

ImageJ and 3D Slicer: open source 2/3D morphometric software

Fiona Pye¹, Nussaibah B. Raja¹, Bryan Shirley¹, Ádám T Kocsis¹, Nick Hohmann¹, Duncan J E Murdock², Emilia Jarochowska¹

¹GeoZentrum Nordbayern, Universität Erlangen–Nürnberg, Erlangen, Bavaria, Germany

²Oxford University Museum of Natural History, Oxford, Oxfordshire, United Kingdom

Corresponding Author:

Fiona Pye¹

Loewenichstraße 28, Erlangen, Bavaria, 91054, Germany

Email address: fiona.pye@outlook.com

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Extended Conference Workshop Abstract

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In a world where an increasing number of resources are hidden behind paywalls and monthly subscriptions, it is becoming crucial for the scientific community to invest energy into freely available, community-maintained systems. Open-source software projects offer a solution, with freely available code which users can utilise and modify, under an open source licence. In addition to software accessibility and methodological repeatability, this also enables and encourages the development of new tools. All software requires some element of maintenance, and with open-source software this often requires voluntary time investment from the users and/or original developers. However, such work encourages collaboration and learning across disciplines, and enables fields to move beyond their original borders to become more interdisciplinary.

As palaeontology moves towards data driven methodologies, it is becoming more important to acquire and provide high quality data through reproducible systematic procedures. Within the field of morphometrics, it is vital to adopt digital methods that help mitigate human bias from data collection. In addition, mathematically founded approaches can reduce subjective decisions which plague classical data. This can be further developed through automation, which increases the efficiency of data collection and analysis, enabling researchers and students with little funding to make greater progress.

With these concepts in mind, we introduce two open-source shape analysis software, that arose from projects within the medical imaging field with funding from the National Institute of Health (NIH), which operate under permissive free software licences. These are ImageJ, an image processing software with batch processing features which processes primarily 2D data, but also contains 3D utilities. 3D Slicer which focuses on 3D informatics and visualisation. Both are designed and utilised for digital data collection and have online guides alongside active support forums. They are easily extensible using common programming languages and additional features created by other users are readily available, on GitHub or through the software itself.

ImageJ. Applied here is FIJI (Fiji Is Just ImageJ), which describes itself as a “batteries included” distribution of ImageJ, bundling many useful plugins for scientific image analysis. ImageJ is Java based and also allows the incorporation of several programming languages (such

as R and Python) within its coding interface. This is alongside its own simplified macro language which can be easily accessed using the macro recorder. The macro utility provides users with easy access to highly repeatable, potentially automated, methods without the coding literacy requirement. A semi-automated plugin, FossilJ has been developed for the digital collection of morphometric data from images, which can be batch processed. In the current pre-release version (v0.2.1, available on GitHub), FossilJ is optimised for bivalve shells (with or without predatory drillholes) in addition to a separate line measurement tool. Some steps are fully automated, and others require user inputs to ensure data quality. Each image is calibrated independently to enable the efficient batch processing of objects with magnitudes of size difference.

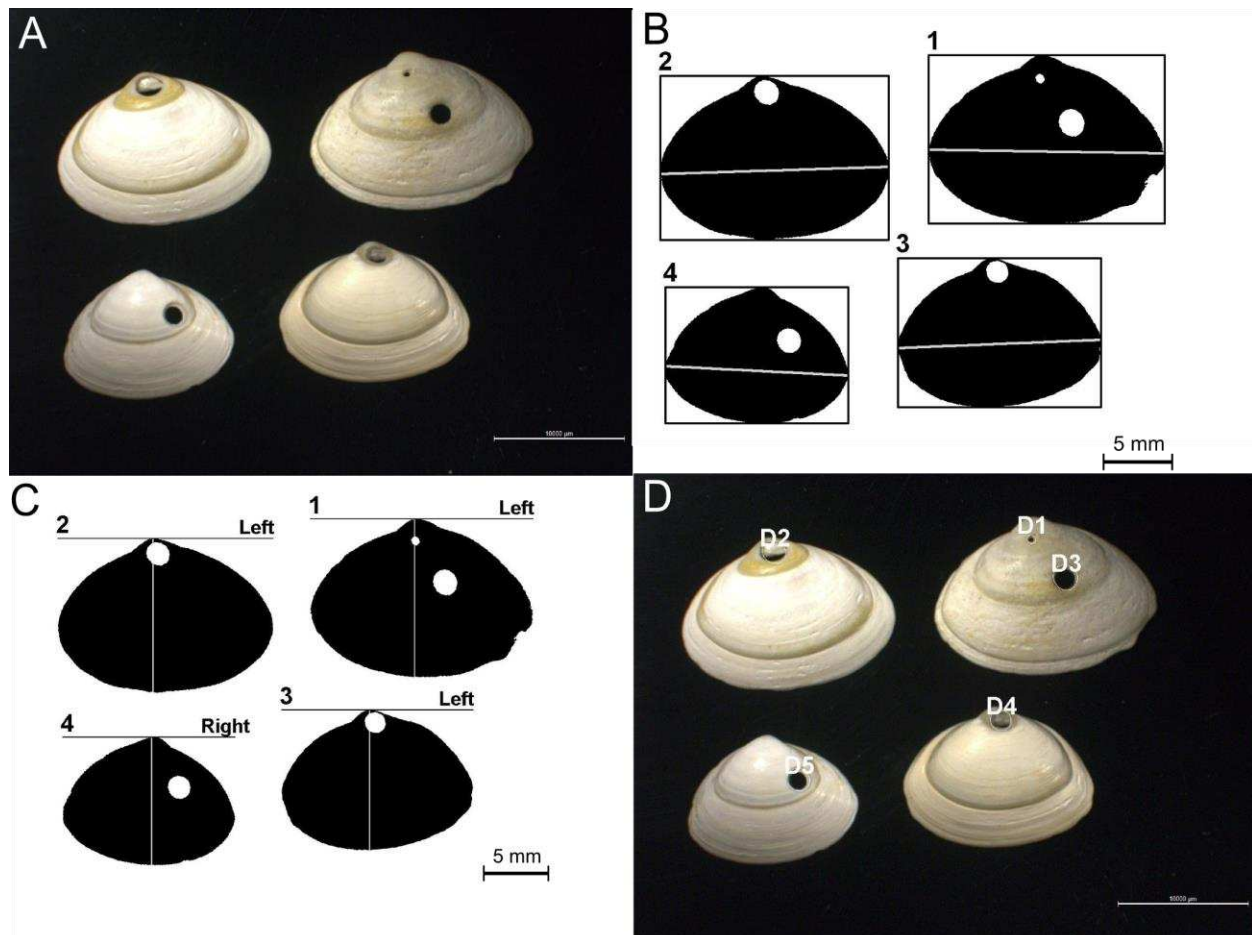


Figure 1: FossilJ process, input (A) and outputs (B, C, D).
(A) Raw image. (B) Bounding box indicating width (posterior-anterior) and height (dorsal-ventral) measurements (C) Labelled valve chirality (D) (C) Unique drillhole references.
Specimen credit: Kenneth de Baets.

Objects are automatically identified and allocated unique specimen numbers (Fig. 1B) which link each specimen to verification images and the data which is compiled and exported in csv format. The data collected is width (posterior-anterior), height (dorsal-ventral) (Fig. 1A), broken, drillhole counts (Fig. 1D, size and location (edge or internal), valve chirality (left or right valve)

(Fig. 1C). Verification experiments show FossilJ to be 2.27 times faster than manual caliper measurement (Table 1). The data produced by FossilJ is equivalent to classical manual caliper data, with regression R^2 values around 0.97 for width and height measurements (Fig. 2).

Table 1: FossilJ verification experiment summary, undertaken on 50 undrilled shells.

Manual Measurement (digital calliper)	Time (minutes)	FossilJ Measurement	Time (minutes)
-	-	Photography	15
Width and height, specimen references	50	Width, height, broken, with verification image production (automatic specimen references)	7
Total	50		22
<i>Shells per minute</i>	<i>1</i>		<i>2.27</i>

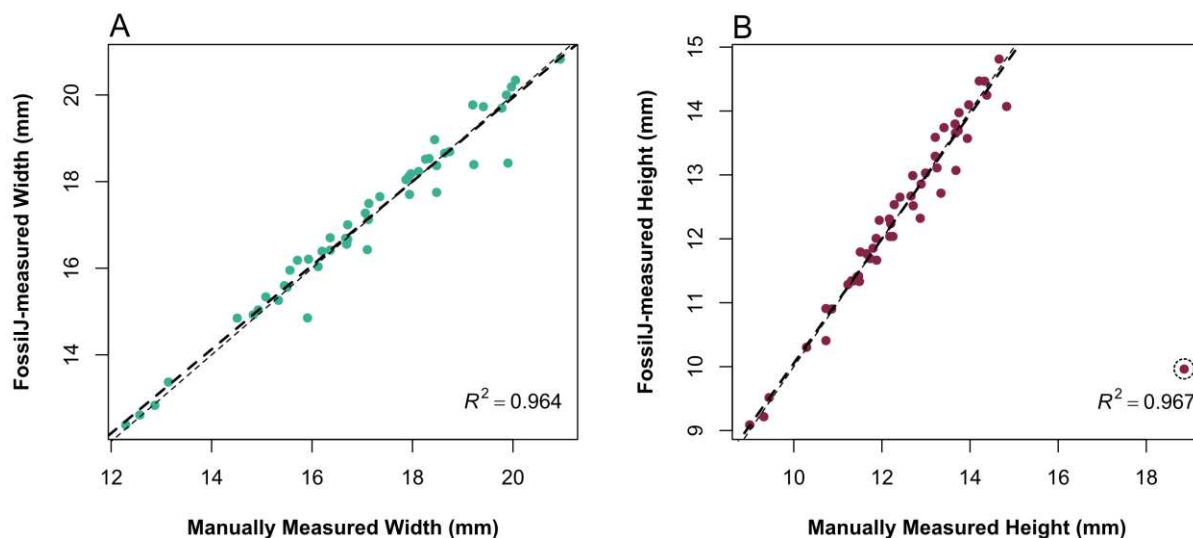


Figure 2: Regression of size measurements, FossilJ against manual caliper measurements. Thick dashed line – regression line (outlier removed), thin dashed line – 1:1 line. (A) Width (posterior-anterior) measurements. (B) Height measurements (dorsal-ventral). Note outlier caused by typing error in manual data collection.

FossilJ is available to download on GitHub at <https://github.com/fionapye/FossilJ>

3D Slicer. 3D Slicer is a useful tool for 3D data processing and visualisation which supports a wide range of file types, for working on stacks, segmentations and models. It comes with many inbuilt tools, and more are available through the extension manager and online repositories such as GitHub. 3D Slicer has a python-based interface and contains a python interactor within the GUI (graphical user interface) which can be used to control slicer. The SPHARM-PDM

extension, has been applied to synchrotron scans of coniform conodonts for the purpose of comparative morphometrics.

Image stacks were imported and resolution downsampled using the Resample Scalar Volume module to improve processing speeds. The resampled stacks were then segmented using the Segment Editor and the specimen axis was generated using the Curve Maker module. All specimens were cut to 90% of their original length perpendicular to the axis, to remove noise around the basal cavity end of the segmentation eye (Fig. 3). This end cutting was undertaken by generating the plane perpendicular to the axis, using a specifically written script which is placed into the python interactor within 3D Slicer. The python interactor provides a valuable tool in this way for users to create repeatable steps, or to achieve accuracies which are unachievable by eye.

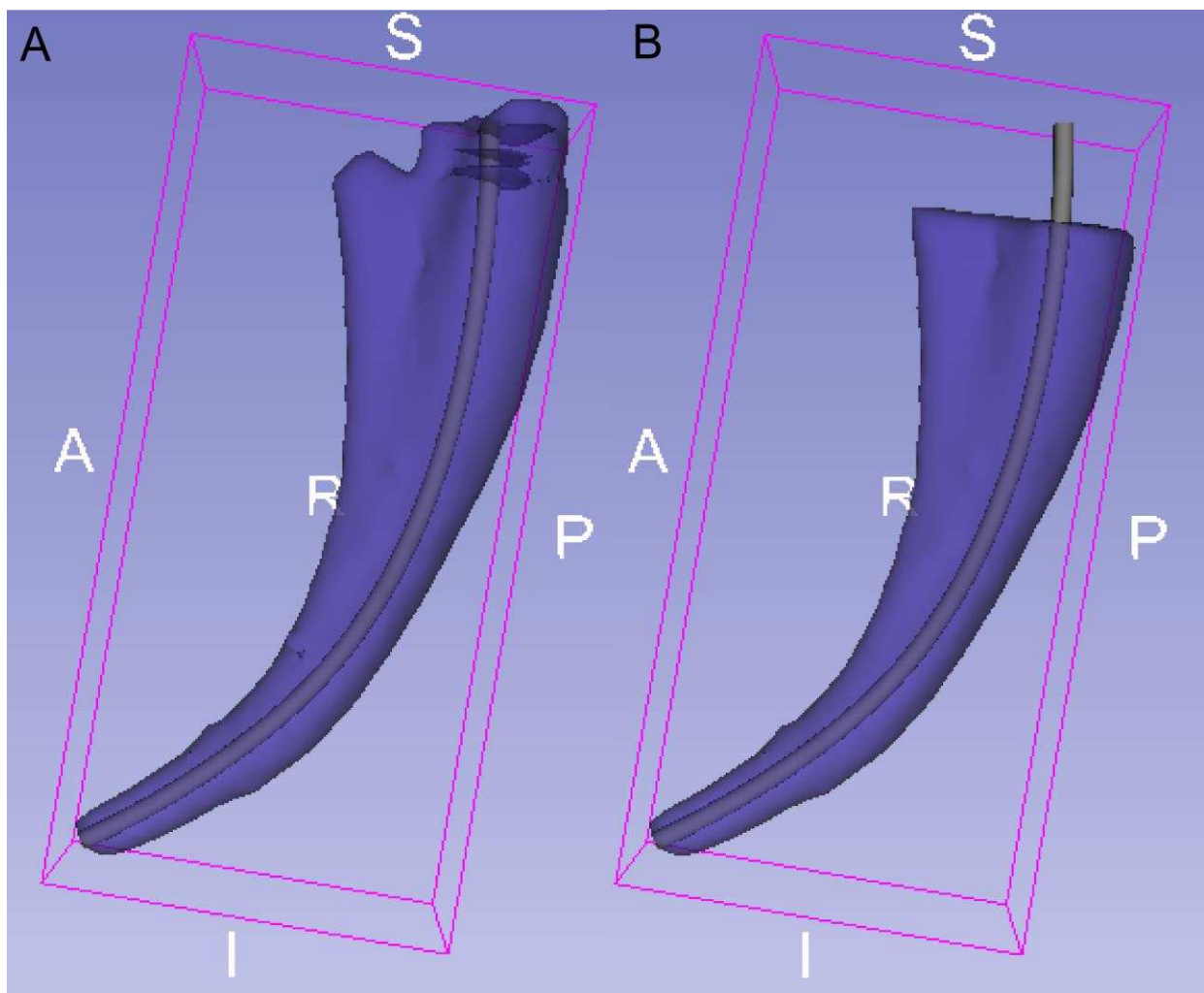


Figure 3: Comparison of original and cut specimen segmentations. (A) Original specimen (cleaned). (B) Cut specimen produced using the python interactor.

The SPHARM-PDM module is developed and maintained by the Neuro Image Research and Analysis Laboratories at University of North Carolina at Chapel Hill in collaboration with

Kitware in the SlicerSALT (Shape AnaLysis Toolbox) project, which brings together shape analysis modules within a lightweight version of 3D Slicer. SPHARM-PDM is also available within the standard 3D Slicer extension manager. It generates spherical harmonic comparative point distribution models, which are suitable for statistical investigation (Fig. 4B). Standard 3D models generated directly from segmentations differ drastically in their resolution and number of polygons/vertices and are often very noisy (Fig. 4A). This makes the data which describes these shapes very difficult to statistically analyse. SPHARM-PDM deals with this issue by generating models which are identical in data structure, with each model reconstructed to a user defined resolution and harmonic detail level which is set inside the GUI. The restriction with this form of spherical harmonics is that it is only applicable to simple shapes.

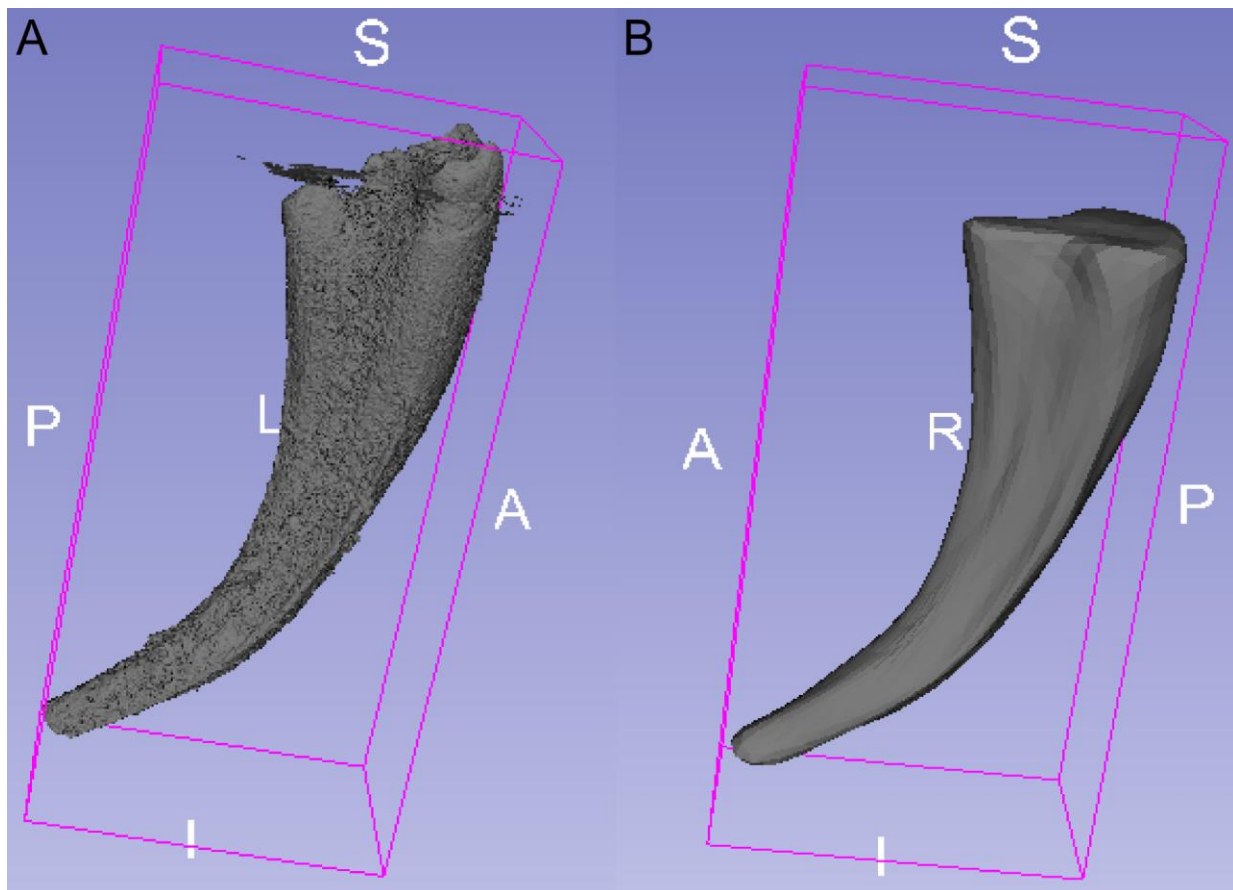


Figure 4: Model comparison of original model and spherical harmonic transform model. (A) Original model from threshold only segmentation, containing ~3.9 million polygons (original as Fig. 3A). (B) SPHARM-PDM generated model (from 15 harmonics) containing 2000 polygons (cut as Fig. 3B). 3D model credit (A): Duncan Murdock.

Spherical harmonic transform can be thought of as a three-dimensional Fourier transform. This is an established method within palaeontology and is even implemented within the PAST statistical software. Spherical harmonics are a series of wavefunctions on the surface of a sphere, which can be used to reconstruct 3D shapes by wave interference. SPHARM-PDM requires clean segmentations or 3D models as an input (containing no loops or holes), resamples all specimens

to equal resolution and generates a parametric mapping, which is then used to create a spherical harmonic reconstructed model of each specimen. It provides a variety of models as outputs (suitable for various purposes) alongside spherical harmonic coefficients, which are global shape descriptors. The module also contains parameters which allow chirality correction by generating mirrored versions and versions of all models aligned by the first order ellipse (first harmonic) which represents the longest axis of the specimens.

For more information and downloads of the tools described, links are provided below.

<https://imagej.net/Fiji>

<https://github.com/fionapye/FossilJ>

<https://www.slicer.org/>

<http://salt.slicer.org/>

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