D model and its accompanying set of fixed landmarks, with users generating and visualizing the patches by specifying triplets of fixed landmarks that form a triangle.
PseudoLMGenerator	This module uses the 3D model's geometry to create a dense template of pseudo-landmarks whose placement is constrained to the 3D model's external surface.
PlaceSemiLMPatches	A utility for applying the generated connectivity table from the **CreateSemiLMPatches** module to other 3D models with the same set of anatomical landmarks. Along with the connectivity table, the input into the module is a 3D model and its accompanying set of fixed landmarks.
ProjectSemiLM	A utility for transferring a template of semi-landmarks to new 3D models using the thin plate splines (TPS) warp. Requires a current set of corresponding anatomical landmarks in the template and target models.
MarkupEditor	A plugin that enables selecting and editing subsets of dense semi-landmarks by drawing an arbitrary closed curve in the 3D viewer using right-click context menus in the 3D viewer. Selected landmarks can be removed from the current node or copied into a new fiducial node. Grouping landmarks into anatomical regions is useful for downstream analyses.
ALPACA	ALPACA provides fast landmark transfer from a 3D model and its associated landmark set to target 3D model(s) through point cloud alignment and deformable registration. Unlike the PlaceSemiLMPatches or ProjectSemiLM modules, it does not require the presence of fixed landmarks to transfer the landmarks.
GPA	Performs generalized Procrustes analysis (GPA) with or without scaling shape configurations to unit size, conducts principle component analysis (PCA) of GPA-aligned shape coordinates, provides graphical output of GPA results and real-time 3D visualization of PC warps, either by using the landmarks of mean shape or a reference model that is transformed into the mean shape.
Animator	A basic keyframe-based animation of 3D volumes. Supports interpolation of regions of interests, rotations, and transfer functions for volume rendering. Output can be either as an image sequence of frames or compiled into mp4 format.
SegmentEndoCranium	Automatically segments the endocranial space in a 3D volume of a mammal skull.

Conclusion

The future of morphology is digital and 3D. With the emergence of machine learning models that use deep learning, the usability of 3D digital datasets, whether from human or non-human organisms, is certain to increase. Even now, most routine segmentation tasks using clinical datasets are fully automated with pretrained AI models of things such as the brain, liver, lung, and many other organs (Diaz-Pinto et al., 2022). Each day, these models are getting faster and better at accurately predicting the locations of these structures in clinical exams. The world is seeing the extensions of these AI applications being applied to model organisms; for example, the MEMOS extension by the SlicerMorph team estimates the segmentation of 50 anatomical structures from a developing mouse fetus (E15) in less than one minute when the pretrained model is run on a GPU (Rolfe & Maga, 2022). Developing similar models for biological anthropology is only a matter of time for (and interest from) the community, whether these are forensic or osteo-archaeological applications (e.g., identifying individuals from skeletal remains, accurately estimating body parts, 3D reconstructions).

Therefore, having the next generation of biological anthropologists be proficient in digital morphology as much as they are proficient in osteology, vertebrate morphology or human physiology is crucial, and this goal is best accomplished by incorporating digital morphology into the curriculum. Obviously, the choice of platform will have a tremendous impact on how the new generation of scientists will be trained. Using an open and extensible platform such as 3D Slicer has the potential to create a transformation in biological anthropology, not unlike the one caused by the emergence of the R statistical language 20 years ago, where within a single generation, R completely transformed how biostatistics courses are taught in the life sciences.

I encourage both instructors and students of biological anthropology to explore the opportunities afforded by the Slicer ecosystem. This starts with being able to work with all the available open-licensed digital specimens on the Internet and continues with being able to collaborate without borders and institutions free of cost. More importantly perhaps, tools such as SlicerMorph and the many other available extensions are not necessarily developed by computer scientists but by domain scientists who are solving a challenge and sharing the solution with their community.

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