





BRIEF COMMUNICATION

morphomap: An R package for long bone landmarking, cortical thickness, and cross-sectional geometry mapping

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Abstract

Objectives: This study describes and demonstrates the functionalities and application of a new R package, *morphomap*, designed to extract shape information as semi-landmarks in multiple sections, build cortical thickness maps, and calculate biomechanical parameters on long bones.

Methods: *morphomap* creates, from a single input (an oriented 3D mesh representing the long bone surface), multiple evenly spaced virtual sections. *morphomap* then directly and rapidly computes morphometric and biomechanical parameters on each of these sections. The R package comprises three modules: (a) to place semilandmarks on the inner and outer outlines of each section, (b) to extract cortical thicknesses for 2D and 3D morphometric mapping, and (c) to compute cross-sectional geometry.

Results: In this article, we apply *morphomap* to femora from *Homo sapiens* and *Pan troglodytes* to demonstrate its utility and show its typical outputs. *morphomap* greatly facilitates rapid analysis and functional interpretation of long bone form and should prove a valuable addition to the osteoarchaeological analysis software toolkit.

Conclusions: Long bone loading history is commonly retrodicted by calculating biomechanical parameters such as area moments of inertia, analyzing external shape and measuring cortical thickness. *morphomap* is a software written in the open source R environment, it integrates the main methodological approaches (geometric morphometrics, cortical morphometric maps, and cross-sectional geometry) used to parameterize long bones.

KEYWORDS

cross-sectional geometry, geometric morphometrics, long bones, morphomap, morphometric maps, R

1 | INTRODUCTION

The study of diaphyseal bone form based on landmarks or measurements between them, cortical thickness variations and cross-sectional

geometry (CSG) are commonly carried to retrodict long bone behavior and adaptation in response to loading. Such analyses are applicable in studies of the impacts on adult form and developing bones of locomotion, the nature, intensity and repetitiveness of physical activity and

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body mass. In the field of specialism of the authors, biological anthropology, many past studies have used parameters of form, cortical thicknesses or CSG, to study past behavior and loading, in primates (Connour, Glander, & Vincent, 2000; Kimura, 2003; Marchi, 2005, 2007, 2010; Marchi, Leischner, Pastor, & Hartstone-Rose, 2018; Patel, Ruff, Simons, & Organ, 2013; Ruff, 2002; Ruff & Runestad, 1992), ancient human populations (Carlson & Marchi, 2014; Holt, 2003; Macintosh, Davies, Pinhasi, & Stock, 2015; Macintosh, Pinhasi, & Stock, 2017; Marchi, Sparacello, Holt, & Formicola, 2006; Niinimäki et al., 2017; Ruff & Hayes, 1983; Ruff & Larsen, 2014; Shaw & Stock, 2013; Sparacello, Marchi, & Shaw, 2014; Stock & Pfeiffer, 2001), and fossil hominins (Friedl et al., 2019; Jungers & Minns, 1979; Marchi, Harper, Chirchir, & Ruff, 2019; Rodríguez, Carretero, García-González, & Arsuaga, 2018; Ruff, Burgess, Ketcham, & Kappelman, 2016; Ruff, Trinkaus, Walker, & Larsen, 1993; Trinkaus & Ruff, 1989, 2012). While parameters describing bone form, cortical thickness variations and CSG have proven to be very useful for reconstructing bone loading patterns (Endo & Takahashi, 1982; Huiskes, 1982; Piziali, Hight, & Nagel, 1976; Uthoff & Jaworski, 1978), the effort in calculation has tended to limit studies to a few cross-sections, although some previous studies have shown the value of finer detailed analysis of whole long bone shafts and multiple sections (Lacoste Jeanson, Santos, Dupej, 2018; Lacoste Jeanson, Santos, Villa, et al., 2018; Puymérail et al., 2012).

Computerized tomography (CT) scanning and advances in three dimensional (3D) reconstruction, visualization, parameterization, and analysis of skeletal form have facilitated the collection, sharing (i.e., morphosource, MorphoMuseum, Digital Morphology museum available at <http://dmm.pri.kyoto-u.ac.jp>, Kupri and NESPOS) (Boyer, Gunnell, Kaufman, & McGeary, 2016; Bradtmöller, Pastoors, Slizewski, & Weniger, 2010; Lebrun & Orliac, 2016) interpretation of large datasets (Davies et al., 2017). These advances underpin a specific subdiscipline within our field of biological anthropology, virtual anthropology (VA; Weber, Recheis, Scholze, & Seidler, 1998; Weber, 2001; Cunningham, Rahman, Lautenschlager, Rayfield, & Donoghue, 2014). The methods of VA are applicable to skeletal studies in all species.

Increasingly, studies utilize skeletal landmark coordinates to investigate form variation using geometric morphometric (GM) methods. However, while landmarks can readily be identified in the cranium (Cardini & O'Higgins, 2004; Mitteroecker, Gunz, & Bookstein, 2005) and epiphyses (Almécija et al., 2019; Arias-Martorell, Potau, Bello-Hellegouarch, Pastor, & Pérez-Pérez, 2012; Brzobohatá, Krajčiček, Velemínský, Poláček, & Velemínská, 2014; Galletta, Stephens, Bardo, Kivell, & Marchi, 2019; Harmon, 2007; Holliday, Hutchinson, Morrow, & Livesay, 2010; Rein, 2019), the diaphysis presents fewer unequivocal matching points between specimens. Therefore, semilandmarks (landmarks placed according to some mathematical rule, e.g., evenly spaced around an outline) offer a potential solution, to characterize both external and internal diaphyseal surface form, albeit with limitations and complications (Brzobohatá et al., 2014; Cardini, O'Higgins, & Rohlf, 2019; De Groote, Lockwood, & Aiello, 2010; Frelat, Katina, Weber, & Bookstein, 2012; Gunz, Mitteroecker, & Bookstein, 2005; Morimoto, De León, & Zollikofer, 2011; Morimoto, Nakatsukasa, de León, & Zollikofer, 2018; Oxnard & O'Higgins, 2009).

One of the most recent developments of VA in functional morphology is the creation of morphometric maps (MMs) aimed at visualizing bone thickness variations along the diaphysis. MMs were first introduced by Amtmann and Schmitt (1968) for visualization in two dimensions (2D). The method was first taken up in medical studies (Benson, Prihoda, & Glass, 1991; Garn, Poznanski, & Nagy, 1971; Poole et al., 2012; Treece, Poole, & Gee, 2012) and only later were MM formalized as color maps and combined with 3D imaging for applications in comparative studies of cortical thickness variation in relation to locomotion (Bondioli et al., 2010; Jashashvili, Dowdeswell, Lebrun, & Carlson, 2015; Puymérail et al., 2012; Puymérail & O'Higgins, 2013; Zollikofer & Ponce de León, 2001). As well as quantitative analyses of diaphyseal cortical thicknesses, MMs allow rapid visual comparison of these among individuals (Lacoste Jeanson, Santos, Dupej, 2018; Lacoste Jeanson, Santos, Villa, et al., 2018).

While landmarks and MMs measure the form of the diaphysis, CSG predicts resistance to particular loading scenarios (e.g., compression, bending, etc.) and has proven effective in retrodicting bone loading history (Endo & Takahashi, 1982; Huiskes, 1982; Piziali et al., 1976; Uthoff & Jaworski, 1978). Analyses of CSG have been widely applied to studies of locomotion, handedness, body mass, and other aspects of habitual loading.

Here, we present *morphomap*, an R package specifically designed to extract cross-sections from long bone meshes at specified intervals along the diaphysis and to site semilandmarks on the periosteal and endosteal outlines of each cross-section and to calculate 2D and 3D MM and CSG parameters. We demonstrate the validity of this computational tool by showing that it obtains the same results as those from manual and other computational approaches. We then demonstrate the functionality of *morphomap* in comparing a human and a chimpanzee femur. The R code and examples are freely distributed in the R-package *morphomap* (Profico, Bondioli, Raia, O'Higgins, & Marchi, 2019). An R vignette with runnable examples is reported in Supporting Information.

2 | MATERIALS AND METHODS

We tested the functionality of the *morphomap* R package on a human and a chimpanzee femur. The human femur (OdN 244) is from a Northern Italian Bronze Age necropolis of Olmo di Nogara (Canci, Tafuri, Fornaciari, Cupito, & Salzani, 2011). It was imaged at the hospital of the University of Pisa using a GE LightSpeed RT16 medical CT scanner (slice thickness 0.625 mm, slice increment 0.625 mm, voltage 120 kV, X-ray tube current 300 mA, standard reconstruction algorithm, pixel size 479 μm). The chimpanzee femur (Kupri 1022) was obtained from the Digital Morphology Museum, KUPRI (<http://dmm.pri.kyoto-u.ac.jp/dmm/WebGallery/index.html>). Its acquisition was performed on a Toshiba Asteio medical CT scanner (slice thickness 1.0 mm, slice increment 0.4 mm, voltage 120 kV, X-ray tube current 150 mA, standard reconstruction algorithm, pixel size 399 μm). The external and internal surfaces extracted from these are included in the *morphomap* R package.

2.1 | The morphomap R package

morphomap is designed to produce by default 61 cross-sections along the diaphysis of the long bone defined at increments of 1% between 20 and 80% of its biomechanical length as it is commonly defined in studies of diaphyseal CSG (Ruff, 2002; Marchi, 2005, 2007; Figure 1a). If required, the number of sections can be changed by the user.

To extract morphometric parameters, the centroid of each cross section is first identified and its coordinates C_x and C_y reported. Next, a set of lines are drawn at equally spaced angles from the centroid of the section. For each line, cortical thickness is calculated as the segment length of the line intersecting the cross-section at the medullary and at the subperiosteal contours. *morphomap* can output the mean cortical thickness (MeanThick), the minimum cortical thickness (MinThick), the standard deviation of the cortical thickness (SdThick), and the maximum cortical thickness (MaxThick). Alternative calculations of thickness can also be derived with *morphomap* (e.g., between points on the medullary outline and their nearest points on the cortex). The coordinates of the points of intersection (semilandmarks) are provided as output for morphometric analysis (Figure 1b,c).

At each cross-section, *morphomap* also calculates the periosteal (ExtP, mm) and endosteal perimeters (MedP), the cortical thickness measured at the four anatomical quadrants (anterior, posterior, medial, and lateral, in mm) and the CSG variables: the total area (TotA, mm²), the medullary area (MedA, mm²), the cortical area (CA, mm²), the area moments of inertia around the y and x axis, (I_x and I_y , mm⁴), the maximum and minimum area moments of inertia (I_{max} and I_{min} , mm⁴), the angle between the major axis and the mediolateral axis of the cross-section, theta (θ , radians), the polar moment of inertia (J, mm⁴), the section moduli ($Z_x, Z_y, Z_{max}, Z_{min},$ and Z_{pol} , mm⁴) and the maximum chord lengths from y and x axes (d_x^* and d_y , mm; see Supporting Information). Table 1 summarizes the main functions of *morphomap*. The

morphomap R package is available for all major platforms (Windows, Linux/Unix and Mac OS X).

2.2 | Automatic segmentation of long bone meshes

morphomap requires an oriented long bone mesh as the input (Figure S1). The orientation of the mesh can be checked using the function *morphomapCheck* which is described in Supporting Information. It may be necessary to mirror long bones to avoid issues of laterality. This can be achieved using the *morphomapMirror* function (Table 1). The first step of the measurement procedure is the automatic separation of the periosteal and endosteal surfaces (Figure 2) by applying the CA-LSE R-tool (Computer Assisted Laser Scanner Emulator; Profico, Schlager, et al., 2018). This is carried out by the function *morphomapSegm* (Table 1).

2.3 | Extraction of cross-sections

Sectioning is carried out using the *morphomapCore* function. First, the user specifies the biomechanical length of the long mesh. Next, *morphomap* extracts by default cross-sections at regular increments of 1% (but the user can choose a different increment) along the shaft between 20 (distal) and 80% (proximal) of the biomechanical length of the bone. The user can choose to change the start and end points by defining these parameters in the function *morphomapCore*. At each level, a transverse plane (perpendicular to the frontal plane) is drawn and the intersection between the transverse plane and the two meshes (periosteal and endosteal) (Figure 2) is used to define the periosteal and endosteal outlines of each cross-section (Figure 1c).

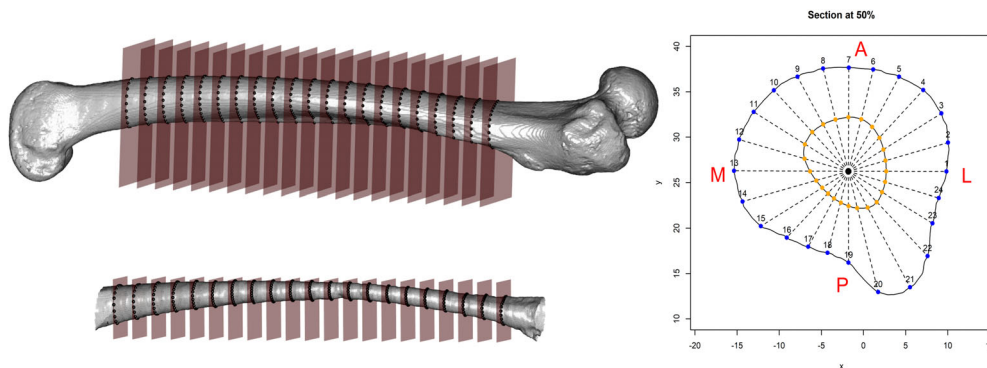


FIGURE 1 (a) Periosteal surface with 21 planes used to obtain the cross-sections; the 24 semilandmarks corresponding to the periosteal contours are reported in blue. (b) Endosteal surface with the 21 planes used to obtain the cross-sections; the 24 semilandmarks corresponding to the endosteal contours are reported in orange. (c) A cross-section at 50% of the bone biomechanical length is shown. Twenty-four lines are drawn at equally spaced angles from the centroid of the cross-section (L, lateral; A, anterior; M, medial, and P, posterior). At each angle, thickness is calculated as the segment length of the intersection of the line with the medullary and subperiosteal contours, and the points of intersection are provided as semilandmarks. In blue are shown the semilandmarks defining the periosteal contour; in orange, the semilandmarks defining the endosteal contour; the centroid of the cross-section is in black

TABLE 1 Description of the main functions of the *morphomap* R package

Function	Description	Notes
<i>morphomapCheck</i>	Check the orientation of the input mesh	Useful to visualize orientation of the mesh axes
<i>morphomapMirror</i>	Mirror a long bone mesh along the yz plane	Useful tool to mirror a long bone, for example, from right to left.
<i>morphomapSegm</i>	Separates a mesh from its visible and not visible components by using CA-LSE method	Creates the periosteal and endosteal long bone meshes
<i>morphomapCore</i>	Tool to slice long bones. The function creates 2D and 3D sections	The core of the <i>morphomap</i> R package. Slices the long bone and extracts cross sections
<i>morphomapShape</i>	Calculates equiangular semilandmarks on each cross section outline. For each cross section it extracts the coordinates of both periosteal and endosteal outlines.	Tool for extracting semilandmarks for morphometric analyses.
<i>morphomapWriteMorphologika</i>	Saves the semilandmark configuration in the morphologika format file	Function to export semilandmarks
<i>morphomapPlotShape</i>	Creates 2D and 3D plots of the semilandmark configuration	Useful to visualize the semilandmark configuration
<i>morphomap2Dmap</i>	Creates and plots a 2D cortical thickness map	Tool for the definition of the 2D cortical thickness map
<i>morphomap3Dmap</i>	Creates and plots a 3D cortical thickness map	Plots the cortical thickness dataset on the long bone mesh
<i>morphomapPic</i>	Saves pictures of the sections with a scale and A, L, P, and M thicknesses.	Function to export cross section
<i>morphomapRaster</i>	Convert a section to a raster image	Useful tool to export a cross-section of actual size
<i>morphomapCSG</i>	Calculates for each section the biomechanical parameters commonly used in studies of cross-sectional geometry	Tool for the calculation of the main parameters used in cross-sectional geometry studies

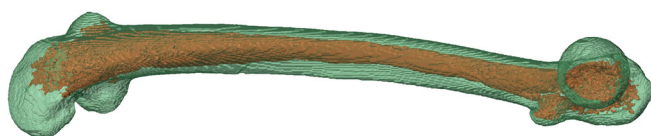


FIGURE 2 The output of the automatic segmentation procedure using the CA-LSE method. The method is part of the Arothron R package (Profico et al., 2018; Profico, Veneziano, Melchionna, Marchi, & Raia, 2018). The periosteal surface is shown in light green, the endosteal surface in purple

2.4 | Shape data module: Semilandmarking of cross-sections

By default, a set of 24 equiangular semilandmark pairs is defined by the intersections of the lines originating from the centroid of the cross-section and the endosteal and periosteal contours (Figure 1c). The *morphomapShape* function is used to output 2D and 3D coordinates of these semilandmarks. For subsequent analyses, the semilandmarks are numbered starting from the most anterior point on both contours, incrementing anticlockwise. The semilandmark

configurations can be exported from *morphomap* in the morphologika format file (O'Higgins & Jones, 1998) using the function *morphomapWriteMorphologika*.

2.5 | MM module: Drawing of two- and three-dimensional MMs

MMs of cortical thickness facilitate visualization of the distribution of cortical bone in long bone diaphyses. They are calculated by the functions *morphomap2Dmap* and *morphomap3Dmap* from the Euclidean distances between each pair of semilandmarks (cortical and the equivalent endosteal one), which is the cortical thickness at each angle. This calculation is carried out between each pair (cortical-endosteal) of semilandmarks in each and every section. In this way, a matrix (by default, 24 distances by 61 slices) of cortical thicknesses is created, which is then converted into 2D and 3D MMs (Figure 3). 2D MMs can be drawn without any interpolation or more smoothly by applying generalized additive modeling (GAM, see Bondioli et al., 2010). 3D MMs are created by allocating to each node of the mesh the weighted (by distance) thickness values associated with its five nearest

semilandmarks (this parameter can be changed by the user). The resolution of the 2D and 3D MMs is fully customizable by the user in order to remove outliers, smooth, and scale the matrix of thickness values.

In functions *morphomap2Dmap* or *morphomap3Dmap* (Table 1) the cortical thicknesses are used to draw topographic maps in 2D or 3D. In these, colors represent thickness, standardized by default (but selectable) from 0 (minimum) to 1 (maximum), on a 100-step color (the color palette is fully customizable by the user) scale from dark red (thickest) to dark blue (thinnest). These colors are plotted in 2D with the x axis corresponding to the unfolded cylinder projection of the diaphysis starting and ending at the anterior (A) border passing through the lateral (L), posterior (P), and medial (M) borders. On the y axis is plotted the diaphyseal length expressed as a percentage of the biomechanical length (Figure 3). In 3D, a plot is returned showing the femur in four anatomical views: anterior, lateral, medial, and posterior (Figure 4).

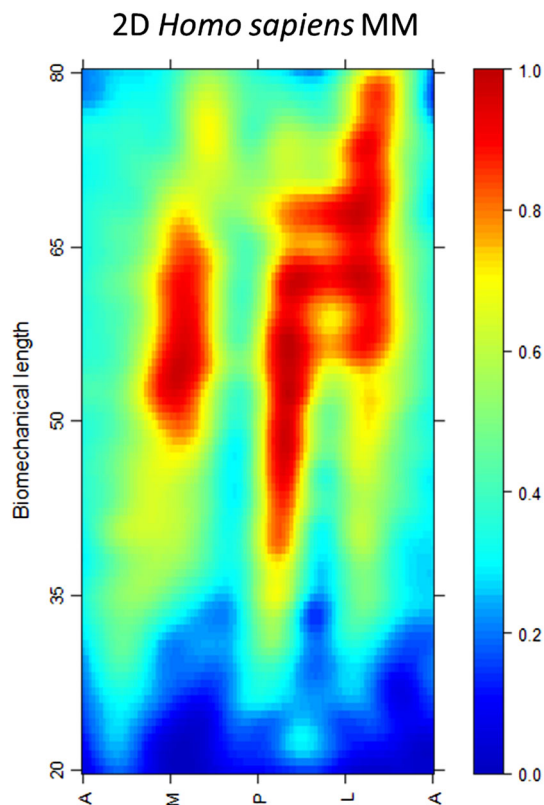


FIGURE 3 2D morphometric maps of cortical thickness along the diaphysis of OdN 244. X axis: unfolded cylinder projection starting and ending at the anterior (A) border, passing through the lateral (L), posterior (P), and medial (M) borders. Y axis: diaphyseal length expressed as a percentage of the biomechanical length from distal (bottom) to proximal (top). The colors indicate the standardized cortical thickness and range from dark red (thickest) to dark blue (thinnest)

2.6 | Exporting images of cross-sections

The *morphomapPic* function (Table 1) exports pictures of each cross-section in TIFF image format. By default, the cortical area is represented in black, the medullary canal in white. A scale bar is drawn to the bottom left (Figure 5). Thickness values at the four quadrants (A, L, P, and M) can be added to the exported cross-section (Figure 5a). The background, the legend and the cortical bone colors are fully customizable by the user.

The *morphomapRaster* function (Table 1) allows the pixel/mm ratio to be adjusted (0.1 by default) and exports the resulting bitmap (raster image) in TIFF format. This is useful to prepare images without a scale bar for importing into other morphometric or reconstruction software.

2.7 | Cross-sectional geometry module and its validation

The *morphomapCSG* function calculates in each section the CSG parameters most commonly used in biomechanical studies: the area, the area moments of inertia (I_x , I_y ; Figure S4), the principal area moments of inertia (I_{max} and I_{min} ; Figure S5), theta (θ), the polar moment of inertia (J) (Figure S6), and the section moduli (Z_x , Z_y , Z_{max} , Z_{min} , and Z_{pol}). The formulae used to calculate each CSG parameter implemented in *morphomap* are given in Table S1. For the calculation of these parameters *morphomap* converts the cortical area defined by periosteal and endosteal contours into picture elements of adjustable side length (delta) (Figure S2). In this way, all the parameters are calculated without interpolation. By default, delta has length 0.1 mm, this is customizable by the user (Figure S3).

We tested the calculation of CSG parameters embedded in *morphomap* by extracting two cross-sections from two surfaces artificially created for this purpose; a hollow circular cross-section and a hollow rectangular cross-section (Figure 6a,b). Table 2 shows the comparison between the values obtained via *morphomap* and those obtained by applying the formulae reported in Supporting Information.

In addition, we compared the values calculated in *morphomap* with the corresponding figures obtained when using BoneJ (Doubé et al., 2010) for diaphyseal cross-sections at 50% of the total biomechanical length of a human femur (OdN 244) and a *Pan troglodytes* (Kupri 1022) femur (Figure 6). Table 3 shows the parameters calculated via *morphomap* and BoneJ.

3 | RESULTS

3.1 | Case study—The human and chimpanzee femora

In this section, we show the application of the main functions embedded in the *morphomap* R functions to a human and a chimpanzee

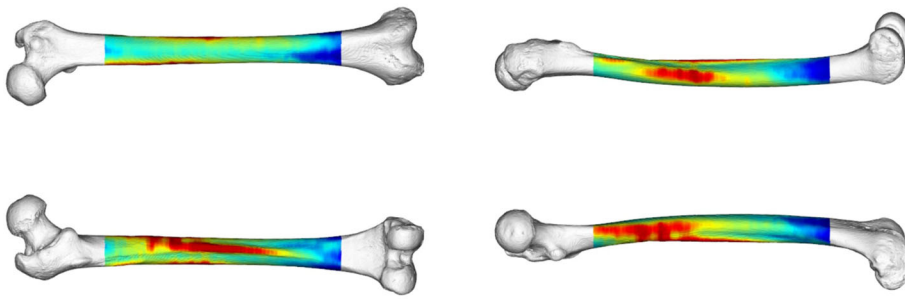


FIGURE 4 3D morphometric map of cortical thickness along the diaphysis of OdN 244. The map is shown in anterior (top left), lateral (top right), medial (bottom right) and posterior (bottom left) views. The colors indicate the standardized cortical thickness associated with each vertex of the mesh and range from dark red (thickest) to dark blue (thinnest)

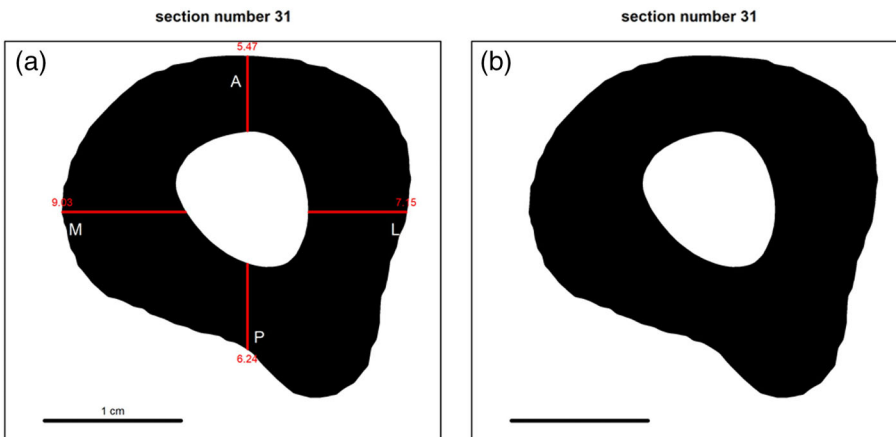


FIGURE 5 Example images of cross-sections exported from *morphomap*. (a) cross-section with anterior, lateral, posterior and medial thicknesses indicated (A, L, P, and M). (b) cross-section with no mark-up, (suitable for import into other software as BoneJ); The bar at the bottom left of each figure is the scale

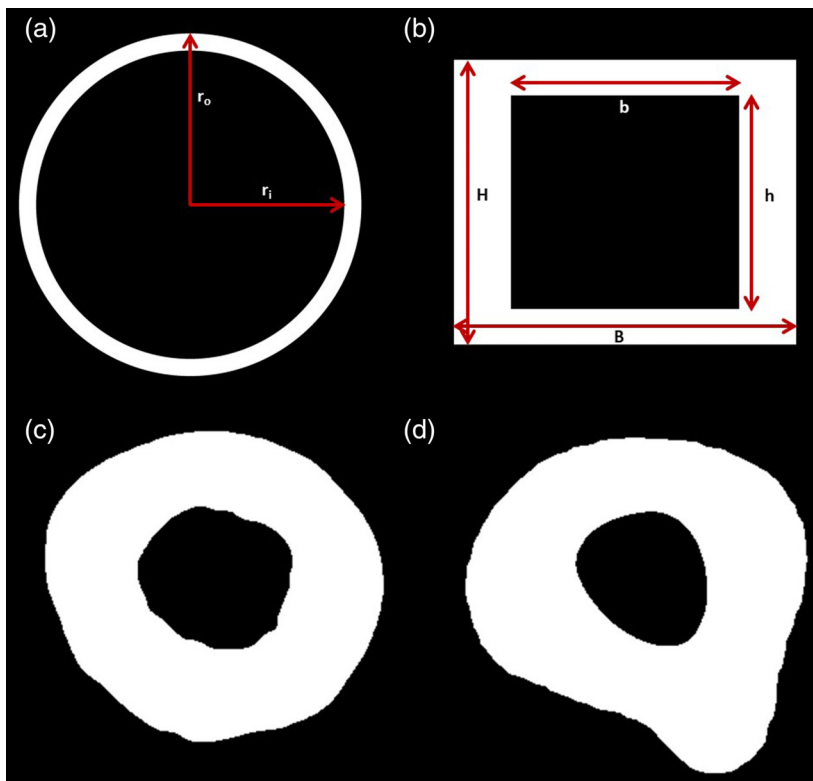


FIGURE 6 Cross-sections used to test the performance of *morphomap*. The parametric cross-sections consist of a hollow circular section (a) ($r_o = 10$ mm, $r_i = 9$ mm) and a hollow rectangular cross-section (b) ($B = 24$ mm, $H = 20$ mm, $b = 16$ mm, $h = 15$ mm). In (c) and (d) two cross-sections extracted at 50% of the biomechanical length of the femur of a chimpanzee (Kupri No. 1022) and a human (OdN 244), respectively, are represented. The pictures were exported using the function *morphomapRaster*

TABLE 2 Cross-sectional geometry of the sections in Figure 6a,b

	Geometric shapes formulae	Morphomap	Difference (%)	BoneJ	Difference (%)
Hollow cylindrical section					
I_x (mm ⁴)	2,700.984	2,700.602	0.01	2,706.6305	-0.21
I_y (mm ⁴)	2,700.984	2,700.602	0.01	2,706.6305	-0.21
CA (mm ²)	59.690	59.690	0.00	59.80	-0.18
Hollow rectangular section					
I_x (mm ⁴)	11,500.00	11,500.00	0.00	11,500.00	0.00
I_y (mm ⁴)	17,920.00	17,920.00	0.00	17,919.8	0.00
CA (mm ²)	240.00	240.00	0.00	240.00	0.00

Note: Parameters are calculated with *morphomap* and directly using the formulae reported in Supporting Information.

TABLE 3 Cross-sectional geometric parameters calculated using *morphomap* and BoneJ on cross sections extracted at the 50% of the biomechanical length of the femur of a human (OdN 244) and of a chimpanzee (Kupri No. 1022)

	<i>Homo sapiens</i>			<i>Pan troglodytes</i>		
	Morphomap	BoneJ	Diff (%)	Morphomap	BoneJ	Diff (%)
Cortical area (mm ²)	386.06	386.17	-0.03	357.00	357.06	-0.02
I_x (mm ⁴)	15,788.98	15,795.66	-0.04	14,093.96	14,109.6	-0.11
I_y (mm ⁴)	18,443.6	18,444.83	-0.01	16,881.29	16,907.60	-0.16
Z_x (mm ³)	1,164.53	1,173.55	-0.77	1,203.09	1,213.32	-0.84
Z_y (mm ³)	1,358.84	1,366.66	-0.57	1,337.16	1,342.81	-0.42
I_{max} (mm ⁴)	19,525.64	19,540.94	-0.08	17,201.32	17,216.36	-0.09
I_{min} (mm ⁴)	14,668.7	14,699.94	-0.21	13,794.83	13,800.50	-0.04
Z_{max} (mm ³)	1,484.86	1,488.25	-0.23	1,312.725	1,315.87	-0.24
Z_{min} (mm ³)	1,208.47	1,213.25	-0.39	1,189.54	1,192.35	-0.24
Theta (rad)	0.50	0.50	0.00	0.31	0.31	0.00

Note: Differences in results are expressed as percentages.

femur. The detailed functionality of the R code is reported in Supporting Information. The 3D femur meshes were aligned using Avizo 6.3 (Visualization Sciences Group, Mérignac, France) following the protocol explained in Ruff (2002). The biomechanical lengths of the bones are 380.23 mm and 277.13 mm for the human and the chimpanzee, respectively. First, the mesh was uploaded into R by using the *file2mesh* function belonging to the Morpho R package (Schlager, 2017). Second, the *morphomapSegm* function was used to separate the periosteal and endosteal contours. The *morphomapSegm* function was used to produce two suitable surfaces for the extraction of the cross-sections. The *morphomapCore* function extracted sixty-one cross-sections from 20 to 80% of the biomechanical length of the two femora (see Figure 1a,b and Figures S7–S8).

Third, the *morphomapShape* function was used to extract from each cross-section 24 equiangular semi-landmarks on the periosteal and endosteal outlines (see Figure 1c). Fourth, the *morphomap2Dmap* function was used to create 2D MMs (Figure S9) and fifth, the *morphomap3Dmap* function was used to create 3D MMs (Figure 7).

In agreement with a previous study (Puyménil, 2013) performed on a sample of 12 modern humans and 10 chimpanzees, the human diaphysis shows greater cortical thickness, resisting posterior bending along the linea aspera, while the chimpanzee femur is characterized by medial and lateral bony reinforcements in the proximal portion of the bone. We have reported in Tables S2 and S3 the CSG parameters computed for the human and chimpanzee femora, respectively. These were calculated for 13 cross-sections taken at 5% increments (for simplicity) from 20 to 80% of the biomechanical length of the femur.

Finally, *morphomap* offers the prospect of rapid processing of large samples. Table 4 shows the CPU time required to process the chimpanzee femur.

4 | DISCUSSION

Cortical bone topographic thickness variation in long bones reflects biomechanical loading history (Kivell, Davenport, Hublin, Thackeray, &

Skinner, 2018; Niinimäki et al., 2017; Ruff, Holt, & Trinkaus, 2006; Shaw & Stock, 2009). The R package, *morphomap* is intended to facilitate the work of functional morphologists in understanding how cortical bone distribution relates to loading history or other factors.

Morphomap is designed to semi-automatically: (a) place semilandmarks on the inner and outer outlines of each section, (b) extract cortical thicknesses for 2D and 3D morphometric mapping, and (c) to compute cross-sectional geometry.

In this article, we detail the algorithms and tools incorporated in *morphomap* and show that its calculations are valid. The tests performed concerning the use of *morphomap* to calculate cross-sectional geometric properties are in agreement with both theoretical expectations and the results obtained using the most popular software for such purpose (i.e., BoneJ) (Doube et al., 2010). Further, we compare 2D and 3D MMs from human and chimpanzee femora and show they are in agreement with those from previous work on larger samples (Puymerail, 2013).

Thus, *morphomap* is a new tool for the study of cortical variation in long bones. It is written in the open source R environment (R Development Core Team, 2016) and is compatible with other R packages commonly used in mesh manipulation, such as Morpho (Schlager, 2017) and Arothron (Profico, Schlager, et al., 2018), morphological studies (Adams & Otárola-Castillo, 2013) and MMs (Adler, Nenadic, & Zucchini, 2003; Sarkar, 2008). *morphomap* semi-automatically processes the entire bone, beginning with an input mesh that is separated into outer and inner cortical meshes using the CAL-SE method from the Arothron R package (Profico, Veneziano, et al., 2018). The R programming language allows for easy editing of the R code for alternative implementations and debugging. The developmental version of the *morphomap* R package is available on github (<https://github.com/AProfico/morphomap>) and the stable version is available on CRAN (<https://CRAN.R-project.org/package=morphomap>). We strongly encourage R developers to propose and code new functionalities to be included in *morphomap*.

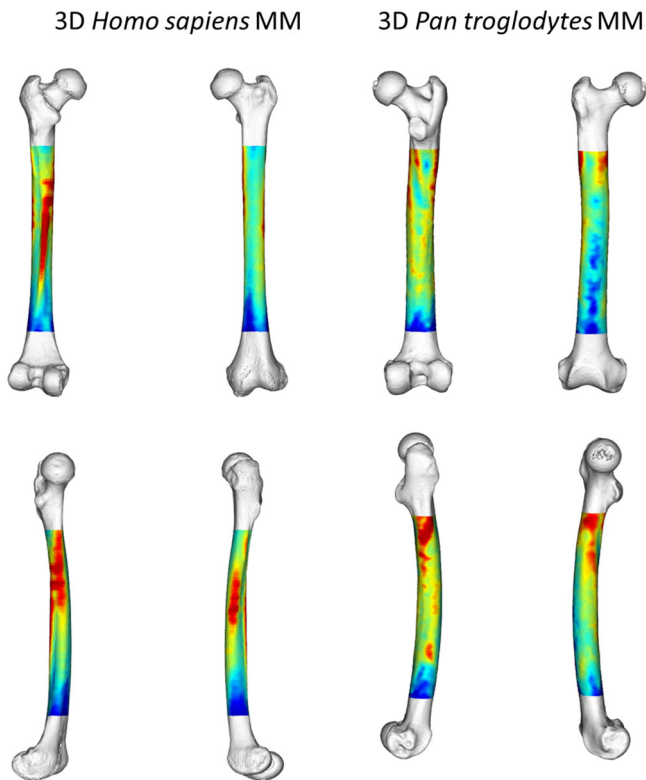


FIGURE 7 Three dimensional morphometric maps calculated on a human (OdN 244) (left) and a chimpanzee (Kupri 1022) femur

TABLE 4 Details on the computation times required by *morphomap* to process the chimpanzee femur. Inter(R) Core (TM) i7-7700HQ CPU 2.80 GHz RAM memory 16.0 GB

Process	Function	Time (s)	Note
Automatic segmentation	<i>morphomapSegm</i>	17.65	347,840 vertices
Cross sections definition	<i>morphomapCore</i>	39.92	61 sections and 1,000 points on each cross section
Definition of equiangular semilandmarks	<i>morphomapShape</i>	22.39	48 semilandmarks on each cross section and definition of the centroid
Creation of 2D morphometric map	<i>morphomapGam</i> <i>morphomap2Dmap</i>	5.94	Creation and plotting of the 2D morphometric map paired with the application of GAM smoothing algorithm
Creation of 3D morphometric map	<i>morphomap3Dmap</i>	7.95	Creation and plotting of the 3D morphometric map paired with the application of GAM smoothing algorithm
Calculation of cross-sectional geometry parameter on the cross section at the 50% of the biomechanical length	<i>morphomapCSG</i>	14.91	Full calculation of the cross-sectional geometry parameters. The speed of execution mainly depends on the definition of the picture elements side length (delta) (for details see Supporting Information).
Entire process		108.76	

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AUTHOR CONTRIBUTIONS

Antonio Profico: Conceptualization; data curation; formal analysis; funding acquisition; investigation; methodology; project administration; resources; software; validation; visualization; writing-original draft; writing-review and editing. **Luca Bondioli:** Software; writing-review and editing. **Pasquale Raia:** Software; writing-review and editing. **Paul O'Higgins:** Conceptualization; funding acquisition; methodology; project administration; software; supervision; writing-original draft; writing-review and editing. **Damiano Marchi:** Conceptualization; methodology; resources; software; supervision; validation; writing-original draft; writing-review and editing.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are included in the R package morphomap. The R package is available on CRAN at <https://CRAN.R-project.org/package=morphomap>.

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SUPPORTING INFORMATION

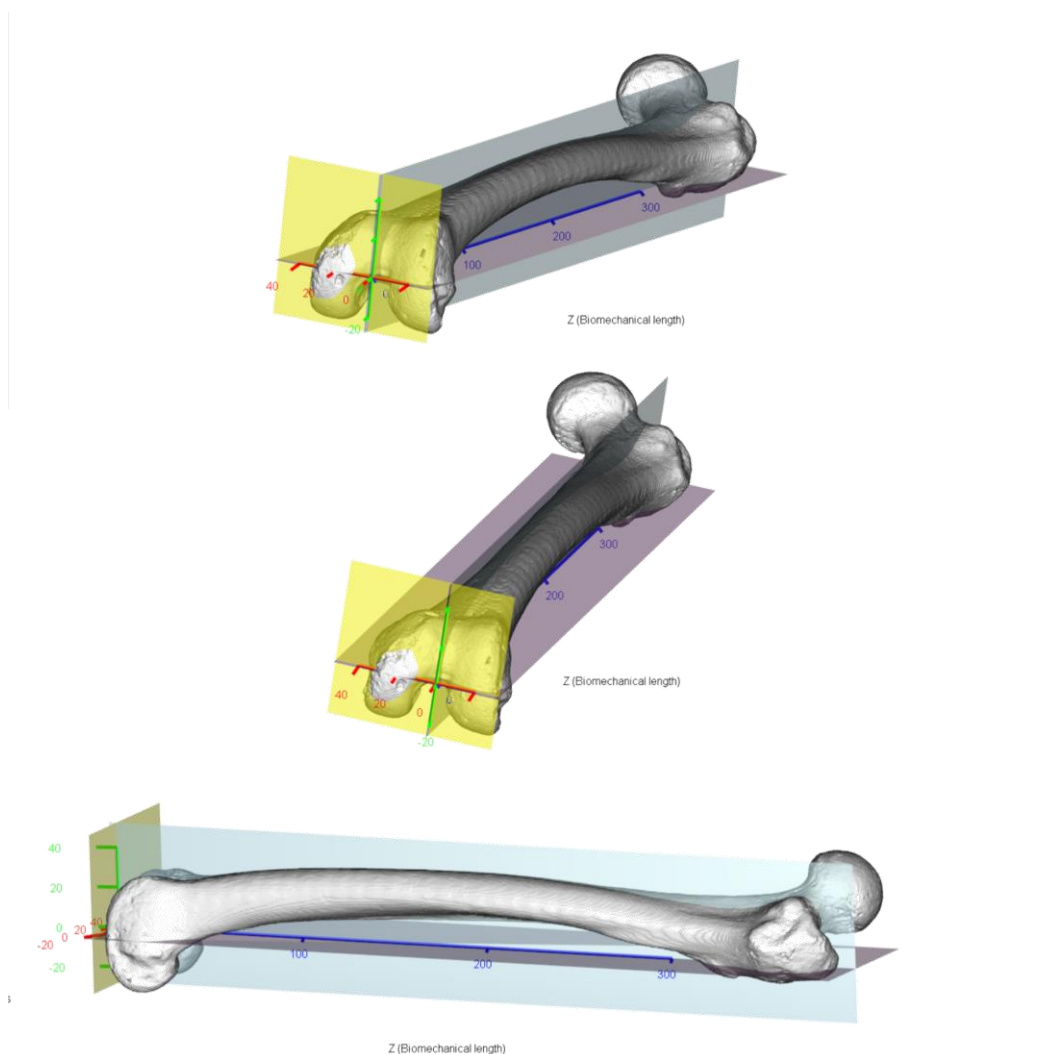
Additional supporting information may be found online in the Supporting Information section at the end of this article.

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Orientation of the long bone 3D model

The input for *morphomap* is an aligned (following Ruff, 2002) long bone mesh, with the origin of its axes (supp. Fig. 1) located distally. The x-y plane defines the transverse plane. The z axis represents the longitudinal axis of the bone. The x-z plane represents the coronal plane and the y-z plane defines the sagittal plane.

In *morphomap* the *morphomapCheck* function allows the orientation of the long bone to be visualised (Supp. Fig. 1) and so, checked before further processing.



Supp. Fig. 1 Output of the function *morphomapCheck*. The coronal plane (x-z) is in violet, the transverse plane (x-y) is in yellow and the sagittal plane (y-z) is in light blue. x axis in red, y axis in green and z axis in blue.

Cross-sectional geometry module

morphomap offers two ways to calculate the area of a cross-section (Supp. Table 1). Equation (1) (shoelace formula) directly estimates the area from the coordinates of the semilandmarks defined on a cross-section (output from *morphomapShape*). The alternative is to discretize the cortical area into picture elements of adjustable side length (*delta*) and to calculate the total area by summation, equation (2) (Supp. Fig. 2). By default, *morphomap* uses the shoelace formula to calculate the cross-sectional area.

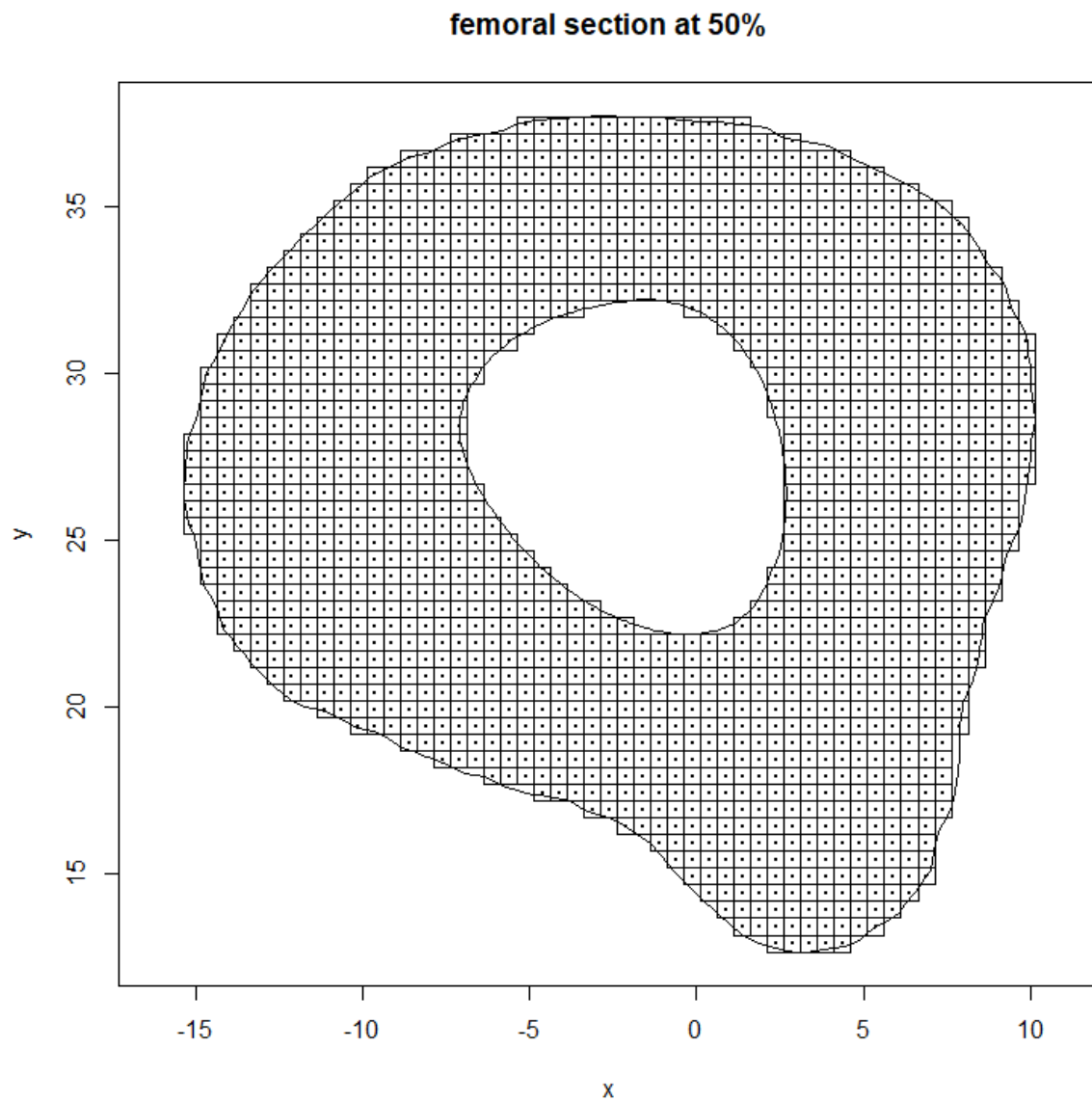
$$A = \frac{1}{2} \left| \sum_{i=1}^{n-1} x_i y_{i+1} + x_n y_1 - \sum_{i=1}^{n-1} x_{i+1} y_i - x_1 y_n \right| \quad \text{[equation (1)]}$$

$$A = \int \text{delta}^2 = \int dA \quad \text{[equation (2)]}$$

With decreasing *delta*, the results of the two equations converge (Supp. Fig. 3).

Supp. Table 1 List of functions embedded in the *morphomap* R package to calculate cross-sectional geometric parameters.

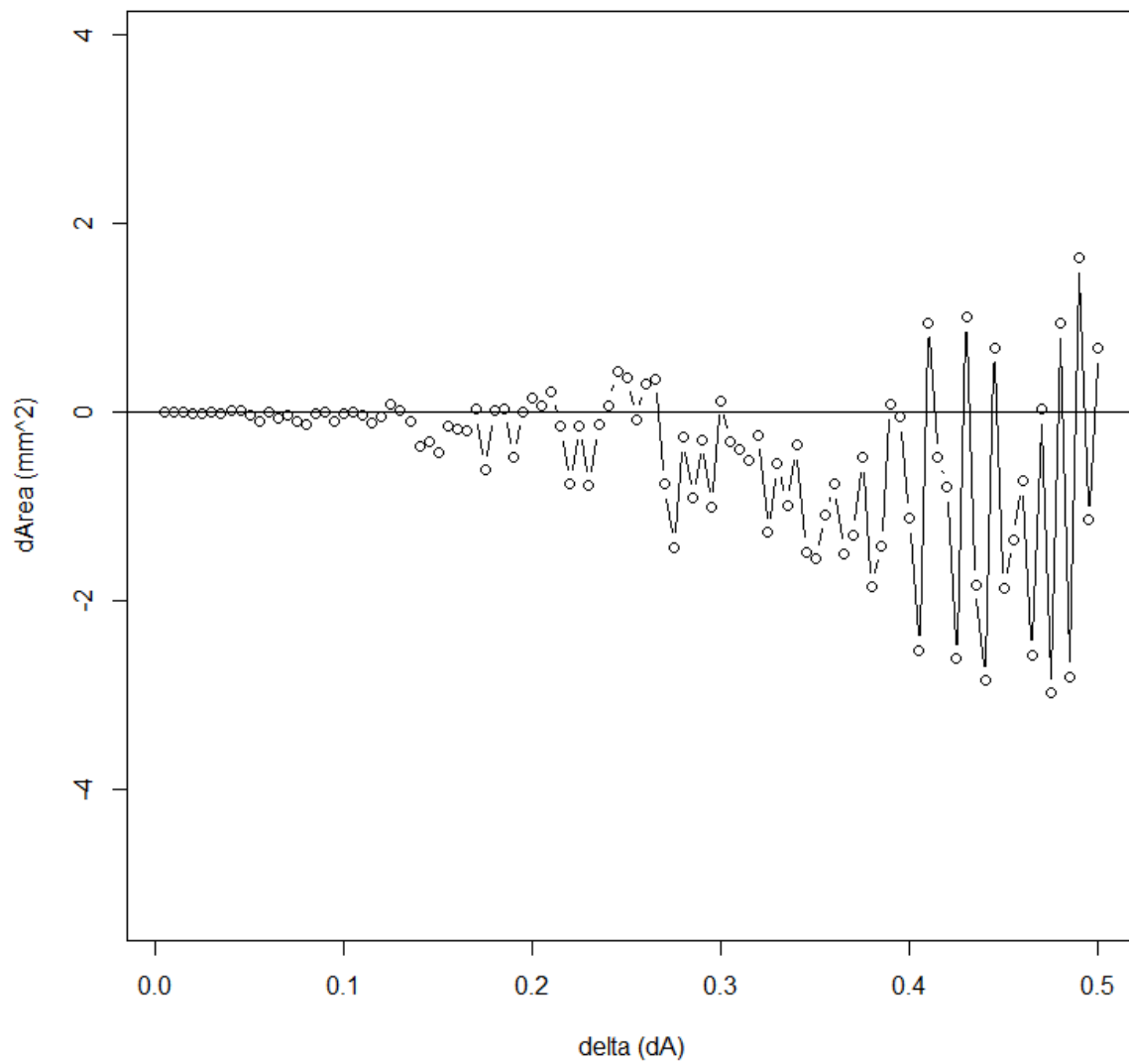
Equation	Label	Formula	R function	Specific setting
Equation (1)	A	Shoelace formula for the calculation of the cross-section area	<i>morphomapArea</i>	By default
Equation (2)	A	Polygon discretization for the calculation of the cross-section area	<i>morphomapArea</i>	Define picture element side length (0.1 mm by default)
Equation (3)	I_x	Area moment of inertia about the x axis	<i>morphomapMoment</i> <i>morphomapCSG</i>	By default
Equation (4)	I_y	Area moment of inertia about the y axis	<i>morphomapMoment</i> <i>morphomapCSG</i>	By default
Equation (5)	I_{xy}	Product of inertia about the x and y axes	<i>morphomapMoment</i> <i>morphomapCSG</i>	By default
Equation (6)	J	Polar moment of inertia	<i>morphomapCSG</i>	By default
Equation (7)	I_{max}	Maximum area moment of inertia	<i>morphomapCSG</i>	Argument I_minmax set on TRUE
Equation (8)	I_{min}	Minimum area moment of inertia	<i>morphomapCSG</i>	Argument I_minmax set on TRUE
Equation (9)	θ	Theta, angle between the maximum moment of inertia (I_x) and the x axis	<i>morphomapCSG</i>	Argument I_minmax set on TRUE
Equation (10)	Z_{pol}	Polar section modulus	<i>morphomapZmoment</i> <i>morphomapCSG</i>	Arguments and Z_{xy} I_minmax set on TRUE
Equation (12)	Z_x	Polar section modulus about the x axis	<i>morphomapZmoment</i> <i>morphomapCSG</i>	Arguments and Z_{xy} I_minmax set on TRUE
Equation (13)	Z_y	Polar section modulus about the y axis	<i>morphomapZmoment</i> <i>morphomapCSG</i>	Arguments and Z_{xy} I_minmax set on TRUE
Equation (14)	Z_{max}	Maximum polar section modulus	<i>morphomapCSG</i>	Arguments and Z_{xy} I_minmax set on TRUE
Equation (15)	Z_{min}	Minimum polar section modulus	<i>morphomapCSG</i>	Arguments and Z_{xy} I_minmax set on TRUE



Supp. Figure 2 Discretization of the cortical area into picture elements (black squares).

Equation (2) is used to calculate the total area by summing the area of each picture element.

The side length of the picture element in this example is set to 0.5 mm.

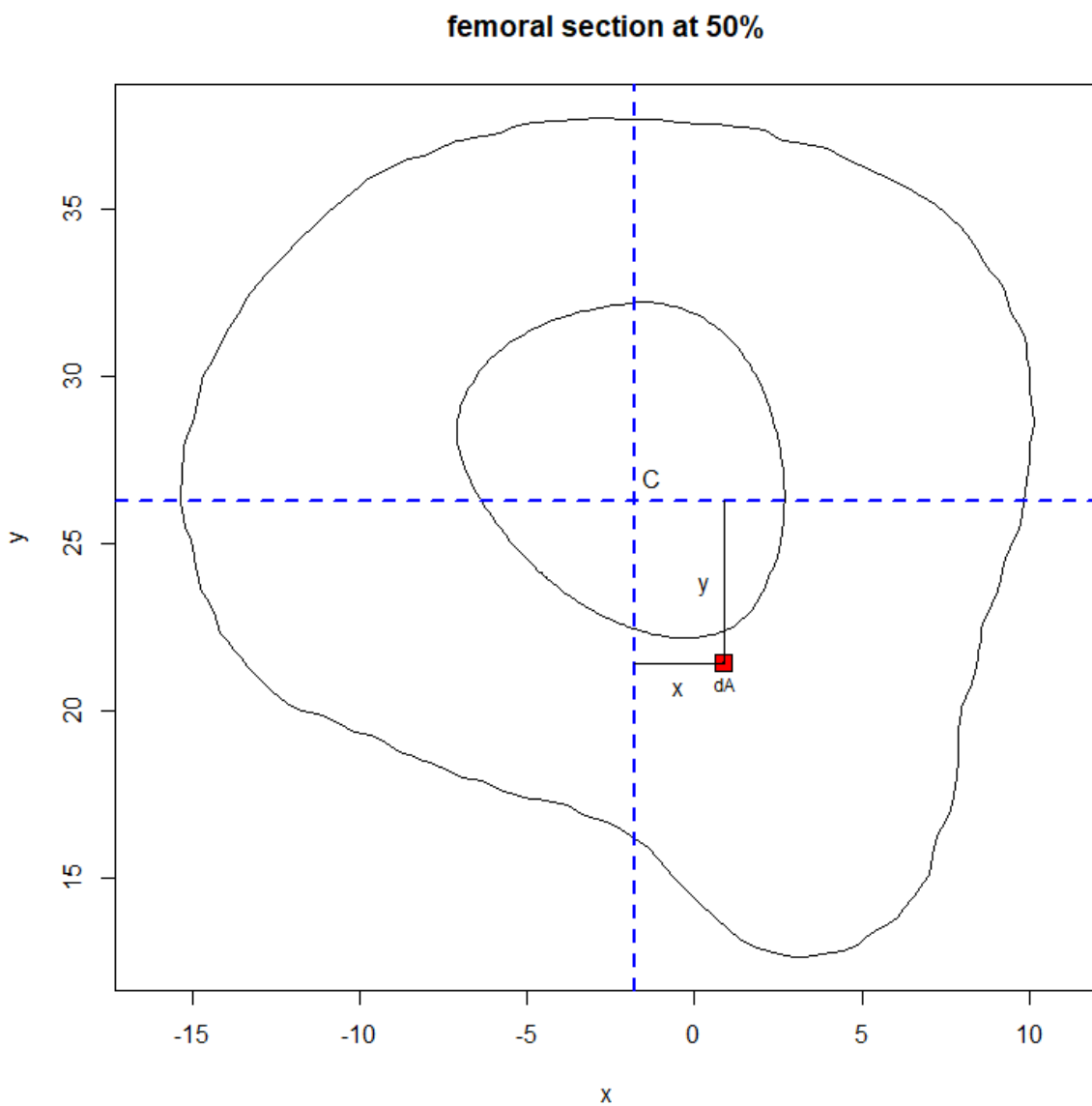


Supp. Figure 3 The horizontal line indicates the area value obtained applying equation (1).
Area calculated using equation (2).

The moment of inertia of each cross section is the sum of squares of the distances y (or x) from the x axis (or y axis) of all of the picture elements (dA) (Supp. Fig. 2 and 4).

$$I_x = \int y^2 dA \quad \text{[equation (3)]}$$

$$I_y = \int x^2 dA \quad \text{[equation (4)]}$$



Supp. Figure 4 The distances x and y between the discretised element dA (in red) and the axes passing through the centroid of the section (C).

The product of inertia is calculated as the sum of the products obtained by multiplying each element of the cross-section, dA , by its coordinates with respect to the x and y axes (with 0,0 at the centroid).

$$I_{xy} = \int xy dA \quad \text{[equation (5)]}$$

The polar moment of inertia is calculated as the sum of the products obtained by multiplying each area of the picture elements, dA by the square of the distances x and y from the axes.

$$J = \int (x^2 + y^2) dA = \int x^2 dA + \int y^2 dA = I_x + I_y \quad \text{[equation (6)]}$$

The maximum and minimum moments of inertia are calculated as I_x and I_y but with respect to the principal axis and the axis perpendicular to it, respectively. The principal axis corresponds to the direction along which the cross-section is most resistant to bending (Supp. Fig. 5).

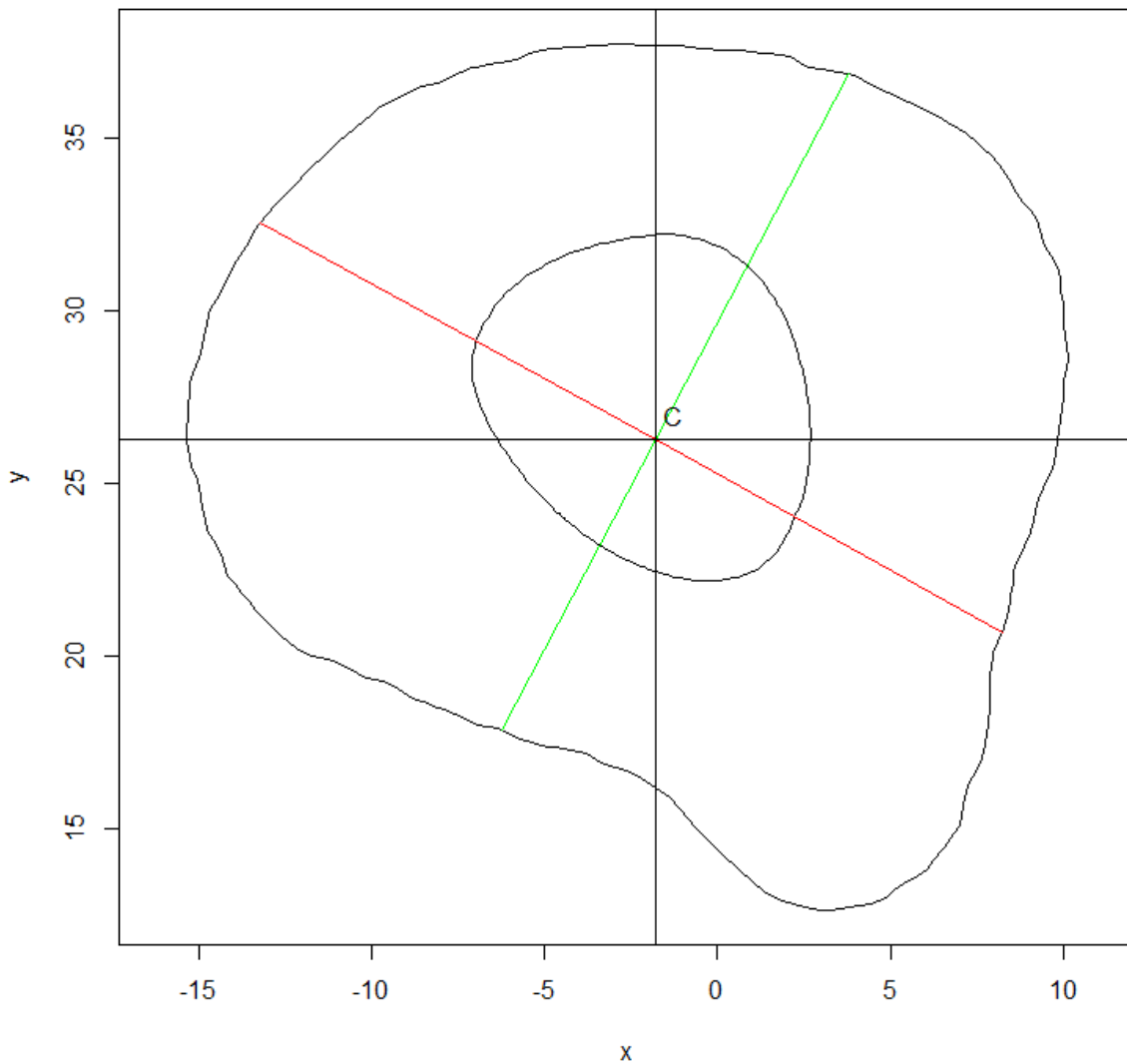
$$I_{max} = \frac{1}{2}(I_x + I_y) + \frac{1}{2}\sqrt{(I_y - I_x)^2 + (4I_{xy})^2} \quad \text{[equation (7)]}$$

$$I_{min} = \frac{1}{2}(I_x + I_y) - \frac{1}{2}\sqrt{(I_y - I_x)^2 + (4I_{xy})^2} \quad \text{[equation (8)]}$$

The angle θ is the angle between the principal axis and the x axis.

$$\theta = \frac{1}{2} \tan^{-1} \frac{2I_{xy}}{I_y - I_x} \quad \text{[equation (9)]}$$

femoral section at 50%



Supp. Figure 5 The principal axis (red line) corresponds to the direction in which the cross-section is most resistant to bending. The axis perpendicular to the principal axis (green line) corresponds to the direction in which the bone is least resistant to bending.

The polar section modulus is calculated as the ratio between the polar moment of inertia and the maximum distance to the outermost fibre of the section from its centroid.

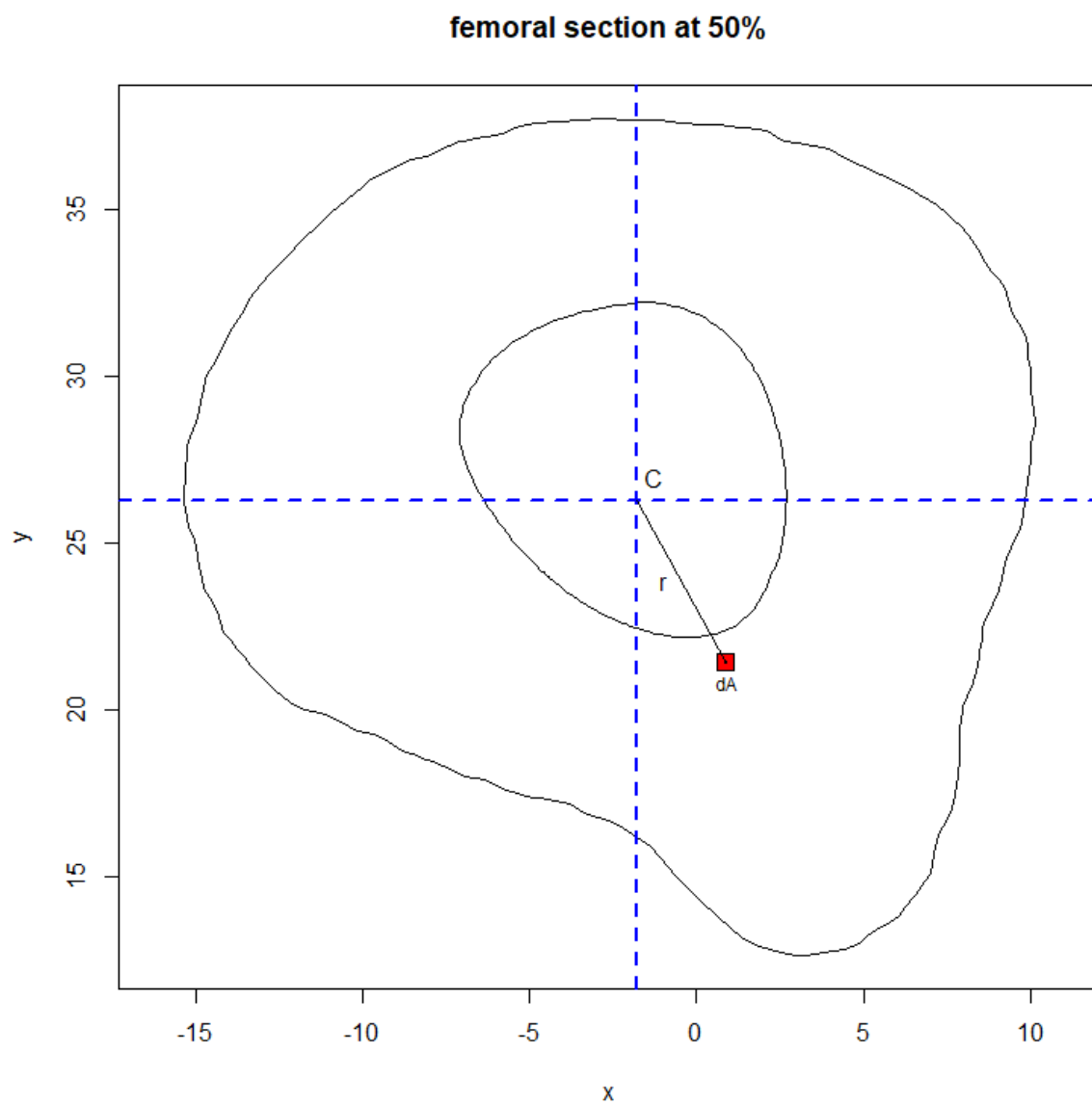
$$Z_{pol} = \frac{\int r^2 dA}{r_{max}}$$

[equation (10)]

where r is the distance from the centroid to dA (Supp. Fig. 6).

$$r = \sqrt{x^2 + y^2}$$

[equation (11)]



Supp. Figure 6 Plot showing how the polar section modulus is calculated. r is the distance from the centroid (C) to the centroid of the picture element (dA).

The section moduli are calculated as the area moments of inertia divided by the maximum chord lengths from the x and y axes passing through the centroid.

$$Z_x = \frac{I_x}{d_y} \text{ and } Z_y = \frac{I_y}{d_x} \quad [\text{equations (12) and (13)}]$$

$$Z_{max} = \frac{I_{max}}{d_{y\theta}} \text{ and } Z_{min} = \frac{I_{min}}{d_{x\theta}} \quad [\text{equations (14) and (15)}]$$

where $d_{x\theta}$ and $d_{y\theta}$ are the maximum chord lengths from the axes rotated by θ to the cross-section.

Calculation of cross-sectional properties for cylindrical and rectangular cross-sections

The area moment of inertia for a hollow circular cross-section is calculated as:

$$I_x = I_y = \frac{\pi(d_o^4 - d_i^4)}{64} \quad [\text{equation (16)}]$$

where d_o is the cylinder external diameter and d_i is the cylinder internal diameter.

The cortical area is calculated as:

$$CCA = \pi r_o^2 - \pi r_i^2 \quad [\text{equation (17)}]$$

where r_o is the cylinder external radius and r_i is the cylinder internal radius.

The area moment of inertia for a hollow rectangular cross-section can be calculated as:

$$I_x = \frac{BH^3}{12} - \frac{bh^3}{12} \quad [\text{equation (18)}]$$

$$I_y = \frac{HB^3}{12} - \frac{hb^3}{12} \quad [\text{equation (19)}]$$

The cortical area is calculated as:

$$CCA = BH - bh \quad \text{[equation (20)]}$$

where B is the width of the external rectangle and b is the width of the internal rectangle. H and h are the heights of the external and internal rectangles, respectively.

Comparing the human and chimpanzee femur bone

Section at 20%



Section at 25%



Section at 30%



Section at 35%



Section at 40%



Section at 45%



Section at 50%



Section at 55%



Section at 60%



Section at 65%



Section at 70%



Section at 75%



Section at 80%



Supp. Figure 7 Cross-sections extracted from the human (OdN 244) femur. For graphical purpose only 13 cross-sections are reported.

Section at 20%



Section at 25%



Section at 30%



Section at 35%



Section at 40%



Section at 45%



Section at 50%



Section at 55%



Section at 60%



Section at 65%



Section at 70%



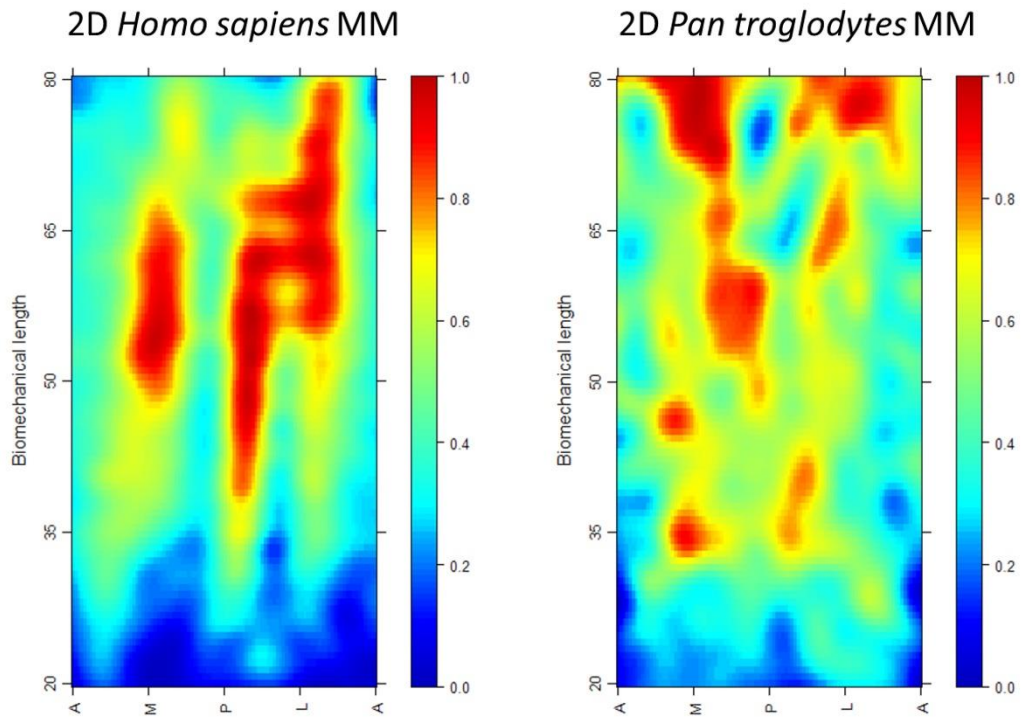
Section at 75%



Section at 80%



Supp. Figure 8 Cross-sections extracted from the chimpanzee (Kupri 1022) femur. For graphical purpose only 16 cross-sections are reported.



Supp. Figure 9 Two dimensional morphometric maps calculated on a) a human (OdN 244) and b) a chimpanzee (Kupri 1022) femur.

Supplementary Table 2. Cross-sectional geometric parameters calculated using *morphomap* on the human (OdN 244) femur. For each cross section the following variables are provided: the coordinates of the centroid (Cx and Cy), the total area (TotA), the medullary area (MedA), the cortical area (CA), the periosteal perimeter (ExtP), the endosteal perimeter (MedP), the mean cortical thickness (MeanThick), the minimum cortical thickness (MinThick), the standard deviation of the cortical thickness (SdThick), the maximum cortical thickness (MaxThick), the area moment of inertia around the Y axis (I_x), the area moment of inertia around the X axis (I_y), the section modulus around the Y and X axis (Z_x and Z_y , respectively), the maximum chord length from the y (dx) and x (dy) axes, the polar section modulus (Z_{pol}), the maximum and minimum area moments of inertia (I_{max} and I_{min} , respectively), the polar moment of inertia (J), the maximum and minimum section modulus (Z_{max} and Z_{min} , respectively) and the theta angle (θ).

Section (%)	Cx	Cy	TotA	MedA	CCA	ExtP	MedP	MeanThick	SdThick	MinThick	MaxThick	I_x
20	-2.97	19.68	717.82	416.72	301.1	98.91	76.43	3.65	0.57	2.66	4.76	21798.41
25	-3.39	22.2	596.71	278.92	317.8	88.52	60.93	4.39	0.48	3.5	5.25	19521.87
30	-3.51	23.94	530.06	198.6	331.45	83.35	50.79	5.05	0.64	3.9	6.74	18402.02
35	-3.21	25.16	496.86	140.86	356	81.76	42.45	5.85	0.78	4.67	7.84	18149.7
40	-2.9	25.86	474.32	105.73	368.59	80.92	36.83	6.47	0.93	4.95	9.25	17161.98
45	-2.25	26.21	463.93	90.67	373.26	80.23	33.94	6.75	1.07	5.32	9.97	16504.33
50	-1.8	26.24	460.37	74.32	386.06	80.29	31.14	7.25	1.27	5.44	10.36	15788.98
55	-1.3	25.97	464.12	58.52	405.6	80.04	27.68	7.97	1.56	5.44	11.1	15177.38
60	-0.88	25.34	461.89	64.45	397.43	78.93	29.01	7.62	1.27	5.39	9.67	14127.82
65	-0.48	24.16	463.16	71.48	391.67	78.02	30.1	7.38	1.07	5.65	9.18	13570.49
70	0.04	22.28	480.61	89.58	391.03	79.5	33.78	7.06	1.1	5.15	9.51	15028.4
75	0.19	19.98	495.04	106.62	388.42	82.74	37.35	6.72	1.09	5.47	9.34	16899.99
80	0.41	17.63	536.85	162.1	374.74	85.65	46.34	5.83	1.07	4.5	8.61	20236.73
Section (%)	I_y	Z_x	Z_y	Z_{pol}	dx	dy	I_{max}	I_{min}	J	Z_{max}	Z_{min}	theta
20	34109.99	1522.82	1834.96	3027.93	18.59	14.31	34120.97	21858.47	55908.4	1836.54	1518.24	0.01
25	25330.93	1439.47	1609.2	2800.06	15.74	13.56	25330.63	19491.45	44852.81	1605.42	1445.16	-0.03
30	20453.84	1324.35	1427.1	2615.41	14.33	13.9	20454.88	18383.19	38855.86	1446.93	1332.39	0.07
35	18791.17	1274.31	1416.63	2534.51	13.26	14.24	19375.85	17554.08	36940.87	1461.54	1363.62	0.61
40	17870.36	1209.87	1369.9	2349.09	13.05	14.19	19280.54	15749.25	35032.35	1423.19	1229.38	0.68
45	17649.17	1168.72	1330.19	2299.06	13.27	14.12	19261.07	14905.41	34153.5	1411.13	1201.94	0.65
50	18443.6	1164.53	1358.84	2311.91	13.57	13.56	19525.64	14668.7	34232.58	1484.86	1208.47	0.5
55	19793.53	1188.03	1435.98	2437.26	13.78	12.78	20494.19	14469.83	34970.9	1514.34	1228.21	0.35
60	20160.18	1190.32	1466.33	2486.69	13.75	11.87	20315.9	13994.71	34288	1490.08	1247.53	0.15
65	20557	1211.8	1468.32	2427.12	14	11.2	20552.4	13551.11	34127.49	1462.25	1201.12	-0.05
70	21414.57	1301.65	1536.83	2542.3	13.93	11.55	22328.74	14101.07	36442.98	1561.35	1228.29	-0.34
75	22246.05	1414.75	1616.42	2521.01	13.76	11.95	25452.39	13729.56	39146.04	1674.67	1214.25	-0.55
80	24511.3	1526.01	1729.81	2721.49	14.17	13.26	30286.59	14520.68	44748.03	1839.31	1293.24	-0.65

Supplementary Table 3. Cross-sectional geometric parameters calculated using *morphomap* on the chimpanzee (No 1022) femur. For each cross section the following variables are provided: the coordinates of the centroid (Cx and Cy), the total area (TotA), the medullary area (MedA), the cortical area (CA), the periosteal perimeter (ExtP), the endosteal perimeter (MedP), the mean cortical thickness (MeanThick), the minimum cortical thickness (MinThick), the standard deviation of the cortical thickness (SdThick), the maximum cortical thickness (MaxThick), the area moment of inertia around the Y axis (Ix), the area moment of inertia around the X axis (Iy), the section modulus around the Y and X axis (Zx and Zy, respectively), the maximum chord length from the y (dx) and x (dy) axes, the polar section modulus (Zpol), the maximum and minimum area moments of inertia (Imax and Imin, respectively), the polar moment of inertia (J), the maximum and minimum section modulus (Zmax and Zmin, respectively) and the theta angle (θ).

Section (%)	Cx	Cy	TotA	MedA	CCA	ExtP	MedP	MeanThick	SdThick	MinThick	MaxThick	Ix
20	1.27	11.12	509.47	165.22	344.26	81.44	48.73	5.51	0.3	4.91	6.14	14625.64
25	1.32	13.26	493.11	142.33	350.78	79.68	45.09	5.83	0.28	5.14	6.49	15138.56
30	1.41	14.99	477.04	122.32	354.72	78.26	41.94	6.12	0.46	5.06	7.25	14623.94
35	1.46	16.13	457.67	93.17	364.51	76.62	36.23	6.66	0.65	5.31	7.63	14028.17
40	1.74	17.29	443.01	94.84	348.16	75.27	37.77	6.41	0.52	5.55	7.71	13458.2
45	1.93	17.86	443.85	87.62	356.23	75.42	35.86	6.62	0.71	5.2	8.72	13846.83
50	2.27	18	449.59	92.59	356.99	75.85	35.06	6.55	0.51	5.53	7.32	14093.96
55	2.4	17.88	449.74	88.28	361.46	75.8	35.49	6.69	0.51	5.75	8.34	13829.39
60	2.39	17.54	446.2	81.89	364.31	75.56	34.07	6.85	0.49	5.97	8.08	13190.49
65	1.9	16.72	446.77	92.87	353.89	75.74	35.03	6.48	0.5	5.58	7.41	12944.62
70	1.27	15.42	440.14	83.5	356.64	75.66	33.53	6.69	0.34	6.03	7.48	13013.99
75	0.59	13.72	447.26	77.03	370.23	76.52	33.95	6.96	0.87	5.49	8.9	12413.38
80	0.32	11.09	492.4	74.21	418.19	80.67	34.46	7.73	1.16	6.49	11.14	15647.78
Section (%)	Iy	Zx	Zy	Zpol	dx	dy	Imax	Imin	J	Zmax	Zmin	theta
20	23362.71	1292.03	1595.86	2581.39	14.64	11.32	23457.9	14539.19	37988.35	1592.25	1269.42	0.1
25	20825.83	1310.57	1517.22	2549.98	13.73	11.55	21138.69	14828	35964.39	1503.19	1262.98	0.22
30	19586.61	1280.08	1449.39	2520.44	13.51	11.42	19944.42	14306.4	34210.56	1470.54	1258.67	0.24
35	18319.22	1213.56	1384.06	2428.78	13.24	11.56	18796.5	13554.25	32347.39	1415.21	1193.09	0.31
40	16638.33	1170.32	1301.91	2294.98	12.78	11.5	17269.48	12835.85	30096.52	1316.33	1142.79	0.39
45	16546.88	1169.01	1295.3	2329.22	12.77	11.84	17204.25	13206.5	30393.71	1314.93	1158.01	0.41
50	16881.29	1203.09	1337.16	2361.89	12.62	11.71	17201.32	13794.83	30975.25	1312.72	1189.54	0.31
55	17305.32	1205.8	1346.62	2416.84	12.85	11.47	17390.69	13737.08	31134.7	1369.51	1206.59	0.14
60	17741.77	1166.74	1372.09	2377.63	12.93	11.31	17746.07	13183.8	30932.26	1371.56	1167.13	-0.01
65	17892.33	1149.77	1365.61	2356.98	13.1	11.26	17957.99	12878	30836.95	1378.2	1156.95	-0.13
70	17192.85	1142.94	1316.36	2276.59	13.06	11.39	17622.01	12571.36	30206.84	1325.71	1081.85	-0.3
75	19410.32	1119.59	1412.57	2312.95	13.74	11.09	19508.6	12302.02	31823.7	1417.89	1113.67	-0.13
80	22851.54	1330.8	1604.37	2621.59	14.24	11.76	22880.93	15621.74	38499.33	1587.35	1324.94	0.06

Reference list

Ruff CB. 2002. Long bone articular and diaphyseal structure in Old World monkeys and apes. I: locomotor effects. *Am J Phys Anthropol Off Publ Am Assoc Phys Anthropol* 119:305–342.

The essential guide to the use of morphomap

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morphomap: an introduction

morphomap is designed to analyse long bone morphology. It virtually sections the bone at n evenly spaced levels along the diaphysis. *morphomap* is organized as three modules: 2D and 3D morphometric maps, bone landmarking and cross-sectional geometry. The stable version of *morphomap* is available on CRAN at <https://CRAN.R-project.org/package=morphomap>, the developmental version is available on GitHub at <https://github.com/morphomap>.

morphomap: list of contents

1. Install *morphomap*
2. Load example data
3. Automatic long bone segmentation
4. Extraction of cross sections
5. Definition of semilandmark configurations
6. Visualization and exporting of the semilandmark configuration
7. 2D morphometric maps
8. 3D morphometric maps
9. Exporting cross section pictures
10. Exporting cross section raster images
11. Cross-sectional geometry
12. Work in progress

1. Install morphomap

To install *morphomap* please type the following code:

```
install.packages("morphomap")
```

To install the developmental version of *morphomap* please type the following code:

```
require(devtools)
```

```
install_github("AProfico/morphomap", local=FALSE)
```

To load the library:

```
library(morphomap)
```

2. Load example data

In *morphomap* we provide two femora ready to be processed. Their names include their biomechanical length (380.23 and 277.13 mm), for ease of reference.

1. HomFem38023

2. PanFem27713

To upload and visualize the two examples data

```
data(HomFem38023)
data(PanFem27713)
library(rgl)
open3d()
wire3d(HomFem38023, col="violet")
open3d()
wire3d(PanFem27713, col="orange")
```



Figure 1. The two femora available as example data in the *morphomap* R package

3. Automatic long bone segmentation

morphomap requires as input an oriented long bone mesh as is deemed appropriate to the study by the user. *morphomap* supports various mesh file formats (i.e., .ply, .obj, .stl).

The user can check the orientation of the long bone by using the function

morphomapCheck.

```
morphomapCheck (HomFem38023)
```

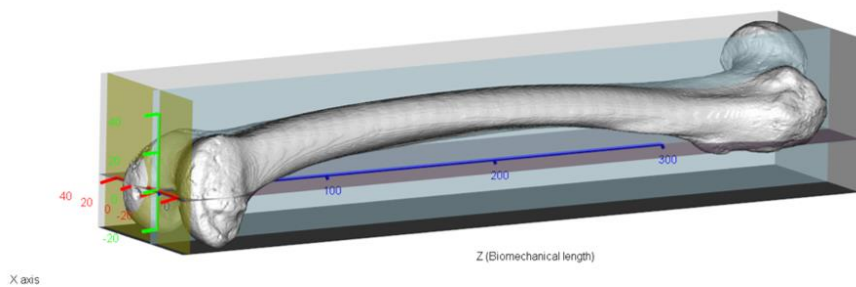


Figure 2. The orientation of the mesh can be checked using the function *morphomapCheck*.

The first step of the procedure is the automatic separation of the periosteal and endosteal surfaces by applying the CA-LSE tool (Computer Assisted Laser Scanner Emulator) (Profico et al., 2018).

```
meshes<-morphomapSegm(HomFem38023)
perMesh<-meshes$external
endMesh<-meshes$internal
open3d()
wire3d(perMesh,col="green")
open3d()
wire3d(endMesh,col="red")
```

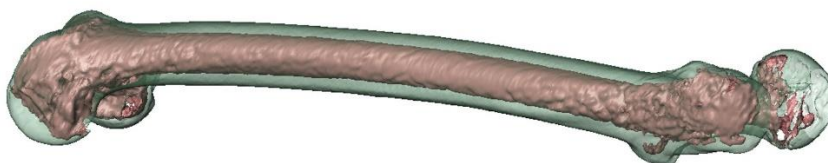


Figure 3. The periosteal and endosteal surfaces are reported in green and red respectively.

Alternatively, the user can import two segmented meshes representing the periosteal and endosteal surfaces.

4. Extraction of cross sections

First the user needs to define the total biomechanical length.

```
mech_length<-380.23
```

In the next step, *morphomapCore* extracts by default the cross sections at regular increments of 1% along the shaft between 20% (distal) to 80% (proximal) of the biomechanical length of the bone. The biomechanical length is defined by the user. At each increment a plane (transverse plane) perpendicular to the frontal plane is drawn and the intersection between the transverse plane and the two meshes (periosteal and endosteal) is used to define the periosteal and endosteal contours of each cross section.

```
rawSections<-morphomapCore(out.sur=perMesh, inn.sur=endMesh,  
num.sect=61,mech.len = mech_length,start = 0.2,end=0.8)
```

5. Definition of semilandmark configurations

The object *rawSections* contains all the information concerning the cross sections. Among other R objects in the output are embedded four arrays containing 2D and 3D coordinates of both periosteal and endosteal cross sections.

```
open3d()  
  
plot3d(rawSections$`3D_out`[, , 1], aspect=FALSE, col="grey",  
type="l",lwd=5,xlab="x", ylab="y",zlab="z")  
  
plot3d(rawSections$`3D_inn`[, , 1], aspect=FALSE,col="red",  
type="l",lwd=5,add=TRUE)  
  
x11()  
  
plot(rawSections$`2D_out`[, , 1], asp=1, col="grey",  
type="l",lwd=5,xlab="x",ylab="y")  
  
points(rawSections$`2D_inn`[, , 1], col="red",type="l",lwd=5)
```

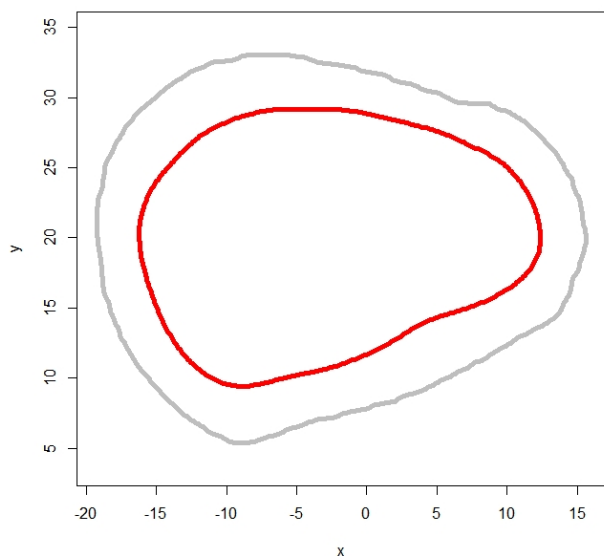


Figure 4. First cross section of the human femur. The periosteal contour is reported in gray, the endosteal contour in red.

The next step is the creation of an array of equiangular semilandmarks, using the function *morphomapShape*.

```
shapeSections<-morphomapShape(rawSections, 21, sects_vector=NULL,
cent.out="CCA",delta=0.1,side="left")

sect1_ext<-shapeSections$`2D_out`[, ,1]
sect1_int<-shapeSections$`2D_inn`[, ,1]

centroid_CCA<-morphomapCentroid(sect1_ext,sect1_int)

plot(sect1_ext,asp=1,xlab="x",ylab="y",main="Section 1 - CCA",col="blue")

points(sect1_int,asp=1,col="red")

start<-c(centroid_CCA[1],centroid_CCA[2])

for(i in 1:21){
to_e<-sect1_ext[i,]
points(rbind(start,to_e),type="l",lty=2)
}

points(centroid_CCA[1],centroid_CCA[2],pch=19,col="orange")
```

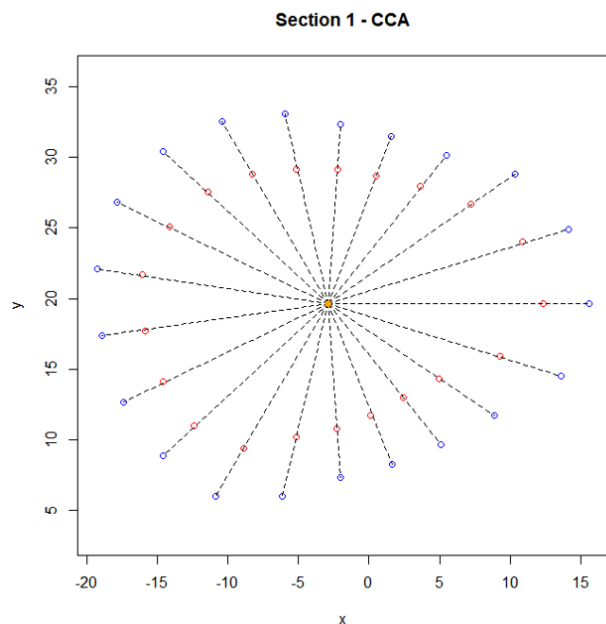


Figure 5. 21 equiangular semilandmarks are sampled on the periosteal (blue) and endosteal (red) contours. The center of cortical area is shown in orange.

The user can decide how to define the centroid of each cross section. The available choices are *CCA* (center of cortical area), *E* (barycenter of the external outline) and *I* (barycenter of the internal outline).

6. Visualization and exporting of the semilandmark configuration

morphomap includes a function (*morphomapPlotShape*) to show the semilandmarks defined on the cross sections.

The user can visualize just a single cross section in 2D or 3D, by setting the argument *dims* on 2 or 3 respectively.

```
morphomapPlotShape(shapeSections,dims=2,vecs=1,lines=TRUE,centroid=TRUE,cent.out="CCA")
```

```
morphomapPlotShape (shapeSections, dims=3, lines=TRUE, centroid=TRUE, lwd=2, vecs
=1)
```

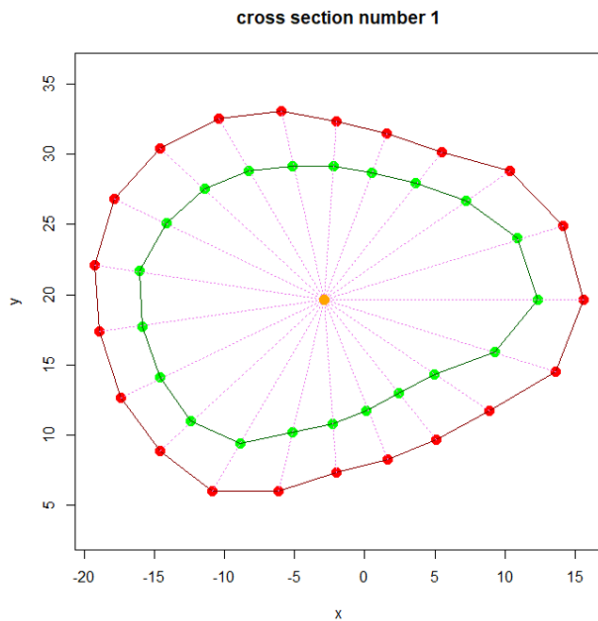


Figure 6. Output of the function *morphomapPlotShape* setting the argument *dims* on 2. The equiangular semilandmarks on the periosteum and on the endosteum are shown respectively in red and green. The center of cortical area is shown in orange. The radii connecting the centroid with the semilandmarks are reported in fuchsia.

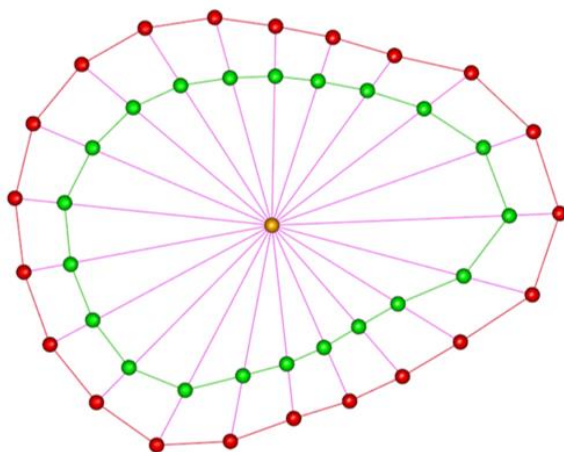


Figure 7. Output of the function *morphomapPlotShape* setting the argument *dims* on 3. The equiangular semilandmarks on the periosteum and on the endosteum are shown respectively in red

and green. The center of cortical area is shown in orange. The radii connecting the centroid with the semilandmarks are reported in fuchsia.

Another possibility is to show the entire semilandmark configuration including a triangulated mesh. In fact, by setting the argument *vecs* to *NULL*, all the cross sections will be considered.

```
morphomapPlotShape(shapeSections, dims=3, size=0.5, lwd=2, lines=FALSE, vecs=NULL)
```

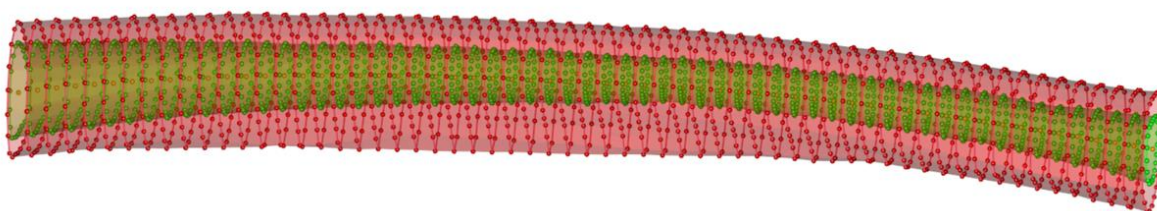


Figure 8. Output of the function *morphomapPlotShape* setting the arguments *dims* and *vecs* on 3 and *NULL* respectively. The equiangular semilandmarks on the periosteum and on the endosteum are shown in red and green respectively. The semilandmark configuration is converted to a triangulated mesh.

The semilandmark configurations can be exported from *morphomap* in the morphologika file format using the function *morphomapWriteMorphologika*.

The user can export single cross sections in two or three dimensions

```
section_1<-shapeSections$`3D_out`[, ,1]
morphomapWriteMorphologika(section_1, file="Sect13D.txt")
section_1<-shapeSections$`2D_out`[, ,1]
morphomapWriteMorphologika(section_1, file="Sect12D.txt")
```

or the entire semilandmark configurations on the periosteal and endosteal contours

```
periosteal_sl<-shapeSections$`3D_out`  
morphomapWriteMorphologika(periosteal_sl,file="periosteal.txt")  
endosteal_sl<-shapeSections$`3D_inn`  
morphomapWriteMorphologika(endosteal_sl,file="endosteal.txt")
```

7. 2D morphometric maps

Morphometric maps of cortical thickness are useful to interpret the distribution of cortical bone in long bones. On the 2D map the cortical thickness distribution, standardised from 0 (minimum) to 1 (maximum), is mapped in an XY plot where the X axis corresponds to the unfolded cross section starting and ending at the anterior (A) border passing through the lateral (L), posterior (P) and medial (M) borders. On the Y axis is reported the diaphyseal length expressed as a percentage of the biomechanical length. By default (*scale=TRUE*), the 2D map is built scaling the thickness values from 0 to 1. Alternatively (*scale=FALSE*) the 2D map is not scaled.

```
library(colorRamps)  
bone2Dmap<- morphomap2Dmap(morphomap.shape=shapeSections, gam=FALSE, plot =  
TRUE, rem.out = TRUE, fac.out = 1.0, pal = blue2green2red(101), aspect=2)  
bone2Dmap<-morphomap2Dmap(morphomap.shape = shapeSections, gam=TRUE, plot  
= TRUE, rem.out = TRUE, fac.out = 1.0, pal = blue2green2red(101), aspect=2)
```

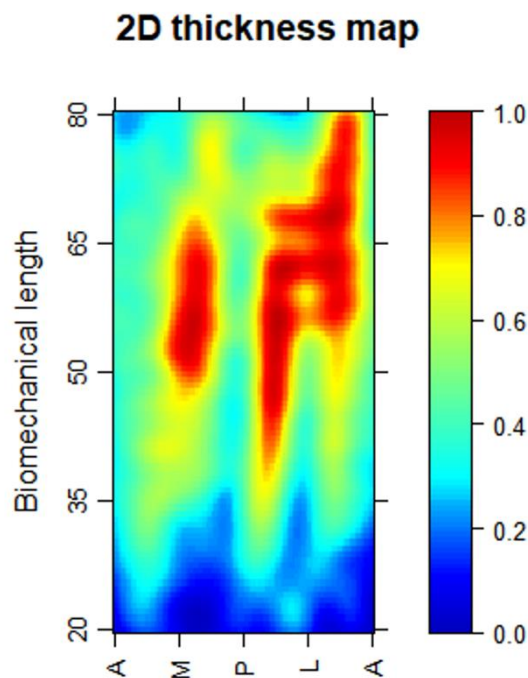


Figure 9. Morphometric map of the human femur. On the right a legend is reported with the scaled values, from 0 to 1, of the cortical thickness.

8. 3D morphometric maps

morphomap produces 3D morphometric maps by colouring the facets of the periosteal surface mesh according to thickness values at their vertices. First, *morphomap* calculates the distances between the coordinates of vertices belonging to the periosteal mesh and the semilandmarks defined on the periosteal contour of the cross sections. *morphomap* estimates the thickness value at each vertex weighting the value according to the distance between the vertex of the mesh and the semilandmark configurations at which the thicknesses are calculated.

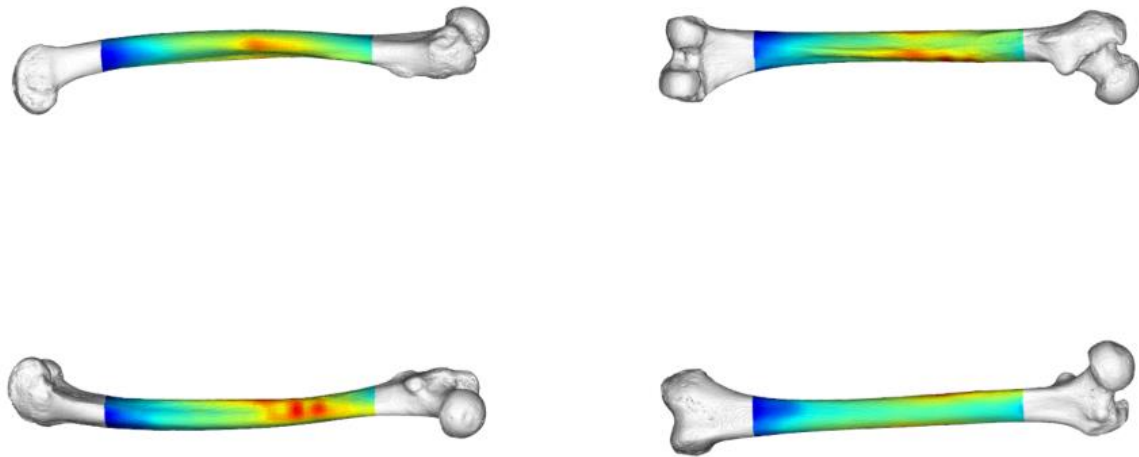


Figure 9. 3D Morphometric map of the human femur. The femur bone is shown in the four principal anatomical views.

9. exporting cross section pictures

In *morphomap*, the user can export a picture of each cross section in TIFF format. In the picture of each cross section the cortical area is represented in black, the medullary canal in white. On the bottom left a metric reference is supplied. Thickness values at the four quadrants (L, A, M e P) can be added to the exported cross section. The background, the legend and the cortical bone colours are fully customizable by the user. The destination folder will be created in the working directory. The name of the directory is defined by the argument *dirpath*.

```
dir.create("picts")
morphomapPic(rawSections,shapeSections, full=TRUE,dirpath="picts",
width=2500,height=2500)
```

10. exporting cross section raster images

Another functionality of *morphomap* is the possibility to export a raster image of a cross section by using the *morphomapRaster* function. The user can define the pixel/mm ratio (0.1 by default) and export the raster image as TIFF format ready to be converted to its real size.

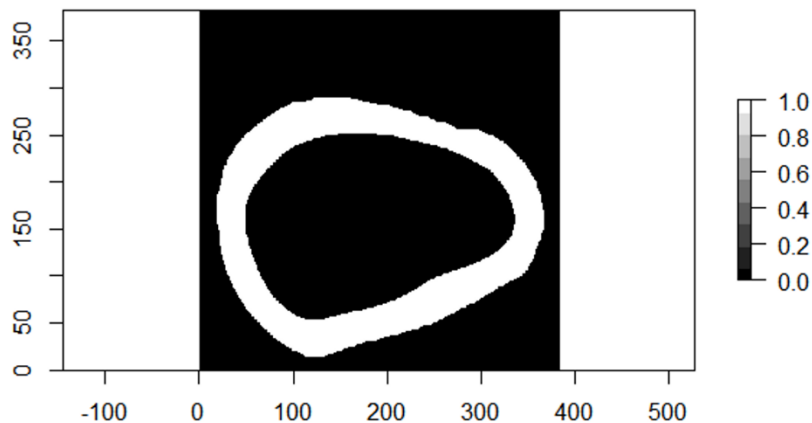


Figure 10. Plot of the raster image of the first cross-section.

11. Cross-sectional geometry

morphomap calculates for each cross section the CSG parameters generally used in biomechanical studies: the area moments of inertia (I_x , I_y), the principal area moments of inertia (I_{max} and I_{min}), theta (θ), the polar moment of inertia (J) and the section modulus (Z_x , Z_y , Z_{max} , Z_{min} and Z_{pol}). In the supplementary information the formula of each CSG parameter implemented in *morphomap* is reported. For the calculation of biomechanical parameters *morphomap* converts the coordinates of the periosteal and endosteal contours into pixel coordinates.

In the following example the CSG parameters are calculated on the section at 50% of the biomechanical length:

```
shapeSectionsCSG<-morphomapShape(rawSections, 100, sects_vector=NULL,
cent.out="CCA",delta=0.1,side="left")

csgSect31<-morphomapCSG(cp = shapeSectionsCSG`2D_out`[, ,31],
mp=shapeSections`2D_inn`[, ,31], translate = FALSE,center="CCA",delta=0.1)
```

The user can easily store a matrix in *morphomap* by writing the calculated CSG parameters for the entire diaphysis by coding a for loop from the first to the last cross section. In the following example from 1 to 61.

```
#Cross sectional geometry along the entire femur bone
results<-matrix(NA,ncol=24,nrow=61)
rownames(results)<-paste("sect",c(1:61))

colnames(results)<-c("Cx","Cy","T_area","M_area","CA",
"Ext_perim","Med_perim","Mean_thick","Sd_thick" ,
"Min_thick","Max_thick","Ix","Iy","Zx" ,"Zy","Zpol" ,
"dx","dy","Imin","Imax","J","Zmax","Zmin","theta")

for(i in 1:61){
results[i,]<-unlist(morphomapCSG(cp = shapeSectionsCSG`2D_out`[, ,i], mp=
shapeSectionsCSG`2D_inn`[, ,i],translate = FALSE,center="CCA",delta = 0.1))
}

fix(results)
```

11. Work in progress

morphomap is always under development. New releases come out regularly.

News and updates will be communicated on Twitter. Feedback from users is very important to us. Your feedback helps us make improvements and drives changes in the next

morphomap release: <https://twitter.com/morphomap>.