

# Package ‘BoneProfileR’

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**Type** Package

**Title** Tools to Study Bone Compactness

**Version** 2.0

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**Depends** imager, HelpersMG (>= 4.7), knitr, rmarkdown, R (>= 4.1),  
shiny

**Suggests** tiff, ijtiff, openxlsx, parallel

**Description** Bone Profiler is a scientific method and a software used to model  
bone section for paleontological and ecological studies. See Girondot and Laurin  
2003 <[https://www.researchgate.net/publication/280021178\\_Bone\\_profiler\\_A\\_tool\\_to\\_quantify\\_model\\_and\\_statistically\\_compare\\_bone-section\\_compactness\\_profiles](https://www.researchgate.net/publication/280021178_Bone_profiler_A_tool_to_quantify_model_and_statistically_compare_bone-section_compactness_profiles)>.

**License** GPL-2

**LazyData** yes

**LazyLoad** yes

**Encoding** UTF-8

**RoxygenNote** 7.1.2

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2021-10-07 10:50:02 UTC

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---

BoneProfileR-package    *A Model for Bone Compactness.*

---

## Description

A Model for Bone Compactness.

The latest version of this package can always be installed using:

```
install.packages(c("imager", "tiff", "ijtiff", "HelpersMG", "knitr", "rmarkdown", "openxlsx", "shiny"))
install.packages("http://www.ese.u-psud.fr/epc/conservation/CRAN/HelpersMG.tar.gz", repos=NULL,
type="source")
install.packages("http://www.ese.u-psud.fr/epc/conservation/CRAN/BoneProfileR.tar.gz", repos=NULL,
type="source")
```

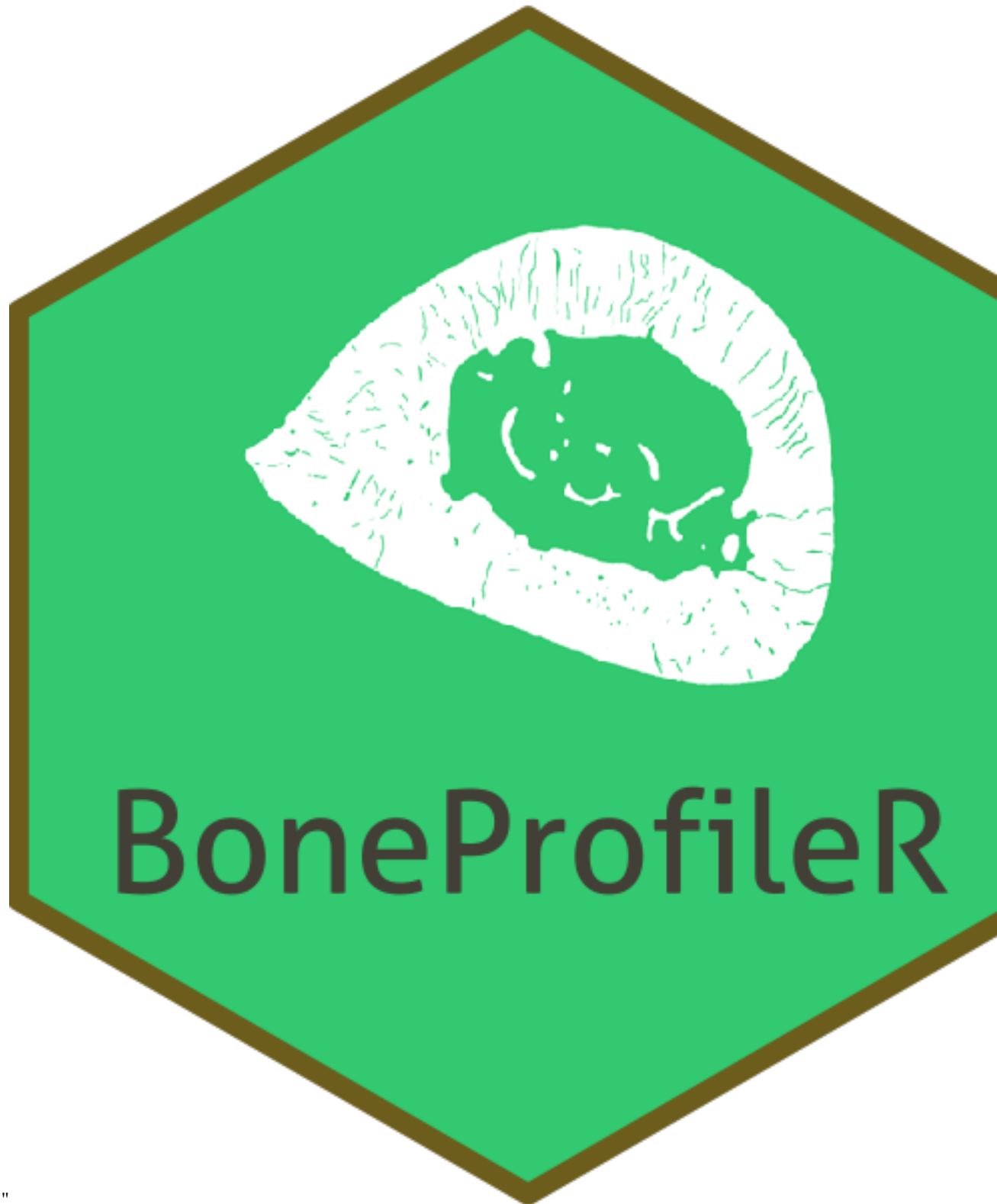
BoneProfileR uses a new results management software that is developed as part of the HelpersMG package. Using this results management system (RM), all the results are stored as part of the analyzed image.

This results management software has been developed to help users to maintain the results associated with the methodology used to obtain it. It is part of the large movement in science of replicative research.

An analysis is then stored with the image in a single file with the following information:

```
name, timestamp, bg, fg, threshold, contour, centers, peripherie, compactness, array.compactness,
cut.distance.center, cut.angle, used.centers, compactness.synthesis, partial, rotation.angle, global.compactness,
optim, optimRadial
```

Several analyses can be stored within a single file.



## Details

A model for bone compactness.

```
Package: BoneProfileR
Type: Package
Version: 2.0 build 693
Date: 2021-10-06
License: GPL (>= 2)
LazyLoad: yes
```

## Author(s)

Marc Girondot <marc.girondot@gmail.com>

## References

Girondot M, Laurin M (2003) Bone Profiler: a tool to quantify, model, and statistically compare bone-section compactness profiles. *Journal of Vertebrate Paleontology* 23: 458-461

Laurin M, Girondot M, Loth M-M (2004) The evolution of long bone microstructure and lifestyle in lissamphibians. *Paleobiology* 30: 589-613

## Examples

```
## Not run:
# Not run:
library(BoneProfileR)
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")

bone <- BP_OpenImage(file=path_Hedgehog)
plot(bone, type="original")
bone <- BP_DetectBackground(bone=bone, analysis="logistic")
bone <- BP_DetectForeground(bone=bone, analysis="logistic")
bone <- BP_DetectCenters(bone=bone, analysis="logistic")
plot(bone, type="original")
plot(bone, type="mineralized")
plot(bone, type="unmineralized")
plot(bone, type="section")
bone <- BP_EstimateCompactness(bone, analysis="logistic", center="ontogenic")
plot(bone, type="original")
plot(bone, type="mineralized")
plot(bone, type="observations")
plot(bone, type="observations+model", analysis=1)
bone <- BP_FitMLCompactness(bone, analysis="logistic")
plot(bone, type="model", analysis=1)
fittedpar <- BP_GetFittedParameters(bone, analysis="logistic")
bone <- BP_DuplicateAnalysis(bone, from="logistic", to="flexit")
bone <- BP_FitMLCompactness(bone,
                           fitted.parameters=c(fittedpar, K1=1, K2=1),
                           fixed.parameters=NULL, analysis="flexit")
```

```

compare_AIC(Logistic=BP_GetFittedParameters(bone, analysis="logistic", alloptim=TRUE),
            Flexit=BP_GetFittedParameters(bone, analysis="flexit", alloptim=TRUE))
# pdf(file = "Figure 2.pdf", width = 8, height = 10, pointsize = 12)
layout(1:2)
plot(bone, type="observations+model", analysis="logistic", restorePar=FALSE, mar=c(4, 4, 2, 5))
plot(bone, type="observations+model", analysis="flexit", restorePar=FALSE, mar=c(4, 4, 2, 5))
layout(1)
# dev.off()

out4p <- plot(bone, type="observations+model", analysis="logistic")
out6p <- plot(bone, type="observations+model", analysis="flexit")
bone <- BP_FitBayesianCompactness(bone, analysis="logistic")
plot(bone, type="observations+model", CI="MCMC")
bone <- BP_FitBayesianCompactness(bone, analysis="flexit")
plot(bone, type="observations+model", CI="MCMC", analysis="flexit")
plot(bone, type="mcmc", parameter="P",
      options.mcmc=list(xlim=c(0.55, 0.57), breaks=seq(from=0, to=1, by=0.001)))
plot(bone, type="mcmc", parameter="S",
      options.mcmc=list(xlim=c(0.02, 0.05), breaks=seq(from=0.02, to=.05, by=0.001)))
plot(bone, type="mcmc", parameter="Min",
      options.mcmc=list(xlim=c(0.05, 0.08), breaks=seq(from=0, to=1, by=0.001)))
plot(bone, type="mcmc", parameter="Max",
      options.mcmc=list(xlim=c(0.95, 0.97), breaks=seq(from=0, to=1, by=0.001)))
outMCMC <- RM_get(x = bone, RM = "RM", RMname = "logistic", valuenam = "mcmc")
summary(outMCMC)
outMCMC <- RM_get(x = bone, RM = "RM", RMname = "flexit", valuenam = "mcmc")
summary(outMCMC)
# pdf(file = "Figure 3.pdf", width = 8, height = 10, pointsize = 12)
layout(1:2)
plot(bone, type="mcmc", parameter="K1", analysis="flexit",
      options.mcmc=list(xlim=c(-1, 3), ylim=c(0,10),
                       breaks=seq(from=-1, to=3, by=0.001),
                       legend = FALSE, show.prior = FALSE, mar=c(4, 4, 1, 6)), restorePar=FALSE)
segments(x0=1, x1=1,
         y0=0, y1=10, lty=4, lwd=3)
text(x=ScalePreviousPlot(x=0.95, y=0.95)$x,
     y=ScalePreviousPlot(x=0.95, y=0.95)$y, labels="A", cex=3)
plot(bone, type="mcmc", parameter="K2", analysis="flexit",
      options.mcmc=list(xlim=c(-1, 3), ylim=c(0,10),
                       breaks=seq(from=-1, to=3, by=0.001),
                       legend = FALSE, show.prior = FALSE, mar=c(4, 4, 1, 6)), restorePar=FALSE)
segments(x0=1, x1=1,
         y0=0, y1=10, lty=4, lwd=3)
text(x=ScalePreviousPlot(x=0.95, y=0.95)$x,
     y=ScalePreviousPlot(x=0.95, y=0.95)$y, labels="B", cex=3)
# dev.off()

bone <- BP_FitMLRadialCompactness(bone, analysis = "flexit")
plot(bone, type="radial", radial.variable=c("P", "S"), analysis = "flexit")
plot(bone, type="radial", radial.variable=c("P", "S", "Min", "Max"), analysis = "flexit")
out <- RM_get(x=bone, RMname="flexit", valuenam = "optimRadial")$synthesis
mean(out[, "P"]); sd(out[, "P"])
range(out[, "S"])
quantile(out[, "S"])

```

```
# pdf(file = "Figure 4.pdf", width=7, height = 9, pointsize = 12)
layout(1:2)
plot(bone, type="radial", radial.variable="P", analysis = "flexit", restorePar=FALSE)
text(x=ScalePreviousPlot(x=0.95, y=0.95)$x,
     y=ScalePreviousPlot(x=0.95, y=0.95)$y, labels="A", cex=3)
plot(bone, type="radial", radial.variable="S", analysis = "flexit", restorePar=FALSE)
text(x=ScalePreviousPlot(x=0.95, y=0.95)$x,
     y=ScalePreviousPlot(x=0.95, y=0.95)$y, labels="B", cex=3)
# dev.off()

## End(Not run)
```

---

BP

*Run a shiny application to fit bone section*

---

## Description

Run a shiny application to fit bone section

## Usage

BP()

## Details

BP runs a shiny application to fit bone section

## Value

Nothing

## Author(s)

Marc Girondot <marc.girondot@gmail.com>

## Examples

```
## Not run:
# Not run:
library(BoneProfileR)
BP()

## End(Not run)
```

---

BP_AutoFit	<i>Fit model automatically</i>
------------	--------------------------------

---

## Description

Open an image, fit a model and generate a report.

## Usage

```
BP_AutoFit(  
  file = file.choose(),  
  xlsx = TRUE,  
  rotation.angle = 0,  
  center = "ontogenic"  
)
```

## Arguments

file	The file to be opened
xlsx	TRUE, FALSE or the name and path of the report
rotation.angle	The angle of rotation for analysis
center	Which center to be used.

## Details

BP\_AutoFit fits model automatically

## Value

Characteristics of an image with all the fit information

## Author(s)

Marc Girondot <marc.girondot@gmail.com>

## See Also

Other BoneProfileR: [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

**Examples**

```
## Not run:
# Not run:
library(BoneProfileR)
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")
bone <- BP_AutoFit(file=path_Hedgehog, xlsx=TRUE)
# or to open a dialog box
bone <- BP_AutoFit()

## End(Not run)
```

---

BP\_ChooseBackground *Let the use to choose the background color of an image*

---

**Description**

Let the user to choose the background color of an image.

**Usage**

```
BP_ChooseBackground(bone, analysis = 1)
```

**Arguments**

bone	The bone image to be used
analysis	The name or rank of analysis

**Details**

BP\_ChooseBackground lets the use to choose the background color of an image

**Value**

The original bone object with a new attribute for background color

**Author(s)**

Marc Girondot <marc.girondot@gmail.com>

**See Also**

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)



## Examples

```
## Not run:
# Not run:
bone <- BP_OpenImage()
bone <- BP_ChooseBackground(bone=bone)
bone <- BP_ChooseForeground(bone=bone)
plot(bone)

## End(Not run)
```

---

BP_ChooseCenter	<i>Let the user to choose the center of the bone</i>
-----------------	--

---

## Description

Let the user to choose the center of the bone.

## Usage

```
BP_ChooseCenter(bone, analysis = 1)
```

## Arguments

bone	The bone image to be used
analysis	The name or rank of analysis

## Details

BP\_ChooseCenter lets the use to choose the center of the bone

## Value

The original bone object with a new attribute for center

## Author(s)

Marc Girondot <marc.girondot@gmail.com>

## See Also

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

**Examples**

```

## Not run:
# Not run:
library(BoneProfileR)
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")
bone <- BP_OpenImage(file=path_Hedgehog)
bone <- BP_DetectBackground(bone=bone)
bone <- BP_DetectForeground(bone=bone)
bone <- BP_ChooseCenter(bone=bone)
# For partial section, only BP_ChooseCenter() must be used
path_Dicynodon <- system.file("extdata", "Dicynodon_tibia_11.11.1.T_b_b-1.png",
                              package = "BoneProfileR")
bone <- BP_OpenImage(file=path_Dicynodon)
bone <- BP_DetectBackground(bone=bone)
bone <- BP_DetectForeground(bone=bone)
bone <- BP_ChooseCenter(bone=bone)
bone <- BP_EstimateCompactness(bone, center="user", partial=TRUE)
bone <- BP_FitMLCompactness(bone, analysis="logistic")
plot(bone, type="observations+model")

## End(Not run)

```

---

BP\_ChooseForeground *Let the user to choose the foreground color of an image*

---

**Description**

Let the user to choose the foreground color of an image.

**Usage**

```
BP_ChooseForeground(bone, analysis = 1)
```

**Arguments**

bone	The bone image to be used
analysis	The name or rank of analysis

**Details**

BP\_ChooseForeground let the user to choose the foreground color of an image

**Value**

The original bone object with a new attribute for foreground color

**Author(s)**

Marc Girondot <marc.girondot@u-psud.fr>

**See Also**

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

**Examples**

```
## Not run:  
# Not run:  
bone <- BP_OpenImage()  
bone <- BP_ChooseBackground(bone=bone)  
bone <- BP_ChooseForeground(bone=bone)  
plot(bone)  
  
## End(Not run)
```

---

BP\_DetectBackground     *Detects the background color of an image*

---

**Description**

Detects the background color of an image.

**Usage**

```
BP_DetectBackground(bone, analysis = 1, show.plot = TRUE)
```

**Arguments**

bone	The bone image to be used
analysis	The name or rank of analysis
show.plot	should plot is shown ?

**Details**

BP\_DetectBackground detects the background color of an image

**Value**

The original bone object with a new attribute for background color

**Author(s)**

Marc Girondot <marc.girondot@gmail.com>

**See Also**

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

**Examples**

```
## Not run:
# Not run:
bone <- BP_OpenImage()
bone <- BP_DetectBackground(bone=bone)
bone <- BP_DetectForeground(bone=bone)
plot(bone)

## End(Not run)
```

---

BP\_DetectCenters      *Detect the centers of an image*

---

**Description**

Detects the centers of an image. Note that this function must not be used with partial bone section.

**Usage**

```
BP_DetectCenters(bone, analysis = 1, show.plot = TRUE)
```

**Arguments**

bone	The bone image to be used
analysis	The name or rank of analysis
show.plot	should plot is shown ?

**Details**

BP\_DetectCenters detects the centers of an image

**Value**

The original bone object with a new attribute for centers

**Author(s)**

Marc Girondot <marc.girondot@gmail.com>

**See Also**

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

**Examples**

```
## Not run:
# Not run:
library(BoneProfileR)
bone <- BP_OpenImage()
# or
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")
bone <- BP_OpenImage(file=path_Hedgehog)
bone <- BP_DetectBackground(bone=bone)
bone <- BP_DetectForeground(bone=bone)
bone <- BP_DetectCenters(bone=bone)
plot(bone, type="ontogenic", show.grid=FALSE)
plot(bone, type="mineralized", show.grid=FALSE)
plot(bone, type="unmineralized", show.grid=FALSE)
plot(bone, type="section", show.grid=FALSE)

## End(Not run)
```

---

BP\_DetectForeground     *Detects the foreground color of an image*

---

**Description**

Detects the foreground color of an image.

**Usage**

```
BP_DetectForeground(bone, analysis = 1, show.plot = TRUE)
```

**Arguments**

bone	The bone image to be used
analysis	The name or rank of analysis
show.plot	should plot is shown ?

**Details**

BP\_DetectForeground detects the foreground color of an image

**Value**

The original bone object with a new attribute for foreground color

**Author(s)**

Marc Girondot <marc.girondot@gmail.com>

**See Also**

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

**Examples**

```
## Not run:  
# Not run:  
bone <- BP_OpenImage()  
bone <- BP_DetectBackground(bone=bone)  
bone <- BP_DetectForeground(bone=bone)  
plot(bone)  
  
## End(Not run)
```

---

BP\_DuplicateAnalysis *Duplicates an analysis stored in an object*

---

**Description**

Duplicates an analysis stored in an object.

**Usage**

```
BP_DuplicateAnalysis(bone, from = 1, to = 2)
```

**Arguments**

bone	The bone image to be used
from	The name or rank of analysis to be duplicated
to	The name or rank of analysis to be created

**Details**

BP\_DuplicateAnalysis duplicates an analysis stored in an object

**Value**

The original bone object with a new analysis

**Author(s)**

Marc Girondot <marc.girondot@gmail.com>

**See Also**

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

**Examples**

```
## Not run:
# Not run:
library(BoneProfileR)
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")
bone <- BP_OpenImage(file=path_Hedgehog)
bone <- BP_DetectBackground(bone=bone, analysis="logistic")
bone <- BP_DetectForeground(bone=bone, analysis="logistic")
bone <- BP_DetectCenters(bone=bone, analysis="logistic")
bone <- BP_EstimateCompactness(bone, analysis="logistic")
bone <- BP_FitMLCompactness(bone, analysis="logistic")
plot(bone)
plot(bone, type="observations")
plot(bone, type="observations+model", analysis=1)
bone <- BP_DuplicateAnalysis(bone, from="logistic", to="flexit")

## End(Not run)
```

---

BP\_EstimateCompactness

*Estimation of the compactness of a bone section*

---

**Description**

Estimation of the compactness of a bone section.

The reference for radial estimation of compactness is the trigonometric circle for rotation.angle=0 in BP\_EstimateCompactness():

- The top of the section is located at  $-\pi/2$ .
- The left of the section is located at  $-\pi$  and  $+\pi$ .
- The bottom of the section is located at  $\pi/2$ .
- The right of the section is 0.

If rotation.angle is different from 0, the value of rotation.angle is added to the angle modulo  $2\pi$ .

**Usage**

```
BP_EstimateCompactness(
  bone,
  center = "ontogenic",
  partial = FALSE,
  cut.angle = 60,
  cut.distance = 100,
  rotation.angle = 0,
  analysis = 1,
  show.plot = TRUE
)
```

**Arguments**

bone	The bone image to be used
center	Which center to be used: user, mineralized, unmineralized, section, ontogenic
partial	Is the section partial?
cut.angle	Number of angles
cut.distance	Number of distances
rotation.angle	The angle of rotation for analysis
analysis	The name or rank of analysis
show.plot	should plot is shown ?

**Details**

BP\_EstimateCompactness estimates the compactness of a bone section

**Value**

The original bone object with a new attribute for compactness

**Author(s)**

Marc Girondot <marc.girondot@gmail.com>



**See Also**

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

**Examples**

```
## Not run:
# Not run:
library(BoneProfileR)
bone <- BP_OpenImage()
# or
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")
bone <- BP_OpenImage(file=path_Hedgehog)
bone <- BP_DetectBackground(bone=bone)
bone <- BP_DetectForeground(bone=bone)
bone <- BP_DetectCenters(bone=bone)
bone <- BP_EstimateCompactness(bone)
plot(bone, type="original", show.grid=FALSE)
plot(bone, type="mineralized", show.grid=FALSE)
plot(bone, type="unmineralized", show.grid=FALSE)
plot(bone, type="section", show.grid=FALSE)

## End(Not run)
```

---

BP\_FitBayesianCompactness

*Estimation of Bayesian model of a bone section*

---

**Description**

Estimation of Bayesian model of a bone section.

**Usage**

```
BP_FitBayesianCompactness(
  bone = stop("A result from BP_FitMLCompactness() must be provided"),
  priors = NULL,
  n.iter = 10000,
  n.chains = 1,
  n.adapt = 100,
  thin = 1,
  analysis = 1,
  silent = TRUE
)
```

**Arguments**

bone	The bone image to be used
priors	Priors
n.iter	Number of iterations
n.chains	Number of chains
n.adapt	Number of iteration to adapt
thin	Thin parameter for analysis
analysis	Name or rank of analysis
silent	Should some information must me shown ?

**Details**

BP\_FitBayesianCompactness estimates Bayesian model of a bone section

**Value**

The  $-\ln L$

**Author(s)**

Marc Girondot <marc.girondot@gmail.com>

**See Also**

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

**Examples**

```
## Not run:
# Not run:
library(BoneProfileR)
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")
bone <- BP_OpenImage(file=path_Hedgehog)
bone <- BP_DetectBackground(bone=bone, analysis="logistic")
bone <- BP_DetectForeground(bone=bone, analysis="logistic")
bone <- BP_DetectCenters(bone=bone, analysis="logistic")
bone <- BP_EstimateCompactness(bone, analysis="logistic")
bone <- BP_FitMLCompactness(bone, analysis="logistic")
plot(bone)
plot(bone, type="observations")
plot(bone, type="observations+model", analysis=1)
fittedpar <- BP_GetFittedParameters(bone, analysis="logistic")
bone <- BP_DuplicateAnalysis(bone, from="logistic", to="flexit")
```

```

bone <- BP_FitMLCompactness(bone,
  fitted.parameters=c(fittedpar, K1=1, K2=1),
  fixed.parameters=NULL, analysis="flexit")
compare_AIC(Logistic=BP_GetFittedParameters(bone, analysis="logistic", alloptim=TRUE),
  Flexit=BP_GetFittedParameters(bone, analysis="flexit", alloptim=TRUE))
out4p <- plot(bone, type="observations+model", analysis="logistic")
out6p <- plot(bone, type="observations+model", analysis="flexit")
bone <- BP_FitBayesianCompactness(bone, analysis="logistic")
plot(bone, type="observations+model", CI="MCMC", analysis="logistic")
bone <- BP_FitBayesianCompactness(bone, analysis="flexit")
plot(bone, type="observations+model", CI="MCMC", analysis="flexit")

## End(Not run)

```

---

BP\_FitMLCompactness     *Estimation of the likelihood of a bone section*

---

## Description

Estimation of the model of compactness of a bone section.

The two-steps analysis performs first a quasi-Newton method, then a Bayesian MCMC and finally again a quasi-Newton method. It generally ensures that global minimum is found. On the other hand, it doubles the time to complete.

## Usage

```

BP_FitMLCompactness(
  bone,
  fitted.parameters = c(P = 0.5, S = 0.05, Min = 0.001, Max = 0.999),
  fixed.parameters = c(K1 = 1, K2 = 1),
  twosteps = TRUE,
  replicates.CI = 10000,
  analysis = 1,
  silent = FALSE
)

```

## Arguments

bone	The bone image to be used
fitted.parameters	Parameters of the model to be fitted
fixed.parameters	Fixed parameters of the model
twosteps	Does a 2-steps analysis be performed?
replicates.CI	Number of replicates to estimate confidence interval
analysis	Name or rank of analysis
silent	Should information be shown?

**Details**

BP\_FitMLCompactness estimates likelihood of model of a bone section

**Value**

The  $-\ln L$

**Author(s)**

Marc Girondot <marc.girondot@gmail.com>

**See Also**

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

**Examples**

```
## Not run:
# Not run:
library(BoneProfileR)
bone <- BP_OpenImage()
# or, to use the package imager to open a tiff image
bone <- BP_OpenImage(ijtiff=TRUE)
library(BoneProfileR)
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")

bone <- BP_OpenImage(file=path_Hedgehog)
bone <- BP_DetectBackground(bone=bone, analysis="logistic")
bone <- BP_DetectForeground(bone=bone, analysis="logistic")
bone <- BP_DetectCenters(bone=bone, analysis="logistic")
bone <- BP_EstimateCompactness(bone, analysis="logistic")
plot(bone, type="ontogenic", show.grid=FALSE)
plot(bone, type="mineralized", show.grid=FALSE)
plot(bone, type="unmineralized", show.grid=FALSE)
plot(bone, type="section", show.grid=FALSE)
bone <- BP_FitMLCompactness(bone, analysis="logistic", twosteps=TRUE)
BP_GetFittedParameters(bone)
plot(bone)
plot(bone, type="observations")
plot(bone, type="observations+model", analysis=1)
bone <- BP_DuplicateAnalysis(bone, from="logistic", to="flexit")
fittedpar <- BP_GetFittedParameters(bone, analysis="logistic")
bone <- BP_DuplicateAnalysis(bone, from="logistic", to="flexit")
BP_ListAnalyses(bone)
bone <- BP_FitMLCompactness(bone,
                           fitted.parameters=c(fittedpar, K1=1, K2=1),
                           fixed.parameters=NULL, analysis="flexit", twosteps=TRUE)
```

```

compare_AIC(Logistic=BP_GetFittedParameters(bone, analysis="logistic", alloptim=TRUE),
            Flexit=BP_GetFittedParameters(bone, analysis="flexit", alloptim=TRUE))
out4p <- plot(bone, type="observations+model", analysis="logistic")
out6p <- plot(bone, type="observations+model", analysis="flexit")

## End(Not run)

```

---

BP\_FitMLRadialCompactness

*Estimation of the likelihood of a bone section*

---

## Description

Estimation of the compactness of a bone section using radial model.

If the fitted.parameters and fixed.parameters are NULL and the analysis includes a BP\_FitMLCompactness() result, the values of this result is used as a reference for fitted.parameters and fixed.parameters.

If no BP\_FitMLCompactness() result is available, it will use:

fitted.parameters=c(P=0.5, S=0.05, Min=-2, Max=5); fixed.parameters=c(K1=1, K2=1).

The reference for radial estimation of compactness is the trigonometric circle for rotation.angle=0 in BP\_EstimateCompactness():

- The top of the section is located at  $-\pi/2$ .
- The left of the section is located at  $-\pi$  and  $+\pi$ .
- The bottom of the section is located at  $\pi/2$ .
- The right of the section is 0.

If rotation.angle is different from 0, the value of rotation.angle is added to the angle modulo  $2\pi$ .

The two-steps analysis performs first a quasi-Newton method, then a Bayesian MCMC and finally again a quasi-Newton method. It generally ensures that global minimum is found. On the other hand, it doubles the time to complete for each angle.

## Usage

```

BP_FitMLRadialCompactness(
  bone,
  fitted.parameters = NULL,
  fixed.parameters = NULL,
  analysis = 1,
  silent = FALSE,
  twosteps = TRUE
)

```

## Arguments

bone	The bone image to be used
fitted.parameters	Parameters of the model to be fitted
fixed.parameters	Fixed parameters of the model

analysis	Name or rank of analysis
silent	Should the function displays some information?
twosteps	Should a 2-steps analysis be performed?

### Details

BP\_FitMLRadialCompactness estimates likelihood of model of a bone section

### Value

The  $-\ln L$

### Author(s)

Marc Girondot <marc.girondot@gmail.com>

### See Also

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

### Examples

```
## Not run:
# Not run
library(BoneProfileR)
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")
bone <- BP_OpenImage(file=path_Hedgehog)
# or
bone <- BP_OpenImage(ijtiff=TRUE)
bone <- BP_DetectBackground(bone=bone, analysis="logistic")
bone <- BP_DetectForeground(bone=bone, analysis="logistic")
bone <- BP_DetectCenters(bone=bone, analysis="logistic")
bone <- BP_EstimateCompactness(bone, analysis="logistic")
bone <- BP_EstimateCompactness(bone, analysis="logistic", cut.angle=30)
bone <- BP_FitMLCompactness(bone, analysis="logistic")
plot(bone)
plot(bone, type="observations")
plot(bone, type="observations+model", analysis=1)
fittedpar <- BP_GetFittedParameters(bone, analysis="logistic")
bone <- BP_DuplicateAnalysis(bone, from="logistic", to="flexit")
bone <- BP_FitMLCompactness(bone,
                           fitted.parameters=c(fittedpar, K1=1.01, K2=1.01),
                           fixed.parameters=NULL, analysis="flexit")
bone <- BP_FitBayesianCompactness(bone, analysis="flexit")
mcmc <- RM_get(bone, RMname = "flexit", value="mcmc")
fittedpar <- as.parameters(mcmc)
```

```

bone <- BP_FitMLCompactness(bone,
  fitted.parameters=fittedpar,
  fixed.parameters=NULL, analysis="flexit")
compare_AIC(Logistic=BP_GetFittedParameters(bone, analysis="logistic", alloptim=TRUE),
  Flexit=BP_GetFittedParameters(bone, analysis="flexit", alloptim=TRUE))
out4p <- plot(bone, type="observations+model", analysis="logistic")
out6p <- plot(bone, type="observations+model", analysis="flexit")
# The twosteps fit is more accurate but is around 100 times slower
bone <- BP_FitMLRadialCompactness(bone, analysis="logistic", twosteps=TRUE)
bone <- BP_FitMLRadialCompactness(bone, analysis="logistic", twosteps=FALSE)
plot(bone, type="observations", angle=0)
plot(bone, type="model", analysis="logistic", angle=0)
plot(bone, type="observations+model", angle=0)
plot(bone, type="observations+model", angle=pi)
plot(bone, type="radial", radial.variable=c("P", "S"), analysis="logistic")
plot(bone, type="radial", radial.variable=c("P", "S", "Min", "Max"), analysis="logistic")
plot(bone, type="radial", radial.variable=c("TRC"), analysis="logistic")
# Test using the change of orientation using default.angle from BP_EstimateCompactness():
bone <- BP_DuplicateAnalysis(bone, from="logistic", to="logistic_rotation_pi")
# With a pi rotation, the top moves to the bottom and the left moves to the right
bone <- BP_EstimateCompactness(bone, rotation.angle=pi, analysis="logistic_rotation_pi")
bone <- BP_FitMLRadialCompactness(bone, analysis="logistic_rotation_pi")
plot(bone, type="radial", radial.variable=c("P", "S"), analysis="logistic")
plot(bone, type="radial", radial.variable=c("P", "S"), analysis="logistic_rotation_pi")
BP_Report(bone=bone,
  analysis=1,
  docx=NULL,
  pdf=NULL,
  xlsx=file.path(getwd(), "report.xlsx"),
  author="Marc Girondot",
  title=attributes(bone)$name)

## End(Not run)

```

---

BP\_GetFittedParameters

*Return the fitted parameters*

---

## Description

Return the fitted parameters.

## Usage

```
BP_GetFittedParameters(bone, analysis = 1, alloptim = FALSE)
```

## Arguments

bone	The bone image to be used
analysis	Name or rank of analysis
alloptim	If TRUE, return the complete object returned by optim

**Details**

BP\_GetFittedParameters returns the fitted parameters

**Value**

The fitted parameters

**Author(s)**

Marc Girondot <marc.girondot@gmail.com>

**See Also**

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

**Examples**

```
## Not run:
# Not run:
library(BoneProfileR)
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")
bone <- BP_OpenImage(file=path_Hedgehog)
bone <- BP_DetectBackground(bone=bone, analysis="logistic")
bone <- BP_DetectForeground(bone=bone, analysis="logistic")
bone <- BP_DetectCenters(bone=bone, analysis="logistic")
bone <- BP_EstimateCompactness(bone, analysis="logistic")
bone <- BP_FitMLCompactness(bone, analysis="logistic")
BP_GetFittedParameters(bone, analysis="logistic")

## End(Not run)
```

---

BP\_ListAnalyses

*List the analyses stored in an object*

---

**Description**

Get the analyses stored in an object.

**Usage**

```
BP_ListAnalyses(bone, silent = TRUE, max.level = FALSE)
```



**Arguments**

bone	The bone image to be used
silent	Should the results be shown ?
max.level	If TRUE, will return all list element of the objects

**Details**

BP\_ListAnalyses lists the analyses stored in an object

**Value**

The list of analyses

**Author(s)**

Marc Girondot <marc.girondot@gmail.com>

**See Also**

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

**Examples**

```
## Not run:
# Not run:
library(BoneProfileR)
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")

bone <- BP_OpenImage(file=path_Hedgehog)
bone <- BP_DetectBackground(bone=bone, analysis="logistic")
bone <- BP_DetectForeground(bone=bone, analysis="logistic")
bone <- BP_DetectCenters(bone=bone, analysis="logistic")
bone <- BP_EstimateCompactness(bone, analysis="logistic")
bone <- BP_FitMLCompactness(bone, analysis="logistic")
plot(bone)
plot(bone, type="observations")
plot(bone, type="observations+model", analysis=1)
bone <- BP_DuplicateAnalysis(bone, from="logistic", to="flexit")
BP_ListAnalyses(bone)

## End(Not run)
```

---

BP\_LnLCompactness      *Estimation of the likelihood of a bone section*

---

### Description

Estimation of the compactness of a bone section.

### Usage

```
BP_LnLCompactness(  
  par,  
  bone = NULL,  
  data_m = NULL,  
  data_nm = NULL,  
  distance.center = NULL,  
  fixed.parameters = NULL,  
  analysis = 1  
)
```

### Arguments

par	Parameters of the model
bone	The bone image to be used
data_m	Number of mineralized pixels
data_nm	Number of non-mineralized pixels
distance.center	Distances to the center
fixed.parameters	Fixed parameters of the model
analysis	Name or rank of analysis

### Details

BP\_LnLCompactness estimates likelihood of model of a bone section

### Value

The  $-\ln L$

### Author(s)

Marc Girondot <marc.girondot@gmail.com>

**See Also**

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

**Examples**

```
## Not run:
# Not run:
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")
bone <- BP_OpenImage(file=path_Hedgehog)
bone <- BP_DetectBackground(bone=bone)
bone <- BP_DetectForeground(bone=bone)
bone <- BP_DetectCenters(bone=bone)
bone <- BP_EstimateCompactness(bone)
plot(bone)

## End(Not run)
```

---

BP_OpenImage	<i>Open an image</i>
--------------	----------------------

---

**Description**

Open an image.

**Usage**

```
BP_OpenImage(file = file.choose(), name = NULL, ijtiff = FALSE)
```

**Arguments**

file	The file to be opened
name	Name of this slice
ijtiff	Should the ijtiff must be used to read tiff image

**Details**

BP\_OpenImage opens an image

**Value**

Characteristics of an image

**Author(s)**

Marc Girondot <marc.girondot@gmail.com>

**See Also**

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

**Examples**

```
## Not run:
# Not run:
library(BoneProfileR)
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")
bone <- BP_OpenImage(file=path_Hedgehog)
plot(bone)
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.tif",
                             package = "BoneProfileR")
bone <- BP_OpenImage(file=path_Hedgehog)
plot(bone)
bone <- BP_OpenImage(file=path_Hedgehog, ijtiff=TRUE)
plot(bone)
# A partial section
path_Dicynodon <- system.file("extdata", "Dicynodon_tibia_11.11.1.T_b_b-1.png",
                              package = "BoneProfileR")
bone <- BP_OpenImage(file=path_Dicynodon)
plot(bone)
# To open a file with a dialog:
bone <- BP_OpenImage()

## End(Not run)
```

---

BP\_Report

*Generate a pdf report for the analyzed bone*

---

**Description**

Generate a docx, xlsx, or pdf report.

**Usage**

```
BP_Report(
  bone = stop("A bone section must be provided"),
  control.plot = list(message = NULL, show.centers = TRUE, show.colors = TRUE,
```

```

    show.grid = TRUE, CI = "ML", show.legend = TRUE),
  analysis = 1,
  docx = file.path(getwd(), "report.docx"),
  pdf = file.path(getwd(), "report.pdf"),
  xlsx = file.path(getwd(), "report.xlsx"),
  author = NULL,
  title = attributes(bone)$name
)

```

### Arguments

bone	The bone image
control.plot	A list with the parameters used for plot
analysis	Indicate analysis name or rank that you want report
docx	Name of Word file
pdf	Name of pdf file
xlsx	Name of Excel file
author	Name indicated in the report
title	Title of the report

### Details

BP\_Report save a pdf report for the analyzed bone

### Value

Nothing

### Author(s)

Marc Girondot <marc.girondot@gmail.com>

### See Also

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

### Examples

```

## Not run:
# Not run:
library(BoneProfileR)
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")
bone <- BP_OpenImage(file=path_Hedgehog)

```

```

bone <- BP_DetectBackground(bone=bone, analysis="logistic")
bone <- BP_DetectForeground(bone=bone, analysis="logistic")
bone <- BP_DetectCenters(bone=bone, analysis="logistic")
bone <- BP_EstimateCompactness(bone, analysis="logistic")
bone <- BP_FitMLCompactness(bone, analysis="logistic")
fittedpar <- BP_GetFittedParameters(bone, analysis="logistic")
bone <- BP_DuplicateAnalysis(bone, from="logistic", to="flexit")
bone <- BP_FitMLCompactness(bone,
                           fitted.parameters=c(fittedpar, K1=1, K2=1),
                           fixed.parameters=NULL, analysis="flexit")
compare_AIC(Logistic=BP_GetFittedParameters(bone, analysis="logistic", alloptim=TRUE),
            Flexit=BP_GetFittedParameters(bone, analysis="flexit", alloptim=TRUE))
bone <- BP_FitMLRadialCompactness(bone, analysis="logistic")
# Test using the change of orientation using default.angle from BP_EstimateCompactness():
bone <- BP_DuplicateAnalysis(bone, from="logistic", to="logistic_rotation_pi")
# With a pi rotation, the top moves to the bottom and the left moves to the right
bone <- BP_EstimateCompactness(bone, rotation.angle=pi, analysis="logistic_rotation_pi")
bone <- BP_FitMLRadialCompactness(bone, analysis="logistic_rotation_pi")
BP_Report(bone=bone,
          analysis=1,
          docx=NULL,
          pdf=NULL,
          xlsx=file.path(getwd(), "report.xlsx"),
          author="Marc Girondot",
          title=attributes(bone)$name)

BP_Report(bone=bone,
          analysis=1,
          docx=NULL,
          pdf=file.path(getwd(), "report.pdf"),
          xlsx=NULL,
          author="Marc Girondot",
          title=attributes(bone)$name)

BP_Report(bone=bone,
          analysis=1,
          docx=file.path(getwd(), "report.docx"),
          pdf=NULL,
          xlsx=NULL,
          author="Marc Girondot",
          title=attributes(bone)$name)

## End(Not run)

```

---

Erinaceus\_europaeus     *Example of hedgehog femur*

---

### Description

Example of hedgehog femur. A drawing produced by Michel Laurin.

## Usage

```
Erinaceus_europaeus
```

## Format

A png image.

## Details

Example of hedgehog femur

## Author(s)

Marc Girondot <marc.girondot@gmail.com>

## See Also

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [plot.BoneProfileR\(\)](#), [summary.BoneProfileR\(\)](#)

## Examples

```
bone <- Erinaceus_europaeus
plot(bone)
```

---

plot.BoneProfileR      *Plot a bone section*

---

## Description

Display a bone section.

type value can be:

Image plot: original, mineralized, unmineralized, section

Original is the original image, mineralized is the mineral interpretation of the section, unmineralized is the unmineralized interpretation of the section, section is the interpretation of the section.

Global analysis: observations, model, observations+model

Radial analysis: radial

If angle is not null and a radial analysis exists, it will show the model for this angle.

mcmc: It will show the posterior distribution of parameter

**Usage**

```
## S3 method for class 'BoneProfileR'
plot(
  x,
  message = NULL,
  type = "original",
  angle = NULL,
  show.centers = TRUE,
  show.colors = TRUE,
  show.grid = TRUE,
  analysis = 1,
  parameter.mcmc = "S",
  options.mcmc = list(),
  restorePar = TRUE,
  mar = NULL,
  CI = "ML",
  radial.variable = "S",
  show.legend = TRUE,
  ...
)
```

**Arguments**

<code>x</code>	The bone image
<code>message</code>	The message to be displayed
<code>type</code>	The type of plot; see description
<code>angle</code>	Which angle model to show
<code>show.centers</code>	Should the centers be shown?
<code>show.colors</code>	Should the background and foreground colors be shown?
<code>show.grid</code>	Should the grid be shown?
<code>analysis</code>	Name or number of analysis to be plotted
<code>parameter.mcmc</code>	The posterior parameter to show for type = "mcmc"
<code>options.mcmc</code>	The option to plot type mcmc output
<code>restorePar</code>	If TRUE, restore the par parameter at the exit
<code>mar</code>	The margin for type = model or observations
<code>CI</code>	Which confidence interval should be plotted: MCMC or ML
<code>radial.variable</code>	Name of the radial variable to plot
<code>show.legend</code>	Should a legend be shown?
<code>...</code>	Not used

**Details**

`plot.BoneProfileR` displays a bone section



**Value**

Nothing

**Author(s)**

Marc Girondot <marc.girondot@gmail.com>

**See Also**

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [summary.BoneProfileR\(\)](#)

**Examples**

```
## Not run:
# Not run:
library(BoneProfileR)
bone <- BP_OpenImage()
# or
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")

bone <- BP_OpenImage(file=path_Hedgehog)
bone <- BP_DetectBackground(bone=bone, analysis="logistic")
bone <- BP_DetectForeground(bone=bone, analysis="logistic")
bone <- BP_DetectCenters(bone=bone, analysis="logistic")
bone <- BP_EstimateCompactness(bone, analysis="logistic", rotation.angle = 1)
bone <- BP_FitMLCompactness(bone, analysis="logistic")
plot(bone)
#
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",
                             package = "BoneProfileR")

bone <- BP_OpenImage(file=path_Hedgehog)
bone <- BP_DetectBackground(bone=bone, analysis="logistic")
bone <- BP_DetectForeground(bone=bone, analysis="logistic")
bone <- BP_DetectCenters(bone=bone, analysis="logistic")
bone <- BP_EstimateCompactness(bone, analysis="logistic")
bone <- BP_FitMLCompactness(bone, analysis="logistic")
plot(bone)
plot(bone, type="observations")
plot(bone, type="observations+model", analysis=1)
bone <- BP_DuplicateAnalysis(bone, from="logistic", to="flexit")
fittedpar <- BP_GetFittedParameters(bone, analysis="logistic")
bone <- BP_DuplicateAnalysis(bone, from="logistic", to="flexit")
bone <- BP_FitMLCompactness(bone,
                           fitted.parameters=c(fittedpar, K1=1, K2=1),
                           fixed.parameters=NULL, analysis="flexit")
compare_AIC(Logistic=BP_GetFittedParameters(bone, analysis="logistic", alloptim=TRUE),
            Flexit=BP_GetFittedParameters(bone, analysis="flexit", alloptim=TRUE))
```

```

out4p <- plot(bone, type="observations+model", analysis="logistic")
out6p <- plot(bone, type="observations+model", analysis="flexit")
bone <- BP_FitBayesianCompactness(bone, analysis="logistic")
plot(bone, type="observations+model", CI="MCMC")
bone <- BP_FitMLRadialCompactness(bone)
plot(bone, type="radial", radial.variable=c("P", "S"))
plot(bone, type="radial", radial.variable=c("P", "S", "Min", "Max"))

## End(Not run)

```

---

summary.BoneProfileR *Plot a bone section*

---

## Description

Display information of bone section

## Usage

```

## S3 method for class 'BoneProfileR'
summary(object, max.level = FALSE, ...)

```

## Arguments

object	The bone image
max.level	If TRUE, will return all list element of the objects
...	Not used

## Details

summary.BoneProfileR displays a bone section

## Value

An invisible list with recorded information

## Author(s)

Marc Girondot <marc.girondot@gmail.com>

## See Also

Other BoneProfileR: [BP\\_AutoFit\(\)](#), [BP\\_ChooseBackground\(\)](#), [BP\\_ChooseCenter\(\)](#), [BP\\_ChooseForeground\(\)](#), [BP\\_DetectBackground\(\)](#), [BP\\_DetectCenters\(\)](#), [BP\\_DetectForeground\(\)](#), [BP\\_DuplicateAnalysis\(\)](#), [BP\\_EstimateCompactness\(\)](#), [BP\\_FitBayesianCompactness\(\)](#), [BP\\_FitMLCompactness\(\)](#), [BP\\_FitMLRadialCompactness\(\)](#), [BP\\_GetFittedParameters\(\)](#), [BP\\_ListAnalyses\(\)](#), [BP\\_LnLCompactness\(\)](#), [BP\\_OpenImage\(\)](#), [BP\\_Report\(\)](#), [Erinaceus\\_europaeus](#), [plot.BoneProfileR\(\)](#)

### **Examples**

```
## Not run:  
# Not run:  
library(BoneProfileR)  
bone <- BP_OpenImage()  
# or  
path_Hedgehog <- system.file("extdata", "Erinaceus_europaeus_fem_2-1_small.png",  
                             package = "BoneProfileR")  
bone <- BP_OpenImage(file=path_Hedgehog)  
summary(bone)  
  
## End(Not run)
```

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