Package 'morphomap'

January 12, 2020

Type Package

Title Morphometric Maps, Bone Landmarking and Cross Sectional Geometry

Version 1.1

Description Extract cross sections from long bone meshes at specified intervals along the diaphysis. Calculate two and three-dimensional morphometric maps, cross-sectional geometric parameters, and semilandmarks on the periosteal and endosteal contours of each cross section.

Depends R (>= 3.4.0)

Imports Arothron (>= 1.0), lattice (>= 0.2), mgcv (>= 1.8), Rvcg (>= 0.18), Morpho (>= 2.0), oce (>= 1.1), rgdal (>= 1.4), raster (>= 3.0), rgl (>= 0.1), sp (>= 1.3), geometry (>= 0.4.0), colorRamps (>= 2.3), DescTools (>= 0.99), grDevices (>= 3.5), graphics (>= 3.5)

License GPL-2

Encoding UTF-8

LazyLoad yes

RoxygenNote 6.1.1

NeedsCompilation no

Author Antonio Profico [aut, cre], Luca Bondioli [aut], Pasquale Raia [aut], Julien Claude [ctb], Paul O'Higgins [aut], Damiano Marchi [aut]

Maintainer Antonio Profico <antonio.profico@gmail.com>

Repository CRAN

Date/Publication 2020-01-12 15:40:06 UTC

R topics documented:

`morphomap-package` *2D and 3D cortical thickness maps and cross sectional geometry*

Description

Tool to process long bone meshes (shape data, morphometric maps and cross-sectional geometry)

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

HomFem38023 *example dataset*

Description

3D mesh of a human femur bone

Usage

```
data(HomFem38023)
```

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

morphomap2Dmap *morphomap2Dmap*

Description

Create a 2D cortical thickness map

Usage

```
morphomap2Dmap(morphomap.shape, rem.out = FALSE, fac.out = 0.5,
  smooth = FALSE, scale = TRUE, smooth.iter = 5, gamMap = FALSE,
  nrow = 90, ncol = 100, gdl = 250, method = "equiangular",
  unwrap = "A", plot = TRUE, pal = blue2green2red(101), aspect = 2)
```

Arguments

morphomap.shape	list: output from morphomapShape function
rem.out	logical: if TRUE the outlier will be removed
fac.out	numeric: parameter to set the threshold in outliers detection
smooth	logical: if TRUE a smooth filter is applied
scale	logical: if TRUE the thichkness matrix is scaled from 0 to 1
smooth.iter	numeric: number of smoothing iterations
gamMap	logical: if TRUE gam smoothing is applied
nrow	numeric: number of rows for gam smoothing
ncol	numeric: number of columns for gam smoothing
gdl	numeric: number of degree of freedom for gam smoothing

method	character: if set on "equiangular" the cortical thickness is meant as the distance of the segment intersecting the external and internal outline starting from the centroid of the section. If set on "closest" the cortical thickness is calculated at each point as the closest distance between external and internal outlines
unwrap	character: starting qaudrant to unwrap the diaphysis ("A"=anterior, "L"=lateral, "P"=posterior, "M"=mesial)
plot	logical: if TRUE the 2D morphometric map is plotted
pal	character vector: colors to be used in the map production
aspect	numeric: axis ratio for 2D morphometric map

Value

dataframe dataframe for colormap production

2Dmap thickness color map

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
library(colorRamps)
#morphomap on a human femur bone
data(HomFem38023)
meshes<-morphomapSegm(HomFem38023)
perMesh<-meshes$external
endMesh<-meshes$internal
mech_length<-380.23
rawSections<-morphomapCore(out.sur=perMesh,
inn.sur=endMesh,num.sect=61,mech.len = mech_length, start = 0.2,end=0.8)
shapeSections<-morphomapShape(rawSections,24,sects_vector=NULL,cent.out="CCA",
delta=0.1, side="left")

#built 2D morphometric map without GAM smoothing
bone2Dmap<-morphomap2Dmap(morphomap.shape=shapeSections,
                    plot = TRUE, rem.out = TRUE,fac.out = 1.0, pal = blue2green2red(101),
                         aspect=2)
#built 2D morphometric map with GAM smoothing
bone2Dmap<-morphomap2Dmap(morphomap.shape=shapeSections,gam=TRUE,
                    plot = TRUE, rem.out = TRUE,fac.out = 1.0, pal = blue2green2red(101),
                         aspect=2)

#morphomap on a chimpanzee femur bone
data(PanFem27713)
meshes<-morphomapSegm(PanFem27713)
perMesh<-meshes$external
endMesh<-meshes$internal
mech_length<-277.13
rawSections<-morphomapCore(out.sur=perMesh,
```

```
                  inn.sur=endMesh,num.sect=61,mech.len = mech_length, start = 0.2,end=0.8)
shapeSections<-morphomapShape(rawSections,24,sects_vector=NULL,cent.out="CCA",
delta=0.1, side="left")
#built 2D morphometric map without GAM smoothing
bone2Dmap<-morphomap2Dmap(morphomap.shape=shapeSections,plot = TRUE,
rem.out = TRUE,fac.out = 1.0,pal = blue2green2red(101),aspect=2)
#built 2D morphometric map with GAM smoothing
bone2Dmap<-morphomap2Dmap(morphomap.shape=shapeSections,gam=TRUE,
                    plot = TRUE, rem.out = TRUE,fac.out = 1.0,pal = blue2green2red(101),
                         aspect=2)
```

`morphomap3Dmap` *morphomap3Dmap*

Description

Plot a 3D thickness map in four different anatomical views

Usage

```
morphomap3Dmap(morphomap.shape, out.sur, method = "equiangular",
  scale = TRUE, rem.out = FALSE, fac.out = 0.5, smooth = FALSE,
  smooth.iter = 5, k = 5, plot = TRUE, pal = blue2green2red(101))
```

Arguments

`morphomap.shape`	list: output from morphomapShape function
`out.sur`	3D mesh: 3D mesh of the long bone
`method`	character: if set on "equiangular" the cortical thickness is meant as the distance of the segment intersecting the external and internal outline starting from the centroid of the section. If set on "closest" the cortical thickness is calculated at each point as the closest distance between external and internal outlines
`scale`	logical: if TRUE the cortical thickness matrix will be scaled from 0 to 1
`rem.out`	logical: if TRUE outliers are identified and removed from thickness matrix
`fac.out`	numeric: parameter to set the threshold in outliers detection
`smooth`	logical: if TRUE the smoothing filter is applied on the thickness matrix
`smooth.iter`	numeric: number of smoothing iterations
`k`	integer: neighbourhood of kd-tree to search the nearest semilandmarks to each vertex
`plot`	logical: if TRUE the 3D map is plotted
`pal`	character vector: colors to be used in the map production

Value

cols color associated at each vertex of 3D mesh

thickmat thickness matrix after smoothing and outliers removal

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
#morphomap on a human femur bone
data(HomFem38023)
meshes<-morphomapSegm(HomFem38023)
perMesh<-meshes$external
endMesh<-meshes$internal
mech_length<-380.23
rawSections<-morphomapCore(out.sur=perMesh,
inn.sur=endMesh,num.sect=61,
mech.len = mech_length,param1 = 0.5,
radius.fact = 2.5,npovs = 100,clean_int_out = TRUE,
num.points = 500, start = 0.2,end=0.8)
shapeSections<-morphomapShape(rawSections,24,secta_vector=NULL,cent.out="CCA",
delta=0.1, side="left")

#built 3D morphometric map
bone3Dmap<-morphomap3Dmap(shapeSections, out.sur=perMesh,
                          plot = TRUE,rem.out=TRUE,
                          fac.out=1.5,smooth=TRUE,
                          smooth.iter=5)
#or
library(rgl)
open3d()
shade3d(perMesh,col=bone3Dmap$cols,specular="black")

#morphomap on a chimpanzee femur bone
data(PanFem27713)
meshes<-morphomapSegm(PanFem27713)
perMesh<-meshes$external
endMesh<-meshes$internal
mech_length<-277.13
rawSections<-morphomapCore(out.sur=perMesh,
                           inn.sur=endMesh,num.sect=61,mech.len = mech_length,
                           start = 0.2,end=0.8)
shapeSections<-morphomapShape(rawSections,24,secta_vector=NULL,cent.out="CCA",
delta=0.1, side="left")
#built 3D morphometric map
bone3Dmap<-morphomap3Dmap(shapeSections, out.sur=perMesh,
                          plot = TRUE,rem.out=TRUE,
                          fac.out=1.5,smooth=TRUE,
                          smooth.iter=5)
#or
```

```
library(rgl)
open3d()
shade3d(perMesh,col=bone3Dmap$cols,specular="black")
```

`morphomapArea` *morphomapArea*

Description

Shoelace formula to calculate the area of a closed outline

Usage

```
morphomapArea(p, delta = 0.1, method = "shoelace")
```

Arguments

`p`	matrix: kx2 matrix
`delta`	numeric: picture elements of adjustable side length
`method`	character: the user can choice to calculate the area applying the "shoelace" formula or discretizing the cross sections in dA areas (method = "delta")

Value

ar numeric: area

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
extsec<-morphomapCircle(10,100)
area<-morphomapArea(extsec, method="shoelace")
```

morphomapCentroid *morphomapCentroid*

Description

Calculate the barycenter of the cortical area

Usage

```
morphomapCentroid(cp, mp, delta = 0.1)
```

Arguments

cp	matrix: coordinates of the external outline of the section
mp	matrix: coordinates of the internal outline of the section
delta	numeric: picture elements of adjustable side length

Value

centroid numeric vector: coordinates of the cortical area

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
extsec<-morphomapCircle(10,100)
intsec<-morphomapCircle(8,100)
plot(extsec,asp=1,type="l")
points(intsec,col=2,type="l")
cent<-morphomapCentroid(extsec,intsec,delta = 0.1)
points(cent[1],cent[2],pch=19,col=3)
```

morphomapCheck *morphomapCheck*

Description

Plot the long bone mesh to check the orientation of the long bone

Usage

```
morphomapCheck(mesh, col = "white")
```

Arguments

mesh	3D mesh: long bone 3D model
col	character: color mesh

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
library(morphomap)
data(HomFem38023)
morphomapCheck(HomFem38023)
```

---

morphomapCircle *morphomapCircle*

Description

Define a circular outline

Usage

```
morphomapCircle(r = 1, n = 1000)
```

Arguments

r	numeric: radius of the outline
n	numeric: number of points along the outline

Value

mat matrix with coordinates

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
extsec<-morphomapCircle(10,100)
intsec<-morphomapCircle(8,100)
plot(extsec,asp=1,type="l")
points(intsec,type="l",col=2)
```

morphomapCore *morphomapCore*

Description

Tool to build 3D and 2D cross sections

Usage

```
morphomapCore(out.sur = out.sur, inn.sur = inn.sur, num.sect = 61,
  mech.len, clean_int_out = TRUE, param1 = 0.5, radius.fact = 2.5,
  npovs = 100, num.points = 500, start = 0.2, end = 0.8,
  print.progress = TRUE)
```

Arguments

out.sur	object of class mesh3d
inn.sur	object of class mesh3d
num.sect	number of sections
mech.len	mechanical length of the long bone
clean_int_out	logical if TRUE the inner section will be cleaned by using spherical flipping
param1	numeric parameter for spherical flipping operator (how much the section will be deformed)
radius.fact	numeric parameter for spherical flipping operator (distance from the center of the outline at which the povs are defined)
npovs	numeric: number of points of view defined around the section
num.points	number of equiengular points to be defined on each section
start	percentage of the mechanical length from which the first section is defined
end	percentage of the mechanical length from which the last section is defined
print.progress	logical: if TRUE a progress bar is printed to the screen

Value

3D_out num.pointsx3xnum.sect array of the external outlines

3D_inn num.pointsx3xnum.sect array of the internal outlines

2D_out num.pointsx2xnum.sect array of the external outlines

2D_inn num.pointsx2xnum.sect array of the internal outlines

mech_length mechanical length of the long bone

start percentage of the mechanical length from which the first section is defined

end percentage of the mechanical length from which the last section is defined

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
#raw section on a human femur bone
data(HomFem38023)
meshes<-morphomapSegm(HomFem38023)
perMesh<-meshes$external
endMesh<-meshes$internal
mech_length<-380.23
rawSections<-morphomapCore(out.sur=perMesh,
                           inn.sur=endMesh,num.sect=61,mech.len = mech_length,
                           start = 0.2,end=0.8)
#2D plot of the first section
plot(rawSections$`2D_out`[,,1],col="grey",asp=1,xlab="x",ylab="y",type="l")
points(rawSections$`2D_inn`[,,1],col="red",type="l")
#3D plot of the first section
library(rgl)
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)

#raw section on a chimpanzee femur bone
data(PanFem27713)
meshes<-morphomapSegm(PanFem27713)
perMesh<-meshes$external
endMesh<-meshes$internal
mech_length<-277.13
rawSections<-morphomapCore(out.sur=perMesh,
                           inn.sur=endMesh,num.sect=61,mech.len = mech_length,
                           start = 0.2,end=0.8)
#2D plot of the first section
plot(rawSections$`2D_out`[,,1],col="grey",asp=1,xlab="x",ylab="y",type="l")
points(rawSections$`2D_inn`[,,1],col="red",type="l")
#3D plot of the first section
library(rgl)
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)
```

---

morphomapCSG *morphomapCSG*

Description

Tool for Cross-sectional geometry

Usage

```
morphomapCSG(cp, mp, translate = FALSE, center = c("I", "E", "CCA"),
  delta = 0.1, Cx = NULL, Cy = NULL, I_xy = TRUE,
  I_minmax = TRUE, Zxy = TRUE)
```

Arguments

cp	matrix: coordinates of the external outline
mp	matrix: coordinates of the internal outline
translate	logical: if TRUE the section will be centered
center	how to define the center of each section. The method allowed are "CCA" (center of cortical area), "E" (barycenter of the external outline) and "I" (barycenter of the internal outline)
delta	numeric: picture elements of adjustable side length
Cx	numeric: new x center coordinate
Cy	numeric: new y center coordinate
I_xy	logical: if TRUE the product of inertia around the x and y axis is calculated
I_minmax	logical: if TRUE the Imin and Imax will be calculated
Zxy	logical: if TRUE the polar moment of inertia will be calculated

Value

Cx x coordinate of the centered section

Cy y coordinate of the centered section

T_area total area

M_area medullar area

CA cortical area

Ext_perim external perimeter

Med_perim medullar perimiter

Mean_thick mean thickness of the section

Sd_thick thickness standard deviation

Min_thick minimum thickness

Max_thick maximum thickness

Ix numeric: moment of inertia around the x axis

Iy numeric: moment of inertia around the y axis

Zx numeric: moment of inertia around the x axis

Zy numeric: moment of inertia around the y axis

Zpol numeric: polar moment of inertia

dx new centered coordinates of the internal outline

dy new centered coordinates of the internal outline

Imin numeric: minimum moment of inertia

Imax numeric: maximum moment of inertia

J numeric: polar moment of inertia

Zmax numeric: the maximum polar section

Zmin numeric: the minimum polar section

theta numeric: theta angle

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
#calculation of csg parameter on a human femur cross section
data(HomFem38023)
meshes<-morphomapSegm(HomFem38023)
perMesh<-meshes$external
endMesh<-meshes$internal
mech_length<-380.23
rawSections<-morphomapCore(out.sur=perMesh,
                           inn.sur=endMesh,num.sect=61,mech.len = mech_length,
                           start = 0.2,end=0.8)
shapeSections<-morphomapShape(rawSections,250,secta_vector=NULL,cent.out="CCA",
delta=0.1, side="left")
csgSect31<-morphomapCSG(cp = shapeSections$`2D_out`[,,31],
                        mp=shapeSections$`2D_inn`[,,31],
                        translate = FALSE,center="CCA")

#Cross sectional geometry along the entire femur bone
results<-matrix(NA,ncol=24,nrow=61)
rownames(results)<-paste("section",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 = shapeSections$`2D_out`[,,i],
                                   mp=shapeSections$`2D_inn`[,,i],
                                  translate = FALSE,center="CCA",delta = 0.5))
}

plot(c(1:61),results[,24],type="b",main="Theta",cex=1,
     xlab="section",ylab="radians")


#calculation of csg parameter on a chimpanzee femur cross section
data(PanFem27713)
meshes<-morphomapSegm(PanFem27713)
```

```
perMesh<-meshes$external
endMesh<-meshes$internal
mech_length<-277.13
rawSections<-morphomapCore(out.sur=perMesh,
                           inn.sur=endMesh,num.sect=61,mech.len = mech_length,
                           start = 0.2,end=0.8)
shapeSections<-morphomapShape(rawSections,250,secs_vector=NULL,cent.out="CCA",
delta=0.1, side="left")
csgSect31<-morphomapCSG(cp = shapeSections$`2D_out`[,,31],
                        mp=shapeSections$`2D_inn`[,,31],
                        translate = FALSE,center="CCA")

#Cross sectional geometry along the entire femur bone
results<-matrix(NA,ncol=24,nrow=61)
rownames(results)<-paste("section",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 = shapeSections$`2D_out`[,,i],
                                   mp=shapeSections$`2D_inn`[,,i],
                                   translate = FALSE,center="CCA",delta = 0.5))
  }

plot(c(1:61),results[,24],type="b",main="Theta",cex=1,
     xlab="section",ylab="radians")
```

---

morphomapDF *morphomapDF*

Description

Tool to build a data.frame suitable for morphometric maps

Usage

```
morphomapDF(morphomap.thickness, rem.out = TRUE, fac.out = 0.5,
  smooth = TRUE, scale = TRUE, smooth.iter = 5,
  method = "equiangular", unwrap = "A")
```

Arguments

morphomap.thickness	list: morphomap.Thickness object
rem.out	logical: if TRUE the outlier will be removed
fac.out	numeric: parameter to set the threshold in outliers detection

smooth	logical: if TRUE the smooth algorithm is applied
scale	logical: if TRUE the thichkness matrix is scaled from 0 to 1
smooth.iter	numeric: number of smoothing iterations
method	character: if set on "equiangular" the cortical thickness is meant as the distance of the segment intersecting the external and internal outline starting from the centroid of the section. If set on "closest" the cortical thickness is calculated at each point as the closest distance between external and internal outlines
unwrap	character: starting qaudrant to unwrap the diaphysis ("A"=anterior, "L"=lateral, "P"=posterior, "M"=mesial)

Value

XYZ data.frame for morphometric map

labels character vector for x labels in the morphometric map

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
library(lattice)
library(colorRamps)
data(HomFem38023)
meshes<-morphomapSegm(HomFem38023)
perMesh<-meshes$external
endMesh<-meshes$internal
mech_length<-380.23
rawSections<-morphomapCore(out.sur=perMesh,
                           inn.sur=endMesh,num.sect=61,mech.len = mech_length,
                           start = 0.2,end=0.8)
shapeSections<-morphomapShape(rawSections,21,sects_vector=NULL,cent.out="CCA",delta=0.1)
femthick<-morphomapThickness(shapeSections)
dataDF<-morphomapDF(femthick)$XYZ
contourplot(dataDF[, 3] ~ dataDF[, 1] + dataDF[, 2],
            col.regions=blue2green2red(101),region=TRUE,
            colorkey=list(at=seq(0,1,length.out = 100)),
        scales = list(x = list(at = seq(0,100,length.out = 5), labels = c("L","A","M","P","L"),
        alternating = 1)),asp=1.5,cuts=20,xlab="femur margin",ylab="biomechanical length")
```

morphomapFlip *morphomapFlip*

Description

Spherical flipping operator for bi-dimensional configuration

Usage

```
morphomapFlip(mat, param1 = 0.8, param2 = 10, radius.fact = 1.5,
  npovs = 100)
```

Arguments

mat	numeric matrix: coordinates of the bi-dimensional configuration
param1	numeric: first parameter for spherical flipping
param2	numeric: second parameter for spherical flipping
radius.fact	mechanical length of the long bone
npovs	number of evenly spaced points to be defined on each section

Value

mat matrix after spherical flipping

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
#create a section
extsec<-morphomapCircle(10,1000)
intsec<-morphomapCircle(8,1000)
#simulate noise
noiseX<-rnorm(1000,mean = 0,sd = 0.2)
noiseY<-rnorm(1000,mean = 0,sd = 0.2)
noise<-cbind(noiseX,noiseY)
noisect<-intsec+noise
#spherical flipping
flipsect<-morphomapFlip(noisect,param1 = 2,radius.fact = 2)
sortsect<-morphomapSort(flipsect)
#original section
plot(extsec,asp=1,type="l",xlim=c(-15,15),ylim=c(-15,15))
points(intsec,asp=1,type="l",xlim=c(-15,15),ylim=c(-15,15))
#noise
points(noisect,col=2)
#new section after spherical flipping
points(sortsect,type="l",col=3,asp=1,lwd=2)
```

morphomapMirror *morphomapMirror*

Description

Mirror a long bone mesh along the yz plane

Usage

```
morphomapMirror(mesh)
```

Arguments

mesh	object of class mesh3d

Value

mesh: object of class mesh3d

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
#a left human femur bone
library(rgl)
data(HomFem38023)
lfem<-HomFem38023
rfem<-morphomapMirror(lfem)
open3d()
wire3d(lfem,col="green")
wire3d(rfem,col="red")
```

morphomapMoment *morphomapMoment*

Description

Calculate the moment of inertia around the x and y axes and the product of inertia

Usage

```
morphomapMoment(cp, mp, delta = 0.1)
```

Arguments

cp	matrix: coordinates of the external outline
mp	matrix: coordinates of the internal outline
delta	numeric: picture elements of adjustable side length

Value

Ix numeric: moment of inertia around the x axis

Iy numeric: moment of inertia around the y axis

Ixy numeric: product of inertia around the x and y axis

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
#create a section
extsec<-morphomapCircle(10,1000)
intsec<-morphomapCircle(8,1000)
InMs<-morphomapMoment(extsec,intsec,delta=0.1)
```

---

morphomapPic *morphomapPic*

Description

Save the sections defined via morphomapShape or morphomapCore

Usage

```
morphomapPic(morphomap.core, morphomap.shape, vector = NULL,
  full = TRUE, width = 1500, height = 1500, pointsize = 12,
  res = 300, dirpath = tempdir())
```

Arguments

morphomap.core	list: morphomap.core object
morphomap.shape	list: morphomap.shape object
vector	numeric: define which sections will be saved
full	logical: if TRUE the thickness at ALPM is reported
width	numeric: width of the picture
height	numeric: height of the picture
pointsize	numeric: pointsize of plotted text
res	numeric: the nominal resolution in ppi which will be recorded
dirpath	character: path of the directory where the pictures will be saved

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
#export picture from a human femur bone
data(HomFem38023)
meshes<-morphomapSegm(HomFem38023)
perMesh<-meshes$external
endMesh<-meshes$internal
mech_length<-380.23
rawSections<-morphomapCore(out.sur=perMesh,
                           inn.sur=endMesh,num.sect=11,mech.len = mech_length,
                           start = 0.2,end=0.8)
shapeSections<-morphomapShape(rawSections,250,secs_vector=NULL,cent.out="CCA",delta=0.5)
morphomapPic(rawSections,shapeSections,full=TRUE,dirpath=tempdir(),
            width=2500,height=2500)

#export picture from a chimpanzee femur bone
data(PanFem27713)
meshes<-morphomapSegm(PanFem27713)
perMesh<-meshes$external
endMesh<-meshes$internal
mech_length<-277.13
rawSections<-morphomapCore(out.sur=perMesh,
                           inn.sur=endMesh,num.sect=11,mech.len = mech_length,
                           start = 0.2,end=0.8)
shapeSections<-morphomapShape(rawSections,250,secs_vector=NULL,cent.out="CCA",delta=0.5)
morphomapPic(rawSections,shapeSections,full=TRUE,dirpath=tempdir(),
             width=2500,height=2500)
```

---

morphomapRaster *morphomapRaster*

Description

Convert a section in a raster image. It is useful to save cross section at the real size

Usage

```
morphomapRaster(cp, mp, pixel = 1, filename, save = FALSE)
```

Arguments

cp	numeric: radius of the outline
mp	numeric: number of points along the outline
pixel	numeric: desired ratio pixel/mm

filename	character: path of the file to be saved
save	logical: if TRUE the raster image will be saved

Value

rimg raster image of the cross section

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
library(raster)
#rectangular section
extsec<-morphomapRectangle(10,6,100)
intsec<-morphomapRectangle(8,4,100)
rimg<-morphomapRaster(extsec,intsec,pixel=0.1,save=FALSE)
plot(rimg)
#circular section
extsec<-morphomapCircle(10,100)
intsec<-morphomapCircle(8,100)
rimg<-morphomapRaster(extsec,intsec,pixel=0.1,save=FALSE)
plot(rimg)
```

---

morphomapRectangle *morphomapRectangle*

Description

Define a rectangular outline

Usage

```
morphomapRectangle(l = 1, h = 1, n = 1000)
```

Arguments

l	numeric: length of the rectangle
h	numeric: height of the rectangle
n	numeric: number of points along the outline

Value

mat matrix with coordinates

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
extsec<-morphomapRectangle(10,6,100)
intsec<-morphomapRectangle(8,4,100)
plot(extsec,asp=1,type="l")
points(intsec,type="l",col=2)
```

`morphomapRegradius` *morphomapRegradius*

Description

Wrapper of the function regularradius written by Julien Claude (Morphometrics with R)

Usage

```
morphomapRegradius(mat, center, n)
```

Arguments

`mat`	a kx2 matrix
`center`	coordinates of the center from which the calculation of regular radius started
`n`	number of points

Value

V2 position of landmarks equi angular spaced

Author(s)

Julien Claude, Antonio Profico

References

Claude, J. (2008). Morphometrics with R. Springer Science & Business Media.

Examples

```
extsec<-morphomapCircle(10,1000)
sel<-morphomapRegradius(extsec,center = c(0,0),n=11)
selcoo<-extsec[sel,]
plot(extsec,type="l",asp=1)
points(selcoo,col="red",pch=19)
```

morphomapSegm *morphomapSegm*

Description

Separate a mesh from its visible and not visible components by using CA-LSE method

Usage

```
morphomapSegm(mesh, views = 30, param1 = 3, num.cores = NULL)
```

Arguments

mesh	object of class mesh3d
views	numeric: number of points of view
param1	numeric: first parameter for spherical flipping
num.cores	numeric: number of cores

Value

external mesh3d of the visible facets from the points of view

internal mesh3d of the not visible facets from the points of view

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

References

Profico A., Schlager S., Valoriani V., Buzi C., Melchionna M., Veneziano A., Raia P., Moggi-Cecchi J. and Manzi G., 2018. Reproducing the internal and external anatomy of fossil bones: Two new automatic digital tools. American Journal of Physical Anthropology 166(4): 979-986.

Examples

```
#automatic separation of external and medullar femur components
library(rgl)
data(HomFem38023)
meshes<-morphomapSegm(HomFem38023)
perMesh<-meshes$external
endMesh<-meshes$internal
open3d()
wire3d(perMesh,col="grey")
wire3d(endMesh,col="red")
```

morphomapShape *morphomapShape*

Description

Tool for the extraction of equiangular landmarks on the entire diaphysis

Usage

```
morphomapShape(morphomap.core, num.land, sects_vector, cent.out = "CCA",
  delta = 0.1, side = "left")
```

Arguments

morphomap.core	list: morphomap.core object
num.land	numeric: number of landmarks defining each section
sects_vector	numeric: number of sections
cent.out	how to define the center of each section. The method allowed are "CCA" (center of cortical area), "E" (barycenter of the external outline) and "I" (barycenter of the internal outline)
delta	pixel size used to calculate the CCA
side	character: specify if the long bone is "left" or "right" side

Value

3D_out num.pointsx3xnum.sect array in which the external outlines are stored

3D_inn num.pointsx3xnum.sect array in which the internal outlines are stored

2D_out num.pointsx2xnum.sect array in which the external outlines are stored

2D_inn num.pointsx2xnum.sect array in which the interal outlines are stored

ALPM_inn array with the coordinates of ALPM coordinates on the external outline

ALPM_out array with the coordinates of ALPM coordinates on the internal outline

mech_length mechanical length of the long bone

start percentage of the mechanical length from which the first section is defined

end percentage of the mechanical length from which the last section is defined

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
data(HomFem38023)
meshes<-morphomapSegm(HomFem38023)
perMesh<-meshes$external
endMesh<-meshes$internal
mech_length<-380.23
rawSections<-morphomapCore(out.sur=perMesh,
inn.sur=endMesh,num.sect=61,
mech.len = mech_length, start = 0.2,end=0.8,num.points = 500)
# Shape coordinates defining as center the barycenter of the cortical area
shapeSections_CCA<-morphomapShape(rawSections,21,secs_vector=NULL, cent.out="CCA",delta=0.1)
sect1_ext<-shapeSections_CCA$`2D_out`[,,1]
sect1_int<-shapeSections_CCA$`2D_inn`[,,1]
centroid_CCA<-morphomapCentroid(rawSections$`2D_out`[,,1],rawSections$`2D_inn`[,,1], delta=0.1)
plot(sect1_ext,type="b",asp=1,xlab="x",ylab="y",main="Section 1 - CCA")
points(sect1_int,type="b",asp=1)
points(centroid_CCA[1],centroid_CCA[2],pch=19)
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")
}

# Shape coordinates defining as center the barycenter of the external perimeter
shapeSections_E<-morphomapShape(rawSections,21,secs_vector=NULL, cent.out="E",
delta=0.1, side="left")
sect1_ext<-shapeSections_E$`2D_out`[,,1]
sect1_int<-shapeSections_E$`2D_inn`[,,1]
centroid_E<-colMeans(rawSections$`2D_out`[,,1])
plot(sect1_ext,type="b",asp=1,xlab="x",ylab="y",main="Section 1 - E")
points(sect1_int,type="b",asp=1)
points(centroid_E[1],centroid_E[2],pch=19)
start<-c(centroid_E[1],centroid_E[2])
for(i in 1:21){
  to_e<-sect1_ext[i,]
  points(rbind(start,to_e),type="l")
}

# Shape coordinates defining as center the barycenter of the internal perimetershape
shapeSections_I<-morphomapShape(rawSections,21,secs_vector=NULL, cent.out="I",
delta=0.1, side="left")
sect1_ext<-shapeSections_I$`2D_out`[,,1]
sect1_int<-shapeSections_I$`2D_inn`[,,1]
centroid_I<-colMeans(rawSections$`2D_inn`[,,1])
plot(sect1_ext,type="b",asp=1,xlab="x",ylab="y",main="Section 1 - I")
points(sect1_int,type="b",asp=1)
points(centroid_I[1],centroid_I[2],pch=19)
start<-c(centroid_I[1],centroid_I[2])
for(i in 1:21){
to_e<-sect1_ext[i,]
points(rbind(start,to_e),type="l")
```

```
}
```

`morphomapSort` *morphomapSort*

Description

Sort a series of points stored as a 2D matrix

Usage

```
morphomapSort(mat)
```

Arguments

`mat`	numeric matrix: a kx2 matrix

Value

mat sorted kx2 matrix

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
rand<-sample(100)
extsec<-morphomapCircle(10,100)[rand,]
plot(extsec,type="l",asp=1)
sorted<-morphomapSort(extsec)
plot(sorted,type="l",asp=1)
```

`morphomapThickness` *morphomapThickness*

Description

Tool for the extraction of equiangular landmarks on the entire diaphysis

Usage

```
morphomapThickness(morphomap.shape)
```

Arguments

morphomap.shape
: list: morphomap.shape object

Value

sect_thickness cortical thickness at each pair of landmarks on the external and internal outlines

ALPM_thickness cortical thickness at ALPM quadrants

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
#morphomap on a human femur bone
data(HomFem38023)
meshes<-morphomapSegm(HomFem38023)
perMesh<-meshes$external
endMesh<-meshes$internal
mech_length<-380.23
rawSections<-morphomapCore(out.sur=perMesh,
                           inn.sur=endMesh,num.sect=61,mech.len = mech_length,
                           start = 0.2,end=0.8)
shapeSections<-morphomapShape(rawSections,21,sects_vector=NULL,cent.out="CCA",delta=0.1)
femthick<-morphomapThickness(shapeSections)
plot(femthick$ALPM_thickness[1,,],type="l",
     main="LAMP thickness",xlab="section",ylab="thickness")
points(femthick$ALPM_thickness[2,,],type="l",col=2)
points(femthick$ALPM_thickness[3,,],type="l",col=3)
points(femthick$ALPM_thickness[4,,],type="l",col=4)
```

---

morphomapTranslate *morphomapTranslate*

Description

Translate a section to a new center defined by the user

Usage

```
morphomapTranslate(corA, medA, Cx, Cy)
```

Arguments

corA	matrix: coordinates of the external outline
medA	matrix: coordinates of the internal outline
Cx	numeric: new x center coordinate
Cy	numeric: new y center coordinate

Value

cortical new centered coordinates of the external outline

medullar new centered coordinates of the internal outline

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
extsec<-morphomapCircle(10,1000)
intsec<-morphomapCircle(8,1000)
plot(extsec,asp=1,type="l",xlim=c(-11,11),ylim=c(-11,11))
points(intsec,type="l")
traSect<-morphomapTranslate(extsec,intsec,1,1)
points(traSect$cortical,type="l",col="red")
points(traSect$medullar,type="l",col="red")
```

---

morphomapZmoment *morphomapZmoment*

Description

Calculate the polar moment of inertia around the x and y axes and the polar section module

Usage

```
morphomapZmoment(cp, mp, Cx = 0, Cy = 0, delta = 0.1)
```

Arguments

cp	matrix: coordinates of the external outline of the section
mp	matrix: coordinates of the internal outline of the section
Cx	numeric: x coordinate of the section center
Cy	numeric: y coordinate of the section center
delta	numeric: picture elements of adjustable side length

Value

Zx numeric: moment of inertia around the x axis

Zy numeric: moment of inertia around the y axis

dx numeric: maximum chord length from y axis

dy numeric: maximum chord length from x axis

Zpol numeric: polar moment of inertia

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Examples

```
extsec<-morphomapCircle(10,1000)
intsec<-morphomapCircle(8,1000)
ZMs<-morphomapZmoment(extsec,intsec,delta=0.1)
```

PanFem27713 *example dataset*

Description

3D mesh of a chimpanzee femur bone

Usage

```
data(PanFem27713)
```

Author(s)

Antonio Profico, Luca Bondioli, Pasquale Raia, Paul O'Higgins, Damiano Marchi

Index