Package 'Momocs'

March 18, 2016

Title Morphometrics using R

Version 1.0.0

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Description A complete toolkit for morphometrics, from data extraction to multivariate analyses.
Most common 2D morphometrics approaches are included:
outlines, open outlines, configurations of landmarks, traditional morphometrics,
and facilities for data preparation, manipulation and visualization
with a consistent grammar throughout.
Momocs allows reproducible, complex morphometric analyses,
paves the way for a pure open-source workflow in R,
and other morphometrics approaches should be easy to plug in,
or develop from, on top of this canvas.

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URL https://github.com/vbonhomme/Momocs/

BugReports https://github.com/vbonhomme/Momocs/issues

Depends R(>= 3.2)

LazyData true

Imports ape, dplyr, magrittr, graphics, geometry, geomorph, ggplot2,
jpeg, MASS, plyr, reshape2, sp, utils

Suggests devtools, knitr, rmarkdown, testthat, covr

VignetteBuilder knitr

RoxygenNote 5.0.1

NeedsCompilation no

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Repository CRAN

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R topics documented:

`a2l` *Converts an array of coordinates to a list of matrices*

Description

Converts a `m x n x k` array of coordinates to a list of `k` matrices with `m` rows and `n` columns matrices.

Usage

```
a2l(a)
```

Arguments

`a`	`array` of coordinates.

Details

May be useful to communicate with other morphometrics packages that use array of coordinates when handling configurations of landmarks.

Value

`list` with 2-cols matrices of (x; y) coordinates.

See Also

Other bridges functions: `a2m`, `as_df`, `l2a`, `l2m`, `m2a`, `m2d`, `m2l1`, `m2l`

Examples

```
data(wings)
l <- wings$coo
l
a <- l2a(l)
a
```

a2m *Converts an array of coordinates to a matrix*

Description

All the individuals (the 3rd dimension of the array) becomes rows, and columns are (all the) x coordinates and (all the) y coordinates, so that we have x1, x2, ..., xn, y1, y2, ..., yn columns. Rows and colums are named anyway.

Usage

```
a2m(a)
```

Arguments

a	array of (x; y) coordinates.

Details

Used in landmarks methods, e.g. for multivariate analysis after a Procrustes alignment.

Value

matrix (see above).

See Also

m2a the reverse function.

Other bridges functions: a2l, as_df, l2a, l2m, m2a, m2d, m2ll, m2l

Examples

```
data(wings)
a <- l2a(wings$coo)
a
```

arrange *Arranges (ala dplyr) on Momocs objects*

Description

Arange shapes by variables, from the $fac. See examples and ?dplyr::arrange.

Usage

```
arrange(.data, ...)
```

Arguments

.data	a Coo, Coe, PCA object
...	logical conditions

Details

dplyr verbs are maintained.

Value

a Momocs object of the same class.

See Also

Other handling functions: at_least, chop, combine, dissolve, filter, mutate, rename, rm_uncomplete, rw_rule, sample_frac, sample_n, select, slice, subset.Coo, transmute

Examples

```
olea
# we create a new column
olea %>% mutate(id=1:length(.)) %$% fac$id
# same but now, shapes are arranged in a desc order, based on id
olea %>% mutate(id=1:length(.)) %>% arrange(desc(id)) %$% fac$id
```

---

as.Out *Convert an OutCoe object into an Out object*

Description

Uses the $method to do the inverse corresponding function. For instance, an OutCoe object obtained with efourier, will be converted to an Out object (outlines from harmonic coefficients), using efourier_i.

Usage

```
as.Out(object, OutCoe, nb.pts = 120)
```

Arguments

object	an OutCoe object
OutCoe	used by as, useless for the front user
nb.pts	number of point for the reconstructed outlines

Details

Note that the 'positionnal' coefficients (ao and co if any) are lost, so for a proper comparison between a raw Out and a Out from Out -> OutCoe -> Out, the raw Out should be centered.

This method is useful since it allows a direct inspection at how Fourier-based methods handle outlines, and in particular how they normalize it (when they do). If you have bad "reconstruction" using as.Out, this probably means that you have to think about alternative alignements on the raw outlines. For instance, it is obvious that normalization does a good job on the bottle example, yet it -pi/2 turns the "outlines" yet neutral for further analysis (and that can be manage with the argument rotate.shp in functions/methods that use reconstructed outlines, e.g. plot.PCA).

Value

an Out object.

Examples

```
data(bot)
bot <- coo_center(bot)
bot.f <- rfourier(bot, 120)
bot.fi <- as.Out(bot.f)
op <- par(mfrow=c(1, 2))
stack(bot, title="raw bot")
stack(bot.fi, title="outlines from bot.f")
par(op)
```

---

as_df *Converts Momocs objects to data.frames*

Description

Used in particular for ggplot2 compatibility.

Usage

```
as_df(x)
```

Arguments

x	an object, typically a Momocs class

Value

a data.frame

See Also

Other bridges functions: a2l, a2m, l2a, l2m, m2a, m2d, m2ll, m2l

Examples

```
data(bot)
head(as_df(bot))
bot.f <- efourier(bot, 10)
head(as_df(bot.f))
bot.p <- PCA(bot.f)
head(as_df(bot.p))
bot.l <- LDA(bot.p, "type")
head(as_df(bot.l))
```

---

at_least *Retains group with at least a certain number of individuals*

Description

Examples are self-speaking.

Usage

```
at_least(x, fac, N)
```

Arguments

x	any Momocs object
fac	the id of name of the $fac column
N	minimal number of individuals to retain the group

Note

if N is too ambitious the original object is returned with a message

See Also

Other handling functions: arrange, chop, combine, dissolve, filter, mutate, rename, rm_uncomplete, rw_rule, sample_frac, sample_n, select, slice, subset.Coo, transmute

Examples

```
data(trilo)
table(trilo, "onto")
at_least(trilo, "onto", 9)
at_least(trilo, "onto", 16)
at_least(trilo, "onto", 2000) # too ambitious !
```

`bezier` *Calculates Bezier coefficients from a shape*

Description

Calculates Bezier coefficients from a shape

Usage

```
bezier(coo, n)
```

Arguments

`coo`	a matrix or a list of (x; y) coordinates
`n`	the degree, by default the number of coordinates.

Value

a list with components:

- `$J` matrix of Bezier coefficients
- `$B` matrix of Bezier vertices.

Note

Directly borrowed for Claude (2008), and also called `bezier` there. Not implemented for open outlines but may be useful for other purposes.

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

See Also

Other bezier functions: `bezier_i`

Examples

```
set.seed(34)
x <- coo_sample(efourier_shape(), 5)
plot(x, ylim=c(-3, 3), asp=1, type='b', pch=20)
b <- bezier(x)
bi <- bezier_i(b$B)
lines(bi, col='red')
```

`bezier_i` *Calculates a shape from Bezier coefficients*

Description

Calculates a shape from Bezier coefficients

Usage

```
bezier_i(B, nb.pts = 120)
```

Arguments

`B`	a matrix of Bezier vertices, such as those produced by bezier
`nb.pts`	the number of points to sample along the curve.

Value

a matrix of (x; y) coordinates

Note

Directly borrowed for Claude (2008), and called `beziercurve` there. Not implemented for open outlines but may be useful for other purposes.

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

See Also

Other bezier functions: `bezier`

Examples

```
set.seed(34)
x <- coo_sample(efourier_shape(), 5)
plot(x, ylim=c(-3, 3), asp=1, type='b', pch=20)
b <- bezier(x)
bi <- bezier_i(b$B)
lines(bi, col='red')
```

bind_db *Binds with a database*

Description

Adds columns to a Coo or Coe object from a data base. Data base must be provided as a data.frame or as a path which will be read.tabled with ... arguments.

Usage

```
bind_db(x, fac_col = "id", db, db_col = "id", ...)
```

Arguments

x	Coo or Coe object
fac_col	character (no numeric here) where to find ids in the fac
db	data.frame with the right number of rows, or a path as character. Then use ... to pass arguments to read.table
db_col	character where to fin ids in db
...	more parameters passed to read.table

Details

Many checks are done on the binding and this is the main advantage of using this method. It requires an "id" on both the Coo/Coe and the database. There is no assumption that shapes/coefficients are in the right order in the Coo/Coe (but a mutate(your_object, id=1:length(your_object)) would do the trick, see examples).

See Also

Other babel functions: chc2Out, chc2pix, import_StereoMorph_curve1, import_jpg, import_tps, nef2Coe, ntsrow2Coo, pix2chc, tie_jpg_txt, tps2coo

Examples

```
# Coo example
df <- data.frame(foo_id=40:1, fake1=rnorm(40), fake2=factor(rep(letters[1:4], 10)))
bot <- mutate(bot, hello=1:length(bot))
bind_db(bot, "hello", df, "foo_id")

# example on a Coe
bf <- efourier(bot, 12)
bind_db(bf, "hello", df, "foo_id")
```

bot *Data: Outline coordinates of beer and whisky bottles.*

Description

Data: Outline coordinates of beer and whisky bottles.

Format

A Out object containing the outlines coordinates and a grouping factor for 20 beer and 20 whisky bottles

Source

Images have been grabbed on the internet and prepared by the package's authors. No particular choice has been made on the dimension of the original images or the brands cited here.

See Also

Other datasets: chaff, charring, flower, hearts, molars, mosquito, oak, olea, shapes, trilo, wings

boxplot.OutCoe *Boxplot of morphometric coefficients*

Description

Explores the distribution of coefficient values.

Usage

```
## S3 method for class 'OutCoe'
boxplot(x, retain = 6, drop = 0, center.y = TRUE, ...)
```

Arguments

x	the Coe object
retain	numeric the number of harmonics to retain
drop	numeric the number of harmonics to drop
center.y	logical whether to center the y-axis
...	useless here but maintain the consistency with generic boxplot

Value

a ggplot2 object

See Also

Other Coe_graphics: hcontrib, hist.OutCoe

Examples

```
data(bot)
bot.f <- efourier(bot, 24)
boxplot(bot.f)

data(olea)
op <- opoly(olea)
boxplot(op)
```

`boxplot.PCA` *Boxplot on PCA objects*

Description

Boxplot on PCA objects

Usage

```
## S3 method for class 'PCA'
boxplot(x, fac = NULL, nax = 1:5, ...)
```

Arguments

x	an object of class "PCA", typically obtained with PCA
fac	factor, or a name or the column id from the $fac slot
nax	the range of PC to plot
...	useless here

Value

a ggplot object

Examples

```
data(bot)
bot.f <- efourier(bot, 12)
bot.p <- PCA(bot.f)
boxplot(bot.p)
p <- boxplot(bot.p, 1)
#p +  theme_minimal() + scale_fill_grey()
#p + facet_wrap(~PC, scales = "free")
```

`breed` *Jitters Coe (and others) objects*

Description

This methods applies column-wise on the `coe` of any Coe object but relies on a function that can be used on any matrix. It simply uses rnorm with the mean and sd calculated for every column (or row). For a `Coe` object, on every colum, randomly generates coefficients values centered on the mean of the column, and with a sd equals to it standard deviates multiplied by `rate`.

Usage

```
breed(x, ...)

## Default S3 method:
breed(x, margin = 2, size, rate = 1, ...)

## S3 method for class 'Coe'
breed(x, size, rate = 1, ...)
```

Arguments

`x`	the object to permute
`...`	useless here
`margin`	numeric whether 1 or 2 (rows or columns)
`size`	numeric the required size for the final object, same size by default
`rate`	numeric the number of sd for rnorm, 1 by default.

See Also

Other farming: `perm`

Examples

```
m <- matrix(1:12, nrow=3)
breed(m, margin=2, size=4)
breed(m, margin=1, size=10)

data(bot)
bot.f <- efourier(bot, 12)
bot.m <- breed(bot.f, 80)
bot.m
panel(bot.m)
```

`calibrate_deviations` *Quantitative calibration, through deviations, for Out and Opn objects*

Description

Calculate deviations from original and reconstructed shapes using a range of harmonic number.

Usage

```
calibrate_deviations(x, method, id, range, norm.centsize, dist.method,
  dist.nbpts)
```

Arguments

`x`	and `Out` or `Opn` object on which to calibrate_deviations
`method`	any method from `c('efourier', 'rfourier', 'tfourier')` and `'dfourier'`.
`id`	the shape on which to perform calibrate_deviations
`range`	vector of harmonics (or degree for opoly and npoly on Opn) on which to perform calibrate_deviations. If not provided, the harmonics corresponding to 0.9, 0.95 and 0.99 are used.
`norm.centsize`	logical whether to normalize deviation by the centroid size
`dist.method`	a method such as edm_nearest to calculate deviations
`dist.nbpts`	numeric the number of points to use for deviations calculations

Details

For *poly methods on Opn objects, the deviations are calculated from a degree 12 polynom.

Value

a ggplot object

See Also

Other calibration: `calibrate_harmonicpower`, `calibrate_r2`, `calibrate_reconstructions`

Examples

```
data(bot)
calibrate_deviations(bot)
## Not run:

# on Opn
data(olea)
camibrate_deviations(olea)

# lets customize the ggplot
```

```
library(ggplot2)
gg <- calibrate_deviations(bot, id=1:20)$gg
gg + geom_hline(yintercept=c(0.001, 0.005), linetype=3)
gg + labs(col="Number of harmonics", fill="Number of harmonics",
          title="Harmonic power") + theme_bw()
gg + coord_polar()

## End(Not run)
```

`calibrate_harmonicpower` *Quantitative calibration, through harmonic power, for Out and Opn objects*

Description

Estimates the number of harmonics required for the four Fourier methods implemented in Momocs: elliptical Fourier analysis (see efourier), radii variation analysis (see rfourier) and tangent angle analysis (see tfourier) and discrete Fourier transform (see dfourier). It returns and can plot cumulated harmonic power whether dropping the first harmonic or not, and based and the maximum possible number of harmonics on the `Coo` object.

Usage

```
calibrate_harmonicpower(x, method, id, nb.h, drop, thresh, plot, verbose)
```

Arguments

`x`	a `Coo` of `Opn` object
`method`	any method from `c('efourier', 'rfourier', 'tfourier')` for `Out`s and `dfourier` for `Out`s.
`id`	the shapes on which to perform calibrate_harmonicpower. All of them by default
`nb.h`	numeric the maximum number of harmonic, on which to base the cumsum
`drop`	numeric the number of harmonics to drop for the cumulative sum
`thresh`	vector of numeric for drawing horizontal lines, and also used for `minh` below
`plot`	logical whether to plot the result or simply return the matrix
`verbose`	whether to print results

Details

The power of a given harmonic n is calculated as follows for elliptical Fourier analysis and the n-th harmonic: $HarmonicPower_n \frac{A_n^2+B_n^2+C_n^2+D_n^2}{2}$ and as follows for radii variation and tangent angle: $HarmonicPower_n = \frac{A_n^2+B_n^2+C_n^2+D_n^2}{2}$

Value

returns a list with component:

- gg a ggplot object, q the quantile matrix
- minh a quick summary that returns the number of harmonics required to achieve a certain proportion of the total harmonic power.

See Also

Other calibration: calibrate_deviations, calibrate_r2, calibrate_reconstructions

Examples

```
data(bot)
cal <- calibrate_harmonicpower(bot)
## Not run:
# for Opn objects
data(olea)
calibrate_harmonicpower(olea, "dfourier")

# let customize the ggplot
library(ggplot2)
cal$gg + theme_minimal() +
coord_cartesian(xlim=c(3.5, 12.5), ylim=c(90, 100)) +
ggtitle("Harmonic power calibration")

## End(Not run)
# if you want to do efourier with 99% calibrate_harmonicpower in one step
# efourier(bot, nb.h=calibrate_harmonicpower(bot, "efourier", plot=FALSE)$minh["99%"])
```

---

calibrate_r2 *Quantitative r2 calibration for Opn objects*

Description

Estimates the r2 to calibrate the degree for npoly and opoly methods. Also returns a plot

Usage

```
calibrate_r2(Opn, method = "opoly", id = 1:length(Opn),
  degree.range = 1:8, thresh = c(0.9, 0.95, 0.99, 0.999), plot = TRUE,
  verbose = TRUE, ...)
```

Arguments

Opn	an Opn object
method	one of 'npoly' or 'opoly'
id	the ids of shapes on which to calculate r2 (all by default)
degree.range	on which to calculate r2
thresh	the threshold to return diagnostic
plot	logical whether to print the plot
verbose	logical whether to print messages
...	useless here

Details

May be long, so you can estimate it on a sample either with id here, or one of sample_n or sample_frac

See Also

Other calibration: calibrate_deviations, calibrate_harmonicpower, calibrate_reconstructions

Examples

```
## Not run:
calibrate_r2(olea, "opoly", degree.range=1:5, thresh=c(0.9, 0.99))

## End(Not run)
```

---

calibrate_reconstructions

Calibrate using reconstructed shapes

Description

Calculate and displays reconstructed shapes using a range of harmonic number. Compare them visually with the maximal fit.

Usage

```
calibrate_reconstructions(x, method, id, range, baseline1, baseline2)
```

Arguments

x	the Coo object on which to calibrate_reconstructions
method	any method from c('efourier', 'rfourier', 'tfourier') for Out, or from c('opoly', 'npoly', 'dfourier') for Opn
id	the shape on which to perform calibrate_reconstructions
range	vector of harmonics on which to perform calibrate_reconstructions
baseline1	$(x; y)$ coordinates for the first point of the baseline
baseline2	$(x; y)$ coordinates for the second point of the baseline
...	only used for the generic

Value

a ggplot object

See Also

Other calibration: calibrate_deviations, calibrate_harmonicpower, calibrate_r2

Examples

```
data(bot)
calibrate_reconstructions(bot, "efourier")

data(olea)
calibrate_reconstructions(olea, "dfourier")
```

---

chaff *Data: Landmark and semilandmark coordinates on cereal glumes*

Description

Data: Landmark and semilandmark coordinates on cereal glumes

Format

An Ldk object with 21 configurations of landmarks and semi-landmarks (4 partitions) sampled on cereal glumes

Source

Research support was provided by the European Research Council (Evolutionary Origins of Agriculture (grant no. 269830-EOA) PI: Glynis Jones, Dept of Archaeology, Sheffield, UK. Data collected by Emily Forster.

See Also

Other datasets: bot, charring, flower, hearts, molars, mosquito, oak, olea, shapes, trilo, wings

charring *Data: Outline coordinates from an experimental charring on cereal grains*

Description

Data: Outline coordinates from an experimental charring on cereal grains

Format

An Out object with 18 grains, 3 views on each, for 2 cereal species, charred at different temperatures for 6 hours (0C (no charring), 230C and 260C).

Source

Research support was provided by the European Research Council (Evolutionary Origins of Agriculture (grant no. 269830-EOA) PI: Glynis Jones, Dept of Archaeology, Sheffield, UK. Data collected by Emily Forster.

See Also

Other datasets: bot, chaff, flower, hearts, molars, mosquito, oak, olea, shapes, trilo, wings

chc2Out *Converts chain-coded coordinates to Out object*

Description

For Shape/ChainCoder files, a wrapper to convert chain-coded coordinates to Out objects.

Usage

```
chc2Out(chc, skip, names)
```

Arguments

chc	a path to the chc file
skip	numeric how many informations before the first chain-coded information
names	an (optional) vector of (skip) names for the fac created. Somehow similar to names in lf_structure

Details

Files from Shape/ChainCoder comes this way:

```
Name_1 fac1 fac2 fac3 [...] 6 6 6 6 6 6 6 6 7 6 [...] -1
Name_2 fac1 fac2 fac3 [...] 6 6 6 6 5 5 7 6 7 6 [...] -1
```

This function does the following:

1. take everything before the first chain-coded coordinate (here a "6") and transform it into a `data.frame`, later used as a `fac`
2. convert all the chain-coded coordinates into (x; y) coordinates using chc2pix (and removes) the "-1" that mark the end of coordinates
3. returns an `Out` object with the corresponding `fac` and with outlines named after the first `fac` column (here with Name_1, Name_2, etc.)

This function needs to know how many information (space-separated there is before) the first coordinate. On the example above, would be 4 id [...] was empty.

Note

I'm not very familiar to other morphometric formats. So if you have troubles importing your datasets, contact me, I can help. Or if you fix something, please let met know!

References

Kuhl, F. P., & Giardina, C. R. (1982). Elliptic Fourier features of a closed contour. *Computer Graphics and Image Processing*, 18(3), 236-258.

See Also

pix2chc

Other babel functions: `bind_db`, `chc2pix`, `import_StereoMorph_curve1`, `import_jpg`, `import_tps`, `nef2Coe`, `ntsrow2Coo`, `pix2chc`, `tie_jpg_txt`, `tps2coo`

Examples

```
## Not run:
# if the file above was called 'coded.chc' in the 'data' folder:
chc2Out("data/coded.chc", skip=4)

## End(Not run)
```

chc2pix *Converts chain-coded coordinates to (x; y) coordinates*

Description

May be useful to convert chain-coded coordinates to (x; y) coordinates. The first point is set at the origin. chc2Out does the job for an entire dataset produced by Shape/ChainCoder, etc.

Usage

```
chc2pix(chc)
```

Arguments

chc	a vector of chain-coded coordinates

References

Kuhl, F. P., & Giardina, C. R. (1982). Elliptic Fourier features of a closed contour. *Computer Graphics and Image Processing*, 18(3), 236-258.

See Also

pix2chc, chc2Out

Other babel functions: `bind_db`, `chc2Out`, `import_StereoMorph_curve1`, `import_jpg`, `import_tps`, `nef2Coe`, `ntsrow2Coo`, `pix2chc`, `tie_jpg_txt`, `tps2coo`

Examples

```
data(shapes)
x <- pix2chc(shapes[1])
coo_plot(chc2pix(x))
```

chop *Chops (rough slicing) Momocs objects*

Description

Rougher slicing that accepts a classifier ie a column name from the `$fac` on Momocs classes. Returns a named (after every level) list that can be lapply-ed and combined. See examples.

Usage

```
chop(.data, fac)
```

Arguments

.data	a Coo or Coe object
fac	a column name from the $fac

Value

a named list of Coo or Coe objects

See Also

Other handling functions: arrange, at_least, combine, dissolve, filter, mutate, rename, rm_uncomplete, rw_rule, sample_frac, sample_n, select, slice, subset.Coo, transmute

Examples

```
data(bot)
```

---

classify *Classify using LDA*

Description

Classify using LDA

Usage

```
classify(x, fac, ref, unk)
```

Arguments

x	a Coe
fac	a standalone factor, or the name or id of the $fac column to use.If it contains NAs, they will also be removed first from the x object
ref	at least two level names from $fac[, "fac"] to use as a training subset of x
unk	same as above for one level name to classify

Value

a list with components:

- $N_ref the number of elements in the training set
- $N_unk the number of elements in the unknown set
- $counts counts of classification of 'unk' in each class of 'ref'
- $pc same thing as percentages
- $probs same thing as posterior probabilities
- $probs same thing as posterior but as a data.frame

Examples

```
data(olea)
table(olea, "var")
x <- opoly(olea, 5, verbose=FALSE)
classify(x, fac="var", ref=c("Aglan","Cypre"), unk="PicMa")
```

CLUST *Hierarchical clustering*

Description

Performs hierarchical clustering through dist and hclust. So far it is mainly a wrapper around these two functions, plus plotting using plot.phylo from the package ape.

Usage

```
CLUST(x, fac, type = "fan", dist_method = "euclidean",
  hclust_method = "complete", retain = 0.99, tip_labels,
  palette = col_qual, ...)

## Default S3 method:
CLUST(x, ...)
```

Arguments

x	a PCA object (Coe method deprecated so far)
fac	the id or column name or formula for columns to use from $fac.
type	to pass to ape::plot.phylo's type argument, one of "cladogram", "phylogram", "radial", "unrooted" or "fan" (by default)
dist_method	to feed dist's method argument, one of "euclidean", "maximum", "manhattan", "canberra", "binary" or "minkowski".
hclust_method	to feed hclust's method argument, one of "ward.D", "ward.D2", "single", "complete" (default), "average", "mcquitty", "median" or "centroid".
retain	number of axis to retain from the PCA as a range of number eg 1:5 to retain the first 5 PCs. If a number <= 1 is passed, then the number of PCs retained will be enough to capture this proportion of variance.
tip_labels	the id or column name in $fac to use as tip_labels rather than rownames. Note that you can also pass a character (or a factor) with the same number of rows of x$x
palette	a color palette to use (col_qual by default). If NULL, par("fg") is used
...	additional parameters to feed plot.phylo

Value

the phylo object, invisibly

See Also

Other multivariate: KMEANS, LDA, MANOVA_PW, MANOVA, PCA

Examples

```
## Not run:

# we prepare a PCA with shorter names
olea_lite <- olea
names(olea_lite) <- as.character(olea$fac$var)
x <- olea_lite %>% opoly(5) %>% PCA()

# By default
CLUST(x)

# With a fac
CLUST(x, 1)

# plot.phylo types
CLUST(x, "var", type="cladogram")
CLUST(x, "var", type="phylogram")
CLUST(x, "var", type="radial")
CLUST(x, "var", type="unrooted")

# other dist/hclust methods
CLUST(x, "var", layout="cladogram", dist_method="minkowski", hclust_method="average")

# With another
CLUST(x, "domes", tip_labels="var", palette=col_india)

# Alternative ways to pass a factor
CLUST(x, 1)
CLUST(x, "var")
CLUST(x, ~var)
# Strict equivalent before but formula allows this:
CLUST(x, ~ domes + var, tip_labels = ~ domes + var)

# More arguments to plot.phylo
CLUST(x, cex=0.5)


## End(Not run)
```

Coe *Coe "super" class*

Description

Coe class is the 'parent' or 'super' class of OutCoe, OpnCoe and LdkCoe classes.

Usage

```
Coe(...)
```

Arguments

...	anything and, anyway, this function will simply returns a message.

Details

Useful shortcuts are described below. See `browseVignettes("Momocs")` for a detail of the design behind Momocs' classes.

`Coe` class is the 'parent' class of the following 'child' classes

- `OutCoe` for coefficients from closed **out**lines morphometrics
- `OpnCoe` for coefficients from **opn** outlines morphometrics
- `LdkCoe` for coefficients from configuration of **l**an**d**mar**k**s morphometrics.

In other words, `OutCoe`, `OpnCoe` and `LdkCoe` classes are all, primarily, `Coe` objects on which we define generic *and* specific methods. See their respective help pages for more help.

You can access all the methods available for `Coe` objects with `methods(class=Coe)`.

See Also

Other Coe objects: `OpnCoe`, `OutCoe`

Examples

```
# to see all methods for Coo objects.
methods(class='Coe')

data(bot)
bot.f<- efourier(bot, 12)
bot.f
class(bot.f)
inherits(bot.f, "Coe")

# if you want to work directly on the matrix of coefficients
bot.f$coe

#getters
bot.f[1]
bot.f[1:5]

#setters
bot.f[1] <- 1:48
bot.f[1]

bot.f[1:5] <- matrix(1:48, nrow=5, ncol=48, byrow=TRUE)
bot.f[1:5]
```

```
# An illustration of Momocs desing. See also browseVignettes("Momocs")
data(olea)
op <- opoly(olea, 5)
op
class(op)
op$coe # same thing

data(wings)
wp <- fgProcrustes(wings, tol=1e-4)
wp
class(wp) # for Ldk methods, LdkCoe objects can also be considered as Coo objects
# so you can apply all Ldk methods available.
wp$coe # Procrustes aligned coordinates
```

`coeff_sel` *Helps to select a given number of harmonics from a numerical vector.*

Description

`coeff_sel` helps to select a given number of harmonics by returning their indices when arranged as a numeric vector. For instance, harmonic coefficients are arranged in the `$coe` slot of `Coe`-objects in that way: $A_1, \ldots, A_n, B_1, \ldots, B_n, C_1, \ldots, C_n, D_1, \ldots, D - n$ after an elliptical Fourier analysis (see efourier and efourier) while $C_n and D_n$ harmonic are absent for radii variation and tangent angle approaches (see rfourier and tfourier respectively). . This function is used internally but might be of interest elwewhere.

Usage

```
coeff_sel(retain = 8, drop = 0, nb.h = 32, cph = 4)
```

Arguments

`retain`	`numeric`. The number of harmonics to retain.
`drop`	`numeric`. The number of harmonics to drop
`nb.h`	`numeric`. The maximum harmonic rank.
`cph`	`numeric`. Must be set to 2 for `rfourier` and `tfourier` were used.

Value

`coeff_sel` returns indices that can be used to select columns from an harmonic coefficient matrix. `coeff_split` returns a named list of coordinates.

Examples

```
data(bot)
bot.f <- efourier(bot, 32)
coe <- bot.f$coe # the raw matrix
coe
# if you want, say the first 8 harmonics but not the first one
retain <- coeff_sel(retain=8, drop=1, nb.h=32, cph=4)
head(coe[, retain])
```

`coeff_split` *Converts a numerical description of harmonic coefficients to a named list.*

Description

`coeff_split` returns a named list of coordinates from a vector of harmonic coefficients. For instance, harmonic coefficients are arranged in the `$coe` slot of `Coe`-objects in that way: $A_1, \ldots, A_n, B_1, \ldots, B_n, C_1, \ldots, C_n, D$ n after an elliptical Fourier analysis (see efourier and efourier) while $C_n and D_n$ harmonic are absent for radii variation and tangent angle approaches (see rfourier and tfourier respectively). This function is used internally but might be of interest elwewhere.

Usage

```
coeff_split(cs, nb.h = 8, cph = 4)
```

Arguments

`cs`	A `vector` of harmonic coefficients.
`nb.h`	`numeric`. The maximum harmonic rank.
`cph`	`numeric`. Must be set to 2 for `rfourier` and `tfourier` were used.

Value

Returns a named list of coordinates.

Examples

```
coeff_split(1:128, nb.h=32, cph=4) # efourier
coeff_split(1:64, nb.h=32, cph=2)  # t/r fourier
```

`col_summer` *Some color palettes*

Description

Colors, colors, colors.

Usage

```
col_summer(n)

col_summer2(n)

col_spring(n)

col_autumn(n)

col_black(n)

col_solarized(n)

col_gallus(n)

col_qual(n)

col_heat(n)

col_hot(n)

col_cold(n)

col_sari(n)

col_india(n)

col_bw(n)

col_grey(n)
```

Arguments

`n`	the number of colors to generate from the color palette

Value

colors (hexadecimal format)

Note

Among available color palettes, `col_solarized` is based on Solarized: http://ethanschoonover.com/solarized; `col_div`, `col_qual`, `col_heat`, `col_cold` and `col_gallus` are based on on ColorBrewer2: http://colorbrewer2.org/.

Examples

```
wheel <- function(palette, n=10){
 op <- par(mar=rep(0, 4)) ; on.exit(par(op))
 pie(rep(1, n), col=palette(n), labels=NA, clockwise=TRUE)}

 # Qualitative
 wheel(col_qual)
 wheel(col_solarized)
 wheel(col_summer)
 wheel(col_summer2)
 wheel(col_spring)
 wheel(col_autumn)

 # Divergent
 wheel(col_gallus)
 wheel(col_india)

 # Sequential
 wheel(col_heat)
 wheel(col_hot)
 wheel(col_cold)
 wheel(col_sari)
 wheel(col_bw)
 wheel(col_grey)

 # Black only for pubs
 wheel(col_black)
```

`col_transp` *Transparency helpers and palettes*

Description

To ease transparency handling.

Usage

```
col_transp(n, col = "#000000", ceiling = 1)

col_alpha(cols, transp = 0)
```

Arguments

n	the number of colors to generate
col	a color in hexadecimal format on which to generate levels of transparency
ceiling	the maximal opacity (from 0 to 1)
cols	on or more colors, provided as hexadecimal values
transp	numeric between 0 and 1, the value of the transparency to obtain

Examples

```
x <- col_transp(10, col='#000000')
x
barplot(1:10, col=x, main='a transparent black is grey')

summer10 <- col_summer(10)
summer10
summer10.transp8 <- col_alpha(summer10, 0.8)
summer10.transp8
summer10.transp2 <- col_alpha(summer10, 0.8)
summer10.transp2
x <- 1:10
barplot(x, col=summer10.transp8)
barplot(x/2, col=summer10.transp2, add=TRUE)
```

---

combine *Combines Momocs objects*

Description

Combine Coo objects after a slicing, either manual or using slice or chop. Note that on Coo object, it combines row-wise (ie, merges shapes as a c would do) ; but on Coe it combines column-wise (merges coefficients). In the latter case, Coe must have the same number of shapes (not necessarily the same number of coefficients). Also the $fac of the first Coe is retrieved. A separate version may come at some point.

Usage

```
combine(...)
```

Arguments

...	a list of Out(Coe), Opn(Coe), Ldk objects (but of the same class)

Note

Note that the order of shapes or their coefficients is not checked, so anything with the same number of rows will be merged.

See Also

Other handling functions: arrange, at_least, chop, dissolve, filter, mutate, rename, rm_uncomplete, rw_rule, sample_frac, sample_n, select, slice, subset.Coo, transmute

Examples

```
data(bot)
w <- filter(bot, type=="whisky")
b <- filter(bot, type=="beer")
combine(w, b)
# or, if you have many levels
bot_s <- chop(bot, type)
bot_s$whisky
# note that you can apply something (single function or a more
# complex pipe) then combine everyone, since combine also works on lists
# eg:
# bot_s2 <- lapply(bot_s, efourier, 10)
# bot_sf <- combine(bot_s2)

# pipe style
lapply(bot_s, efourier, 10) %>% combine()
```

---

conf_ell *Confidence ellipses*

Description

Draw (gaussian) confidence ellipses

Usage

```
conf_ell(x, y, conf = 0.95, nb.pts = 60)
```

Arguments

x	numeric values on the x axis
y	numeric values on the y axis
conf	the level of confidence
nb.pts	the number of points to return, to draw the ellipsis

Value

a list with $ell coordinates of the ellipse and $seg coordinates of its vertices

a matrix of (x; y) coordinates to draw the ellipsis

See Also

Other plotting functions: Ntable, coo_arrows, coo_draw, coo_listpanel, coo_lolli, coo_plot, coo_ruban, ldk_chull, ldk_confell, ldk_contour, ldk_labels, ldk_links, plot_devsegments

Examples

```
x <- rnorm(100, sd=3)
y <- rnorm(100)
plot(x, y, asp=1)
ce095 <- conf_ell(x, y, conf=0.95) # no need for conf arg since it's .95 by default
ce090 <- conf_ell(x, y, conf=0.90)
ce050 <- conf_ell(x, y, conf=0.50)
cols <- col_hot(10)
lines(ce050$ell, col=cols[5]) # you can also coo_close(ce050$ell)
lines(ce090$ell, col=cols[8])
lines(ce095$ell, col=cols[9])
segments(ce095$seg[1, 1], ce095$seg[1, 2], ce095$seg[2, 1], ce095$seg[2, 2])
segments(ce095$seg[3, 1], ce095$seg[3, 2], ce095$seg[4, 1], ce095$seg[4, 2])
```

Coo *Coo "super" class*

Description

Coo class is the 'parent' or 'super' class of Out, Opn and Ldk classes.

Usage

```
Coo(...)
```

Arguments

...	anything and, anyway, this function will simply returns a message.

Details

Useful shortcuts are described below. See `browseVignettes("Momocs")` for a detail of the design behind Momocs' classes.

Coo class is the 'parent' class of the following 'child' classes

- Out for closed **out**lines
- Opn for **opn** outlines
- Ldk for configuration of **l**an**d**mar**k**s

Since all 'child classes' of them handle $(x; y)$ coordinates among other generic methods, but also all have their specificity, this architecture allow to recycle generic methods and to use specific methods.

In other words, Out, Opn and Ldk classes are all, primarily, Coo objects on which we define generic *and* specific methods. See their respective help pages for more help.

You can access all the methods available for Coo objects with `methods(class=Coo)`.

See Also

Other Coo objects: Opn, Out

Examples

```
## Not run:
# to see all methods for Coo objects.
methods(class='Coo')
# Let's take an Out example. But all methods shown here
# work on Ldk (try data(wings) ) and on Opn (try data(olea))
data(bot)

# Primarily a 'Coo' object, but also an 'Out'
class(bot)
inherits(bot, "Coo")
panel(bot)
stack(bot)
plot(bot)

# Getters (you can also use it to set data)
bot[1] %>% coo_plot()
bot[1:5] %>% str()

# Setters
bot[1] <- shapes[4]
panel(bot)

bot[1:5] <- shapes[4:8]
panel(bot)

# access the different components
# $coo coordinates
head(bot$coo)
# $fac grouping factors
head(bot$fac)
# or if you know the name of the column of interest
bot$type
# table
table(bot$fac)
# an internal view of an Out object
str(bot)

# subsetting
# see ?filter, ?select, and their 'see also' section for the
# complete list of dplyr-like verbs implemented in Momocs

length(bot) # the number of shapes
names(bot) # access all individual names
bot2 <- bot
names(bot2) <- paste0('newnames', 1:length(bot2)) # define new names

## End(Not run)
```

coo_align *Aligns coordinates*

Description

Aligns the coordinates along their longer axis using var-cov matrix and eigen values.

Usage

```
coo_align(coo)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.

Value

a matrix of (x; y) coordinates, or a Coo object.

See Also

Other aligning functions: coo_aligncalliper, coo_alignminradius, coo_alignxax

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Examples

```
coo_plot(bot[1])
coo_plot(coo_align(bot[1]))
# on a Coo
stack(bot)
stack(coo_align(bot))
```

coo_aligncalliper *Aligns shapes along their 'calliper length'*

Description

And returns them registered on bookstein coordinates. See coo_bookstein.

Usage

```
coo_aligncalliper(coo)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.

Value

a matrix of (x; y) coordinates, or any Coo object.

See Also

Other aligning functions: coo_alignminradius, coo_alignxax, coo_align

Other coo_ utilities: coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Examples

```
## Not run:
b <- bot[1]
coo_plot(b)
coo_plot(coo_aligncalliper(b))
bot.al <- coo_aligncalliper(bot)
stack(bot.al)

## End(Not run)
```

coo_alignminradius *Aligns shapes using their shortest radius*

Description

And returns them slided with the first coordinate on the east. May be used as an aligning strategy on shapes with a clear 'invaginate' part.

Usage

```
coo_alignminradius(coo)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.

Value

a matrix of (x; y) coordinates, or a Coo object.

See Also

Other aligning functions: coo_aligncalliper, coo_alignxax, coo_align

Other coo_ utilities: coo_aligncalliper, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Examples

```
## Not run:
stack(coo_alignminradius(hearts))

## End(Not run)
```

coo_alignxax *Aligns shapes along the x-axis*

Description

Align the longest axis of a shape along the x-axis.

Usage

```
coo_alignxax(coo)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.

Details

If some shapes are upside-down (or mirror of each others), try redefining a new starting point (eg with coo_slidedirection) before the alignment step. This may solve your problem because coo_calliper orders the $arr.ind used by coo_aligncalliper.

Value

a matrix of (x; y) coordinates, or any Coo object.

See Also

Other aligning functions: coo_aligncalliper, coo_alignminradius, coo_align

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Examples

```
## Not run:
b <- bot[1]
coo_plot(b)
coo_plot(coo_alignxax(b))

## End(Not run)
```

coo_area *Calculates the area of a shape*

Description

Calculates the area for a (non-crossing) shape.

Usage

```
coo_area(coo)
```

Arguments

coo	a matrix of (x; y) coordinates.

Value

numeric, the area.

Note

Using area.poly in gpc package is a good idea, but their licence impedes Momocs to rely on it. but here is the function to do it, once gpc is loaded: `area.poly(as(coo, 'gpc.poly'))`

See Also

Other coo_ descriptors: coo_chull, coo_circularityharalick, coo_circularitynorm, coo_circularity, coo_convexity, coo_eccentricityboundingbox, coo_eccentricityeigen, coo_elongation, coo_length, coo_lw, coo_rectangularity, coo_rectilinearity, coo_solidity, coo_tangle, coo_theta3, coo_thetapts, coo_width

Examples

```
data(bot)
coo_area(bot[1])
# for the distribution of the area of the bottles dataset
hist(sapply(bot$coo, coo_area), breaks=10)
```

coo_arrows *Plots (lollipop) differences between two configurations*

Description

Draws 'arrows' between two configurations.

Usage

```
coo_arrows(coo1, coo2, length = coo_centsize(coo1)/15, angle = 20, ...)
```

Arguments

coo1	A list or a matrix of coordinates.
coo2	A list or a matrix of coordinates.
length	a length for the arrows.
angle	an angle for the arrows
...	optional parameters to fed arrows.

See Also

Other plotting functions: Ntable, conf_ell, coo_draw, coo_listpanel, coo_lolli, coo_plot, coo_ruban, ldk_chull, ldk_confell, ldk_contour, ldk_labels, ldk_links, plot_devsegments

Examples

```
data(olea)
coo_arrows(coo_sample(olea[3], 50), coo_sample(olea[6], 50))
title("Hi there !")
```

coo_baseline *Register new baselines*

Description

A non-exact baseline registration on t1 and t2 coordinates, for the ldk1-th and ldk2-th points. By default it returns Bookstein's coordinates.

Usage

```
coo_baseline(coo, ldk1, ldk2, t1, t2)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.
ldk1	numeric the id of the first point of the new baseline
ldk2	numeric the id of the second point of the new baseline
t1	numeric the (x; y) coordinates of the 1st point of the new baseline
t2	numeric the (x; y) coordinates of the 2nd point of the new baseline

Value

a matrix of (x; y) coordinates or a Coo object.

See Also

Other baselining functions: coo_bookstein

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Examples

```
stack(hearts)
stack(coo_baseline(hearts, 2, 4, c(-1, 0), c(1, 1)))
```

---

coo_bookstein *Register Bookstein's coordinates*

Description

Registers a new baseline for the shape, with the ldk1-th and ldk2-th points being set on $(x = -0.5; y = 0)$ and $(x = 0.5; y = 0)$, respectively.

Usage

```
coo_bookstein(coo, ldk1, ldk2)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.
ldk1	numeric the id of the first point of the new baseline (the first, by default)
ldk2	numeric the id of the second point of the new baseline (the last, by default)

Details

For Out, it tries to do it using $ldk slot. Also the case for Opn, but if no landmark is defined, it will do it on the first and the last point of the shape.

For Out and Opn defines the first landmark as the first point of the new shapes with coo_slide.

Value

a matrix of (x; y) coordinates, or a Coo object.

See Also

Other baselining functions: coo_baseline

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Examples

```
stack(hearts)
stack(coo_bookstein(hearts, 2, 4))
h <- hearts[1]
coo_plot(h)
coo_plot(coo_bookstein(h, 20, 57), border='red')
```

---

coo_calliper *Calculates the calliper length*

Description

Also called the Feret's diameter, the longest distance between two points of the shape provided.

Usage

```
coo_calliper(coo, arr.ind = FALSE)
```

Arguments

coo	a matrix of (x; y) coordinates.
arr.ind	logical, see below.

Value

numeric, the centroid size. If arr.ind=TRUE, a list with the calliper length $length and the two points $arr.ind. If arr.ind=TRUE, only the calliper length as a numeric.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Examples

```
b <- bot[1]
coo_calliper(b)
p <- coo_calliper(b, arr.ind=TRUE)
p$length
ids <- p$arr.ind
coo_plot(b)
segments(b[ids[1], 1], b[ids[1], 2], b[ids[2], 1], b[ids[2], 2], lty=2)
```

---

coo_centdist *Returns the distance between everypoints and the centroid*

Description

For every point of the shape, returns the (centroid-points) distance.

Usage

```
coo_centdist(coo)
```

Arguments

coo	a matrix of (x; y) coordinates.

Value

a matrix of (x; y) coordinates.

See Also

Other centroid functions: coo_centpos, coo_centsize

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Examples

```
b <- coo_sample(bot[1], 64)
d <- coo_centdist(b)
barplot(d, xlab="Points along the outline", ylab="Distance to the centroid (pixels)")
```

`coo_center` *Centers coordinates*

Description

Returns a shape centered on the origin. The two functions are strictly equivalent.

Usage

```
coo_center(coo)

coo_centre(coo)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.

Value

a `matrix` of (x; y) coordinates, or a Coo object.

See Also

Other coo_ utilities: `coo_aligncalliper`, `coo_alignminradius`, `coo_alignxax`, `coo_align`, `coo_baseline`, `coo_bookstein`, `coo_calliper`, `coo_centdist`, `coo_centpos`, `coo_centsize`, `coo_close`, `coo_down`, `coo_dxy`, `coo_extract`, `coo_flipx`, `coo_force2close`, `coo_interpolate`, `coo_jitter`, `coo_left`, `coo_nb`, `coo_perimcum`, `coo_perimpts`, `coo_perim`, `coo_rev`, `coo_right`, `coo_rotatecenter`, `coo_rotate`, `coo_samplerr`, `coo_sample`, `coo_scalex`, `coo_scale`, `coo_shearx`, `coo_slice`, `coo_slidedirection`, `coo_slidegap`, `coo_slide`, `coo_smoothcurve`, `coo_smooth`, `coo_template`, `coo_trans`, `coo_trim`, `coo_up`, `is_closed`

Examples

```
coo_plot(bot[1])
# same as
coo_plot(coo_centre(bot[1]))
# this
coo_plot(coo_center(bot[1]))
# on Coo objects
stack(bot)
stack(coo_center(bot))
```

coo_centpos *Calculate centroid coordinates*

Description

Returns the (x; y) centroid coordinates of a shape.

Usage

```
coo_centpos(coo)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.

Value

(x; y) coordinates of the centroid as a vector or a matrix.

See Also

Other centroid functions: coo_centdist, coo_centsize

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Examples

```
b <- bot[1]
coo_plot(b)
xy <- coo_centpos(b)
points(xy[1], xy[2], cex=2, col='blue')
# on a Coo
coo_centpos(bot)
```

`coo_centsize` *Calculates centroid size*

Description

Calculates centroid size

Usage

```
coo_centsize(coo)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.

Details

This function can be used to integrate size - if meaningful - to Coo objects. See also coo_length and rescale.

Value

`numeric`, the centroid size.

See Also

Other centroid functions: `coo_centdist`, `coo_centpos`

Other coo_ utilities: `coo_aligncalliper`, `coo_alignminradius`, `coo_alignxax`, `coo_align`, `coo_baseline`, `coo_bookstein`, `coo_calliper`, `coo_centdist`, `coo_center`, `coo_centpos`, `coo_close`, `coo_down`, `coo_dxy`, `coo_extract`, `coo_flipx`, `coo_force2close`, `coo_interpolate`, `coo_jitter`, `coo_left`, `coo_nb`, `coo_perimcum`, `coo_perimpts`, `coo_perim`, `coo_rev`, `coo_right`, `coo_rotatecenter`, `coo_rotate`, `coo_samplerr`, `coo_sample`, `coo_scalex`, `coo_scale`, `coo_shearx`, `coo_slice`, `coo_slidedirection`, `coo_slidegap`, `coo_slide`, `coo_smoothcurve`, `coo_smooth`, `coo_template`, `coo_trans`, `coo_trim`, `coo_up`, `is_closed`

Examples

```
coo_centsize(bot[1])
# on a Coo
coo_centsize(bot)
# add it to $fac
mutate(bot, size=coo_centsize(bot))
```

coo_check *Checks shapes*

Description

A simple utility, used internally, mostly in the coo functions and methods. Returns a matrix of coordinates, when passed with either a list or a `matrix` of coordinates.

Usage

```
coo_check(coo)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.

Value

a `matrix` of (x; y) coordinates or a Coo object.

Examples

```
#coo_check('Not a shape')
#coo_check(matrix(1:10, ncol=2))
#coo_check(list(x=1:5, y=6:10))
```

coo_chull *Calculates the convex hull of a shape*

Description

Returns the ids of points that define the convex hull of a shape. A simple wrapper around chull, mainly used in graphical functions.

Usage

```
coo_chull(coo)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates.

Value

a `matrix` of ids defining the convex hull of the shape.

See Also

Other coo_ descriptors: coo_area, coo_circularityharalick, coo_circularitynorm, coo_circularity, coo_convexity, coo_eccentricityboundingbox, coo_eccentricityeigen, coo_elongation, coo_length, coo_lw, coo_rectangularity, coo_rectilinearity, coo_solidity, coo_tangle, coo_theta3, coo_thetapts, coo_width

Examples

```
data(hearts)
h <- coo_sample(hearts[4], 32)
coo_plot(h)
ch <- coo_chull(h)
lines(ch, col='red', lty=2)
```

---

coo_circularity *Calculates the circularity of a shape*

Description

Returns the 'circularity measure'. Also called 'compactness' and 'shape factor' sometimes.

Usage

```
coo_circularity(coo)
```

Arguments

coo	a matrix of (x; y) coordinates.

Value

numeric, the circularity.

See Also

Other coo_ descriptors: coo_area, coo_chull, coo_circularityharalick, coo_circularitynorm, coo_convexity, coo_eccentricityboundingbox, coo_eccentricityeigen, coo_elongation, coo_length, coo_lw, coo_rectangularity, coo_rectilinearity, coo_solidity, coo_tangle, coo_theta3, coo_thetapts, coo_width

Examples

```
data(bot)
coo_circularity(bot[1])
```

coo_circularityharalick *Calculates the Haralick's circularity of a shape*

Description

Returns Haralick's circularity which is less sensible to digitalization noise than coo_circularity

Usage

```
coo_circularityharalick(coo)
```

Arguments

coo	a matrix of (x; y) coordinates.

Value

numeric, the Haralick's circularity.

Source

Rosin PL. 2005. Computing global shape measures. Handbook of Pattern Recognition and Computer Vision. 177-196.

See Also

Other coo_ descriptors: coo_area, coo_chull, coo_circularitynorm, coo_circularity, coo_convexity, coo_eccentricityboundingbox, coo_eccentricityeigen, coo_elongation, coo_length, coo_lw, coo_rectangularity, coo_rectilinearity, coo_solidity, coo_tangle, coo_theta3, coo_thetapts, coo_width

Examples

```
data(bot)
coo_circularityharalick(bot[1])
```

coo_circularitynorm *Calculates the 'normalized' circularity of a shape*

Description

Returns the 'circularity', also called compactness and shape factor, but normalized to the unit circle.

Usage

```
coo_circularitynorm(coo)
```

Arguments

coo	a matrix of (x; y) coordinates.

Value

numeric, the circularity normalized to the unit circle.

Source

Rosin PL. 2005. Computing global shape measures. Handbook of Pattern Recognition and Computer Vision. 177-196.

See Also

Other coo_ descriptors: coo_area, coo_chull, coo_circularityharalick, coo_circularity, coo_convexity, coo_eccentricityboundingbox, coo_eccentricityeigen, coo_elongation, coo_length, coo_lw, coo_rectangularity, coo_rectilinearity, coo_solidity, coo_tangle, coo_theta3, coo_thetapts, coo_width

Examples

```
data(bot)
coo_circularitynorm(bot[1])
```

coo_close *Closes/uncloses shapes*

Description

Returns a closed shape from (un)closed shapes. See also coo_unclose.

Returns a unclosed shape from (un)closed shapes. See also coo_close.

Usage

```
coo_close(coo)

coo_unclose(coo)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.

Value

a matrix of (x; y) coordinates, or a Coo object.

a matrix of (x; y) coordinates, or a Coo object.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Examples

```
x <- (matrix(1:10, ncol=2))
x2 <- coo_close(x)
x3 <- coo_unclose(x2)
x
is_closed(x)
x2
is_closed(x2)
x3
is_closed(x3)
x <- (matrix(1:10, ncol=2))
x2 <- coo_close(x)
x3 <- coo_unclose(x2)
x
is_closed(x)
x2
is_closed(x2)
x3
```

```
is_closed(x3)
```

`coo_convexity` *Calculates the convexity of a shape*

Description

Calculated using a ratio of the eigen values (inertia axis)

Usage

```
coo_convexity(coo)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates.

Value

numeric, the convexity.

Source

Rosin PL. 2005. Computing global shape measures. Handbook of Pattern Recognition and Computer Vision. 177-196.

See Also

Other coo_ descriptors: `coo_area`, `coo_chull`, `coo_circularityharalick`, `coo_circularitynorm`, `coo_circularity`, `coo_eccentricityboundingbox`, `coo_eccentricityeigen`, `coo_elongation`, `coo_length`, `coo_lw`, `coo_rectangularity`, `coo_rectilinearity`, `coo_solidity`, `coo_tangle`, `coo_theta3`, `coo_thetapts`, `coo_width`

Examples

```
data(bot)
coo_convexity(bot[1])
```

coo_down *coo_down ———— Retains coordinates with negative y-coordinates*

Description

Useful when shapes are aligned along the x-axis (e.g. because of a bilateral symmetry) and when one wants to retain just the lower side.

Usage

```
coo_down(coo, slidegap = FALSE)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.
slidegap	logical whether to apply coo_slidegap after coo_down

Value

a matrix of (x; y) coordinates or a Coo object (Out are returned as Opn)

Note

When shapes are "sliced" along the x-axis, it usually results on open curves and thus to huge/artefactual gaps between points neighboring this axis. This is usually solved with coo_slidegap. See examples there.

Also, when apply a coo_left/right/up/down on an Out object, you then obtain an Opn object, which is done automatically.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Other opening functions: coo_left, coo_right, coo_up

Examples

```
b <- coo_alignxax(bot[1])
coo_plot(b)
coo_draw(coo_down(b), border='red')
```

coo_draw *Adds a shape to the current plot*

Description

coo_draw is simply a coo_plot with plot.new=FALSE, ie that adds a shape on the active plot.

Usage

```
coo_draw(coo, ...)
```

Arguments

coo	a list or a matrix of coordinates.
...	optional parameters for coo_plot

See Also

Other plotting functions: Ntable, conf_ell, coo_arrows, coo_listpanel, coo_lolli, coo_plot, coo_ruban, ldk_chull, ldk_confell, ldk_contour, ldk_labels, ldk_links, plot_devsegments

Examples

```
data(bot)
b1 <- bot[4]
b2 <- bot[5]
coo_plot(b1)
coo_draw(b2, border='red') # all coo_plot arguments will work for coo_draw
```

coo_dxy *Calculate abscissa and ordinate on a shape*

Description

A simple wrapper to calculate dxi - dx1 and dyi - dx1.

Usage

```
coo_dxy(coo)
```

Arguments

coo	a matrix (or a list) of (x; y) coordinates

Value

a list with two components dx and dy

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Examples

```
coo_dxy(bot[1])
```

---

coo_eccentricityboundingbox

Calculates the eccentricity (bounding box) of a shape

Description

Calculated using the width / length ratio. See coo_lw

Usage

```
coo_eccentricityboundingbox(coo)
```

Arguments

coo	a matrix of (x; y) coordinates.

Value

numeric, the eccentricity (boundingbox)

Source

Rosin PL. 2005. Computing global shape measures. Handbook of Pattern Recognition and Computer Vision. 177-196.

See Also

coo_eccentricityeigen

Other coo_ descriptors: coo_area, coo_chull, coo_circularityharalick, coo_circularitynorm, coo_circularity, coo_convexity, coo_eccentricityeigen, coo_elongation, coo_length, coo_lw, coo_rectangularity, coo_rectilinearity, coo_solidity, coo_tangle, coo_theta3, coo_thetapts, coo_width

Examples

```
data(bot)
coo_eccentricityboundingbox(bot[1])
```

`coo_eccentricityeigen` *Calculates the eccentricity (using eigenvalues) of a shape*

Description

Calculated using a ratio of the eigen values (inertia axes oof coordinates.)

Usage

```
coo_eccentricityeigen(coo)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates.

Value

numeric, the eccentricity (eigenvalues)

Source

Rosin PL. 2005. Computing global shape measures. Handbook of Pattern Recognition and Computer Vision. 177-196.

See Also

coo_eccentricityboundingbox

Other coo_ descriptors: coo_area, coo_chull, coo_circularityharalick, coo_circularitynorm, coo_circularity, coo_convexity, coo_eccentricityboundingbox, coo_elongation, coo_length, coo_lw, coo_rectangularity, coo_rectilinearity, coo_solidity, coo_tangle, coo_theta3, coo_thetapts, coo_width

Examples

```
data(bot)
coo_eccentricityeigen(bot[1])
```

coo_elongation *Calculates the elongation of a shape*

Description

Calculates the elongation of a shape

Usage

```
coo_elongation(coo)
```

Arguments

coo	a matrix of (x; y) coordinates.

Value

numeric, the circularity normalized to the unit circle.

Source

Rosin PL. 2005. Computing global shape measures. Handbook of Pattern Recognition and Computer Vision. 177-196.

See Also

Other coo_ descriptors: coo_area, coo_chull, coo_circularityharalick, coo_circularitynorm, coo_circularity, coo_convexity, coo_eccentricityboundingbox, coo_eccentricityeigen, coo_length, coo_lw, coo_rectangularity, coo_rectilinearity, coo_solidity, coo_tangle, coo_theta3, coo_thetapts, coo_width

Examples

```
data(bot)
coo_elongation(bot[1])
```

coo_extract *Extract coordinates from a shape*

Description

Extract ids coordinates from a single shape or a Coo object.

Usage

```
coo_extract(coo, ids)
```

Arguments

coo	either a matrix of (x; y) coordinates or a Coo object.
ids	integer, the ids of points to sample.

Details

It probably only make sense for Coo objects with the same number of coordinates and them being homologous, typically on Ldk.

Value

a matrix of (x; y) coordinates, or a Coo object.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Other sampling functions: coo_interpolate, coo_samplerr, coo_sample

Examples

```
b <- bot[1]
stack(bot)
stack(coo_sample(bot, 24))
coo_plot(b)
coo_plot(coo_sample(b, 24))
```

---

coo_flipx *Flips shapes*

Description

coo_flipx flips shapes about the x-axis; coo_flipy about the y-axis.

Usage

```
coo_flipx(coo)

coo_flipy(coo)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.

Value

a matrix of (x; y) coordinates

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Other transforming functions: coo_shearx

Examples

```
cat <- shapes[4]
cat <- coo_center(cat)
coo_plot(cat)
coo_draw(coo_flipx(cat), border="red")
coo_draw(coo_flipy(cat), border="blue")

#' # to flip an entire Coo:
shapes2 <- shapes
shapes$coo <- lapply(shapes2$coo, coo_flipx)
```

---

coo_force2close *Forces shapes to close*

Description

An exotic function that distribute the distance between the first and the last points of unclosed shapes, so that they become closed. May be useful (?) e.g. for t/rfourier methods where reconstructed shapes may not be closed.

Usage

```
coo_force2close(coo)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.

Value

a matrix of (x; y) coordinates, or a Coo object.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Examples

```
b <- coo_sample(bot[1], 64)
b <- b[1:40,]
coo_plot(b)
coo_draw(coo_force2close(b), border='red')
```

---

coo_interpolate *Interpolates coordinates*

Description

Interpolates n coordinates 'among existing points'between' existing points, along the perimeter of the coordinates provided and keeping the first point

Usage

```
coo_interpolate(coo, n)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.
n	codeinteger, the number fo points to interpolate.

Value

a matrix of (x; y) coordinates, or a Coo object.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Other sampling functions: coo_extract, coo_samplerr, coo_sample

Examples

```
b <- bot[1]
stack(bot)
stack(coo_scale(bot))
coo_plot(b)
coo_plot(coo_scale(b))
stack(bot)
stack(coo_interpolate(coo_sample(bot, 12), 120))
coo_plot(bot[1])
coo_plot(coo_interpolate(coo_sample(bot[1], 12), 120))
```

`coo_jitter` *Jitters shapes*

Description

A simple wrapper around jitter.

Usage

```
coo_jitter(coo, ...)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.
`...`	additional parameter for jitter

Value

a `matrix` of (x; y) coordinates or a Coo object

See Also

get_pairs

Other coo_ utilities: `coo_aligncalliper`, `coo_alignminradius`, `coo_alignxax`, `coo_align`, `coo_baseline`, `coo_bookstein`, `coo_calliper`, `coo_centdist`, `coo_center`, `coo_centpos`, `coo_centsize`, `coo_close`, `coo_down`, `coo_dxy`, `coo_extract`, `coo_flipx`, `coo_force2close`, `coo_interpolate`, `coo_left`, `coo_nb`, `coo_perimcum`, `coo_perimpts`, `coo_perim`, `coo_rev`, `coo_right`, `coo_rotatecenter`, `coo_rotate`, `coo_samplerr`, `coo_sample`, `coo_scalex`, `coo_scale`, `coo_shearx`, `coo_slice`, `coo_slidedirection`, `coo_slidegap`, `coo_slide`, `coo_smoothcurve`, `coo_smooth`, `coo_template`, `coo_trans`, `coo_trim`, `coo_up`, `is_closed`

Examples

```
b <-bot[1]
coo_plot(b, zoom=0.2)
coo_draw(coo_jitter(b, amount=3), border="red")

# for a Coo example, see \link{get_pairs}
```

coo_ldk *Defines landmarks interactively*

Description

Allows to interactively define a `nb.ldk` number of landarks on a shape. Used in other facilities to acquire/manipulate data.

Usage

```
coo_ldk(coo, nb.ldk)
```

Arguments

`coo`	a `matrix` or a list of (x; y) coordinates.
`nb.ldk`	`integer`, the number of landmarks to define

Value

`numeric` that corresponds to the closest ids, on the shape, from cliked points.

Examples

```
## Not run:
b <- bot[1]
coo_ldk(b, 3) # run this, and click 3 times
coo_ldk(bot, 2) # this also works on Out

## End(Not run)
```

coo_left *Retains coordinates with negative x-coordinates*

Description

Useful when shapes are aligned along the y-axis (e.g. because of a bilateral symmetry) and when one wants to retain just the lower side.

Usage

```
coo_left(coo, slidegap = FALSE)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.
`slidegap`	`logical` whether to apply coo_slidegap after coo_left

Value

a matrix of (x; y) coordinates or a Coo object (Out are returned as Opn)

Note

When shapes are "sliced" along the y-axis, it usually results on open curves and thus to huge/artefactual gaps between points neighboring this axis. This is usually solved with coo_slidegap. See examples there.

Also, when apply a coo_left/right/up/down on an Out object, you then obtain an Opn object, which is done automatically.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Other opening functions: coo_down, coo_right, coo_up

Examples

```
b <- coo_center(bot[1])
coo_plot(b)
coo_draw(coo_left(b), border='red')
```

---

coo_length *Calculates the length of a shape*

Description

Nothing more than coo_lw(coo)[1].

Usage

```
coo_length(coo)
```

Arguments

coo	a matrix of (x; y) coordinates or a Coo object

Details

This function can be used to integrate size - if meaningful - to Coo objects. See also coo_centsize and rescale.

Value

the length (in pixels) of the shape

See Also

coo_lw, coo_width

Other coo_ descriptors: coo_area, coo_chull, coo_circularityharalick, coo_circularitynorm, coo_circularity, coo_convexity, coo_eccentricityboundingbox, coo_eccentricityeigen, coo_elongation, coo_lw, coo_rectangularity, coo_rectilinearity, coo_solidity, coo_tangle, coo_theta3, coo_thetapts, coo_width

Examples

```
data(bot)
coo_length(bot[1])
coo_length(bot)
mutate(bot, size=coo_length(bot))
```

---

coo_listpanel *Plots sets of shapes.*

Description

coo_listpanel plots a list of shapes if passed with a list of coordinates. Mainly used by panel.Coo functions. If used outside the latter, shapes must be "templated", see coo_template. If you want to reorder shapes according to a factor, use arrange.

Usage

```
coo_listpanel(coo.list, dim, byrow = TRUE, fromtop = TRUE, cols, borders,
  poly = TRUE, points = FALSE, points.pch = 3, points.cex = 0.2,
  points.col = "#333333")
```

Arguments

coo.list	A list of coordinates
dim	A vector of the form (nb.row, nb.cols) to specify the panel display. If missing, shapes are arranged in a square.
byrow	logical. Whether to succesive shape by row or by col.
fromtop	logical. Whether to display shapes from the top of the plotting region.
cols	A vector of colors to fill shapes.
borders	A vector of colors to draw shape borders.
poly	logical whether to use polygon or lines to draw shapes. mainly for use for outlines and open outlines.
points	logical if poly is set to FALSE whether to add points

points.pch	if points is TRUE, a pch for these points
points.cex	if points is TRUE, a cex for these points
points.col	if points is TRUE, a col for these points

Value

Returns (invisibly) a data.frame with position of shapes that can be used for other sophisticated plotting design.

See Also

Other plotting functions: Ntable, conf_ell, coo_arrows, coo_draw, coo_lolli, coo_plot, coo_ruban, ldk_chull, ldk_confell, ldk_contour, ldk_labels, ldk_links, plot_devsegments

Examples

```
coo_listpanel(bot$coo) # equivalent to panel(bot)
```

---

coo_lolli *Plots (lollipop) differences between two configurations*

Description

Draws 'lollipops' between two configurations.

Usage

```
coo_lolli(coo1, coo2, pch = NA, cex = 0.5, ...)
```

Arguments

coo1	A list or a matrix of coordinates.
coo2	A list or a matrix of coordinates.
pch	a pch for the points (default to NA)
cex	a cex for the points
...	optional parameters to fed points and segments.

See Also

Other plotting functions: Ntable, conf_ell, coo_arrows, coo_draw, coo_listpanel, coo_plot, coo_ruban, ldk_chull, ldk_confell, ldk_contour, ldk_labels, ldk_links, plot_devsegments

Examples

```
data(olea)
coo_lolli(coo_sample(olea[3], 50), coo_sample(olea[6], 50))
title("A nice title !")
```

coo_lw *Calculates length and width of a shape*

Description

Returns the length and width of a shape based on their iniertia axis i.e. alignment to the x-axis. The length is defined as the range along the x-axis; the width as the range on the y-axis.

Usage

```
coo_lw(coo)
```

Arguments

coo	a matrix of (x; y) coordinates.

Value

a vector of two numeric: the length and the width.

See Also

coo_length, coo_width.

Other coo_ descriptors: coo_area, coo_chull, coo_circularityharalick, coo_circularitynorm, coo_circularity, coo_convexity, coo_eccentricityboundingbox, coo_eccentricityeigen, coo_elongation, coo_length, coo_rectangularity, coo_rectilinearity, coo_solidity, coo_tangle, coo_theta3, coo_thetapts, coo_width

Examples

```
data(bot)
coo_lw(bot[1])
```

coo_nb *Counts coordinates*

Description

Returns the number of coordinates, for a single shape or a Coo object

Usage

```
coo_nb(coo)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.

Value

either a single numeric or a vector of numeric

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Examples

```
# single shape
coo_nb(bot[1])
# Coo object
coo_nb(bot)
```

---

coo_oscillo *Momocs' 'oscilloscope' for Fourier-based approaches*

Description

Shape analysis deals with curve fitting, whether $x(t)$ and $y(t)$ positions along the curvilinear abscissa and/or radius/tangent angle variation. These functions are mainly intended for (self-)teaching of Fourier-based methods.

Usage

```
coo_oscillo(coo, method = c("efourier", "rfourier", "tfourier", "all")[4],
  nb.pts = 24)
```

Arguments

coo	A list or a matrix of coordinates.
method	character among c('efourier', 'rfourier', 'tfourier', 'all'). 'all' by default
nb.pts	integer. The number or reference points, sampled equidistantly along the curvilinear abscissa and added on the oscillo curves.

See Also

exemplifying functions

Examples

```
data(shapes)
coo_oscillo(shapes[4])
coo_oscillo(shapes[4], 'efourier')
coo_oscillo(shapes[4], 'rfourier')
coo_oscillo(shapes[4], 'tfourier')
#tfourier is prone to high-frequency noise but smoothing can help
coo_oscillo(coo_smooth(shapes[4], 10), 'tfourier')
```

`coo_perim` *Calculates the perimeter*

Description

Calculates the perimeter

Usage

```
coo_perim(coo)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates.

Value

`numeric`, the perimeter.

See Also

Other coo_ utilities: `coo_aligncalliper`, `coo_alignminradius`, `coo_alignxax`, `coo_align`, `coo_baseline`, `coo_bookstein`, `coo_calliper`, `coo_centdist`, `coo_center`, `coo_centpos`, `coo_centsize`, `coo_close`, `coo_down`, `coo_dxy`, `coo_extract`, `coo_flipx`, `coo_force2close`, `coo_interpolate`, `coo_jitter`, `coo_left`, `coo_nb`, `coo_perimcum`, `coo_perimpts`, `coo_rev`, `coo_right`, `coo_rotatecenter`, `coo_rotate`, `coo_samplerr`, `coo_sample`, `coo_scalex`, `coo_scale`, `coo_shearx`, `coo_slice`, `coo_slidedirection`, `coo_slidegap`, `coo_slide`, `coo_smoothcurve`, `coo_smooth`, `coo_template`, `coo_trans`, `coo_trim`, `coo_up`, `is_closed`

Other perimeter functions: `coo_perimcum`, `coo_perimpts`

Examples

```
coo_perim(bot[1])
hist(sapply(bot$coo, coo_perim), breaks=10)
```

coo_perimcum *Calculates the cumulative chordal distance along a shape.*

Description

Just a wrapper for `cumsum(coo_perimpts)`. See coo_perimpts.

Usage

```
coo_perimcum(coo)
```

Arguments

coo	a `matrix` of (x; y) coordinates.

Value

`numeric` the cumulate sum of chrodal distances

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Other perimeter functions: coo_perimpts, coo_perim

Examples

```
b <- coo_sample(bot[1], 24)
coo_perimcum(b)
```

coo_perimpts *Calculates the chordal distance along a shape.*

Description

Calculates the euclidean distance between every points of a shape for coo_perimpts. The cumulative sum for coo_perimcum

Usage

```
coo_perimpts(coo)
```

Arguments

coo	matrix of (x; y) coordinates.

Value

numeric the distance between every point.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Other perimeter functions: coo_perimcum, coo_perim

Examples

```
b <- coo_sample(bot[1], 24)
coo_perimpts(b)
```

---

coo_plot *Plots a single shape*

Description

A simple wrapper around plot for plotting shapes. Widely used in Momocs in other graphical functions, in methods, etc.

Usage

```
coo_plot(coo, ...)

## Default S3 method:
coo_plot(coo, xlim, ylim, border = "#333333", col = NA,
  lwd = 1, lty = 1, points = FALSE, first.point = TRUE,
  centroid = TRUE, xy.axis = TRUE, pch = 1, cex = 0.5, main = NA,
  poly = TRUE, plot.new = TRUE, plot = TRUE, zoom = 1, ...)

ldk_plot(coo, ...)
```

Arguments

coo	A list or a matrix of coordinates.
...	further arguments for use in coo_plot methods. See examples.
xlim	If coo_plot is called and coo is missing, then a vector of length 2 specifying the ylim of the ploting area.
ylim	If coo_plot is called and coo is missing, then a vector of length 2 specifying the ylim of the ploting area.
border	A color for the shape border.
col	A color to fill the shape polygon.
lwd	The lwd for drawing shapes.
lty	The lty for drawing shapes.
points	logical. Whether to display points. If missing and number of points is < 100, then points are plotted.
first.point	logical whether to plot or not the first point.
centroid	logical. Whether to display centroid.
xy.axis	logical. Whether to draw the xy axis.
pch	The pch for points.
cex	The cex for points.
main	character. A title for the plot.
poly	logical whether to use polygon and lines to draw the shape, or just points. In other words, whether the shape should be considered as a configuration of landmarks or not (eg a closed outline).
plot.new	logical whether to plot or not a new frame.
plot	logical whether to plot something or just to create an empty plot.
zoom	a numeric to take your distances.

Value

No returned value.

See Also

Other plotting functions: Ntable, conf_ell, coo_arrows, coo_draw, coo_listpanel, coo_lolli, coo_ruban, ldk_chull, ldk_confell, ldk_contour, ldk_labels, ldk_links, plot_devsegments

Examples

```
data(bot)
b <- bot[1]
coo_plot(b)
coo_plot(bot[2], plot.new=FALSE) # equivalent to coo_draw(bot[2])
coo_plot(b, zoom=2)
coo_plot(b, border='blue')
coo_plot(b, first.point=FALSE, centroid=FALSE)
coo_plot(b, points=TRUE, pch=20)
coo_plot(b, xy.axis=FALSE, lwd=2, col='#F2F2F2')
```

coo_rectangularity *Calculates the rectangularity of a shape*

Description

Calculates the rectangularity of a shape

Usage

```
coo_rectangularity(coo)
```

Arguments

coo	a matrix of (x; y) coordinates.

Value

numeric, the rectangularity.

Source

Rosin PL. 2005. Computing global shape measures. Handbook of Pattern Recognition and Computer Vision. 177-196.

See Also

Other coo_ descriptors: coo_area, coo_chull, coo_circularityharalick, coo_circularitynorm, coo_circularity, coo_convexity, coo_eccentricityboundingbox, coo_eccentricityeigen, coo_elongation, coo_length, coo_lw, coo_rectilinearity, coo_solidity, coo_tangle, coo_theta3, coo_thetapts, coo_width

Examples

```
data(bot)
coo_rectangularity(bot[1])
```

coo_rectilinearity *Calculates the rectilinearity of a shape*

Description

As proposed by Zunic and Rosin (see below). May need some testing/review.

Usage

```
coo_rectilinearity(coo)
```

Arguments

coo	a matrix of (x; y) coordinates.

Value

numeric, the rectilinearity

Note

due to the laborious nature of the algorithm (in nb.pts^2), and of its implementation, it may be very long to compute.

Source

Zunic J, Rosin PL. 2003. Rectilinearity measurements for polygons. IEEE Transactions on Pattern Analysis and Machine Intelligence 25: 1193-1200.

See Also

Other coo_ descriptors: coo_area, coo_chull, coo_circularityharalick, coo_circularitynorm, coo_circularity, coo_convexity, coo_eccentricityboundingbox, coo_eccentricityeigen, coo_elongation, coo_length, coo_lw, coo_rectangularity, coo_solidity, coo_tangle, coo_theta3, coo_thetapts, coo_width

Examples

```
data(bot)
b <- coo_sample(bot[1], 32)
coo_rectilinearity(b)
```

---

coo_rev *Reverses coordinates*

Description

Returns the reverse suite of coordinates, i.e. change shape's orientation

Usage

```
coo_rev(coo)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.

Value

a matrix of (x; y) coordinates or a Coo object

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Examples

```
b <- coo_sample(bot[1], 4)
b
coo_rev(b)
```

---

coo_right *Retains coordinates with positive x-coordinates*

Description

Useful when shapes are aligned along the y-axis (e.g. because of a bilateral symmetry) and when one wants to retain just the upper side.

Usage

```
coo_right(coo, slidegap = FALSE)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.
slidegap	logical whether to apply coo_slidegap after coo_right

Value

a matrix of (x; y) coordinates or a Coo object (Out are returned as Opn)

Note

When shapes are "sliced" along the y-axis, it usually results on open curves and thus to huge/artefactual gaps between points neighboring this axis. This is usually solved with coo_slidegap. See examples there.

Also, when apply a coo_left/right/up/down on an Out object, you then obtain an Opn object, which is done automatically.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Other opening functions: coo_down, coo_left, coo_up

Examples

```
b <- coo_center(bot[1])
coo_plot(b)
coo_draw(coo_right(b), border='red')
```

`coo_rotate` *Rotates coordinates*

Description

Rotates the coordinates by a 'theta' angle (in radians) in the trigonometric direction (anti-clockwise). If not provided, assumed to be the centroid size. It involves three steps: centering from current position, dividing coordinates by 'scale', translating to the original position.

Usage

```
coo_rotate(coo, theta = 0)
```

Arguments

`coo`	either a `matrix` of (x; y) coordinates, or any Coo object.
`theta`	`numeric`the angle (in radians) to rotate shapes.

Value

a `matrix` of (x; y) coordinates, or a Coo object.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Other rotation functions: coo_rotatecenter

Examples

```
coo_plot(bot[1])
coo_plot(coo_rotate(bot[1], pi/2))
# on Coo
stack(bot)
stack(coo_rotate(bot, pi/2))
```

`coo_rotatecenter` *Rotates shapes with a custom center*

Description

rotates a shape of 'theta' angles (in radians) and with a (x; y) 'center'.

Usage

```
coo_rotatecenter(coo, theta, center = c(0, 0))
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.
`theta`	`numeric` the angle (in radians) to rotate shapes.
`center`	`numeric` the (x; y) position of the center

Value

a `matrix` of (x; y) coordinates, or a Coo object.

See Also

Other coo_ utilities: `coo_aligncalliper`, `coo_alignminradius`, `coo_alignxax`, `coo_align`, `coo_baseline`, `coo_bookstein`, `coo_calliper`, `coo_centdist`, `coo_center`, `coo_centpos`, `coo_centsize`, `coo_close`, `coo_down`, `coo_dxy`, `coo_extract`, `coo_flipx`, `coo_force2close`, `coo_interpolate`, `coo_jitter`, `coo_left`, `coo_nb`, `coo_perimcum`, `coo_perimpts`, `coo_perim`, `coo_rev`, `coo_right`, `coo_rotate`, `coo_samplerr`, `coo_sample`, `coo_scalex`, `coo_scale`, `coo_shearx`, `coo_slice`, `coo_slidedirection`, `coo_slidegap`, `coo_slide`, `coo_smoothcurve`, `coo_smooth`, `coo_template`, `coo_trans`, `coo_trim`, `coo_up`, `is_closed`

Other rotation functions: `coo_rotate`

Other rotation functions: `coo_rotate`

Examples

```
b <- bot[1]
coo_plot(b)
coo_draw(coo_rotatecenter(b, -pi/2, c(200, 200)), border='red')
```

coo_ruban *Plots differences as (colored) segments aka a ruban*

Description

Useful to display differences between shapes

Usage

```
coo_ruban(coo, dev, palette = col_heat, normalize = TRUE, ...)
```

Arguments

coo	a shape, typically a mean shape
dev	numeric a vector of distances or anythinh relevant
palette	the color palette to use or any palette
normalize	logical whether to normalize (TRUE by default) distances
...	other paremeters to fed segments, eg lwd (see examples)

Value

nothing

See Also

Other plotting functions: Ntable, conf_ell, coo_arrows, coo_draw, coo_listpanel, coo_lolli, coo_plot, ldk_chull, ldk_confell, ldk_contour, ldk_labels, ldk_links, plot_devsegments

Other plotting functions: Ntable, conf_ell, coo_arrows, coo_draw, coo_listpanel, coo_lolli, coo_plot, ldk_chull, ldk_confell, ldk_contour, ldk_labels, ldk_links, plot_devsegments

Examples

```
data(bot)
ms <- mshapes(efourier(bot , 10), "type")
b <- ms$shp$beer
w <- ms$shp$whisky
# we obtain the mean shape, then euclidean distances between points
m <- mshapes(list(b, w))
d <- edm(b, w)
# First plot
coo_plot(m, plot=FALSE)
coo_draw(b)
coo_draw(w)
coo_ruban(m, d, lwd=5)

#Another example
coo_plot(m, plot=FALSE)
```

```
coo_ruban(m, d, palette=col_summer2, lwd=5)

#If you want linewidth rather than color
coo_plot(m, plot=FALSE)
coo_ruban(m, d, palette=col_black, lwd=.normalize(d)*10)
```

`coo_sample` *Sample coordinates (among points)*

Description

Sample n coordinates among existing points.

Usage

```
coo_sample(coo, n)
```

Arguments

`coo`	either a `matrix` of (x; y) coordinates or an Out or an Opn object.
`n`	`integer`, the number fo points to sample.

Details

For the Out an Opn methods (pointless for Ldk), in an `$ldk` component is defined, it is changed accordingly by multiplying the ids by n over the number of coordinates.

Value

a `matrix` of (x; y) coordinates, or an Out or an Opn object.

See Also

Other coo_ utilities: `coo_aligncalliper`, `coo_alignminradius`, `coo_alignxax`, `coo_align`, `coo_baseline`, `coo_bookstein`, `coo_calliper`, `coo_centdist`, `coo_center`, `coo_centpos`, `coo_centsize`, `coo_close`, `coo_down`, `coo_dxy`, `coo_extract`, `coo_flipx`, `coo_force2close`, `coo_interpolate`, `coo_jitter`, `coo_left`, `coo_nb`, `coo_perimcum`, `coo_perimpts`, `coo_perim`, `coo_rev`, `coo_right`, `coo_rotatecenter`, `coo_rotate`, `coo_samplerr`, `coo_scalex`, `coo_scale`, `coo_shearx`, `coo_slice`, `coo_slidedirection`, `coo_slidegap`, `coo_slide`, `coo_smoothcurve`, `coo_smooth`, `coo_template`, `coo_trans`, `coo_trim`, `coo_up`, `is_closed`

Other sampling functions: `coo_extract`, `coo_interpolate`, `coo_samplerr`

Examples

```
b <- bot[1]
stack(bot)
stack(coo_sample(bot, 24))
coo_plot(b)
coo_plot(coo_sample(b, 24))
```

`coo_samplerr` *Samples coordinates (regular radius)*

Description

Samples n coordinates with a regular angle.

Usage

```
coo_samplerr(coo, n)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.
`n`	`integer`, the number of points to sample.

Value

a `matrix` of (x; y) coordinates or a Coo object.

See Also

Other coo_ utilities: `coo_aligncalliper`, `coo_alignminradius`, `coo_alignxax`, `coo_align`, `coo_baseline`, `coo_bookstein`, `coo_calliper`, `coo_centdist`, `coo_center`, `coo_centpos`, `coo_centsize`, `coo_close`, `coo_down`, `coo_dxy`, `coo_extract`, `coo_flipx`, `coo_force2close`, `coo_interpolate`, `coo_jitter`, `coo_left`, `coo_nb`, `coo_perimcum`, `coo_perimpts`, `coo_perim`, `coo_rev`, `coo_right`, `coo_rotatecenter`, `coo_rotate`, `coo_sample`, `coo_scalex`, `coo_scale`, `coo_shearx`, `coo_slice`, `coo_slidedirection`, `coo_slidegap`, `coo_slide`, `coo_smoothcurve`, `coo_smooth`, `coo_template`, `coo_trans`, `coo_trim`, `coo_up`, `is_closed`

Other sampling functions: `coo_extract`, `coo_interpolate`, `coo_sample`

Examples

```
stack(bot)
bot <- coo_center(bot)
stack(coo_samplerr(bot, 12))
coo_plot(bot[1])
coo_plot(rr <- coo_samplerr(bot[1], 12))
cpos <- coo_centpos(bot[1])
segments(cpos[1], cpos[2], rr[, 1], rr[, 2])
```

`coo_scale` *Scales coordinates*

Description

Scales the coordinates by a 'scale' factor. If not provided, assumed to be the centroid size. It involves three steps: centering from current position, dividing coordinates by 'scale', pusing back to the original position.

Usage

```
coo_scale(coo, scale)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.
`scale`	the scaling factor, by default, the centroid size.

Value

a `matrix` of (x; y) coordinates, or a Coo object.

See Also

Other coo_ utilities: `coo_aligncalliper`, `coo_alignminradius`, `coo_alignxax`, `coo_align`, `coo_baseline`, `coo_bookstein`, `coo_calliper`, `coo_centdist`, `coo_center`, `coo_centpos`, `coo_centsize`, `coo_close`, `coo_down`, `coo_dxy`, `coo_extract`, `coo_flipx`, `coo_force2close`, `coo_interpolate`, `coo_jitter`, `coo_left`, `coo_nb`, `coo_perimcum`, `coo_perimpts`, `coo_perim`, `coo_rev`, `coo_right`, `coo_rotatecenter`, `coo_rotate`, `coo_samplerr`, `coo_sample`, `coo_scalex`, `coo_shearx`, `coo_slice`, `coo_slidedirection`, `coo_slidegap`, `coo_slide`, `coo_smoothcurve`, `coo_smooth`, `coo_template`, `coo_trans`, `coo_trim`, `coo_up`, `is_closed`

Other scaling functions: `coo_scalex`, `coo_template`

Examples

```
coo_plot(bot[1])
coo_plot(coo_scale(bot[1]))
# on Coo objects
stack(coo_center(bot))
stack(coo_scale(coo_center(bot)))
```

`coo_scalex` *Shrinks coordinates in one direction*

Description

`coo_scalex` applies a scaling parallel to the x-axis to a matrix of (x; y) or a list of coordinates or any Coo object, `coo_scaley` does it parallel to the y-axis.

Usage

```
coo_scalex(coo, k = 1)

coo_scaley(coo, k = 1)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.
`k`	`numeric` scaling factor

Value

a `matrix` of (x; y) coordinates, or a Coo object.

See Also

Other coo_ utilities: `coo_aligncalliper`, `coo_alignminradius`, `coo_alignxax`, `coo_align`, `coo_baseline`, `coo_bookstein`, `coo_calliper`, `coo_centdist`, `coo_center`, `coo_centpos`, `coo_centsize`, `coo_close`, `coo_down`, `coo_dxy`, `coo_extract`, `coo_flipx`, `coo_force2close`, `coo_interpolate`, `coo_jitter`, `coo_left`, `coo_nb`, `coo_perimcum`, `coo_perimpts`, `coo_perim`, `coo_rev`, `coo_right`, `coo_rotatecenter`, `coo_rotate`, `coo_samplerr`, `coo_sample`, `coo_scale`, `coo_shearx`, `coo_slice`, `coo_slidedirection`, `coo_slidegap`, `coo_slide`, `coo_smoothcurve`, `coo_smooth`, `coo_template`, `coo_trans`, `coo_trim`, `coo_up`, `is_closed`

Other scaling functions: `coo_scale`, `coo_template`

Examples

```
coo <- shapes[11] %>% coo_template()
coo_plot(coo, xlim=c(-1, 1))
coo %>% coo_scalex(1.5) %>% coo_draw(border="blue")
coo %>% coo_scaley(1.5) %>% coo_draw(border="red")
coo %>% coo_scalex(0.5) %>% coo_draw(border="blue", lty=2)
coo %>% coo_scaley(0.5) %>% coo_draw(border="red", lty=2)
```

coo_shearx *Shears shapes*

Description

coo_shearx applies a shear mapping on a matrix of (x; y) coordinates (or a list), parallel to the x-axis (i.e. x' = x + ky; y' = y + kx). coo_sheary does it parallel to the y-axis.

Usage

```
coo_shearx(coo, k)

coo_sheary(coo, k)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.
k	numeric shear factor

Value

a matrix of (x; y) coordinates.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Other transforming functions: coo_flipx

Examples

```
coo <- coo_template(shapes[11])
coo_plot(coo)
coo_draw(coo_shearx(coo, 0.5), border="blue")
coo_draw(coo_sheary(coo, 0.5), border="red")
```

`coo_slice` *Slices shapes between successive coordinates*

Description

Takes a shape with n coordinates. When you pass this function with at least two ids (<= n), the shape will be open on the corresponding coordinates and slices returned as a list

Usage

```
coo_slice(coo, ids)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.
`ids`	`numeric` of length >= 2, where to slice the shape(s)

Value

a list of shapes or a list of Opn

See Also

Other coo_ utilities: `coo_aligncalliper`, `coo_alignminradius`, `coo_alignxax`, `coo_align`, `coo_baseline`, `coo_bookstein`, `coo_calliper`, `coo_centdist`, `coo_center`, `coo_centpos`, `coo_centsize`, `coo_close`, `coo_down`, `coo_dxy`, `coo_extract`, `coo_flipx`, `coo_force2close`, `coo_interpolate`, `coo_jitter`, `coo_left`, `coo_nb`, `coo_perimcum`, `coo_perimpts`, `coo_perim`, `coo_rev`, `coo_right`, `coo_rotatecenter`, `coo_rotate`, `coo_samplerr`, `coo_sample`, `coo_scalex`, `coo_scale`, `coo_shearx`, `coo_slidedirection`, `coo_slidegap`, `coo_slide`, `coo_smoothcurve`, `coo_smooth`, `coo_template`, `coo_trans`, `coo_trim`, `coo_up`, `is_closed`

Examples

```
# single shape, a list of matrices is returned
sh <- coo_slice(hearts[1], c(12, 24, 36, 48))
coo_plot(sh[[1]])
panel(Opn(sh))
# on a Coo, a list of Opn is returned
# makes no sense if shapes are not normalized first
sh2 <- coo_slice(hearts, c(12, 24, 36, 48))
panel(sh2[[1]])
```

`coo_slide` *Slides coordinates*

Description

Slides the coordinates so that the id1-th point become the first one.

Usage

```
coo_slide(coo, id1, ldk)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.
`id1`	`numeric` the id(s) of the point that will become the new first point. See details below for the method on Coo objects.
`ldk`	`numeric` the id of the ldk to use as id1, only on `Out`

Details

For Coo objects, and in particular for Out and Opn three different ways of coo_sliding are available:

- **no ldk passed and a single id1 is passed**: all id1-th points within the shapes will become the first points. $ldk will be slided accordingly.
- **no ldk passed and a vector of ids matching the length of the Coo**: for every shape, the id1-th point will be used as the id1-th point. $ldk will be slided accordingly.
- **a single ldk is passed**: the ldk-th ldk will be used to slide every shape. If an ldk is passed, id1 is ignored with a message.

See examples.

Value

a `matrix` of (x; y) coordinates, or a Coo object.

See Also

Other coo_ utilities: `coo_aligncalliper`, `coo_alignminradius`, `coo_alignxax`, `coo_align`, `coo_baseline`, `coo_bookstein`, `coo_calliper`, `coo_centdist`, `coo_center`, `coo_centpos`, `coo_centsize`, `coo_close`, `coo_down`, `coo_dxy`, `coo_extract`, `coo_flipx`, `coo_force2close`, `coo_interpolate`, `coo_jitter`, `coo_left`, `coo_nb`, `coo_perimcum`, `coo_perimpts`, `coo_perim`, `coo_rev`, `coo_right`, `coo_rotatecenter`, `coo_rotate`, `coo_samplerr`, `coo_sample`, `coo_scalex`, `coo_scale`, `coo_shearx`, `coo_slice`, `coo_slidedirection`, `coo_slidegap`, `coo_smoothcurve`, `coo_smooth`, `coo_template`, `coo_trans`, `coo_trim`, `coo_up`, `is_closed`

Other sliding functions: `coo_slidedirection`, `coo_slidegap`

Examples

```
stack(hearts)
# set the first landmark as the starting point
stack(coo_slide(hearts, ldk=1))
# set the 50th point as the starting point (everywhere)
stack(coo_slide(hearts, id1=50))
# set the id1-random-th point as the starting point (everywhere)
set.seed(123) # just for the reproducibility
id1_random <- sample(x=min(sapply(hearts$coo, nrow)), size=length(hearts),
replace=TRUE)
stack(coo_slide(hearts, id1=id1_random))
```

`coo_slidedirection` *Slides coordinates in a particular direction*

Description

Shapes are centered and then, according to direction, the point northwards, southwards, eastwards or westwards the centroid, becomes the first point with coo_slide.

Usage

```
coo_slidedirection(coo, direction, center, id)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.
`direction`	`character` among `'N'` (by default), `'S'`, `'E'`, or `'W'`.
`center`	`logical` whether to center or not before sliding
`id`	`numeric` whether to return the id of the point or the slided shapes

Value

a `matrix` of (x; y) coordinates, or a Coo object.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Other sliding functions: coo_slidegap, coo_slide

Examples

```
b <- coo_rotate(bot[1], pi/6) # dummy example just to make it obvious
coo_plot(b) # not the first point
coo_plot(coo_slidedirection(b, 'N'))
coo_plot(coo_slidedirection(b, 'E'))
coo_plot(coo_slidedirection(b, 'W'))
coo_plot(coo_slidedirection(b, 'S'))

# on Coo objects
stack(bot)
stack(coo_slidedirection(bot, 'E'))
```

---

coo_slidegap *Slides coordinates using the widest gap*

Description

When slicing a shape using two landmarks, or functions such as coo_up, an open curve is obtained and the rank of points make wrong/artefactual results. If the widest gap is > 5 * median of other gaps, then the couple of coordinates forming this widest gap is used as starting and ending points. This switch helps to deal with open curves. Examples are self-speaking. Use `force=TRUE` to bypass this check

Usage

```
coo_slidegap(coo, force)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.
`force`	`logical` whether to use the widest gap, with no check, as the real gap

Value

a `matrix` of (x; y) coordinates or a Coo object.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, coo_up, is_closed

Other sliding functions: coo_slidedirection, coo_slide

Examples

```
cat <- coo_center(shapes[4])
coo_plot(cat)

# we only retain the bottom of the cat
cat_down <- coo_down(cat, slidegap=FALSE)

# see? the segment on the x-axis coorespond to the widest gap.
coo_plot(cat_down)

# that's what we meant
coo_plot(coo_slidegap(cat_down))
```

`coo_smooth` *Smoothes coordinates*

Description

Smoothes coordinates using a simple moving average. May be useful to remove digitization noise, mainly on outlines and open outlines.

Usage

```
coo_smooth(coo, n)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.
`n`	`integer` the number of smoothing iterations

Value

a `matrix` of (x; y) coordinates, or a Coo object.

See Also

Other coo_ utilities: `coo_aligncalliper`, `coo_alignminradius`, `coo_alignxax`, `coo_align`, `coo_baseline`, `coo_bookstein`, `coo_calliper`, `coo_centdist`, `coo_center`, `coo_centpos`, `coo_centsize`, `coo_close`, `coo_down`, `coo_dxy`, `coo_extract`, `coo_flipx`, `coo_force2close`, `coo_interpolate`, `coo_jitter`, `coo_left`, `coo_nb`, `coo_perimcum`, `coo_perimpts`, `coo_perim`, `coo_rev`, `coo_right`, `coo_rotatecenter`, `coo_rotate`, `coo_samplerr`, `coo_sample`, `coo_scalex`, `coo_scale`, `coo_shearx`, `coo_slice`, `coo_slidedirection`, `coo_slidegap`, `coo_slide`, `coo_smoothcurve`, `coo_template`, `coo_trans`, `coo_trim`, `coo_up`, `is_closed`

Other smoothing functions: `coo_smoothcurve`

Examples

```
b <- bot[1]
stack(bot)
stack(coo_smooth(bot, 10))
coo_plot(bot[1])
coo_plot(coo_smooth(bot[1], 30))
```

`coo_smoothcurve` *Smoothes coordinates on curves*

Description

Smoothes coordinates using a simple moving average but let the first and last points unchanged. May be useful to remove digitization noise on curves.

Usage

```
coo_smoothcurve(coo, n)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.
`n`	`integer` to specify the number of smoothing iterations

Value

a `matrix` of (x; y) coordinates, or a Coo object.

See Also

Other coo_ utilities: `coo_aligncalliper`, `coo_alignminradius`, `coo_alignxax`, `coo_align`, `coo_baseline`, `coo_bookstein`, `coo_calliper`, `coo_centdist`, `coo_center`, `coo_centpos`, `coo_centsize`, `coo_close`, `coo_down`, `coo_dxy`, `coo_extract`, `coo_flipx`, `coo_force2close`, `coo_interpolate`, `coo_jitter`, `coo_left`, `coo_nb`, `coo_perimcum`, `coo_perimpts`, `coo_perim`, `coo_rev`, `coo_right`, `coo_rotatecenter`, `coo_rotate`, `coo_samplerr`, `coo_sample`, `coo_scalex`, `coo_scale`, `coo_shearx`, `coo_slice`, `coo_slidedirection`, `coo_slidegap`, `coo_slide`, `coo_smooth`, `coo_template`, `coo_trans`, `coo_trim`, `coo_up`, `is_closed`

Other smoothing functions: `coo_smooth`

Examples

```
o <- olea[1]
coo_plot(o, border='grey50', points=FALSE)
coo_draw(coo_smooth(o, 24), border='blue', points=FALSE)
coo_draw(coo_smoothcurve(o, 24), border='red', points=FALSE)
```

coo_solidity *Calculates the solidity of a shape*

Description

Returns the ids of points that define the convex hull of a shape.

Usage

```
coo_solidity(coo)
```

Arguments

coo	a matrix of (x; y) coordinates.

Value

numeric, the solidity of a shape.

Source

Rosin PL. 2005. Computing global shape measures. Handbook of Pattern Recognition and Computer Vision. 177-196.

See Also

Other coo_ descriptors: coo_area, coo_chull, coo_circularityharalick, coo_circularitynorm, coo_circularity, coo_convexity, coo_eccentricityboundingbox, coo_eccentricityeigen, coo_elongation, coo_length, coo_lw, coo_rectangularity, coo_rectilinearity, coo_tangle, coo_theta3, coo_thetapts, coo_width

Examples

```
data(bot)
coo_solidity(bot[1])
```

coo_tangle *Calculates the tangent angle along the perimeter of a shape*

Description

Calculated using complex numbers and returned in radians minus the first one (modulo 2*pi).

Usage

```
coo_tangle(coo)
```

Arguments

coo	a matrix of coordinates

Value

a numeric, the tangent angle along the perimeter

See Also

tfourier

Other coo_ descriptors: coo_area, coo_chull, coo_circularityharalick, coo_circularitynorm, coo_circularity, coo_convexity, coo_eccentricityboundingbox, coo_eccentricityeigen, coo_elongation, coo_length, coo_lw, coo_rectangularity, coo_rectilinearity, coo_solidity, coo_theta3, coo_thetapts, coo_width

Examples

```
data(bot)
b <- bot[1]
phi  <- coo_tangle(b)
phi2 <- coo_tangle(coo_smooth(b, 2))
plot(phi, type='l')
plot(phi2, type='l', col='red') # ta is very sensible to noise
```

---

coo_template *'Templates' shapes*

Description

coo_template returns shape centered on the origin and inscribed in a size-side square

Usage

```
coo_template(coo, size)
```

Arguments

coo	A list or a matrix of coordinates.
size	numeric. Indicates the length of the side 'inscribing' the shape.

Details

See coo_listpanel for an illustration of this function. The morphospaces functions also take profit of this function. May be useful to develop other graphical functions.

Value

Returns a matrix of (x; y)coordinates.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_trans, coo_trim, coo_up, is_closed

Other scaling functions: coo_scalex, coo_scale

Examples

```
data(bot)
coo <- bot[1]
coo_plot(coo_template(coo), xlim=c(-1, 1), ylim=c(-1, 1))
rect(-0.5, -0.5, 0.5, 0.5)

s <- 0.01
coo_plot(coo_template(coo, s))
rect(-s/2, -s/2, s/2, s/2)
```

---

coo_theta3 *Calculate the angle formed by three (x; y) coordinates*

Description

Returns the angle (in radians) defined by a triplet of points either signed ('atan2') or not ('acos').

Usage

```
coo_theta3(m, method = c("atan2", "acos")[1])
```

Arguments

m	a 3x2 matrix of 3 points (rows) and (x; y) coordinates
method	one of 'atan2' or 'acos' for a signed or not angle.

Value

numeric the angle in radians.

See Also

Other coo_ descriptors: coo_area, coo_chull, coo_circularityharalick, coo_circularitynorm, coo_circularity, coo_convexity, coo_eccentricityboundingbox, coo_eccentricityeigen, coo_elongation, coo_length, coo_lw, coo_rectangularity, coo_rectilinearity, coo_solidity, coo_tangle, coo_thetapts, coo_width

Examples

```
data(bot)
b <- coo_sample(bot[1], 64)
b <- b[c(1, 14, 24), ]
coo_plot(b)
coo_theta3(b)
coo_theta3(b, method='acos')
```

`coo_thetapts` *Calculates the angle of every edge of a shape*

Description

Returns the angle (in radians) of every edge of a shape,

Usage

```
coo_thetapts(coo, method = c("atan2", "acos")[1])
```

Arguments

`coo`	a `matrix` or a list of (x; y) coordinates.
`method`	one of 'atan2' or 'acos' for a signed or not angle.

Value

`numeric` the angles in radians for every edge.

See Also

Other coo_ descriptors: `coo_area`, `coo_chull`, `coo_circularityharalick`, `coo_circularitynorm`, `coo_circularity`, `coo_convexity`, `coo_eccentricityboundingbox`, `coo_eccentricityeigen`, `coo_elongation`, `coo_length`, `coo_lw`, `coo_rectangularity`, `coo_rectilinearity`, `coo_solidity`, `coo_tangle`, `coo_theta3`, `coo_width`

Examples

```
data(bot)
b <- coo_sample(bot[1], 64)
coo_thetapts(b)
```

coo_trans *Translates coordinates*

Description

Translates the coordinates by a 'x' and 'y' value

Usage

```
coo_trans(coo, x = 0, y = 0)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.
x	numeric translation along the x-axis.
y	numeric translation along the y-axis.

Value

a matrix of (x; y) coordinates, or a Coo object.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trim, coo_up, is_closed

Examples

```
coo_plot(bot[1])
coo_plot(coo_trans(bot[1], 50, 100))
# on Coo
stack(bot)
stack(coo_trans(bot, 50, 100))
```

coo_trim *Trims coordinates from shape*

Description

Removes `trim` coordinates at both ends of a shape, ie from top and bottom of the shape matrix.

Usage

```
coo_trim(coo, trim = 1)
```

Arguments

`coo`	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.
`trim`	`numeric`, the number of coordinates to trim

See Also

Other coo_ utilities: `coo_aligncalliper`, `coo_alignminradius`, `coo_alignxax`, `coo_align`, `coo_baseline`, `coo_bookstein`, `coo_calliper`, `coo_centdist`, `coo_center`, `coo_centpos`, `coo_centsize`, `coo_close`, `coo_down`, `coo_dxy`, `coo_extract`, `coo_flipx`, `coo_force2close`, `coo_interpolate`, `coo_jitter`, `coo_left`, `coo_nb`, `coo_perimcum`, `coo_perimpts`, `coo_perim`, `coo_rev`, `coo_right`, `coo_rotatecenter`, `coo_rotate`, `coo_samplerr`, `coo_sample`, `coo_scalex`, `coo_scale`, `coo_shearx`, `coo_slice`, `coo_slidedirection`, `coo_slidegap`, `coo_slide`, `coo_smoothcurve`, `coo_smooth`, `coo_template`, `coo_trans`, `coo_up`, `is_closed`

Examples

```
olea[1] %>% coo_sample(12) %T>%
   print() %T>% ldk_plot() %>%
   coo_trim(1) %T>% print() %>% points(col="red")
```

coo_up *Retains coordinates with positive y-coordinates*

Description

Useful when shapes are aligned along the x-axis (e.g. because of a bilateral symmetry) and when one wants to retain just the upper side.

Usage

```
coo_up(coo, slidegap = FALSE)
```

Arguments

coo	a matrix of (x; y) coordinates or a list, or any Coo object.
slidegap	logical whether to apply coo_slidegap after coo_down

Value

a matrix of (x; y) coordinates or a Coo object (Out are returned as Opn)

Note

When shapes are "sliced" along the x-axis, it usually results on open curves and thus to huge/artefactual gaps between points neighboring this axis. This is usually solved with coo_slidegap. See examples there.

Also, when apply a coo_left/right/up/down on an Out object, you then obtain an Opn object, which is done automatically.

See Also

Other coo_ utilities: coo_aligncalliper, coo_alignminradius, coo_alignxax, coo_align, coo_baseline, coo_bookstein, coo_calliper, coo_centdist, coo_center, coo_centpos, coo_centsize, coo_close, coo_down, coo_dxy, coo_extract, coo_flipx, coo_force2close, coo_interpolate, coo_jitter, coo_left, coo_nb, coo_perimcum, coo_perimpts, coo_perim, coo_rev, coo_right, coo_rotatecenter, coo_rotate, coo_samplerr, coo_sample, coo_scalex, coo_scale, coo_shearx, coo_slice, coo_slidedirection, coo_slidegap, coo_slide, coo_smoothcurve, coo_smooth, coo_template, coo_trans, coo_trim, is_closed

Other opening functions: coo_down, coo_left, coo_right

Examples

```
b <- coo_alignxax(bot[1])
coo_plot(b)
coo_draw(coo_up(b), border='red')
```

---

coo_width *Calculates the width of a shape*

Description

Nothing more than coo_lw(coo)[2].

Usage

```
coo_width(coo)
```

Arguments

coo	a matrix of (x; y) coordinates.

Value

the width (in pixels) of the shape

See Also

coo_lw, coo_length.

Other coo_ descriptors: coo_area, coo_chull, coo_circularityharalick, coo_circularitynorm, coo_circularity, coo_convexity, coo_eccentricityboundingbox, coo_eccentricityeigen, coo_elongation, coo_length, coo_lw, coo_rectangularity, coo_rectilinearity, coo_solidity, coo_tangle, coo_theta3, coo_thetapts

Examples

```
data(bot)
coo_width(bot[1])
```

---

d *A wrapper to calculates euclidean distances between two points*

Description

The main advantage over ed is that it is a method that can be passed to different objects and used in combination with measure. See examples.

Usage

```
d(x, id1, id2)
```

Arguments

x	a Ldk (typically), an Out or a matrix
id1	id of the 1st row
id2	id of the 2nd row

Note

On Out objects, we first get_ldk.

See Also

if you want all pairwise combinations, see truss

Examples

```
# single shape
d(wings[1], 1, 4)
# Ldk object
d(wings, 1, 4)
# Out object
d(hearts, 2, 4)
```

`def_ldk` *Defines landmarks on Out and Opn objects*

Description

Helps to define landmarks on a `Coo` object. The number of landmarks must be specified and rows indices that correspond to the nearest points clicked on every outlines are stored in the `$ldk` slot of the `Coo` object.

Usage

```
def_ldk(Coo, nb.ldk)
```

Arguments

`Coo`	an Out or Opn object
`nb.ldk`	the number of landmarks to define on every shape

Value

an Out or an Opn object with some landmarks defined

See Also

Other ldk/slidings methods: `def_slidings`, `get_ldk`, `get_slidings`, `slidings_scheme`

Examples

```
## Not run:
data(bot)
bot <- bot[1:5] # to make it shorter to try
# click on 3 points, 5 times.
# Don't forget to save the object returned by def_ldk...
bot2 <- def_ldk(bot, 3)
stack(bot2)
bot2$ldk

## End(Not run)
```

def_links *Defines links between landmarks*

Description

Works on Ldk objects, on 2cols matrices, 3dim arrays (msshapes turns it into a matrix).

Usage

```
def_links(x, nb.ldk)
```

Arguments

x	Ldk, matric or array
nb.ldk	numeric the iterative procedure is stopped when the user click on the top of the graphical window.

See Also

Other ldk helpers: ldk_check, links_all, links_delaunay

Examples

```
## Not run:
data(wings)
wm <- mshapes(wings)
links <- def_links(wm, 3) # click to define pairs of landmarks
ldk_links(wm, links)

## End(Not run)
```

def_slidings *Defines sliding landmarks matrix*

Description

Defines sliding landmarks matrix

Usage

```
def_slidings(Coo, slidings)
```

Arguments

Coo	an Ldk object
slidings	a matrix, a numeric or a list of numeric. See Details

Details

`$slidings` in Ldk must be a 'valid' matrix: containing ids of coordinates, none of them being lower than 1 and higher the number of coordinates in `$coo`.

`slidings` matrix contains 3 columns (`before`, `slide`, `after`). It is inspired by `geomorph` and should be compatible with it.

This matrix can be passed directly if the `slidings` argument is a matrix. Of course, it is strictly equivalent to `Ldk$slidings <- slidings`.

`slidings` can also be passed as "partition(s)", when sliding landmarks identified by their ids (which are a row number) are consecutive in the `$coo`.

A single partition can be passed either as a numeric (eg `4:12`), if points 5 to 11 must be considered as sliding landmarks (4 and 12 being fixed); or as a list of numeric.

See examples below.

See Also

Other ldk/slidings methods: `def_ldk`, `get_ldk`, `get_slidings`, `slidings_scheme`

Examples

```
#waiting for a sliding dataset...
```

`dfourier` *Discrete cosinus transform*

Description

Calculates discrete cosine transforms, as introduced by Dommergues and colleagues, on a shape (mainly open outlines).

Usage

```
dfourier(coo, nb.h, verbose = TRUE)

## Default S3 method:
dfourier(coo, nb.h, verbose = TRUE)

## S3 method for class 'Opn'
dfourier(coo, nb.h, verbose = TRUE)

## S3 method for class 'Coo'
dfourier(coo, nb.h, verbose = TRUE)
```

Arguments

coo	a matrix (or a list) of (x; y) coordinates
nb.h	numeric the number of harmonics to calculate
verbose	whether to print messages and progress bar.

Value

a list with the following components:

- an the A harmonic coefficients
- bn the B harmonic coefficients
- mod the modules of the points
- arg the arguments of the points

Note

This method has been only poorly tested in Momocs and should be considered as experimental. Yet improved by a factor 10, this method is still long to execute. It will be improved in further releases but it should not be so painful right now. It also explains that a progress bar is printed when 'verbose' is TRUE. Shapes should be aligned before performing the dct transform.

References

- Dommergues, C. H., Dommergues, J.-L., & Verrecchia, E. P. (2007). The Discrete Cosine Transform, a Fourier-related Method for Morphometric Analysis of Open Contours. *Mathematical Geology*, 39(8), 749-763. doi:10.1007/s11004-007-9124-6
- Many thanks to Remi Laffont for the translation in R).

See Also

Other dfourier: dfourier_i, dfourier_shape

Examples

```
data(olea)
## Not run:  # because it's long
od <- dfourier(olea)
od
op <- PCA(od)
plot(op, 1)

## End(Not run)
# dfourier and inverse dfourier
o <- olea[1]
o <- coo_bookstein(o)
coo_plot(o)
o.dfourier <- dfourier(o, nb.h=12)
o.dfourier
o.i <- dfourier_i(o.dfourier)
```

```
o.i <- coo_bookstein(o.i)
coo_draw(o.i, border='red')

#future calibrate_reconstructions
o <- olea[1]
h.range <- 2:13
coo <- list()
for (i in seq(along=h.range)){
coo[[i]] <- dfourier_i(dfourier(o, nb.h=h.range[i]))}
names(coo) <- paste0('h', h.range)
panel(Opn(coo), borders=col_india(12), names=TRUE)
title('Discrete Cosine Transforms')
```

`dfourier_i` *Investe discrete cosinus transform*

Description

Calculates inverse discrete cosine transforms (see dfourier), given a list of A and B harmonic coefficients, typically such as those produced by dfourier.

Usage

```
dfourier_i(df, nb.h, nb.pts = 60)
```

Arguments

`df`	a list with `$A` and `$B` components, containing harmonic coefficients.
`nb.h`	a custom number of harmonics to use
`nb.pts`	numeric the number of pts for the shape reconstruction

Value

a matrix of (x; y) coordinates

Note

Only the core functions so far. Will be implemented as an Opn method soon.

References

- Dommergues, C. H., Dommergues, J.-L., & Verrecchia, E. P. (2007). The Discrete Cosine Transform, a Fourier-related Method for Morphometric Analysis of Open Contours. *Mathematical Geology*, 39(8), 749-763. doi:10.1007/s11004-007-9124-6
- Many thanks to Remi Laffont for the translation in R).

See Also

Other dfourier: `dfourier_shape`, `dfourier`

Examples

```
# dfourier and inverse dfourier
data(olea)
o <- olea[1]
o <- coo_bookstein(o)
coo_plot(o)
o.dfourier <- dfourier(o, nb.h=12)
o.dfourier
o.i <- dfourier_i(o.dfourier)
o.i <- coo_bookstein(o.i)
coo_draw(o.i, border='red')

o <- olea[1]
h.range <- 2:13
coo <- list()
for (i in seq(along=h.range)){
coo[[i]] <- dfourier_i(dfourier(o, nb.h=h.range[i]))}
names(coo) <- paste0('h', h.range)
panel(Opn(coo), borders=col_india(12), names=TRUE)
title('Discrete Cosine Transforms')
```

---

dfourier_shape *Calculates and draws 'dfourier' shapes*

Description

Calculates shapes based on 'Discrete cosine transforms' given harmonic coefficients (see dfourier) or can generate some random 'dfourier' shapes. Mainly intended to generate shapes and/or to understand how dfourier works.

Usage

```
dfourier_shape(A, B, nb.h, nb.pts = 60, alpha = 2, plot = TRUE)
```

Arguments

A	vector of harmonic coefficients
B	vector of harmonic coefficients
nb.h	if A and/or B are not provided, the number of harmonics to generate
nb.pts	if A and/or B are not provided, the number of points to use to reconstruct the shapes
alpha	tThe power coefficient associated with the (usually decreasing) amplitude of the harmonic coefficients (see efourier_shape)
plot	logical whether to plot the shape

See Also

Other dfourier: dfourier_i, dfourier

Examples

```
# some signatures
panel(coo_align(Opn(replicate(48, dfourier_shape(alpha=0.5, nb.h=6)))))
# some worms
panel(coo_align(Opn(replicate(48, dfourier_shape(alpha=2, nb.h=6)))))
```

`dissolve` *Dissolves Coe objects*

Description

the opposite of combine, typically used after it. Note that the `$fac` slot may be wrong since combine...well combines... this `$fac`. See examples.

Usage

```
dissolve(x, retain)
```

Arguments

`x`	a Coe object
`retain`	the partition id to retain. Or their name if the partitions are named (see x$method) eg after a chop

See Also

Other handling functions: `arrange`, `at_least`, `chop`, `combine`, `filter`, `mutate`, `rename`, `rm_uncomplete`, `rw_rule`, `sample_frac`, `sample_n`, `select`, `slice`, `subset.Coo`, `transmute`

Examples

```
data(bot)
w <- filter(bot, type=="whisky")
b <- filter(bot, type=="beer")
wf <- efourier(w, 10)
bf <- efourier(b, 10)
wbf <- combine(wf, bf)
dissolve(wbf, 1)
dissolve(wbf, 2)
```

ed *Calculates euclidean distance between two points.*

Description

ed simply calculates euclidean distance between two points defined by their (x; y) coordinates.

Usage

```
ed(pt1, pt2)
```

Arguments

pt1	(x; y) coordinates of the first point.
pt2	(x; y) coordinates of the second point.

Value

Returns the euclidean distance between the two points.

See Also

edm, edm_nearest, dist.

Examples

```
ed(c(0,1), c(1,0))
```

edi *Calculates euclidean intermediate between two points.*

Description

edi simply calculates coordinates of a points at the relative distance r on the pt1-pt2 defined by their (x; y) coordinates. This function is used internally but may be of interest for other analyses.

Usage

```
edi(pt1, pt2, r = 0.5)
```

Arguments

pt1	$(x; y)$ coordinates of the first point.
pt2	$(x; y)$ coordinates of the second point.
r	the relative distance from pt1 to pt2.

Value

returns the $(x; y)$ interpolated coordinates.

See Also

ed, edm.

Examples

```
edi(c(0,1), c(1,0), r = 0.5)
```

---

edm *Calculates euclidean distance every pairs of points in two matrices.*

Description

edm returns the euclidean distances between points $1- > n$ of two 2-col matrices of the same dimension. This function is used internally but may be of interest for other analyses.

Usage

```
edm(m1, m2)
```

Arguments

m1	The first matrix of coordinates.
m2	The second matrix of coordinates.

Details

If one wishes to align two (or more shapes) Procrustes surimposition may provide a better solution.

Value

Returns a vector of euclidean distances between pairwise coordinates in the two matrices.

See Also

ed, edm_nearest, dist.

Examples

```
x <- matrix(1:10, nc=2)
edm(x, x)
edm(x, x+1)
```

edm_nearest *Calculates the shortest euclidean distance found for every point of one matrix among those of a second.*

Description

edm_nearest calculates the shortest euclidean distance found for every point of one matrix among those of a second. In other words, if m1, m2 have n rows, the result will be the shortest distance for the first point of m1 to any point of m2 and so on, n times. This function is used internally but may be of interest for other analyses.

Usage

```
edm_nearest(m1, m2, full = FALSE)
```

Arguments

m1	The first list or matrix of coordinates.
m2	The second list or matrix of coordinates.
full	logical. Whether to returns a condensed version of the results.

Details

So far this function is quite time consumming since it performs $n \times n$ euclidean distance computation. If one wishes to align two (or more shapes) Procrustes surimposition may provide a better solution.

Value

If full is TRUE, returns a list with two components: d which is for every point of m1 the shortest distance found between it and any point in m2, and pos the (m2) row indices of these points. Otherwise returns d as a numeric vector of the shortest distances.

See Also

ed, edm, dist.

Examples

```
x <- matrix(1:10, nc=2)
edm_nearest(x, x+rnorm(10))
edm_nearest(x, x+rnorm(10), full=TRUE)
```

`efourier` *Elliptical Fourier transform*

Description

`efourier` computes Elliptical Fourier Analysis (or Transforms or EFT) from a matrix (or a list) of (x; y) coordinates.

Usage

```
efourier(x, ...)

## Default S3 method:
efourier(x, nb.h, smooth.it = 0, verbose = TRUE, ...)

## S3 method for class 'Out'
efourier(x, nb.h, smooth.it = 0, norm = TRUE, start = FALSE,
  verbose = TRUE, ...)
```

Arguments

`x`	A `list` or a `matrix` of coordinates or a `Out` object
`...`	useless here
`nb.h`	`integer`. The number of harmonics to use. If missing 99pc harmonic power is used.
`smooth.it`	`integer`. The number of smoothing iterations to perform.
`verbose`	`logical`. Whether to print or not diagnosis messages.
`norm`	whether to normalize the coefficients using efourier_norm
`start`	logical whether to consider the first point as homologous

Details

For the maths behind see the paper in JSS.

Normalization of coefficients has long been a matter of trouble, and not only for newcomers. There are two ways of normalizing outlines: the first, and by far the msot used, is to use a "numerical" alignment, directly on the matrix of coefficients. The coefficients of the first harmonic are consumed by this process but harmonics of higher rank are normalized in terms of size and rotation. This is sometimes referred as using the "first ellipse", as the harmonics define an ellipse in the plane, and the first one is the mother of all ellipses, on which all others "roll" along. This approach is really convenient as it is done easily by most software (if not the only option) and by Momocs too. It is the default option of `efourier`.

But here is the pitfall: if your shapes are prone to bad aligments among all the first ellipses, this will result in poorly (or even not at all) "homologous" coefficients. The shapes prone to this are either (at least roughly) circular and/or with a strong bilateral symmetry. You can try to use `stack` on the `Coe` object returned by `efourier`. Also, when plotting PCA using Momocs, this will be strikingly

clear though. This phenomenon will result in two clusters, and more strikingly into upside-down (or 180 degrees rotated) shapes on the morphospace. If this happen, you should seriously consider aligning your shapes *before* the `efourier` step, and performing the latter with no normalization (`norm = FALSE`), since it has been done before.

You have several options to align your shapes, using control points (or landmarks), of Procrustes alignment (see `fgProcrustes`) through their calliper length (see `coo_aligncalliper`), etc. You should also make the first point homologous either with `coo_slide` or `coo_slidedirection` to minimize any subsequent problems.

I will dedicate (some day) a vignette or a paper to this problem.

Value

A list with these components:

`an`	`vector` of $a_{1->n}$ harmonic coefficients.
`bn`	`vector` of $b_{1->n}$ harmonic coefficients.
`cn`	`vector` of $c_{1->n}$ harmonic coefficients.
`dn`	`vector` of $d_{1->n}$ harmonic coefficients.
`ao`	`ao` Harmonic coefficient.
`co`	`co` Harmonic coefficient.

Note

Directly borrowed for Claude (2008), and also called `efourier` there.

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp. Ferson S, Rohlf FJ, Koehn RK. 1985. Measuring shape variation of two-dimensional outlines. *Systematic Biology* **34**: 59-68.

See Also

Other efourier: `efourier_i`, `efourier_norm`, `efourier_shape`

Examples

```
data(bot)
coo <- bot[1]
coo_plot(coo)
ef <- efourier(coo, 12)
ef
efi <- efourier_i(ef)
coo_draw(efi, border='red', col=NA)
```

`efourier_i` *Inverse elliptical Fourier transform*

Description

`efourier_i` uses the inverse elliptical Fourier transformation to calculate a shape, when given a list with Fourier coefficients, typically obtained computed with efourier.

Usage

```
efourier_i(ef, nb.h, nb.pts = 120)
```

Arguments

`ef`	`list`. A list containing a_n, b_n, c_n and d_n Fourier coefficients, such as returned by `efourier`.
`nb.h`	`integer`. The number of harmonics to use. If not specified, `length(ef$an)` is used.
`nb.pts`	`integer`. The number of points to calculate.

Details

See efourier for the mathematical background.

Value

A matrix of (x; y) coordinates.

Note

Directly borrowed for Claude (2008), and also called `iefourier` there.

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp. Ferson S, Rohlf FJ, Koehn RK. 1985. Measuring shape variation of two-dimensional outlines. *Systematic Biology* **34**: 59-68.

See Also

Other efourier: `efourier_norm`, `efourier_shape`, `efourier`

Examples

```
data(bot)
coo <- bot[1]
coo_plot(coo)
ef  <- efourier(coo, 12)
ef
efi <- efourier_i(ef)
coo_draw(efi, border='red', col=NA)
```

`efourier_norm` *Normalizes harmonic coefficients.*

Description

`efourier_norm` normalizes Fourier coefficients for rotation, tranlation, size and orientation of the first ellipse.

Usage

```
efourier_norm(ef, start = FALSE)
```

Arguments

`ef`	`list`. A list containing a_n, b_n, c_n and d_n Fourier coefficients, such as returned by `efourier`.
`start`	`logical`. Whether to conserve the position of the first point of the outline.

Details

See efourier for the mathematical background of the normalization.

Sometimes shapes do not 'align' well each others, and this is usually detectable on a morphospace on a regular PCA. You mat find 180 degrees rotated shapes or bizarre clustering. Most of the time this is due to a poor normalization on the matrix of coefficients, and the variability you observe may mostly be due to the variability in the alignment of the 'first' ellipsis which is defined by the first harmonic, used for the normalization. In that case, you should align shapes *before* efourier and with `norm = FALSE`. You have several options: coo_align, coo_aligncalliper, fgProcrustes either directly on the coordinates or on some landmarks along the outline or elsewhere on your original shape, depending of what shall provide a good alignment. Have a look to Momocs' vignette for some illustration of these pitfalls and how to manage them.

Value

A list with the following components:

- `A` vector of $A_{1->n}$ *normalized* harmonic coefficients
- `B` vector of $B_{1->n}$ *normalized* harmonic coefficients
- `C` vector of $C_{1->n}$ *normalized* harmonic coefficients

- D vector of $D_{1->n}$ *normalized* harmonic coefficients
- size Magnitude of the semi-major axis of the first fitting ellipse
- theta angle, in radians, between the starting point and the semi-major axis of the first fitting ellipse
- psi orientation of the first fitting ellipse
- ao ao harmonic coefficient
- co co Harmonic coefficient
- lnef a list with A, B, C and D concatenated in a vector.

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

Ferson S, Rohlf FJ, Koehn RK. 1985. Measuring shape variation of two-dimensional outlines. *Systematic Biology* **34**: 59-68.

See Also

Other efourier: efourier_i, efourier_shape, efourier

Examples

```
data(bot)
q <- efourier(bot[1], 24)
efourier_i(q) # equivalent to efourier_shape(q$an, q$bn, q$cn, q$dn)
efourier_norm(q)
efourier_shape(nb.h=5, alpha=1.2)
efourier_shape(nb.h=12, alpha=0.9)
```

---

efourier_shape *Calculates and draw 'efourier' shapes.*

Description

efourier_shape calculates a 'Fourier elliptical shape' given Fourier coefficients (see Details) or can generate some 'efourier' shapes. Mainly intended to generate shapes and/or to understand how efourier works.

Usage

```
efourier_shape(an, bn, cn, dn, nb.h, nb.pts = 60, alpha = 2, plot = TRUE)
```

Arguments

an	numeric. The a_n Fourier coefficients on which to calculate a shape.
bn	numeric. The b_n Fourier coefficients on which to calculate a shape.
cn	numeric. The c_n Fourier coefficients on which to calculate a shape.
dn	numeric. The d_n Fourier coefficients on which to calculate a shape.
nb.h	integer. The number of harmonics to use.
nb.pts	integer. The number of points to calculate.
alpha	numeric. The power coefficient associated with the (usually decreasing) amplitude of the Fourier coefficients (see **Details**).
plot	logical. Whether to plot or not the shape.

Details

efourier_shape can be used by specifying nb.h and alpha. The coefficients are then sampled in an uniform distribution $(-\pi; \pi)$ and this amplitude is then divided by $harmonicrank^alpha$. If alpha is lower than 1, consecutive coefficients will thus increase. See efourier for the mathematical background.

Value

A list with components:

- x vector of x-coordinates
- y vector of y-coordinates.

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

Ferson S, Rohlf FJ, Koehn RK. 1985. Measuring shape variation of two-dimensional outlines. *Systematic Biology* **34**: 59-68.

See Also

Other efourier: efourier_i, efourier_norm, efourier

Examples

```
data(bot)
ef <- efourier(bot[1], 24)
efourier_shape(ef$an, ef$bn, ef$cn, ef$dn) # equivalent to efourier_i(ef)
efourier_shape() # is autonomous

panel(Out(a2l(replicate(100,
efourier_shape(nb.h=6, alpha=2.5, plot=FALSE))))) # Bubble family
```

export *Exports Coe objects and shapes*

Description

Writes a `.txt` or `.xls` or whatever readable from a Coe, or PCA object, along with individual names and grouping factors. A simple wrapper around write.table.

Usage

```
export(x, file, sep, dec)
```

Arguments

`x`	a Coe object
`file`	the filenames `data.txt` by default
`sep`	the field separator string (see `sep` in write.table). A tab by default
`dec`	the string to use for decimal points (see `dec` in write.table). A dot by default.

Note

Default parameters will write a `.txt` file, directly readable by MS Excel and other programs. With default parameters, numbers will dots as decimal points, which is considered as a character chain in Excel in many countries (locale versions.) this can be solved using `dec=','` as in the examples below.

If you are new to R, you may be looking for where this damn file has been saved. With the defaults settings, `getwd()` will provide the answer.

I have to mention that everytime you use this function, escape from R to use Excel and do 'statistics' there, an adorable kitten is probably murdered somewhere. Use R, not Excel!

See Also

babel functions

Examples

```
## Not run:
# Will write files on your machine!
data(bot)
bot.f <- efourier(bot, 6)
export(bot.f) # data.txt which can be opened by every software including MS Excel
# If you are French, or another country that has not been invaded by anglo-american rules.
# and for use in Excel.
export(bot.f, dec=',')
export(bot.f, file='data.xls', dec=',')

# for shapes (matrices)
```

```
 export(bot[1], file='bot1.txt')

## End(Not run)
```

`fgProcrustes` *Full Generalized Procrustes alignment between shapes*

Description

Directly borrowed from Claude (2008), called there the `fgpa2` function.

Usage

```
fgProcrustes(x, tol, verbose, coo)
```

Arguments

`x`	an array, a list of configurations, or an Out, Opn or Ldk object
`tol`	numeric when to stop iterations
`verbose`	logical whether to print outputs (iteration number, and gain)
`coo`	logical, when working on `Out` or `Opn`, whether to use `$coo` rather than `$ldk`

Details

If performed on an Out or an Opn object, will try to use the `$ldk` slot, if landmarks have been previousy defined, then (with a message) on the `$coo` slot, but in that case, all shapes must have the same number of coordinates (coo_sample may help).

Value

a list with components:

- `rotated` array of superimposed configurations
- `iterationnumber` number of iterations
- `Q` convergence criterion
- `Qi` full list of Q
- `Qd` difference between succesive Q
- `interproc.dist` minimal sum of squared norms of pairwise differences between all shapes in the superimposed sample
- `mshape` mean shape configuration
- `cent.size` vector of centroid sizes.

or an Out, Opn or an Ldk object.

Note

Slightly less optimized than procGPA in the shapes package (~20

References

Claude, J. (2008). Morphometrics with R. Analysis (p. 316). Springer.

See Also

Other procrustes functions: `fProcrustes`, `fgsProcrustes`, `pProcrustes`

Examples

```
## Not run:
# on Ldk
stack(wings)
fgProcrustes(wings, tol=0.1) %>% stack()

# on Out
stack(hearts)
fgProcrustes(hearts) %>%  stack()

## End(Not run)
```

`fgsProcrustes` *Full Generalized Procrustes alignment between shapes with sliding landmarks*

Description

Directly wrapped around `geomorph::gpagen`.

Usage

```
fgsProcrustes(x)
```

Arguments

`x`	Ldk object with some `$slidings`

Note

Landmarks methods are the less tested in Momocs. Keep in mind that some features are still experimental and that your help is welcome.

Source

See `?gpagen` in `geomorph` package

See Also

Other procrustes functions: fProcrustes, fgProcrustes, pProcrustes

Examples

```
chaffp <- fgsProcrustes(chaff)
chaffp
chaffp %>% PCA() %>% plot("taxa")
```

---

filter *Filters (ala dplyr) on Momocs objects*

Description

Return shapes with matching conditions, from the $fac. See examples and ?dplyr::filter.

Usage

```
filter(.data, ...)
```

Arguments

.data	a Coo, Coe, PCA object
...	logical conditions

Details

dplyr verbs are maintained.

Value

a Momocs object of the same class.

See Also

Other handling functions: arrange, at_least, chop, combine, dissolve, mutate, rename, rm_uncomplete, rw_rule, sample_frac, sample_n, select, slice, subset.Coo, transmute

Examples

```
olea
# we retain on dorsal views
filter(olea, view=="VD")
# only dorsal views and Aglan+PicMa varieties
filter(olea, view=="VD", var %in% c("Aglan", "PicMa"))
# we create an id column and retain the 120 first shapes
olea %>% mutate(id=1:length(olea)) %>% filter(id > 120)
```

flower *Data: Measurement of iris flowers*

Description

Data: Measurement of iris flowers

Format

A TraCoe object with 150 measurements of 4 variables (petal + sepal) x (length x width) on 3 species of iris. This dataset is the classical iris formatted for Momocs.

Source

see linkiris

See Also

Other datasets: bot, chaff, charring, hearts, molars, mosquito, oak, olea, shapes, trilo, wings

fProcrustes *Full Procrustes alignment between two shapes*

Description

Directly borrowed from Claude (2008), called there the fPsup function.

Usage

```
fProcrustes(coo1, coo2)
```

Arguments

coo1	configuration matrix to be superimposed onto the centered preshape of coo2.
coo2	reference configuration matrix.

Value

a list with components:

- coo1 superimposed centered preshape of coo1 onto the centered preshape of coo2
- coo2 centered preshape of coo2
- rotation rotation matrix
- scale scale parameter
- DF full Procrustes distance between coo1 and coo2.

References

Claude, J. (2008). Morphometrics with R. Analysis (p. 316). Springer.

See Also

Other procrustes functions: `fgProcrustes`, `fgsProcrustes`, `pProcrustes`

`get_chull_area` *Calculates convex hull area/volume of PCA scores*

Description

May be useful to compare shape diversity. Expressed in PCA units that should only be compared within the same PCA.

Usage

```
get_chull_area(x, fac, xax = 1, yax = 2)

get_chull_volume(x, fac, xax = 1, yax = 2, zax = 3)
```

Arguments

`x`	a PCA object
`fac`	(optionnal) column name or ID from the $fac slot.
`xax`	the first PC axis to use (1 by default)
`yax`	the second PC axis (2 by default)
`zax`	the third PC axis (3 by default only for volume)

Details

get_chull_area is calculated using coo_chull followed by coo_area; get_chull_volume is calculated using geometry::convexhulln

Value

If fac is not provided global area/volume is returned; otherwise a named list for every level of fac

Examples

```
data(bot)
bp <- PCA(efourier(bot, 12))
get_chull_area(bp)
get_chull_area(bp, 1)

get_chull_volume(bp)
get_chull_volume(bp, 1)
```

get_ldk *Retrieves landmarks coordinates*

Description

See Details for the different behaviors implemented.

Usage

```
get_ldk(Coo)
```

Arguments

Coo	an Out, Opn or Ldk object

Details

Different behaviors depending on the class of the object:

- Ldk: retrieves landmarks.
- Ldk with slidings defined: retrieves only the fixed landmarks, not the sliding ones. See also get_slidings.
- Out landmarks from $ldk and $coo, if any.
- Opn: same as above.

Value

a list of shapes

See Also

Other ldk/slidings methods: def_ldk, def_slidings, get_slidings, slidings_scheme

Examples

```
# Out example
ldk.h <- get_ldk(hearts)
stack(Ldk(ldk.h))

# on Ldk (no slidings)
get_ldk(wings) # equivalent to wings$coo

# on Ldk (slidings)
get_ldk(chaff)
get_ldk(chaff) %>% Ldk %>% fgProcrustes(tol=0.1) %>% stack
```

get_pairs *Get paired individual on a Coe, PCA or LDA objects*

Description

If you have paired individuals, i.e. before and after a treatment or for repeated measures, and if you have coded coded it into `$fac`, this methods allows you to retrieve the cooresponding PC/LD scores, or coefficients for Coe objects.

Usage

```
get_pairs(x, fac, range)
```

Arguments

`x`	any Coe, PCA of LDA object.
`fac`	factor or column name or id corresponding to the pairing factor.
`range`	numeric the range of coefficients for `Coe`, or PC (LD) axes on which to return scores.

Value

a list with components `x1` all coefficients/scores corresponding to the first level of the `fac` provided; `x2` same thing for the second level; `fac` the corresponding `fac`.

Examples

```
data(bot)
bot2 <- bot1 <- coo_scale(coo_center(coo_sample(bot, 60)))
bot1$fac$session <- factor(rep("session1", 40))
# we simulate an measurement error
bot2 <- coo_jitter(bot1, amount=0.01)
bot2$fac$session <- factor(rep("session2", 40))
botc <- combine(bot1, bot2)
botcf <- efourier(botc, 12)

# we gonna plot the PCA with the two measurement sessions and the two types
botcp <- PCA(botcf)
plot(botcp, "type", col=col_summer(2), pch=rep(c(1, 20), each=40), eigen=FALSE)
bot.pairs <- get_pairs(botcp, fac = "session", range=1:2)
segments(bot.pairs$session1[, 1], bot.pairs$session1[, 2],
       bot.pairs$session2[, 1], bot.pairs$session2[, 2],
       col=col_summer(2)[bot.pairs$fac$type])
```

get_slidings *Extracts sliding landmarks coordinates*

Description

From an Ldk object.

Usage

```
get_slidings(Coo, partition)
```

Arguments

Coo	an Ldk object
partition	numeric which one(s) to get.

Value

a list of list(s) of coordinates.

See Also

Other ldk/slidings methods: def_ldk, def_slidings, get_ldk, slidings_scheme

Examples

```
# for each example below a list with partition containign shapes is returned
# extracts the first partition
get_slidings(chaff, 1) %>% names()
# the first and the fourth
get_slidings(chaff, c(1, 4)) %>%  names()
# all of them
get_slidings(chaff) %>%  names
# here we want to see it
get_slidings(chaff, 1)[[1]] %>%  Ldk %>% stack
```

harm_pow *Calculates harmonic power given a list from e/t/rfourier*

Description

Given a list with an, bn (and eventually cn and dn), returns the harmonic power.

Usage

```
harm_pow(xf)
```

Arguments

xf	A list with an, bn (and cn, dn) components, typically from a e/r/tfourier passed on coo_

Value

Returns a vector of harmonic power

Examples

```
data(bot)
ef <- efourier(bot[1], 24)
rf <- efourier(bot[1], 24)
harm_pow(ef)
harm_pow(rf)

plot(cumsum(harm_pow(ef)[-1]), type='o',
  main='Cumulated harmonic power without the first harmonic',
  ylab='Cumulated harmonic power', xlab='Harmonic rank')
```

---

hcontrib *Harmonic contribution to shape*

Description

Calculates contribution of harmonics to shape. The amplitude of every coefficients of a given harmonic is multiplied by the coefficients provided and the resulting shapes are reconstructed and plotted. Naturally, only works on Fourier-based methods.

Usage

```
hcontrib(Coe, ...)

## S3 method for class 'OutCoe'
hcontrib(Coe, id, harm.r, amp.r = c(0, 0.5, 1, 2, 5, 10),
  main = "Harmonic contribution to shape", xlab = "Harmonic rank",
  ylab = "Amplification factor", ...)
```

Arguments

Coe	a Coe object (either OutCoe or (soon) OpnCoe)
...	additional parameter to pass to coo_draw
id	the id of a particular shape, otherwise working on the meanshape
harm.r	range of harmonics on which to explore contributions
amp.r	a vector of numeric for multiplying coefficients

main	a title for the plot
xlab	a title for the x-axis
ylab	a title for the y-axis

See Also

Other Coe_graphics: boxplot.OutCoe, hist.OutCoe

Examples

```
data(bot)
bot.f <- efourier(bot, 12)
hcontrib(bot.f)
hcontrib(bot.f, harm.r=3:10, amp.r=1:8, col="grey20",
   main="A huge panel")
```

---

hearts *Data: Outline coordinates of hand-drawn hearts*

Description

Data: Outline coordinates of hand-drawn hearts

Format

A Out object with the outline coordinates of 240 hand-drawn hearts by 8 different persons, with 4 landmarks.

Source

We thank the fellows of the Ecology Department of the French Institute of Pondicherry that drawn the hearts, that then have been smoothed, scaled, centered, and downsampled to 80 coordinates per outline.

See Also

Other datasets: bot, chaff, charring, flower, molars, mosquito, oak, olea, shapes, trilo, wings

`hist.OutCoe` *Histogram of morphometric coefficients*

Description

Explores the distribution of coefficient values.

Usage

```
## S3 method for class 'OutCoe'
hist(x, retain = 4, drop = 0, bw = 20, ...)
```

Arguments

`x`	the Coe object
`retain`	numeric the number of harmonics to retain
`drop`	numeric the number of harmonics to drop
`bw`	the number of bins (range/bw) to display
`...`	useless here but maintain the consistency with generic hist

Value

a ggplot2 object

See Also

Other Coe_graphics: `boxplot.OutCoe`, `hcontrib`

Examples

```
data(bot)
bot.f <- efourier(bot, 24)
hist(bot.f)

data(olea)
op <- opoly(olea)
hist(op)
```

img_plot *Plots a .jpg image*

Description

A very simple image plotter. If provided with a path, reads the .jpg and plots it. If not provided with an imagematrix, will ask you to choose interactively a `.jpeg` image.

Usage

```
img_plot(img)

img_plot0(img)
```

Arguments

`img`	a matrix of an image, such as those obtained with readJPEG.

Details

`img_plot` is used in import functions such as import_jpg1; `img_plot0` does the same job but preserves the `par` and plots axes.

import_Conte *Extracts outlines coordinates from an image silhouette*

Description

Provided with an image 'mask' (i.e. black pixels on a white background), and a point form where to start the algorithm, returns the (x; y) coordinates of its outline.

Usage

```
import_Conte(img, x)
```

Arguments

`img`	a matrix of a binary image mask.
`x`	numeric the (x; y) coordinates of a starting point within the shape.

Details

Used internally by import_jpg1 but may be useful for other purposes.

Value

a matrix the (x; y) coordinates of the outline points.

References

- The original algorithm is due to: Pavlidis, T. (1982). *Algorithms for graphics and image processing*. Computer science press.
- is detailed in: Rohlf, F. J. (1990). An overview of image processing and analysis techniques for morphometrics. In *Proceedings of the Michigan Morphometrics Workshop*. Special Publication No. 2 (pp. 47-60). University of Michigan Museum of Zoology: Ann Arbor.
- and translated in R by: Claude, J. (2008). *Morphometrics with R*. (p. 316). Springer.

See Also

babel functions.

`import_jpg` *Extracts outline coordinates from multiple .jpg files*

Description

This function is used to import outline coordinates and is built around import_jpg1.

Usage

```
import_jpg(jpg.paths = NULL, auto.notcentered = TRUE,
  fun.notcentered = NULL, threshold = 0.5, verbose = TRUE)
```

Arguments

`jpg.paths`	a vector of paths corresponding to the .jpg files to import. If not provided (or `NULL`), switches to the automatic version. See Details below.
`auto.notcentered`	logical if TRUE random locations will be used until. one of them is (assumed) to be within the shape (because of a black pixel); if FALSE a locator will be called, and you will have to click on a point within the shape.
`fun.notcentered`	NULL by default. Is your shapes are not centered and if a random pick of a black pixel is not satisfactory. See import_jpg1 help and examples.
`threshold`	the threshold value use to binarize the images. Above, pixels are turned to 1, below to 0.
`verbose`	whether to print which file is being treated. Useful to detect problems.

Details

see import_jpg1 for important informations about how the outlines are extracted, and import_Conte for the algorithm itself.

If `jpg.paths` is not provided (or `NULL`), you will have to select any `.jpg` file in the folder taht contains all your files. All the outlines should be imported then.

Value

a list of matrices of (x; y) coordinates that can be passed to Out

See Also

Other babel functions: `bind_db`, `chc2Out`, `chc2pix`, `import_StereoMorph_curve1`, `import_tps`, `nef2Coe`, `ntsrow2Coo`, `pix2chc`, `tie_jpg_txt`, `tps2coo`

Examples

```
## Not run:

# if your images are in the folder '/foo/jpgs/'
lf <- list.files('/foo/jpegs', full.names=TRUE)
coo <- import_jpg(lf)
Out(coo)

# 'automatic' version
coo <- import_jpg()

## End(Not run)
```

`import_jpg1` *Extracts outline coordinates from a single .jpg file*

Description

Used to import outline coordinates from .jpg files. This function is used for single images and is wrapped by import_jpg. It relies itself on import_Conte

Usage

```
import_jpg1(jpg.path, auto.notcentered = TRUE, fun.notcentered = NULL,
  threshold = 0.5)
```

Arguments

`jpg.path`	vector of paths corresponding to the .jpg files to import, such as those obtained with list.files.
`auto.notcentered`	logical if TRUE random locations will be used until one of them is (assumed) to be within the shape (because it corresponds to a black pixel) and only if the middle point is not black; if FALSE a locator will be called, and you will have to click on a point within the shape.
`fun.notcentered`	NULL by default but can accept a function that, when passed with an image-matrix and returns a numeric of length two that corresponds to a starting point on the imagematrix for the Conte algorithm. A `while` instruction wraps it, so the function may be wrong in proposing this starting position. See the examples below for a quick example.
`threshold`	the threshold value use to binarize the images. Above, pixels are turned to 1, below to 0.
`...`	arguments to be passed to read.table, eg. 'skip', 'dec', etc.

Details

jpegs can be provided either as RVB or as 8-bit greylevels or monochrome. The function binarizes pixels values using the 'threshold' argument. It will try to start to apply the import_Conte algorithm from the center of the image and 'looking' downwards for the first black/white 'frontier' in the pixels. This point will be the first of the outlines. The latter may be useful if you align manually the images and if you want to retain this information in the consequent morphometric analyses.

If the point at the center of the image is not within the shape, i.e. is 'white' you have two choices defined by the 'auto.notcentered' argument. If it's TRUE, some random starting points will be tried until on of them is 'black' and within the shape; if FALSE you will be asked to click on a point within the shape.

If some pixels on the borders are not white, this functions adds a 2-pixel border of white pixels; otherwise import_Conte would fail and return an error.

Finally, remember that if the images are not in your working directory, list.files must be called with the argument `full.names=TRUE`!

Note that the use of the `fun.notcentered` argument will probably leads to serious headaches and will probably imply the dissection of these functions: import_Conte, img_plot and `import_jpg` itself

Value

a matrix of (x; y) coordinates that can be passed to Out

See Also

import_jpg, import_Conte, import_txt, lf_structure. See also Momocs' vignettes for data import.

babel functions.

`import_StereoMorph_curve1` *Imports files creates by StereoMorph into Momocs*

Description

Helps to read `.txt` files created by StereoMorph into (x; y) coordinates or Momocs objects. Can be applied to 'curves' or 'ldk' text files.

Usage

```
import_StereoMorph_curve1(path)

import_StereoMorph_curve(path, names)

import_StereoMorph_ldk1(path)

import_StereoMorph_ldk(path, names)
```

Arguments

`path`	toward a single file or a folder containing `.txt` files produced by StereoMorph
`names`	to feed lf_structure

Details

*1 functions import a single `.txt` file. Their counterpart (no '1') work when path indicates the folder, i.e. 'curves' or 'ldk'. They then return a list of Opn or Ldk objects, respectively. Please do not hesitate to contact me should you have a particular case or need something.

See Also

Other babel functions: `bind_db`, `chc2Out`, `chc2pix`, `import_jpg`, `import_tps`, `nef2Coe`, `ntsrow2Coo`, `pix2chc`, `tie_jpg_txt`, `tps2coo`

Other babel functions: `bind_db`, `chc2Out`, `chc2pix`, `import_jpg`, `import_tps`, `nef2Coe`, `ntsrow2Coo`, `pix2chc`, `tie_jpg_txt`, `tps2coo`

import_tps *Imports a tps file*

Description

And returns a list of coordinates, curves, scale

Usage

```
import_tps(tps.path, curves = TRUE)
```

Arguments

tps.path	lines, typically from readLines, describing a single shape in tps-like format
curves	logical whether to read curves, if any

Value

a list with components: coo a matrix of coordinates; cur a list of matrices; scale the scale as a numeric.

See Also

Other babel functions: bind_db, chc2Out, chc2pix, import_StereoMorph_curve1, import_jpg, nef2Coe, ntsrow2Coo, pix2chc, tie_jpg_txt, tps2coo

import_txt *Imports coordinates from a .txt file*

Description

A wrapper around read.table that can be used to import outline/landmark coordinates.

Usage

```
import_txt(txt.paths = NULL, ...)
```

Arguments

txt.paths	a vector of paths corresponding to the .txt files to import. If not provided (or NULL), switches to the automatic version, just as inimport_jpg. See Details there.
...	arguments to be passed to read.table, eg. 'skip', 'dec', etc.

Details

By default, it works with the default arguments of read.table, e.g. assumes that the columns are not named in the `.txt` files. You can tune this using the `...` argument. Define the read.table arguments that allow to import a single file, and then pass them to this function.

Value

a list of matrix(ces) of (x; y) coordinates that can be passed to Out, Opn and Ldk.

See Also

babel functions.

`is` *Various class/component testers*

Description

Class testers test if any of the classes of an object is of a given class. For instance is.PCA on a PCA object (both 'PCA' and 'prcomp') will return TRUE. Component testers check if a particular component (eg $fac, etc.) is present.

Usage

```
is.Coo(x)

is.PCA(x)

is.LDA(x)

is.Out(x)

is.Opn(x)

is.Ldk(x)

is.Coe(x)

is.OutCoe(x)

is.OpnCoe(x)

is.LdkCoe(x)

is.shp(x)

is.fac(x)
```

```
is.ldk(x)

is.slidings(x)

is.links(x)
```

Arguments

x	the object to test

Value

TRUE/FALSE

Examples

```
data(bot)
is.Coo(bot)
is.Out(bot)
is.Ldk(bot)
```

`is_closed` *Tests if shapes are closed*

Description

Returns TRUE/FALSE whether the last coordinate of the shapes is the same as the first one.

Usage

```
is_closed(coo)
```

Arguments

coo	a `matrix` of (x; y) coordinates or a `list`, or any Coo object.

Value

a single or a vector of `logical`.

See Also

Other coo_ utilities: `coo_aligncalliper`, `coo_alignminradius`, `coo_alignxax`, `coo_align`, `coo_baseline`, `coo_bookstein`, `coo_calliper`, `coo_centdist`, `coo_center`, `coo_centpos`, `coo_centsize`, `coo_close`, `coo_down`, `coo_dxy`, `coo_extract`, `coo_flipx`, `coo_force2close`, `coo_interpolate`, `coo_jitter`, `coo_left`, `coo_nb`, `coo_perimcum`, `coo_perimpts`, `coo_perim`, `coo_rev`, `coo_right`, `coo_rotatecenter`, `coo_rotate`, `coo_samplerr`, `coo_sample`, `coo_scalex`, `coo_scale`, `coo_shearx`, `coo_slice`, `coo_slidedirection`, `coo_slidegap`, `coo_slide`, `coo_smoothcurve`, `coo_smooth`, `coo_template`, `coo_trans`, `coo_trim`, `coo_up`

Examples

```
is_closed(matrix(1:10, ncol=2))
is_closed(coo_close(matrix(1:10, ncol=2)))
is_closed(bot)
is_closed(coo_close(bot))
```

KMEANS *KMEANS on PCA objects*

Description

A very basic implementation of k-means. Beware that morphospaces are calculated so far for the 1st and 2nd component.

Usage

```
KMEANS(x, ...)

## S3 method for class 'PCA'
KMEANS(x, centers, nax = 1:2, pch = 20, cex = 0.5, ...)
```

Arguments

x	PCA object
...	additional arguments to be passed to kmeans
centers	numeric number of centers
nax	numeric the range of PC components to use (1:2 by default)
pch	to draw the points
cex	to draw the points

Value

the same thing as kmeans

See Also

Other multivariate: CLUST, LDA, MANOVA_PW, MANOVA, PCA

Examples

```
data(bot)
bp <- PCA(efourier(bot, 10))
KMEANS(bp, 2)
```

`l2a` *Converts a list of coordinates to an array of coordinates*

Description

l2a converts a list of `k` matrices with `m` rows and `n` columns matrices to a `m x n x k` array.

Usage

```
l2a(l)
```

Arguments

`l`	`list` of matrices of the same dimension.

Details

May be useful to communicate with other morphometrics packages that use array of coordinates when handling configurations of landmarks.

Value

an array of coordinates.

See Also

Other bridges functions: `a2l`, `a2m`, `as_df`, `l2m`, `m2a`, `m2d`, `m2ll`, `m2l`

Other bridges functions: `a2l`, `a2m`, `as_df`, `l2m`, `m2a`, `m2d`, `m2ll`, `m2l`

Examples

```
data(wings)
l <- wings$coo
l
a <- l2a(l)
a
```

l2m *Converts a list of coordinates to a matrix of coordinates.*

Description

Converts a `list` with x and y components to a two-columns (colnamed) `matrix` of coordinates. Also, if l is a list with a single matrix, then l[[1]] is returned.

Usage

```
l2m(l)
```

Arguments

`l`	`list` with x and y coordinates as components.

Value

`matrix` of (x; y) coordinates.

See Also

m2l.

Other bridges functions: `a2l`, `a2m`, `as_df`, `l2a`, `m2a`, `m2d`, `m2l1`, `m2l`

Examples

```
data(wings)
l <- m2l(wings[1])
l
m <- l2m(l)
m
```

LDA *Linear Discriminant Analysis on Coe objects*

Description

Performs a LDA on Coe objects. Relies on lda in MASS.

Usage

```
LDA(x, fac, retain, ...)

## Default S3 method:
LDA(x, fac, retain, ...)

## S3 method for class 'PCA'
LDA(x, fac, retain = 0.99, verbose = TRUE, ...)
```

Arguments

x	a PCA object
fac	the grouping factor (names of one of the $fac column or column id)
retain	the proportion of the total variance to retain (if retain<1) using scree, or the number of PC axis (if retain>1).
...	additional arguments to feed lda
verbose	logical whether to print messages

Value

a 'LDA' object on which to apply plot.LDA, which is a list with components:

- x any Coe object (or a matrix)
- fac grouping factor used
- removed ids of columns in the original matrix that have been removed since constant (if any)
- mod the raw lda mod from lda
- mod.pred the predicted model using x and mod
- CV.fac cross-validated classification
- CV.tab cross-validation tabke
- CV.correct proportion of correctly classified individuals
- CV.ce class error
- LDs unstandardized LD scores see Claude (2008)
- mshape mean values of coefficients in the original matrix
- method inherited from the Coe object (if any)

Note

For LDA.PCA, retain can be passed as a vector (eg: 1:5, and retain=1, retain=2, ..., retain=5) will be tried, or as "best" (same as before but retain=1:number_of_pc_axes is used).

See Also

Other multivariate: CLUST, KMEANS, MANOVA_PW, MANOVA, PCA

Examples

```
data(bot)
bot.f <- efourier(bot, 24)
bot.p <- PCA(bot.f)
LDA(bot.p, 'type', retain=0.99) # retains 0.99 of the total variance
LDA(bot.p, 'type', retain=5) # retain 5 axis
bot.l <- LDA(bot.p, 'type', retain=0.99)
bot.l
plot(bot.l)
bot.f$fac$plop <- factor(rep(letters[1:4], each=10))
bot.l <- LDA(PCA(bot.f), 'plop')
bot.l
plot(bot.l)
```

Ldk *Builds an Ldk object*

Description

In Momocs, Ldk classes objects are lists of configurations of **l**an**d**mar**k**s, with optionnal components, on which generic methods such as plotting methods (e.g. stack) and specific methods (e.g. todo-Procrustes can be applied. Ldk objects are primarily Coo objects.

Usage

```
Ldk(coo, links = NULL, slidings = NULL, fac = data.frame())
```

Arguments

coo	a list of matrices of (x; y) coordinates, or an array, an Ldk object.
links	(optionnal) a 2-columns matrix of 'links' between landmarks, mainly for plotting
slidings	(optionnal) a 3-columns matrix defining (if any) sliding landmarks
fac	(optionnal) a data.frame of factors and/or numerics specifying the grouping structure

Details

All the shapes in x must have the same number of landmarks. If you are trying to make an Ldk object from an Out or an Opn object, try coo_sample beforehand to homogeneize the number of coordinates among shapes.

implementation of $slidings is inspired by geomorph

Value

an Ldk object

Examples

```
#Methods on Ldk
methods(class=Ldk)
```

---

ldk_check *Checks 'ldk' shapes*

Description

A simple utility, used internally, mostly by Ldk methods, in some graphical functions, and notably in l2a. Returns an array of landmarks arranged as `(nb.ldk) x (x; y) x (nb.shapes)`, when passed with either a list, a matrix or an array of coordinates. If a list is provided, checks that the number of landmarks is consistent.

Usage

```
ldk_check(ldk)
```

Arguments

ldk	a `matrix` of (x; y) coordinates, a list, or an array.

Value

an `array` of (x; y) coordinates.

See Also

Other ldk helpers: `def_links`, `links_all`, `links_delaunay`

Examples

```
#coo_check('Not a shape')
#coo_check(matrix(1:10, ncol=2))
#coo_check(list(x=1:5, y=6:10))
```

ldk_chull *Draws convex hulls around landmark positions*

Description

A wrapper that uses coo_chull

Usage

```
ldk_chull(ldk, col = "grey40", lty = 1)
```

Arguments

ldk	an array (or a list) of landmarks
col	a color for drawing the convex hull
lty	an lty for drawing the convex hulls

See Also

coo_chull, chull, ldk_confell, ldk_contour

Other ldk plotters: ldk_confell, ldk_contour, ldk_labels, ldk_links

Other plotting functions: Ntable, conf_ell, coo_arrows, coo_draw, coo_listpanel, coo_lolli, coo_plot, coo_ruban, ldk_confell, ldk_contour, ldk_labels, ldk_links, plot_devsegments

Examples

```
data(wings)
coo_plot(mshapes(wings))
ldk_chull(wings$coo)
```

ldk_confell *Draws confidence ellipses for landmark positions*

Description

Draws confidence ellipses for landmark positions

Usage

```
ldk_confell(ldk, conf = 0.5, col = "grey40", ell.lty = 1, ax = TRUE,
  ax.lty = 2)
```

Arguments

ldk	an array (or a list) of landmarks
conf	the confidence level (normal quantile, 0.5 by default)
col	the color for the ellipse
ell.lty	an lty for the ellipse
ax	logical whether to draw ellipses axes
ax.lty	an lty for ellipses axes

See Also

Other ldk plotters: ldk_chull, ldk_contour, ldk_labels, ldk_links

Other plotting functions: Ntable, conf_ell, coo_arrows, coo_draw, coo_listpanel, coo_lolli, coo_plot, coo_ruban, ldk_chull, ldk_contour, ldk_labels, ldk_links, plot_devsegments

Examples

```
data(wings)
coo_plot(mshapes(wings))
ldk_confell(wings$coo)
```

---

ldk_contour *Draws kernel density contours around landmark*

Description

Using kde2d in the MASS package.

Usage

```
ldk_contour(ldk, nlevels = 5, grid.nb = 50, col = "grey60")
```

Arguments

ldk	an array (or a list) of landmarks
nlevels	the number of contour lines
grid.nb	the grid.nb
col	a color for drawing the contour lines

See Also

kde2d, ldk_confell, ldk_chull

Other ldk plotters: ldk_chull, ldk_confell, ldk_labels, ldk_links

Other plotting functions: Ntable, conf_ell, coo_arrows, coo_draw, coo_listpanel, coo_lolli, coo_plot, coo_ruban, ldk_chull, ldk_confell, ldk_labels, ldk_links, plot_devsegments

Examples

```
data(wings)
coo_plot(mshapes(wings))
ldk_contour(wings$coo)
```

`ldk_labels` *Add landmarks labels*

Description

Add landmarks labels

Usage

```
ldk_labels(ldk, d = 0.05, cex = 2/3, ...)
```

Arguments

`ldk`	a matrix of (x; y) coordinates: where to plot the labels
`d`	how far from the coordinates, on a (centroid-landmark) segment
`cex`	the cex for the label
`...`	additional parameters to fed text

See Also

Other ldk plotters: `ldk_chull`, `ldk_confell`, `ldk_contour`, `ldk_links`

Other plotting functions: `Ntable`, `conf_ell`, `coo_arrows`, `coo_draw`, `coo_listpanel`, `coo_lolli`, `coo_plot`, `coo_ruban`, `ldk_chull`, `ldk_confell`, `ldk_contour`, `ldk_links`, `plot_devsegments`

Examples

```
data(wings)
coo_plot(wings[1])
ldk_labels(wings[1])
# closer and smaller
coo_plot(wings[1])
ldk_labels(wings[1], d=0.05, cex=0.5)
```

ldk_links *Draws links between landmarks*

Description

Cosmetics only but useful to visualize shape variation.

Usage

```
ldk_links(ldk, links, ...)
```

Arguments

ldk	a matrix of (x; y) coordinates
links	a matrix of links. On the first column the starting-id, on the second column the ending-id (id= the number of the coordinate)
...	additional parameters to fed segments

See Also

Other ldk plotters: ldk_chull, ldk_confell, ldk_contour, ldk_labels

Other plotting functions: Ntable, conf_ell, coo_arrows, coo_draw, coo_listpanel, coo_lolli, coo_plot, coo_ruban, ldk_chull, ldk_confell, ldk_contour, ldk_labels, plot_devsegments

lf_structure *Extracts structure from filenames*

Description

If filenames are consistently named with the same character serating factors, and with every individual including its belonging levels, e.g.:

- 001_speciesI_siteA_ind1_dorsalview
- 002_speciesI_siteA_ind2_lateralview

etc., this function returns a data.frame from it that can be passed to Out, Opn, Ldk objects.

Usage

```
lf_structure(lf, names = character(), split = "_", trim.extension = FALSE)
```

Arguments

lf	a list (its names are used, except if it is a list from import_tps in this case names(lf$coo) is used) of a list of filenames, as characters, typically such as those obtained with list.files. Alternatively, a path to a folder containing the files. Actually, if lf is of length 1 (a single character), the function assumes it is a path and do a list.files on it.
names	the names of the groups, as a vector of characters which length corresponds to the number of groups.
split	character, the spliting factor used for the file names.
trim.extension	logical. Whether to remove the last for characters in filenames, typically their extension, e.g. '.jpg'.

Details

The number of groups must be consistent accross filenames.

Value

data.frame with, for every individual, the corresponding level for every group.

Note

This is, to my view, a good practice to 'store' the grouoing structure in filenames, but it is of course not mandatory.

Note also that you can: i) do a import_jpg and save is a list, say 'foo'; then ii) pass 'names(foo)' to lf_structure. See Momocs' vignette for an illustration.

See Also

import_jpg1, import_Conte, import_txt, lf_structure. See also Momocs' vignettes for data import.

---

links_all *Creates links (all pariwise combinations) between landmarks*

Description

Creates links (all pariwise combinations) between landmarks

Usage

```
links_all(coo)
```

Arguments

coo	a matrix (or a list) of (x; y) coordinates

Value

a matrix that can be passed to ldk_links, etc. The columns are the row ids of the original shape.

See Also

Other ldk helpers: def_links, ldk_check, links_delaunay

Examples

```
data(wings)
w <- wings[1]
coo_plot(w)
links <- links_all(w)
ldk_links(w, links)
```

---

links_delaunay *Creates links (Delaunay triangulation) between landmarks*

Description

Creates links (Delaunay triangulation) between landmarks

Usage

```
links_delaunay(coo)
```

Arguments

coo	a matrix (or a list) of (x; y) coordinates

Details

uses delaunayn in the geometry package.

Value

a matrix that can be passed to ldk_links, etc. The columns are the row ids of the original shape.

See Also

Other ldk helpers: def_links, ldk_check, links_all

Examples

```
data(wings)
w <- wings[1]
coo_plot(w, poly=FALSE)
links <- links_delaunay(w)
ldk_links(w, links)
```

m2a *Converts a matrix of coordinates to an array of coordinates*

Description

Converts a matrix arranged with the individuals (the 3rd dimension of the array) as rows, and (all) x coordinates and (all) y coordinates as columns, into an array built as follows: nb.of.landmarks x 2 (x; y) x nb.of.individuals.

Usage

```
m2a(m)
```

Arguments

m	a matrix (see above).

Details

Used in landmarks methods.

Value

an array (see above).

See Also

a2m the reverse function.

Other bridges functions: a2l, a2m, as_df, l2a, l2m, m2d, m2ll, m2l

Examples

```
data(wings)
m <- a2m(l2a(wings$coo))
m2a(m)
```

m2d *Converts a matrix of coordinates to a data.frame*

Description

Converts a `m x 2` matrix of coordinates named data.frame.

Usage

```
m2d(m)
```

Arguments

`m`	a matrix (see above).

Value

a data.frame (see above).

See Also

m2d the reverse function.

Other bridges functions: `a2l`, `a2m`, `as_df`, `l2a`, `l2m`, `m2a`, `m2ll`, `m2l`

Examples

```
data(wings)
m2d(wings[3])
```

m2l *Converts a matrix of coordinates to a list of coordinates.*

Description

Converts a matrix of (x; y) coordinates to a list with x and y components.

Usage

```
m2l(m)
```

Arguments

`m`	a two-columns `matrix` of x and y coordinates.

Value

a `list` with x and y components.

See Also

l2m.

Other bridges functions: a2l, a2m, as_df, l2a, l2m, m2a, m2d, m2ll

Examples

```
data(wings)
l <- m2l(wings[1])
l
m <- l2m(l)
m
```

`m2ll` *Converts a matrix of coordinates into a list of matrices*

Description

Used internally to hanle coo and cur in Ldk objects but may be useful elsewhere

Usage

```
m2ll(m, index = NULL)
```

Arguments

`m`	`matrix`, typically of (x; y) coordinates
`index`	`numeric`, the number of coordinates for every slice.

See Also

Other bridges functions: a2l, a2m, as_df, l2a, l2m, m2a, m2d, m2l

Examples

```
m2ll(wings[1], c(6, 4, 3, 5))
```

`MANOVA` *Multivariate analysis of variance on Coe objects*

Description

Performs multivariate analysis of variance on PCA objects.

Usage

```
MANOVA(x, fac, test = "Hotelling", retain, drop, verbose)

## S3 method for class 'OpnCoe'
MANOVA(x, fac, test = "Hotelling", retain, drop,
  verbose = TRUE)

## S3 method for class 'OutCoe'
MANOVA(x, fac, test = "Hotelling", retain, drop,
  verbose = TRUE)

## S3 method for class 'PCA'
MANOVA(x, fac, test = "Hotelling", retain = 0.99, drop,
  verbose = TRUE)
```

Arguments

`x`	a Coe object
`fac`	a name of a colum in the `$fac` slot, or its id, or a formula
`test`	a test for manova (`'Hotelling'` by default)
`retain`	how many harmonics (or polynomials) to retain, for PCA the highest number of PC axis to retain, or the proportion of the variance to capture.
`drop`	how many harmonics (or polynomials) to drop
`verbose`	logical whether to print messages

Details

Performs a MANOVA on PC scores. Just a wrapper around manova. See examples for multifactorial manova and summary.manova for more details and examples.

Value

a list of matrices of (x,y) coordinates.

Note

Needs a review and should be considered as experimental.

See Also

Other multivariate: CLUST, KMEANS, LDA, MANOVA_PW, PCA

Examples

```
data(bot)
bot.p <- PCA(efourier(bot, 12))
MANOVA(bot.p, 'type')

data(olea)
op <- PCA(npoly(olea, 5))
MANOVA(op, 'domes')

 m <- manova(op$x[, 1:5] ~  op$fac$domes * op$fac$var)
 summary(m)
 summary.aov(m)
```

MANOVA_PW *Pairwise Multivariate analyses of variance*

Description

A wrapper for pairwise MANOVAs on Coe objects. Calculates a MANOVA for every pairwise combination of the factor provided.

Usage

```
MANOVA_PW(x, ...)

## S3 method for class 'PCA'
MANOVA_PW(x, fac, verbose = FALSE, retain = 0.99, ...)
```

Arguments

x	a PCA object
...	more arguments to feed MANOVA
fac	a name (or its id) of a grouping factor in $fac or a factor or a formula.
verbose	to feed MANOVA
retain	the number of PC axis to retain (1:retain) or the proportion of variance to capture (0.99 par default).

Value

a list with the following components is returned (invisibly because $manovas may be very long, see examples):

- manovas a list containing all the raw manovas
- summary a matrix with all important statists
- stars.tab a table with 'significance star', discutable but useful: '***' if Pr(>F) < 0.001; '**' of < 0.01; '*' if < 0.05; '.' if < 0.10 and '-' if above.

Note

Needs a review and should be considered as experimental. If the fac passed has only two levels, there is only pair and it is equivalent to MANOVA. `MANOVA_PW.PCA` works with the regular manova.

See Also

MANOVA, manova.

Other multivariate: `CLUST`, `KMEANS`, `LDA`, `MANOVA`, `PCA`

Examples

```
data(bot)
# we create a fake factor with 4 levels
bot$fac$fake <- factor(rep(letters[1:4], each=10))
bot.p <- PCA(efourier(bot, 8))
MANOVA_PW(bot.p, 'fake') # or MANOVA_PW(bot.p, 2)

# an example on open outlines
data(olea)
op <- PCA(npoly(olea))
MANOVA_PW(op, 'domes')
# to get the results
res <- MANOVA_PW(op, 'domes')
res$manovas
res$stars.tab
res$summary
```

`measure` *Measures shape descriptors*

Description

Calculates shape descriptors on Coo and other objects. Any function that returns a scalar when fed coordinates can be passed and naturally those of Momocs (pick some there `apropos("coo_")`). Functions without arguments (eg coo_area) have to be passed without brackets but functions with arguments (eg d) have to be passed "entirely". See examples.

Usage

```
measure(x, ...)
```

Arguments

x	any Coo object, or a list of shapes, or a shape as a matrix.
...	a list of functions. See examples.

Value

a TraCoe object, or a raw data.frame

See Also

Other premodern: truss

Examples

```
# lets write a custom function
coo_ellipse_area <- function(x){
  prod(coo_lw(x))*pi
}
bm <- measure(bot, coo_area, coo_perim, coo_ellipse_area)
bm
bm$coe

# how to use arguments, eg with the d() function
measure(wings, coo_area, d(1, 3), d(4, 5))

# alternatively
measure(bot$coo, coo_area, coo_perim, coo_ellipse_area)

# and also
measure(bot[1], coo_area, coo_perim, coo_ellipse_area)
```

---

molars *Data: Outline coordinates of 360 molars*

Description

Courtesy of Julien Corny and Florent Detroit.

Format

A Out object containing 79 equilinearly spaced (x; y) coordinates for 360 crown outlines, of modern human molars, along with their type ($type) - 90 first upper molars (UM1), 90 second upper molars (UM2), 90 first lower molars (LM1), 90 second lower molars (LM2) - and the individual (ind) they come from (the data of the 360 molars are taken from 180 individuals).

Source

Corny, J., & Detroit, F. (2014). Technical Note: Anatomic identification of isolated modern human molars: testing Procrustes aligned outlines as a standardization procedure for elliptic fourier analysis. *American Journal of Physical Anthropology*, 153(2), 314-22. doi:10.1002/ajpa.22428 http://onlinelibrary.wiley.com/doi/10.1002/ajpa.22428/abstract

See Also

Other datasets: bot, chaff, charring, flower, hearts, mosquito, oak, olea, shapes, trilo, wings

---

`Momocs` *Momocs*

Description

A complete toolkit for morphometrics, from data extraction to multivariate analyses. Most common 2D morphometrics approaches are included: outlines, open outlines, configurations of landmarks, traditional morphometrics, and facilities for data preparation, manipulation and visualization with a consistent grammar throughout. Momocs allows reproducible, complex morphometric analyses, paves the way for a pure open-source workflow in R, and other morphometrics approaches should be easy to plug in, or develop from, on top of this canvas.

Details

To cite Momocs in publications: `citation("Momocs")`.

Cheers

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References

- Bonhomme V, Picq S, Gaucherel C, Claude J. 2014. Momocs: Outline Analysis Using R. *Journal of Statistical Software* **56**. http://www.jstatsoft.org/v56/i13.
- Claude J. 2008. *Morphometrics with R*. Springer-Verlag, New-York.

See Also

- **Homepage**: https://github.com/vbonhomme/Momocs
- **Issues**: https://github.com/vbonhomme/Momocs/issues
- **Tutorial**: `browseVignettes("Momocs")`
- **Email**: `bonhomme.vincent@gmail.com` to contribute to dev, ask for something, share your data, etc.

Momocs_help *Browse Momocs online doc*

Description

Launch a browser to an online version of the manual

Usage

```
Momocs_help(topic = NULL)
```

Arguments

topic	the function name to access. If not specified the homepage of the online manual is accessed.

Momocs_lastversion *Install and load the last version of Momocs*

Description

Download the last version of Momocs from its GitHub account from http://www.github.com/vbonhomme/Momocs), install it and load it (library(Momocs)). You need devtools, but it is checked anyway.

Usage

```
Momocs_lastversion()
```

Momocs_version *Get Momocs version*

Description

A simple wrapper around packageVersion("Momocs").

Usage

```
Momocs_version()
```

mosquito *Data: Outline coordinates of mosquito wings.*

Description

Data: Outline coordinates of mosquito wings.

Format

A Out object with the 126 mosquito wing outlines outlines used Rohlf and Archie (1984). Note that the links defined here are quite approximate.

Source

Rohlf F, Archie J. 1984. A comparison of Fourier methods for the description of wing shape in mosquitoes (Diptera: Culicidae). *Systematic Biology*: 302-317. Arranged from: http://life.bio.sunysb.edu/morph/data/RohlfArchieWingOutlines.nts.

See Also

Other datasets: bot, chaff, charring, flower, hearts, molars, oak, olea, shapes, trilo, wings

mshapes *Mean shape calculation for Coo, Coe, etc.*

Description

Quite a versatile function that calculates mean (or median, or whatever function) on list or an array of shapes, an Ldk object. It can also be used on OutCoe and OpnCoe objects. In that case, the reverse transformation (from coefficients to shapes) is calculated, (within groups defined with the fac argument if provided) and the Coe object is returned.

Usage

```
mshapes(x, ...)

## S3 method for class 'list'
mshapes(x, FUN = mean, ...)

## S3 method for class 'array'
mshapes(x, FUN = mean, ...)

## S3 method for class 'Ldk'
mshapes(x, FUN = mean, ...)

## S3 method for class 'OutCoe'
```

```
mshapes(x, fac, FUN = mean, nb.pts = 120, ...)

## S3 method for class 'OpnCoe'
mshapes(x, fac, FUN = mean, nb.pts = 120, ...)

## S3 method for class 'LdkCoe'
mshapes(x, fac, FUN = mean, ...)

## S3 method for class 'PCA'
mshapes(x, fac, ...)

MSHAPES(x, ...)
```

Arguments

x	a list, array, Ldk, LdkCoe, OutCoe or OpnCoe or PCA object
...	useless here.
FUN	a function to compute the mean shape (mean by default, by median can be considered)
fac	factor from the $fac slot (only for Coe objects). See examples below.
nb.pts	numeric the number of points for calculated shapes (only Coe objects)

Details

Note that on Coe objects, the average can be made within levels of the passed $fac (if any); in that case, the other columns of the fac are also returned, usingthe first row within every level, but they may not be representive of the group. Also notice that for PCA objects, mean scores are returned within a PCA object (accesible with PCA$x) that can be plotted directly but other slots are left unchanged.

Value

the averaged shape; on Coe objects, a list with two components: $Coe object of the same class, and $shp a list of matrices of (x, y) coordinates.

Examples

```
#### on shapes
data(wings)
mshapes(wings)
mshapes(wings$coo)
data(bot)
mshapes(coo_sample(bot, 24)$coo)
stack(wings)
coo_draw(mshapes(wings))

data(bot)
bot.f <- efourier(bot, 12)
mshapes(bot.f) # the mean (global) shape
```

```
ms <- mshapes(bot.f, 'type')
ms$Coe
class(ms$Coe)
ms <- ms$shp
coo_plot(ms$beer)
coo_draw(ms$whisky, border='forestgreen')
tps_arr(ms$whisky, ms$beer) #etc.

data(olea)
op <- npoly(filter(olea, view=='VL'), 5)
ms <- mshapes(op, 'var') #etc
ms$Coe
panel(Opn(ms$shp), names=TRUE)

data(wings)
wp <- fgProcrustes(wings, tol=1e-4)
ms <- mshapes(wp, 1)
ms$Coe
panel(Ldk(ms$shp), names=TRUE) #etc.
panel(ms$Coe) # equivalent (except the $fac slot)
```

`mutate` *Mutates (ala dplyr) on Momocs objects*

Description

Add new variables to the `$fac`. See examples and `?dplyr::mutate`.

Usage

```
mutate(.data, ...)
```

Arguments

`.data`	a `Coo`, `Coe`, `PCA` object
`...`	comma separated list of unquoted expressions

Details

dplyr verbs are maintained.

Value

a Momocs object of the same class.

See Also

Other handling functions: `arrange`, `at_least`, `chop`, `combine`, `dissolve`, `filter`, `rename`, `rm_uncomplete`, `rw_rule`, `sample_frac`, `sample_n`, `select`, `slice`, `subset.Coo`, `transmute`

Examples

```
olea
mutate(olea, id=factor(1:length(olea)))
```

`nef2Coe` *Imports .nef to Coe objects*

Description

Useful to convert .nef files into Coe objects. It returns a matrix of coefficients that can be passed to Coe.

Usage

```
nef2Coe(nef.path)
```

Arguments

`nef.path`	the path to the .nef file

Note

I'm not very familiar to other morphometric formats. So if you have troubles importing your datasets, contact me, I can help. Or if you fix something, please let met know!

See Also

Other babel functions: `bind_db`, `chc2Out`, `chc2pix`, `import_StereoMorph_curve1`, `import_jpg`, `import_tps`, `ntsrow2Coo`, `pix2chc`, `tie_jpg_txt`, `tps2coo`

`npoly` *Calculate natural polynomial fits on open outlines*

Description

Calculates natural polynomial coefficients, through a linear model fit (see lm), from a matrix of (x; y) coordinates or an Opn object

Usage

```
npoly(x, ...)

## Default S3 method:
npoly(x, degree, ...)

## S3 method for class 'Opn'
npoly(x, degree, baseline1 = c(-0.5, 0), baseline2 = c(0.5,
  0), nb.pts = 120, ...)
```

Arguments

x	a matrix (or a list) of (x; y) coordinates or an Opn object
...	useless here
degree	polynomial degree for the fit (the Intercept is also returned)
baseline1	numeric the $(x; y)$ coordinates of the first baseline by default $(x = -0.5; y = 0)$
baseline2	numeric the $(x; y)$ coordinates of the second baseline by default $(x = 0.5; y = 0)$
nb.pts	number of points to sample and on which to calculate polynomials

Value

when applied on a single shape, a list with components:

- coeff the coefficients (includint the intercept)
- ortho whether orthogonal or natural polynomials were fitted
- degree degree of the fit (could be retrieved through coeff though)
- baseline1 the first baseline point (so far the first point)
- baseline2 the second baseline point (so far the last point)
- r2 the r2 from the fit
- mod the raw lm model

otherwise, an OpnCoe object.

See Also

Other polynomials: opoly_i, opoly

Examples

```
data(olea)
o <- olea[1]
op <- opoly(o, degree=4)
op
# shape reconstruction
opi <- opoly_i(op)
lines(opi, col='red')
# R2 for degree 1 to 10
r <- numeric()
for (i in 1:10) { r[i] <- npoly(o, degree=i)$r2 }
plot(2:10, r[2:10], type='b', pch=20, col='red', main='R2 / degree')
```

`Ntable` *Plots confusion matrix of sample sizes within $fac*

Description

An utility that plots a confusion matrix of sample size (or a barplot) for every object with a $fac. Useful to visually how large are sample sizes, how (un)balanced are designs, etc.

Usage

```
Ntable(x, fac1, fac2 = fac1, rm0 = FALSE)
```

Arguments

`x`	any object with a $fac slot (Coo, Coe, PCA, etc.)
`fac1`	the name or id of the first factor
`fac2`	the name of id of the second factor
`rm0`	logical whether to print zeros

Value

a ggplot2 object

See Also

Other plotting functions: `conf_ell`, `coo_arrows`, `coo_draw`, `coo_listpanel`, `coo_lolli`, `coo_plot`, `coo_ruban`, `ldk_chull`, `ldk_confell`, `ldk_contour`, `ldk_labels`, `ldk_links`, `plot_devsegments`

Examples

```
data(olea)
Ntable(olea, "var")
Ntable(olea, "domes", "var")
gg <- Ntable(olea, "domes", "var", rm0 = TRUE)
gg
library(ggplot2)
gg + coord_equal()
gg + scale_fill_gradient(low="green", high = "red")
gg + coord_flip()
```

ntsrow2Coo *Imports .nts to Coo objects*

Description

Useful to convert .nts files into Coo objects. For .nts provided as rows, use ntsrow2Coo; for .nts provided as columns of coordinates, try ntscol2Coo. It returns a list of matrices of coordinates that can be passed to Coo (Out, Opn or Ldk).

Usage

```
ntsrow2Coo(nts.path, sep = "\t")
```

Arguments

nts.path	the path to the .nts file
sep	the separator between data

Note

I'm not very familiar to other morphometric formats. So if you have troubles importing your datasets, contact me, I can help. Or if you fix something, please let met know!

See Also

Other babel functions: bind_db, chc2Out, chc2pix, import_StereoMorph_curve1, import_jpg, import_tps, nef2Coe, pix2chc, tie_jpg_txt, tps2coo

Examples

```
# That's how wings dataset was created
# made a local copy from http://life.bio.sunysb.edu/morph/data/RohlfSlice1990Mosq.nts
# then :
# coo_list  <- ntscol2Coo('~/Desktop/mosquitowings.nts)
# fac       <- data.frame(fac=factor(substr(names(coo_list), 1, 2)))
# wings <- Ldk(coo_list, fac=fac)
```

oak *Data: Configuration of landmarks of oak leaves*

Description

From Viscosi and Cardini (2001).

Format

A Ldk object containing 11 (x; y) landmarks from 176 oak leaves wings, from

Source

Viscosi, V., & Cardini, A. (2011). Leaf morphology, taxonomy and geometric morphometrics: a simplified protocol for beginners. PloS One, 6(10), e25630. doi:10.1371/journal.pone.0025630

See Also

Other datasets: bot, chaff, charring, flower, hearts, molars, mosquito, olea, shapes, trilo, wings

---

`olea` *Data: Outline coordinates of olive seeds open outlines.*

Description

Data: Outline coordinates of olive seeds open outlines.

Format

An Opn object with the outline coordinates of olive seeds.

Source

We thank Jean-Frederic Terral and Sarah Ivorra (UMR CBAE, Montpellier, France) from allowing us to share the data.

You can have a look to the original paper: Terral J-F, Alonso N, Capdevila RB i, Chatti N, Fabre L, Fiorentino G, Marinval P, Jorda GP, Pradat B, Rovira N, et al. 2004. Historical biogeography of olive domestication (*Olea europaea* L.) as revealed by geometrical morphometry applied to biological and archaeological material. *Journal of Biogeography* **31**: 63-77.

See Also

Other datasets: bot, chaff, charring, flower, hearts, molars, mosquito, oak, shapes, trilo, wings

---

`Opn` *Builds an Opn object*

Description

In Momocs, `Opn` classes objects are lists of **open** outlines, with optionnal components, on which generic methods such as plotting methods (e.g. stack) and specific methods (e.g. npoly can be applied. `Opn` objects are primarily `Coo` objects.

Usage

```
Opn(x, fac = data.frame(), ldk = list())
```

Arguments

x	list of matrices of (x; y) coordinates
fac	(optionnal) a data.frame of factors and/or numerics specifying the grouping structure
ldk	(optionnal) list of landmarks as row number indices

Value

an Opn object

See Also

Other Coo objects: Coo, Out

Examples

```
#Methods on Opn
methods(class=Opn)
# we load some open outlines. See ?olea for credits
data(olea)
olea
panel(olea)
# orthogonal polynomials
op <- opoly(olea, degree=5)
# we print the Coe
op
# Let's do a PCA on it
op.p <- PCA(op)
plot(op.p, 'domes')
plot(op.p, 'var')
# and now an LDA after a PCA
olda <- LDA(PCA(op), 'var')
# for CV table
olda
plot(olda)
```

OpnCoe *Builds an OpnCoe object*

Description

In Momocs, OpnCoe classes objects are wrapping around lists of morphometric coefficients, along with other informations, on which generic methods such as plotting methods (e.g. boxplot) and specific methods can be applied. OpnCoe objects are primarily Coe objects.

Usage

```
OpnCoe(coe = matrix(), fac = data.frame(), method = character(),
  baseline1 = numeric(), baseline2 = numeric(), mod = list(),
  r2 = numeric())
```

Arguments

coe	matrix of morphometric coefficients
fac	(optionnal) a data.frame of factors, specifying the grouping structure
method	used to obtain these coefficients
baseline1	$(x; y)$ coordinates of the first baseline point
baseline2	$(x; y)$ coordinates of the second baseline point
mod	an R lm object, used to reconstruct shapes
r2	numeric, the r-squared from every model

Value

an OpnCoe object

See Also

Other Coe objects: Coe, OutCoe

Examples

```
# all OpnCoe classes
methods(class='OpnCoe')
```

---

opoly *Calculate orthogonal polynomial fits on open outlines*

Description

Calculates orthogonal polynomial coefficients, through a linear model fit (see lm), from a matrix of (x; y) coordinates or a Opn object

Usage

```
opoly(x, ...)

## Default S3 method:
opoly(x, degree, ...)

## S3 method for class 'Opn'
opoly(x, degree, baseline1 = c(-0.5, 0), baseline2 = c(0.5,
  0), nb.pts = 120, ...)
```

Arguments

x	a matrix (or a list) of (x; y) coordinates
...	useless here
degree	polynomial degree for the fit (the Intercept is also returned)
baseline1	numeric the $(x; y)$ coordinates of the first baseline by default $(x = -0.5; y = 0)$
baseline2	numeric the $(x; y)$ coordinates of the second baseline by default $(x = 0.5; y = 0)$
nb.pts	number of points to sample and on which to calculate polynomials

Value

a list with components when applied on a single shape:

- coeff the coefficients (including the intercept)
- ortho whether orthogonal or natural polynomials were fitted
- degree degree of the fit (could be retrieved through coeff though)
- baseline1 the first baseline point (so far the first point)
- baseline2 the second baseline point (so far the last point)
- r2 the r2 from the fit
- mod the raw lm model

otherwise an OpnCoe object.

Note

Orthogonal polynomials are sometimes called Legendre's polynomials. They are preferred over natural polynomials since adding a degree do not change lower orders coefficients.

See Also

Other polynomials: npoly, opoly_i

Examples

```
data(olea)
o <- olea[1]
op <- opoly(o, degree=4)
op
# shape reconstruction
opi <- opoly_i(op)
lines(opi, col='red')
# R2 for degree 1 to 10
r <- numeric()
for (i in 1:10) { r[i] <- opoly(o, degree=i)$r2 }
plot(2:10, r[2:10], type='b', pch=20, col='red', main='R2 / degree')
```

opoly_i *Calculates shape from a polynomial model*

Description

Returns a matrix of (x; y) coordinates when passed with a list obtained with opoly or npoly.

Usage

```
opoly_i(pol, nb.pts = 120, reregister = TRUE)

npoly_i(pol, nb.pts = 120, reregister = TRUE)
```

Arguments

pol	a pol list such as created by npoly or opoly
nb.pts	the number of points to predict. By default (and cannot be higher) the number of points in the original shape.
reregister	logical whether to reregister the shape with the original baseline.

Value

a matrix of (x; y) coordinates.

See Also

Other polynomials: npoly, opoly

Examples

```
data(olea)
o <- olea[5]
coo_plot(o)
for (i in 2:7){
x <- opoly_i(opoly(o, i))
coo_draw(x, border=col_summer(7)[i], points=FALSE)  }
```

Out *Builds an Out object*

Description

In Momocs, Out-classes objects are lists of closed **out**lines, with optionnal components, and on which generic methods such as plotting methods (e.g. stack) and specific methods (e.g. efourier can be applied. Out objects are primarily Coo objects.

Usage

```
Out(x, fac = data.frame, ldk = list())
```

Arguments

x	a list of matrices of $(x; y)$ coordinates, or an array or an Out object or an Ldk object
fac	(optionnal) a data.frame of factors and/or numerics specifying the grouping structure
ldk	(optionnal) list of landmarks as row number indices

Value

an Out object

See Also

Other Coo objects: Coo, Opn

Examples

```
methods(class=Out)
```

OutCoe *Builds an OutCoe object*

Description

In Momocs, OutCoe classes objects are wrapping around lists of morphometric coefficients, along with other informations, on which generic methods such as plotting methods (e.g. boxplot) and specific methods can be applied. OutCoe objects are primarily Coe objects.

Usage

```
OutCoe(coe = matrix(), fac = data.frame(), method, norm)
```

Arguments

coe	matrix of harmonic coefficients
fac	(optionnal) a data.frame of factors, specifying the grouping structure
method	used to obtain these coefficients
norm	the normalisation used to obtain these coefficients

Details

These methods can be applied on Out objects:

Value

an OutCoe object

See Also

Other Coe objects: Coe, OpnCoe

Examples

```
# all OutCoe methods
methods(class='OutCoe')
```

---

panel *Family picture of shapes*

Description

Plots all the outlines, side by side, from a Coo (Out, Opn or Ldk) objects.

Usage

```
panel(x, ...)

## S3 method for class 'Out'
panel(x, dim, cols, borders, fac, palette = col_summer,
  coo_sample = 120, names = NULL, cex.names = 0.6, points = TRUE,
  points.pch = 3, points.cex = 0.2, points.col, ...)

## S3 method for class 'OutCoe'
panel(x, nb.pts = 120, ...)

## S3 method for class 'Opn'
panel(x, cols, borders, fac, palette = col_summer,
  coo_sample = 120, names = NULL, cex.names = 0.6, points = TRUE,
  points.pch = 3, points.cex = 0.2, points.col, ...)
```

```
## S3 method for class 'Ldk'
panel(x, cols, borders, fac, palette = col_summer,
  names = NULL, cex.names = 0.6, points = TRUE, points.pch = 3,
  points.cex = 0.2, points.col = "#333333", ...)
```

Arguments

x	The Coo object to plot.
...	further arguments to maintain consistency with the generic plot.
dim	for coo_listpanel: a numeric of length 2 specifying the dimensions of the panel
cols	A vector of colors for drawing the outlines. Either a single value or of length exactly equal to the number of coordinates.
borders	A vector of colors for drawing the borders. Either a single value or of length exactly equals to the number of coordinates.
fac	a factor within the $fac slot for colors
palette	a color palette
coo_sample	if not NULL the number of point per shape to display (to plot quickly)
names	whether to plot names or not. If TRUE uses shape names, a column name or number from $fac can be supllied, or even a character of the same length of the Coo
cex.names	a cex for the names
points	logical (for Ldk) whether to draw points
points.pch	(for Ldk) and a pch for these points
points.cex	(for Ldk) and a cex for these points
points.col	(for Ldk) and a col for these points
nb.pts	the number of points to use for the shape reconstruction

Note

If you want to reorder shapes according to a factor, use arrange.

See Also

Other Coo_graphics: panel2, plot.Coo, stack.Coo

Examples

```
data(mosquito)
panel(mosquito, names=TRUE, cex.names=0.5)
data(olea)
panel(olea)
data(bot)
panel(bot, c(4, 10))
bot.f <- efourier(bot, 12)
panel(bot.f)
# an illustration of the use of fac
panel(bot, fac='type', palette=col_spring, names=TRUE)
```

panel2 *Family picture of shapes (ggplot2)*

Description

May replace panel one day.

Usage

```
panel2(Coo)
```

Arguments

Coo	a Coo object

Value

a ggplot2 object

See Also

Other Coo_graphics: panel, plot.Coo, stack.Coo

Examples

```
data(shapes)
panel2(shapes)
```

PCA *Principal component analysis on Coe objects*

Description

Performs a PCA on Coe objects, using prcomp.

Usage

```
PCA(x, scale., center, fac)

## S3 method for class 'OutCoe'
PCA(x, scale. = FALSE, center = TRUE, fac)

## S3 method for class 'OpnCoe'
PCA(x, scale. = FALSE, center = TRUE, fac)

## S3 method for class 'LdkCoe'
```

```
PCA(x, scale. = FALSE, center = TRUE, fac)

## S3 method for class 'TraCoe'
PCA(x, scale. = TRUE, center = TRUE, fac)

## Default S3 method:
PCA(x, scale. = TRUE, center = TRUE, fac = data.frame())

as.PCA(x, fac)
```

Arguments

x	a Coe object or an appropriate object (eg prcomp) for as.PCA
scale.	logical whether to scale the input data
center	logical whether to center the input data
fac	any factor or data.frame to be passed to as.PCA and for use with plot.PCA

Details

By default, methods on Coe object do not scale the input data but center them. There is also a generic method (eg for traditional morphometrics) that centers and scales data.

Value

a 'PCA' object on which to apply plot.PCA

See Also

Other multivariate: CLUST, KMEANS, LDA, MANOVA_PW, MANOVA

Examples

```
data(bot)
bot.f <- efourier(bot, 12)
bot.p <- PCA(bot.f)
bot.p
plot(bot.p, morpho=FALSE)
plot(bot.p, 'type')

data(olea)
op <- npoly(olea, 5)
op.p <- PCA(op)
op.p
plot(op.p, 1, morpho=TRUE)

data(wings)
wp <- fgProcrustes(wings, tol=1e-4)
wpp <- PCA(wp)
wpp
plot(wpp, 1)
```

```
# "foreign prcomp"
head(iris)
iris.p <- prcomp(iris[, 1:4])
iris.p <- as.PCA(iris.p, iris[, 5])
class(iris.p)
plot(iris.p, 1)
```

PCcontrib *Shape variation along PC axes*

Description

Calculates and plots shape variation along Principal Component axes.

Usage

```
PCcontrib(PCA, ...)

## S3 method for class 'PCA'
PCcontrib(PCA, nax = 1:4, sd.r = c(-2, -1, -0.5, 0, 0.5, 1,
  2), gap = 1, ...)
```

Arguments

PCA	a PCA object
...	additional parameter to pass to coo_draw
nax	a single or a range of PC axes
sd.r	a single or a range of mean +/- sd values (eg: c(-1, 0, 1))
gap	for combined-Coe, an adjustment variable for gap between shapes. (bug)Default to 1 (whish should never superimpose shapes), reduce it to get a more compact plot.

Value

a ggplot object

Examples

```
data(bot)
bot.p <- PCA(efourier(bot, 12))
PCcontrib(bot.p)
## Not run:
library(ggplot2)
gg <- PCcontrib(bot.p, nax=1:8, sd.r=c(-5, -3, -2, -1, -0.5, 0, 0.5, 1, 2, 3, 5))
gg + geom_polygon(fill="slategrey", col="black") + ggtitle("A nice title")

## End(Not run)
```

perm *Permutes and breed Coe (and others) objects*

Description

This methods applies permutations column-wise on the coe of any Coe object but relies on a function that can be used on any matrix. For a Coe object, it uses sample on every column (or row) with (or without) replacement.

Usage

```
perm(x, ...)

## Default S3 method:
perm(x, margin = 2, size, replace = TRUE, ...)

## S3 method for class 'Coe'
perm(x, size, replace = TRUE, ...)
```

Arguments

x	the object to permute
...	useless here
margin	numeric whether 1 or 2 (rows or columns)
size	numeric the required size for the final object, same size by default.
replace	logical, whether to use sample with replacement

See Also

Other farming: breed

Examples

```
m <- matrix(1:12, nrow=3)
m
perm(m, margin=2, size=5)
perm(m, margin=1, size=10)

data(bot)
bot.f <- efourier(bot, 12)
bot.m <- perm(bot.f, 80)
bot.m
panel(bot.m)
```

pix2chc *Converts (x; y) coordinates to chaincoded coordinates*

Description

Useful to convert (x; y) coordinates to chain-coded coordinates.

Usage

```
pix2chc(coo)
```

Arguments

coo	(x; y) coordinates passed as a matrix

References

Kuhl, F. P., & Giardina, C. R. (1982). Elliptic Fourier features of a closed contour. *Computer Graphics and Image Processing*, 18(3), 236-258.

See Also

chc2pix

Other babel functions: bind_db, chc2Out, chc2pix, import_StereoMorph_curve1, import_jpg, import_tps, nef2Coe, ntsrow2Coo, tie_jpg_txt, tps2coo

Examples

```
data(shapes)
pix2chc(shapes[1])
```

plot.Coo *Graphical inspection of shapes*

Description

Allows to plot shapes, individually, for Coo (Out, Opn or Ldk) objects.

Usage

```
## S3 method for class 'Coo'
plot(x, id, ...)
```

Arguments

x	the Coo object
id	the id of the shape to plot, if not provided a random shape is plotted. If passed with 'all' all shapes are plotted, one by one.
...	further arguments to be passed to coo_plot

See Also

Other Coo_graphics: panel2, panel, stack.Coo

Examples

```
## Not run:
data(bot)
plot(bot, 5)
plot(bot)
plot(bot, 5, pch=3, points=TRUE) # an example of '...' use

## End(Not run)
```

---

plot.LDA *Plots Linear Discriminant Analysis*

Description

The Momocs' LDA plotter with many graphical options.

Usage

```
## S3 method for class 'LDA'
plot(x, fac = x$fac, xax = 1, yax = 2, points = TRUE,
  col = "#000000", pch = 20, cex = 0.5, palette = col_solarized,
  center.origin = FALSE, zoom = 1, bg = par("bg"), grid = TRUE,
  nb.grids = 3, morphospace = FALSE, pos.shp = c("range", "full",
  "circle", "xy", "range_axes", "full_axes")[1], amp.shp = 1, size.shp = 1,
  nb.shp = 12, nr.shp = 6, nc.shp = 5, rotate.shp = 0,
  flipx.shp = FALSE, flipy.shp = FALSE, pts.shp = 60,
  border.shp = col_alpha("#000000", 0.5), lwd.shp = 1,
  col.shp = col_alpha("#000000", 0.95), stars = FALSE, ellipses = FALSE,
  conf.ellipses = 0.5, ellipsesax = TRUE, conf.ellipsesax = c(0.5, 0.9),
  lty.ellipsesax = 1, lwd.ellipsesax = sqrt(2), chull = FALSE,
  chull.lty = 1, chull.filled = FALSE, chull.filled.alpha = 0.92,
  density = FALSE, lev.density = 20, contour = FALSE, lev.contour = 3,
  n.kde2d = 100, delaunay = FALSE, loadings = FALSE,
  labelspoints = FALSE, col.labelspoints = par("fg"),
  cex.labelspoints = 0.6, abbreviate.labelspoints = TRUE,
  labelsgroups = TRUE, cex.labelsgroups = 0.8, rect.labelsgroups = FALSE,
```

```
abbreviate.labelsgroups = FALSE, color.legend = FALSE, axisnames = TRUE,
axisvar = TRUE, eigen = TRUE, rug = TRUE, title = substitute(x),
box = TRUE, old.par = TRUE, ...)
```

Arguments

x	an object of class "LDA", typically obtained with LDA
fac	name or the column id from the $fac slot, or a formula combining colum names from the $fac slot (cf. examples). A factor or a numeric of the same length can also be passed on the fly.
xax	the first PC axis
yax	the second PC axis
points	logical whether to plot points
col	a color for the points (either global, for every level of the fac or for every individual, see examples)
pch	a pch for the points (either global, for every level of the fac or for every individual, see examples)
cex	the size of the points
palette	a palette
center.origin	logical whether to center the plot onto the origin
zoom	to keep your distances
bg	color for the background
grid	logical whether to draw a grid
nb.grids	and how many of them
morphospace	logical whether to add the morphological space
pos.shp	passed to pos.shapes, one of "range", "full", "circle", "xy", "range_axes", "full_axes". Or directly a matrix of positions. See pos.shapes
amp.shp	amplification factor for shape deformation
size.shp	the size of the shapes
nb.shp	(pos.shp="circle") the number of shapes on the compass
nr.shp	(pos.shp="full" or "range) the number of shapes per row
nc.shp	(pos.shp="full" or "range) the number of shapes per column
rotate.shp	angle in radians to rotate shapes (if several methods, a vector of angles)
flipx.shp	same as above, whether to apply coo_flipx
flipy.shp	same as above, whether to apply coo_flipy
pts.shp	the number of points fro drawing shapes
border.shp	the border color of the shapes
lwd.shp	the line width for these shapes
col.shp	the color of the shapes
stars	logical whether to draw "stars"

ellipses	logical whether to draw confidence ellipses
conf.ellipses	numeric the quantile for the (bivariate gaussian) confidence ellipses
ellipsesax	logical whether to draw ellipse axes
conf.ellipsesax	one or more numeric, the quantiles for the (bivariate gaussian) ellipses axes
lty.ellipsesax	if yes, the lty with which to draw these axes
lwd.ellipsesax	if yes, one or more numeric for the line widths
chull	logical whether to draw a convex hull
chull.lty	if yes, its linetype
chull.filled	logical whether to add filled convex hulls
chull.filled.alpha	numeric alpha transparency
density	whether to add a 2d density kernel estimation (based on kde2d)
lev.density	if yes, the number of levels to plot (through image)
contour	whether to add contour lines based on 2d density kernel
lev.contour	if yes, the (approximate) number of lines to draw
n.kde2d	the number of bins for kde2d, ie the 'smoothness' of density kernel
delaunay	logical whether to add a delaunay 'mesh' between points
loadings	logical whether to add loadings for every variables
labelspoints	if TRUE rownames are used as labels, a colname from $fac can also be passed
col.labelspoints	a color for these labels, otherwise inherited from fac
cex.labelspoints	a cex for these labels
abbreviate.labelspoints	logical whether to abbreviate
labelsgroups	logical whether to add labels for groups
cex.labelsgroups	ifyes, a numeric for the size of the labels
rect.labelsgroups	logical whether to add a rectangle behind groups names
abbreviate.labelsgroups	logical, whether to abbreviate group names
color.legend	logical whether to add a (cheap) color legend for numeric fac
axisnames	logical whether to add PC names
axisvar	logical whether to draw the variance they explain
eigen	logical whether to draw a plot of the eigen values
rug	logical whether to add rug to margins
title	character a name for the plot
box	whether to draw a box around the plotting region
old.par	whether to restore the old par. Set it to FALSE if you want to reuse the graphical window.
...	useless here, just to fit the generic plot

Details

Widely inspired by the "layers" philosophy behind graphical functions of the ade4 R package.

Note

Morphospaces are deprecated so far. 99 is shared with plot.PCA waiting for a general rewriting of a multivariate plotter. See https://github.com/vbonhomme/Momocs/issues/121

See Also

LDA, plot_CV, plot_CV2, plot.PCA.

Examples

```
data(bot)
bot.f <- efourier(bot, 24)
bot.l <- LDA(PCA(bot.f), "type")
plot(bot.l)

bot.f$fac$fake <- factor(rep(letters[1:4], each=10))
bot.l <- LDA(PCA(bot.f), "fake")
plot(bot.l)
```

---

plot.PCA *Plots Principal Component Analysis*

Description

The Momocs' PCA plotter with morphospaces and many graphical options.

Usage

```
## S3 method for class 'PCA'
plot(x, fac, xax = 1, yax = 2, points = TRUE,
  col = "#000000", pch = 20, cex = 0.5, palette = col_solarized,
  center.origin = FALSE, zoom = 1, bg = par("bg"), grid = TRUE,
  nb.grids = 3, morphospace = TRUE, pos.shp = c("range", "full", "circle",
  "xy", "range_axes", "full_axes")[1], amp.shp = 1, size.shp = 1,
  nb.shp = 12, nr.shp = 6, nc.shp = 5, rotate.shp = 0,
  flipx.shp = FALSE, flipy.shp = FALSE, pts.shp = 60,
  border.shp = col_alpha("#000000", 0.5), lwd.shp = 1,
  col.shp = col_alpha("#000000", 0.95), stars = FALSE, ellipses = FALSE,
  conf.ellipses = 0.5, ellipsesax = TRUE, conf.ellipsesax = c(0.5, 0.9),
  lty.ellipsesax = 1, lwd.ellipsesax = sqrt(2), chull = FALSE,
  chull.lty = 1, chull.filled = FALSE, chull.filled.alpha = 0.92,
  density = FALSE, lev.density = 20, contour = FALSE, lev.contour = 3,
  n.kde2d = 100, delaunay = FALSE, loadings = FALSE,
  labelspoints = FALSE, col.labelspoints = par("fg"),
```

```
cex.labelspoints = 0.6, abbreviate.labelspoints = TRUE,
labelsgroups = TRUE, cex.labelsgroups = 0.8, rect.labelsgroups = FALSE,
abbreviate.labelsgroups = FALSE, color.legend = FALSE, axisnames = TRUE,
axisvar = TRUE, eigen = TRUE, rug = TRUE, title = substitute(x),
box = TRUE, old.par = TRUE, ...)
```

Arguments

x	an object of class "PCA", typically obtained with PCA
fac	name or the column id from the $fac slot, or a formula combining colum names from the $fac slot (cf. examples). A factor or a numeric of the same length can also be passed on the fly.
xax	the first PC axis
yax	the second PC axis
points	logical whether to plot points
col	a color for the points (either global, for every level of the fac or for every individual, see examples)
pch	a pch for the points (either global, for every level of the fac or for every individual, see examples)
cex	the size of the points
palette	a palette
center.origin	logical whether to center the plot onto the origin
zoom	to keep your distances
bg	color for the background
grid	logical whether to draw a grid
nb.grids	and how many of them
morphospace	logical whether to add the morphological space
pos.shp	passed to pos.shapes, one of "range", "full", "circle", "xy", "range_axes", "full_axes". Or directly a matrix of positions. See pos.shapes
amp.shp	amplification factor for shape deformation
size.shp	the size of the shapes
nb.shp	(pos.shp="circle") the number of shapes on the compass
nr.shp	(pos.shp="full" or "range) the number of shapes per row
nc.shp	(pos.shp="full" or "range) the number of shapes per column
rotate.shp	angle in radians to rotate shapes (if several methods, a vector of angles)
flipx.shp	same as above, whether to apply coo_flipx
flipy.shp	same as above, whether to apply coo_flipy
pts.shp	the number of points fro drawing shapes
border.shp	the border color of the shapes
lwd.shp	the line width for these shapes

`col.shp` the color of the shapes

`stars` logical whether to draw "stars"

`ellipses` logical whether to draw confidence ellipses

`conf.ellipses` numeric the quantile for the (bivariate gaussian) confidence ellipses

`ellipsesax` logical whether to draw ellipse axes

`conf.ellipsesax` one or more numeric, the quantiles for the (bivariate gaussian) ellipses axes

`lty.ellipsesax` if yes, the lty with which to draw these axes

`lwd.ellipsesax` if yes, one or more numeric for the line widths

`chull` logical whether to draw a convex hull

`chull.lty` if yes, its linetype

`chull.filled` logical whether to add filled convex hulls

`chull.filled.alpha` numeric alpha transparency

`density` whether to add a 2d density kernel estimation (based on kde2d)

`lev.density` if yes, the number of levels to plot (through image)

`contour` whether to add contour lines based on 2d density kernel

`lev.contour` if yes, the (approximate) number of lines to draw

`n.kde2d` the number of bins for kde2d, ie the 'smoothness' of density kernel

`delaunay` logical whether to add a delaunay 'mesh' between points

`loadings` logical whether to add loadings for every variables

`labelspoints` if TRUE rownames are used as labels, a colname from $fac can also be passed

`col.labelspoints` a color for these labels, otherwise inherited from fac

`cex.labelspoints` a cex for these labels

`abbreviate.labelspoints` logical whether to abbreviate

`labelsgroups` logical whether to add labels for groups

`cex.labelsgroups` ifyes, a numeric for the size of the labels

`rect.labelsgroups` logical whether to add a rectangle behind groups names

`abbreviate.labelsgroups` logical, whether to abbreviate group names

`color.legend` logical whether to add a (cheap) color legend for numeric fac

`axisnames` logical whether to add PC names

`axisvar` logical whether to draw the variance they explain

`eigen` logical whether to draw a plot of the eigen values

`rug` logical whether to add rug to margins

title	character a name for the plot
box	whether to draw a box around the plotting region
old.par	whether to restore the old par. Set it to FALSE if you want to reuse the graphical window.
...	useless here, just to fit the generic plot

Details

Widely inspired by the "layers" philosophy behind graphical functions of the ade4 R package.

See Also

plot.LDA

Examples

```
## Not run:
data(bot)
bot.f <- efourier(bot, 12)
bot.p <- PCA(bot.f)

### Morphospace options
plot(bot.p, pos.shp="full")
plot(bot.p, pos.shp="range")
plot(bot.p, pos.shp="xy")
plot(bot.p, pos.shp="circle")
plot(bot.p, pos.shp="range_axes")
plot(bot.p, pos.shp="full_axes")

plot(bot.p, morpho=FALSE)

### Passing factors to plot.PCA
# 3 equivalent methods
plot(bot.p, "type")
plot(bot.p, 1)
plot(bot.p, ~type)

# let's create a dummy factor of the correct length
# and another added to the $fac with mutate
# and a numeric of the correct length
data(bot)
f <- factor(rep(letters[1:2], 20))
z <- factor(rep(LETTERS[1:2], 20))
bot %<>% mutate(cs=coo_centsize(.), z=z)
bp <- bot %>% efourier %>% PCA
# so bp contains type, cs (numeric) and z; not f
# yet f can be passed on the fly
plot(bp, f)
# numeric fac are allowed
plot(bp, "cs", cex=3, color.legend=TRUE)
# numeric can also be passed on the fly
```

```
plot(bp, 1:40, cex=2)
# formula allows combinations of factors
plot(bp, ~type+z)

### other morphometric approaches works the same
# open curves
data(olea)
op <- npoly(olea, 5)
op.p <- PCA(op)
op.p
plot(op.p, ~ domes + var, morpho=TRUE) # use of formula

# landmarks
data(wings)
wp <- fgProcrustes(wings, tol=1e-4)
wpp <- PCA(wp)
wpp
plot(wpp, 1)

# traditionnal measurements
data(flower)
flower %>% PCA %>% plot(1)

# plot.PCA can be used after a PCA
data(iris)
PCA(iris[, 1:4], fac=iris$Species)  %>% plot(1)

### Cosmetic options
# window
plot(bp, 1, zoom=2)
plot(bp, zoom=0.5)
plot(bp, center.origin=FALSE, grid=FALSE)

# ellipses
plot(bp, 1, conf.ellipsesax=2/3)
plot(bp, 1, ellipsesax=FALSE)
plot(bp, 1, ellipsesax=TRUE, ellipses=TRUE)

# stars
plot(bp, 1, stars=TRUE, ellipsesax=FALSE)

# convex hulls
plot(bp, 1, chull=TRUE)
plot(bp, 1, chull.lty=3)

# filled convex hulls
plot(bp, 1, chull.filled=TRUE)
plot(bp, 1, chull.filled.alpha = 0.8, chull.lty =1) # you can omit chull.filled=TRUE

# density kernel
plot(bp, 1, density=TRUE, contour=TRUE, lev.contour=10)

# delaunay
```

```
plot(bp, 1, delaunay=TRUE)

# loadings
flower %>% PCA %>% plot(1, loadings=TRUE)

# point/group labelling
plot(bp, 1, labelspoint=TRUE) # see options for abbreviations
plot(bp, 1, labelsgroup=TRUE) # see options for abbreviations

# clean axes, no rug, no border, random title
plot(bp, axisvar=FALSE, axisnames=FALSE, rug=FALSE, box=FALSE, title="random")

# no eigen
plot(bp, eigen=FALSE) # eigen cause troubles to graphical window
# eigen may causes troubles to the graphical window. you can try old.par = TRUE

## End(Not run)
```

`plot2` *Plots Principal Component Analysis ala ggplot2*

Description

Displays a PCA object with many useful layers in morphometrics, notably morphological space.

Usage

```
plot2(x, ...)

## S3 method for class 'PCA'
plot2(x, fac = NULL, xax = "PC1", yax = "PC2",
  points = TRUE, shapes = TRUE, shapes_pos = "full", ellipse = FALSE,
  ellipseax = FALSE, ellipse_type = "t", ellipse_level = 0.5,
  stars = FALSE, chull = FALSE, text, text_abbreviatemin = 1,
  text_size = 5, center = TRUE, legend_position = "bottom",
  title = substitute(x), return_df = FALSE, ...)
```

Arguments

`x`	a PCA object
`...`	more arguments to be passed to xxx.
`fac`	(optionnal)
`xax`	the name of the component to plot on the x-axis, eg "PC1"
`yax`	the name of the component to plot on the y-axis, eg "PC2"
`points`	logical whether to draw points
`shapes`	logical whether to draw shapes

shapes_pos	a position parameter xxx either "axes", "full", "range", "circle", "xy" or a custom data.frame of positions
ellipse	logical whether to draw confidence ellipses
ellipseax	logical whether to draw confidence ellipses axes
ellipse_type	character one of the available type in ggplot2::stat_ellipse
ellipse_level	numeric the confidence level for ellipses
stars	logical whether to draw segments between every point and their group centroid
chull	logical whether to draw convex hull
text	numeric : 1 is for labelling every shape, 2 for group centroids, 3 is for evry shape using group names
text_abbreviatemin	numeric if not missing, the min.length sensu abbreviate
text_size	numeric to adjust the size of labels
center	logical whether to center the plot
legend_position	character for theme(legend.position), either "none", "top", "bottom", "left", "right"
title	character a title for the plot
return_df	logical whether to return ggplot or the data_frames behind

Details

Detail the df_s. Detail the calculations.

Value

a ggplot object or a list of data.frames :

- df0
- df_shp
- df_ellipseax
- df_stars
- df_chull

Examples

```
data(bot)
bp <- PCA(efourier(bot, 8))
plot2(bp)
plot2(bp, "type")
plot2(bp, "type", ellipse=TRUE)
# data(bot)

# bot$fac$fake <- factor(rep(letters[1:4], 10))
# bot$fac$fake2 <- c(runif(20), runif(20, 5, 10))
# xx + stat_density2d(aes(fill = ..level..), geom="polygon", alpha=0.1)
```

plot3 *#' @describeIn plot.PCA #' @export mplot <- plot.PCA Plots a combination of the three first PCs*

Description

Creates a 2 x 3 layout with, from top to bottom and form left to right: PC1-PC2, PC1-PC3, PC2-3, and the barplot of eigenvalues percentages.

Usage

```
plot3(PCA, ...)

## S3 method for class 'PCA'
plot3(PCA, ...)
```

Arguments

PCA	a PCA object
...	additional arguments to fed plot.PCA

Examples

```
data(bot)
bot.f <- efourier(bot, 12)
bot.p <- PCA(bot.f)
plot3(bot.p) # no groups
plot3(bot.p, 1) # groups
plot3(bot.p, "type", pos.shp="circle") # all plot.PCA args should work
```

plot_CV *Plots a cross-validation table as an heatmap*

Description

Either with frequencies (or percentages) plus marginal sums, and values as heatmaps. Used in Momocs for plotting cross-validation tables but may be used for any table (likely with freq=FALSE).

Usage

```
plot_CV(x, ...)

## Default S3 method:
plot_CV(x, freq = TRUE, rm0 = TRUE, cex = 5,
  round = 2, labels = TRUE, ...)
```

```
## S3 method for class 'LDA'
plot_CV(x, freq = TRUE, rm0 = TRUE, cex = 5, round = 2,
  labels = TRUE, ...)
```

Arguments

x	a (cross-validation table) or an LDA object
...	only used for the generic
freq	logical whether to display frequencies or counts
rm0	logical whether to remove zeros
cex	numeric to adjust labels in every cell. NA to remove them
round	numeric, when freq=TRUE how many decimals should we display
labels	logical whether to display freq or counts as text labels

Value

a ggplot object

See Also

LDA, plot.LDA, and (pretty much the same) Ntable.

Examples

```
data(olea)
ol <- LDA(PCA(opoly(olea, 5)), "domes")
gg <- plot_CV(ol) # just a wrapper for plot_CV(ol$CV.tab) though
gg
```

---

plot_CV2 *Plots a cross-correlation table*

Description

Or any contingency/confusion table. A simple graphic representation based on variable width and/or color for arrows or segments, based on the relative frequencies.

Usage

```
plot_CV2(x, ...)

## S3 method for class 'LDA'
plot_CV2(x, ...)

## S3 method for class 'table'
plot_CV2(x, links.FUN = arrows, col = TRUE,
  col0 = "black", col.breaks = 5, palette = col_heat, lwd = TRUE,
  lwd0 = 5, gap.dots = 0.2, pch.dots = 20, gap.names = 0.25,
  cex.names = 1, legend = TRUE, ...)
```

Arguments

x	an LDA object, a table or a squared matrix
...	useless here.
links.FUN	a function to draw the links: eg segments (by default), arrows, etc.
col	logical whether to vary the color of the links
col0	a color for the default link (when col = FALSE)
col.breaks	the number of different colors
palette	a color palette, eg col_summer, col_hot, etc.
lwd	logical whether to vary the width of the links
lwd0	a width for the default link (when lwd = FALSE)
gap.dots	numeric to set space between the dots and the links
pch.dots	a pch for the dots
gap.names	numeric to set the space between the dots and the group names
cex.names	a cex for the names
legend	logical whether to add a legend

See Also

LDA, plot.LDA, plot_CV.

Examples

```
# Below various table that you can try. We will use the last one for the examples.
## Not run:
#pure random
a <- sample(rep(letters[1:4], each=10))
b <- sample(rep(letters[1:4], each=10))
tab <- table(a, b)

# veryhuge + some structure
a <- sample(rep(letters[1:10], each=10))
b <- sample(rep(letters[1:10], each=10))
tab <- table(a, b)
diag(tab) <- round(runif(10, 10, 20))

tab <- matrix(c(8, 3, 1, 0, 0,
                2, 7, 1, 2, 3,
                3, 5, 9, 1, 1,
                1, 1, 2, 7, 1,
                0, 9, 1, 4, 5), 5, 5, byrow=TRUE)
tab <- as.table(tab)

## End(Not run)
# good prediction
tab <- matrix(c(8, 1, 1, 0, 0,
               1, 7, 1, 0, 0,
```

```
                1, 2, 9, 1, 0,
                1, 1, 1, 7, 1,
                0, 0, 0, 1, 8), 5, 5, byrow=TRUE)
tab <- as.table(tab)


plot_CV2(tab)
plot_CV2(tab, arrows) # if you prefer arrows
plot_CV2(tab, lwd=FALSE, lwd0=1, palette=col_india) # if you like india but not lwds
plot_CV2(tab, col=FALSE, col0='pink') # only lwd
plot_CV2(tab, col=FALSE, lwd0=10, cex.names=2) # if you're getting old
plot_CV2(tab, col=FALSE, lwd=FALSE) # pretty but useless
plot_CV2(tab, col.breaks=2) # if you think it's either good or bad
plot_CV2(tab, pch=NA) # if you do not like dots
plot_CV2(tab, gap.dots=0) # if you want to 'fill the gap'
plot_CV2(tab, gap.dots=1) # or not

#trilo examples
data(trilo)
trilo.f <- efourier(trilo, 8)
trilo.l <- LDA(PCA(trilo.f), 'onto')
trilo.l
plot_CV2(trilo.l)

# olea example
data(olea)
op <- opoly(olea, 5)
opl <- LDA(PCA(op), 'var')
plot_CV2(opl)
```

`plot_devsegments` *Draws colored segments from a matrix of coordinates.*

Description

Given a matrix of (x; y) coordinates, draws segments between every points defined by the row of the matrix and uses a color to display an information.

Usage

```
plot_devsegments(coo, cols, lwd = 1)
```

Arguments

`coo`	A matrix of coordinates.
`cols`	A vector of color of `length = nrow(coo)`.
`lwd`	The `lwd` to use for drawing segments.

See Also

Other plotting functions: Ntable, conf_ell, coo_arrows, coo_draw, coo_listpanel, coo_lolli, coo_plot, coo_ruban, ldk_chull, ldk_confell, ldk_contour, ldk_labels, ldk_links

Examples

```
# we load some data
data(bot)
guinness <- coo_sample(bot[9], 100)

# we calculate the diff between 48 harm and one with 6 harm.
out.6    <- efourier_i(efourier(guinness, nb.h=6), nb.pts=120)

# we calculate deviations, you can also try 'edm'
dev <- edm_nearest(out.6, guinness) / coo_centsize(out.6)

# we prepare the color scale
d.cut <- cut(dev, breaks=20, labels=FALSE, include.lowest=TRUE)
cols  <- paste0(col_summer(20)[d.cut], 'CC')

# we draw the results
coo_plot(guinness, main='Guiness fitted with 6 harm.', points=FALSE)
par(xpd=NA)
plot_devsegments(out.6, cols=cols, lwd=4)
coo_draw(out.6, lty=2, points=FALSE, col=NA)
par(xpd=FALSE)
```

---

pos.shapes *Calculates nice positions on a plane for drawing shapes*

Description

Calculates nice positions on a plane for drawing shapes

Usage

```
pos.shapes(xy, pos.shp = c("range", "full", "circle", "xy", "range_axes",
  "full_axes")[1], nb.shp = 12, nr.shp = 6, nc.shp = 5, circle.r.shp)
```

Arguments

xy	todo
pos.shp	how shapes should be positionned: `range` of xy, `full` extent of the plane, `circle` as a rosewind, on xy values provided, `range_axes` on the range of xy but on the axes, `full_axes` same thing but on (0.85) range of the axes. You can also directly pass a matrix (or a data.frame) with columns named `("x", "y")`.
nb.shp	the total number of shapes

nr.shp	the number of rows to position shapes
nc.shp	the number of cols to position shapes
circle.r.shp	if circle, its radius

Details

See plot.PCA for self-speaking examples

---

pProcrustes *Partial Procrustes alignment between two shapes*

Description

Directly borrowed from Claude (2008), and called pPsup there.

Usage

```
pProcrustes(coo1, coo2)
```

Arguments

coo1	Configuration matrix to be superimposed onto the centered preshape of coo2.
coo2	Reference configuration matrix.

Value

a list with components

- coo1 superimposed centered preshape of coo1 onto the centered preshape of coo2
- coo2 centered preshape of coo2
- rotation rotation matrix
- DP partial Procrustes distance between coo1 and coo2
- rho trigonometric Procrustes distance.

References

Claude, J. (2008). Morphometrics with R. Analysis (p. 316). Springer.

See Also

Other procrustes functions: fProcrustes, fgProcrustes, fgsProcrustes

`Ptolemy` *Ptolemaic ellipses and illustration of efourier*

Description

Calculate and display Ptolemaic ellipses which illustrates intuitively the principle behing elliptical Fourier analysis.

Usage

```
Ptolemy(coo, t = seq(0, 2 * pi, length = 7)[-1], nb.h = 3, nb.pts = 360,
  palette = col_heat, zoom = 5/4, legend = TRUE, ...)
```

Arguments

`coo`	a matrix of (x; y) coordinates
`t`	A `vector` af angles (in radians) on which to display ellipses
`nb.h`	`integer`. The number of harmonics to display
`nb.pts`	`integer`. The number of points to use to display shapes
`palette`	a color palette
`zoom`	numeric a zoom factor for coo_plot
`legend`	`logical`. Whether to plot the legend box
`...`	additional parameters to feed coo_plot

References

This method has been inspired by the figures found in the followings papers. Kuhl FP, Giardina CR. 1982. Elliptic Fourier features of a closed contour. *Computer Graphics and Image Processing* **18**: 236-258. Crampton JS. 1995. Elliptical Fourier shape analysis of fossil bivalves: some practical considerations. *Lethaia* **28**: 179-186.

See Also

An intuitive explanation of elliptic Fourier analysis can be found in the **Details** section of the efourier function.

exemplifying functions

Examples

```
data(shapes)
cat <- shapes[4]
Ptolemy(cat, main="An EFT cat")
```

`reLDA` *"Redo" a LDA on new data*

Description

Basically a wrapper around predict.lda from the package MASS. Uses a LDA model to classify new data.

Usage

```
reLDA(newdata, LDA)

## Default S3 method:
reLDA(newdata, LDA)

## S3 method for class 'PCA'
reLDA(newdata, LDA)

## S3 method for class 'Coe'
reLDA(newdata, LDA)
```

Arguments

`newdata`	to use, a PCA or any Coe object
`LDA`	a LDA object

Value

a list with components (from ?predict.lda).

- class factor of classification
- posterior posterior probabilities for the classes
- x the scores of test cases
- res data.frame of the results
- CV.tab a confusion matrix of the results
- CV.correct proportion of the diagonal of CV.tab
- newdata the data used to calculate passed to predict.lda

Note

Uses the same number of PC axis as the LDA object provided. You should probably use rePCA in conjonction with reLDA to get 'homologous' scores.

Examples

```
data(bot)
# We select the first 10 individuals in bot,
# for whisky and beer bottles. It will be our referential.
bot1   <- slice(bot, c(1:10, 21:30))
# Same thing for the other 10 individuals.
# It will be our unknown dataset on which we want
# to calculate classes.
bot2   <- slice(bot, c(11:20, 31:40))

# We calculate efourier on these two datasets
bot1.f <- efourier(bot1, 8)
bot2.f <- efourier(bot2, 8)

# Here we obtain our LDA model: first, a PCA, then a LDA
bot1.p <- PCA(bot1.f)
bot1.l <- LDA(bot1.p, "type")

# we redo the same PCA since we worked with scores
bot2.p <- rePCA(bot1.p, bot2.f)

# we finally "predict" with the model obtained before
bot2.l <- reLDA(bot2.p, bot1.l)
bot2.l
```

---

rename *Renames (ala dplyr) on Momocs objects*

Description

Rename variables by name, from the `$fac`. See examples and `?dplyr::rename`.

Usage

```
rename(.data, ...)
```

Arguments

`.data`	a `Coo`, `Coe`, `PCA` object
`...`	comma separated list of unquoted expressions

Details

dplyr verbs are maintained.

Value

a Momocs object of the same class.

See Also

Other handling functions: arrange, at_least, chop, combine, dissolve, filter, mutate, rm_uncomplete, rw_rule, sample_frac, sample_n, select, slice, subset.Coo, transmute

Examples

```
olea
rename(olea, Ind=ind, View=view)
```

---

rePCA *"Redo" a PCA on a new Coe*

Description

Basically reapply rotation to a new Coe object.

Usage

```
rePCA(PCA, Coe)
```

Arguments

PCA	a PCA object
Coe	a Coe object

Note

Quite experimental. Dimensions of the matrices and methods must match.

Examples

```
data(bot)
b <- filter(bot, type=="beer")
w <- filter(bot, type=="whisky")

bf <- efourier(b, 8)
bp <- PCA(bf)

wf <- efourier(w, 8)

# and we use the "beer" PCA on the whisky coefficients
wp <- rePCA(bp, wf)

plot(wp)

plot(bp, eig=FALSE)
points(wp$x[, 1:2], col="red", pch=4)
```

rescale *Rescale coordinates from pixels to real length units*

Description

Most of the time, (x, y) coordinates are recorded in pixels. If we want to have them in mm, cm, etc. we need to convert them and to rescale them. This functions does the job for the two cases: i) either an homogeneous rescaling factor, e.g. if all pictures were taken using the very same magnification or ii) with various magnifications. More in the Details section

Usage

```
rescale(x, scaling_factor, scale_mapping, magnification_col, ...)
```

Arguments

x	any Coo object
scaling_factor	numeric an homogeneous scaling factor. If all you (x, y) coordinates have the same scale
scale_mapping	either a data.frame or a path to read such a data.frame. It MUST contain three columns in that order: magnification found in $fac[, "magnification_col"], pixels, real length unit. Column names do not matter but must be specified, as read.table reads with header=TRUE Every different magnification level found in $fac[, "magnification_col"] must have its row.
magnification_col	the name or id of the $fac column to look for magnification levels for every image
...	additional arguments (besides header=TRUE) to pass to read.table if 'scale_mapping' is a path

Details

The i) case above is straightforward, if 1cm is 500pix long on all your pictures, just call `rescale(your_Coo, scaling_factc` and all coordinates will be in cm.

The ii) second case is more subtle. First you need to code in your /linkCoo object, in the fac slot, a column named, say "mag", for magnification. Imagine you have 4 magnifications: 0.5, 1, 2 and 5, we have to indicate for each magnification, how many pixels stands for how many units in the real world.

This information is passed as a data.frame, built externally or in R, that must look like this:

```
mag   pix    cm
0.5   1304   10
1     921    10
2     816    5
5     1020   5
```

.

We have to do that because, for optical reasons, the ratio pix/real_unit, is not a linear function of the magnification.

All shapes will be centered to apply (the single or the different) scaling_factor.

Note

This function is simple but quite complex to detail. Feel free to contact me should you have any problem with it. You can just access its code (type `rescale`) and reply it yourself.

`rfourier` *Radii variation Fourier transform*

Description

`rfourier` computes radii variation Fourier analysis from a matrix or a list of coordinates.

Usage

```
rfourier(x, ...)

## Default S3 method:
rfourier(x, nb.h, smooth.it = 0, norm = FALSE,
  verbose = TRUE, ...)

## S3 method for class 'Out'
rfourier(x, nb.h = 40, smooth.it = 0, norm = TRUE,
  verbose = TRUE, ...)
```

Arguments

`x`	A `list` or `matrix` of coordinates or an `Out` object
`...`	useless here
`nb.h`	`integer`. The number of harmonics to use. If missing 99pc harmonic power is used.
`smooth.it`	`integer`. The number of smoothing iterations to perform.
`norm`	`logical`. Whether to scale the outlines so that the mean length of the radii used equals 1.
`verbose`	`logical`. Whether to display diagnosis messages.

Details

see the JSS paper for the maths behind.

Value

A list with following components:

- an vector of $a_{1->n}$ harmonic coefficients
- bn vector of $b_{1->n}$ harmonic coefficients
- ao ao harmonic coefficient.
- r vector of radii lengths.

Note

Directly borrowed for Claude (2008), and called `fourier1` there.

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

See Also

Other rfourier: `rfourier_i`, `rfourier_shape`

Examples

```
data(bot)
coo <- coo_center(bot[1]) # centering is almost mandatory for rfourier family
coo_plot(coo)
rf  <- rfourier(coo, 12)
rf
rfi <- rfourier_i(rf)
coo_draw(rfi, border='red', col=NA)
```

---

rfourier_i *Inverse radii variation Fourier transform*

Description

`rfourier_i` uses the inverse radii variation transformation to calculate a shape, when given a list with Fourier coefficients, typically obtained computed with rfourier.

Usage

```
rfourier_i(rf, nb.h, nb.pts = 120)
```

Arguments

rf	A `list` with ao, an and bn components, typically as returned by `rfourier`.
nb.h	`integer`. The number of harmonics to calculate/use.
nb.pts	`integer`. The number of points to calculate.

Details

See the JSS paper for the maths behind.

Value

A list with components:

x	vector of x-coordinates.
y	vector of y-coordinates.
angle	vector of angles used.
r	vector of radii calculated.

Note

Directly borrowed for Claude (2008), and called ifourier1 there.

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

See Also

Other rfourier: rfourier_shape, rfourier

Examples

```
data(bot)
coo <- coo_center(bot[1]) # centering is almost mandatory for rfourier family
coo_plot(coo)
rf  <- rfourier(coo, 12)
rf
rfi <- rfourier_i(rf)
coo_draw(rfi, border='red', col=NA)
```

---

rfourier_shape *Calculates and draw 'rfourier' shapes.*

Description

rfourier_shape calculates a 'Fourier radii variation shape' given Fourier coefficients (see Details) or can generate some 'rfourier' shapes.

Usage

```
rfourier_shape(an, bn, nb.h, nb.pts = 80, alpha = 2, plot = TRUE)
```

Arguments

an	numeric. The a_n Fourier coefficients on which to calculate a shape.
bn	numeric. The b_n Fourier coefficients on which to calculate a shape.
nb.h	integer. The number of harmonics to use.
nb.pts	integer. The number of points to calculate.
alpha	numeric. The power coefficient associated with the (usually decreasing) amplitude of the Fourier coefficients (see **Details**).
plot	logical. Whether to plot or not the shape.

Details

rfourier_shape can be used by specifying nb.h and alpha. The coefficients are then sampled in an uniform distribution $(-\pi; \pi)$ and this amplitude is then divided by $harmonicrank^{a}lpha$. If alpha is lower than 1, consecutive coefficients will thus increase. See rfourier for the mathematical background.

Value

A matrix of (x; y) coordinates.

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

See Also

Other rfourier: rfourier_i, rfourier

Examples

```
data(bot)
rf <- rfourier(bot[1], 24)
rfourier_shape(rf$an, rf$bn) # equivalent to rfourier_i(rf)
rfourier_shape() # not very interesting

rfourier_shape(nb.h=12) # better
rfourier_shape(nb.h=6, alpha=0.4, nb.pts=500)

# Butterflies of the vignette' cover
panel(Out(a2l(replicate(100,
rfourier_shape(nb.h=6, alpha=0.4, nb.pts=200, plot=FALSE)))))
```

`rm_asym` *Removes asymmetric and symmetric variation on OutCoe objects*

Description

Only for those obtained with efourier, otherwise a message is returned. `rm_asym` sets all B and C coefficients to 0; `rm_sym` sets all A and D coefficients to 0.

Usage

```
rm_asym(OutCoe)

## Default S3 method:
rm_asym(OutCoe)

## S3 method for class 'OutCoe'
rm_asym(OutCoe)

rm_sym(OutCoe)

## Default S3 method:
rm_sym(OutCoe)

## S3 method for class 'OutCoe'
rm_sym(OutCoe)
```

Arguments

`OutCoe`	an OutCoe object

Value

an OutCoe object

References

Below: the first mention, and two applications.

#'

- Iwata, H., Niikura, S., Matsuura, S., Takano, Y., & Ukai, Y. (1998). Evaluation of variation of root shape of Japanese radish (Raphanus sativus L.) based on image analysis using elliptic Fourier descriptors. Euphytica, 102, 143-149.
- Iwata, H., Nesumi, H., Ninomiya, S., Takano, Y., & Ukai, Y. (2002). The Evaluation of Genotype x Environment Interactions of Citrus Leaf Morphology Using Image Analysis and Elliptic Fourier Descriptors. Breeding Science, 52(2), 89-94. doi:10.1270/jsbbs.52.89
- Yoshioka, Y., Iwata, H., Ohsawa, R., & Ninomiya, S. (2004). Analysis of petal shape variation of Primula sieboldii by elliptic fourier descriptors and principal component analysis. Annals of Botany, 94(5), 657-64. doi:10.1093/aob/mch190

See Also

symmetry.

Examples

```
data(bot)
botf <- efourier(bot, 12)
botSym <- rm_asym(botf)
boxplot(botSym)
botSymp <- PCA(botSym)
plot(botSymp)
plot(botSymp, amp.shp=5)

# Asymmetric only
botAsym <- rm_sym(botf)
boxplot(botAsym)
botAsymp <- PCA(botAsym)
plot(botAsymp)
# strange shapes because the original shape was mainly symmetric and would need its
# symmetric (eg its average) for a proper reconstruction. Should only be used like that:
plot(botAsymp, morpho=FALSE)
```

---

rm_harm *Removes harmonics from Coe objects*

Description

Useful to drop harmonics on Coe objects. Should only work for Fourier-based approached since it looks for `[A-D][1-drop]` pattern.

Usage

```
rm_harm(x, drop = 1)
```

Arguments

x	Coe object
drop	numeric number of harmonics to drop

Examples

```
data(bot)
bf <- efourier(bot)
colnames(rm_harm(bf, 1)$coe)
```

`rm_uncomplete` *Removes shapes with incomplete slices*

Description

Imagine you take three views of every object you study. Then, you can slice, filter or chop your entire dataset, do morphometrics on it, then want to combine it. But if you have forgotten one view, or if it was impossible to obtain, for one or more objects, combine will not work. This function helps you to remove those ugly ducklings. See examples

Usage

```
rm_uncomplete(x, id, by)
```

Arguments

`x`	the object on which to remove uncomplete "by"
`id`	of the objects, within the $fac slot
`by`	which column of the $fac should objects have complete views

See Also

Other handling functions: `arrange`, `at_least`, `chop`, `combine`, `dissolve`, `filter`, `mutate`, `rename`, `rw_rule`, `sample_frac`, `sample_n`, `select`, `slice`, `subset.Coo`, `transmute`

Examples

```
# we load olea
data(olea)
# we select the var Aglan since it is the only one complete
ol <- filter(olea, var == "Aglan")
# everything seems fine
table(ol, "view", "ind")
# indeed
rm_uncomplete(ol, id="ind", by="view")

# we mess the ol object by removing a single shape
ol.pb <- slice(ol, -1)
table(ol.pb, "view", "ind")
# the counterpart has been removed with a notice
ol.ok <- rm_uncomplete(ol.pb, "ind", "view")
# now you can combine them
table(ol.ok, "view", "ind")
```

rw_rule *Renames levels on Momocs objects*

Description

rw_rule stands for 'rewriting rule'. Typically useful to correct typos at the import, or merge some levels within covariates. Drops levels silently.

Usage

```
rw_rule(x, fac, from, to)
```

Arguments

x	any Momocs object
fac	the id of the name of the $fac column to look for
from	which level(s) should be renamed; passed as a single or several characters
to	which name ?

Value

a Momocs object of the same type

See Also

Other handling functions: arrange, at_least, chop, combine, dissolve, filter, mutate, rename, rm_uncomplete, sample_frac, sample_n, select, slice, subset.Coo, transmute

Examples

```
data(bot)
# single renaming
rw_rule(bot, "type", "whisky", "agua_de_fuego") # 1 instead of "type" is fine too
# several renaming
bot2 <- mutate(bot, fake=factor(rep(letters[1:4], 10)))
rw_rule(bot2, "fake", c("a", "e"), "ae")$fake
```

`sample_frac` *Samples a fraction of shapes in Momocs objects*

Description

Sample a fraction of shapes from a Momocs object. See examples and `?dplyr::sample_n`.

Usage

```
sample_frac(tbl, size, replace, fac, ...)
```

Arguments

`tbl`	a Momocs object (Coo, Coe)
`size`	numeric (0 < numeric <= 1) the fraction of shapes to select
`replace`	logical whether sample should be done with ot without replacement
`fac`	a column name if a `$fac` is defined; size is then applied within levels of this factor
`...`	additional arguments to dplyr::sample_frac and to maintain generic compatibility

Note

the resulting fraction is rounded with ceiling.

See Also

Other handling functions: `arrange`, `at_least`, `chop`, `combine`, `dissolve`, `filter`, `mutate`, `rename`, `rm_uncomplete`, `rw_rule`, `sample_n`, `select`, `slice`, `subset.Coo`, `transmute`

Examples

```
data(bot)
bot
# samples 50% of the bottles no matter their type
sample_frac(bot, 0.5)
# 80% bottles of beer and of whisky
table(sample_frac(bot, 0.8, fac="type"))
# bootstrap the same number of bootles of each type but with replacement
table(names(sample_frac(bot, 1, replace=TRUE)))
```

`sample_n` *Samples n shapes on Momocs objects*

Description

Sample n shapes from a Momocs object. See examples and `?dplyr::sample_n`.

Usage

```
sample_n(tbl, size, replace, fac, ...)
```

Arguments

`tbl`	a Momocs object (Coo, Coe)
`size`	numeric how many shapes should we sample
`replace`	logical whether sample should be done with ot without replacement
`fac`	a column name if a `$fac` is defined; size is then applied within levels of this factor
`...`	additional arguments to dplyr::sample_n and to maintain generic compatibility

See Also

Other handling functions: `arrange`, `at_least`, `chop`, `combine`, `dissolve`, `filter`, `mutate`, `rename`, `rm_uncomplete`, `rw_rule`, `sample_frac`, `select`, `slice`, `subset.Coo`, `transmute`

Examples

```
data(bot)
bot
# samples 5 bottles no matter their type
sample_n(bot, 5)
# 5 bottles of beer and of whisky
table(sample_n(bot, 5, fac="type"))
# many repetitions
table(names(sample_n(bot, 400, replace=TRUE)))
```

scree *Methods for PCA eigen values*

Description

A set of functions around PCA/LDA eigen/trace. `scree` calculates their proportion and cumulated proportion; `scree_min` returns the minimal number of axis to use to retain a given proportion; `scree_plot` displays a screeplot.

Usage

```
scree(x, nax)

## S3 method for class 'PCA'
scree(x, nax = 1:10)

## S3 method for class 'LDA'
scree(x, nax = 1:10)

scree_min(x, prop = 0.99)

scree_plot(x, nax = 1:10)
```

Arguments

x	a PCA object
nax	numeric range of axis to consider
prop	numeric how many axis are enough this proportion of variance, if too high then number of axis is returned.

Value

scree returns a data.frame, scree_min a numeric, scree_plot a ggplot.

Examples

```
data(bot)
# On PCA
bp <- PCA(efourier(bot))
scree(bp)
scree_min(bp, 0.99)
scree_min(bp, 1)

scree_plot(bp)
scree_plot(bp, 1:5)

# on LDA, it uses svd
data(olea)
```

```
bl <- LDA(PCA(opoly(olea)), "var")
scree(bl)
```

`select` *Selects (ala dplyr) on Momocs objects*

Description

Select variables by name, from the `$fac`. See examples and `?dplyr::select`.

Usage

```
select(.data, ...)
```

Arguments

`.data`	a `Coo`, `Coe`, `PCA` object
`...`	comma separated list of unquoted expressions

Details

dplyr verbs are maintained.

Value

a Momocs object of the same class.

See Also

Other handling functions: `arrange`, `at_least`, `chop`, `combine`, `dissolve`, `filter`, `mutate`, `rename`, `rm_uncomplete`, `rw_rule`, `sample_frac`, `sample_n`, `slice`, `subset.Coo`, `transmute`

Examples

```
data(olea)
olea
select(olea, var, view) # drops domes and ind
select(olea, variety=var, domesticated_status=domes, view)
# combine with filter with magrittr pipes
# only dorsal views, and 'var' and 'domes' columns
filter(olea, view=="VD") %>% select(var, domes)
```

shapes *Data: Outline coordinates of various shapes*

Description

Data: Outline coordinates of various shapes

Format

An Out object with the outline coordinates of some various shapes.

Source

Borrowed default shapes from (c) Adobe Photoshop. Do not send me to jail.

See Also

Other datasets: bot, chaff, charring, flower, hearts, molars, mosquito, oak, olea, trilo, wings

slice *Slices (ala dplyr) on Momocs objects*

Description

Select rows by position, based on `$fac`. See examples and `?dplyr::slice`.

Usage

```
slice(.data, ...)
```

Arguments

.data	a Coo, Coe, PCA object
...	logical conditions

Details

dplyr verbs are maintained.

Value

a Momocs object of the same class.

See Also

Other handling functions: arrange, at_least, chop, combine, dissolve, filter, mutate, rename, rm_uncomplete, rw_rule, sample_frac, sample_n, select, subset.Coo, transmute

Examples

```
olea
slice(olea, 1) # if you only want the coordinates, try bot[1]
slice(olea, 1:20)
slice(olea, 21:30)
```

---

slidings_scheme *Extracts partitions of sliding coordinates*

Description

Helper function that deduces (likely to be a reminder) partition scheme from $slidings of Ldk objects.

Usage

```
slidings_scheme(Coo)
```

Arguments

Coo	an Ldk object

Value

a list with two components: n the number of partition; id their position. Or a NULL if no slidings are defined

See Also

Other ldk/slidings methods: def_ldk, def_slidings, get_ldk, get_slidings

Examples

```
# no slidings defined a NULL is returned with a message
slidings_scheme(wings)

# slidings defined
slidings_scheme(chaff)
```

stack.Coo *Family picture of shapes*

Description

Plots all the outlines, on the same graph, from a Coo (Out, Opn or Ldk) object.

Usage

```
## S3 method for class 'Coo'
stack(x, cols, borders, fac, palette = col_summer,
  coo_sample = 120, points = FALSE, first.point = TRUE, centroid = TRUE,
  ldk = TRUE, ldk_pch = 3, ldk_col = "#FF000055", ldk_cex = 0.5,
  ldk_links = FALSE, ldk_confell = FALSE, ldk_contour = FALSE,
  ldk_chull = FALSE, ldk_labels = FALSE, xy.axis = TRUE,
  title = substitute(x), ...)

## S3 method for class 'Ldk'
stack(x, cols, borders, first.point = TRUE, centroid = TRUE,
  ldk = TRUE, ldk_pch = 20, ldk_col = col_alpha("#000000", 0.5),
  ldk_cex = 0.3, meanshape = FALSE, meanshape_col = "#FF0000",
  ldk_links = FALSE, ldk_confell = FALSE, ldk_contour = FALSE,
  ldk_chull = FALSE, ldk_labels = FALSE, slidings = TRUE,
  slidings_pch = "", xy.axis = TRUE, title = substitute(x), ...)
```

Arguments

x	The Coo object to plot.
cols	A vector of colors for drawing the outlines. Either a single value or of length exactly equals to the number of coordinates.
borders	A vector of colors for drawing the borders. Either a single value or of length exactly equals to the number of coordinates.
fac	a factor within the $fac slot for colors
palette	a color palette to use when fac is provided
coo_sample	if not NULL the number of point per shape to display (to plot quickly)
points	logical whether to draw or not points
first.point	logical whether to draw or not the first point
centroid	logical whether to draw or not the centroid
ldk	logical. Whether to display landmarks (if any).
ldk_pch	pch for these landmarks
ldk_col	color for these landmarks
ldk_cex	cex for these landmarks
ldk_links	logical whether to draw links (of the mean shape)

ldk_confell	logical whether to draw conf ellipses
ldk_contour	logical whether to draw contour lines
ldk_chull	logical whether to draw convex hull
ldk_labels	logical whether to draw landmark labels
xy.axis	whether to draw or not the x and y axes
title	a title for the plot. The name of the Coo by default
...	further arguments to be passed to coo_plot
meanshape	logical whether to add meanshape related stuff (below)
meanshape_col	a color for everything meanshape
slidings	logical whether to draw slidings semi landmarks
slidings_pch	pch for semi landmarks

See Also

Other Coo_graphics: panel2, panel, plot.Coo

Examples

```
## Not run:
data(bot)
stack(bot)
bot.f <- efourier(bot, 12)
stack(bot.f)
data(mosquito)
stack(mosquito, borders='#1A1A1A22', first.point=FALSE)
data(hearts)
stack(hearts)
stack(hearts, ldk=FALSE)
stack(hearts, borders='#1A1A1A22', ldk=TRUE, ldk_col=col_summer(4), ldk_pch=20)
stack(hearts, fac="aut", palette=col_sari)

chaffal <- fgProcrustes(chaff)
stack(chaffal, slidings=FALSE)
stack(chaffal, meanshape=TRUE, meanshape_col="blue")

## End(Not run)
```

---

stack2 *Family picture of shapes (ggplot2)*

Description

Will replace stack soon.

Usage

```
stack2(Coo)
```

Arguments

Coo	a Coo object Family picture of shapes

Value

a ggplot2 object

Examples

```
data(bot)
stack2(bot)
```

---

subset.Coo *Subsets on Momocs objects*

Description

Subset is a wrapper around dplyr's verbs and should NOT be used directly.

Usage

```
## S3 method for class 'Coo'
subset(x, subset, ...)

## S3 method for class 'Coe'
subset(x, subset, ...)

## S3 method for class 'PCA'
subset(x, subset, ...)
```

Arguments

x	a Coo or a Coe object.
subset	logical taken from the $fac slot, or indices. See examples.
...	useless here but maintains consistence with the generic subset.

See Also

Other handling functions: arrange, at_least, chop, combine, dissolve, filter, mutate, rename, rm_uncomplete, rw_rule, sample_frac, sample_n, select, slice, transmute

Examples

```
# Do not use subset directly
```

`symmetry` *Calcuates symmetry indices on OutCoe objects*

Description

For OutCoe objects obtained with efourier, calculates several indices on the matrix of coefficients: `AD`, the sum of absolute values of harmonic coefficients A and D; `BC` same thing for B and C; `amp` the sum of the absolute value of all harmonic coefficients and `sym` which is the ratio of `AD` over `amp`. See references below for more details.

Usage

```
symmetry(OutCoe)
```

Arguments

`OutCoe`	[efourier] objects

Value

a matrix with 4 colums described above.

References

Below: the first mention, and two applications.

#'

- Iwata, H., Niikura, S., Matsuura, S., Takano, Y., & Ukai, Y. (1998). Evaluation of variation of root shape of Japanese radish (Raphanus sativus L.) based on image analysis using elliptic Fourier descriptors. Euphytica, 102, 143-149.
- Iwata, H., Nesumi, H., Ninomiya, S., Takano, Y., & Ukai, Y. (2002). The Evaluation of Genotype x Environment Interactions of Citrus Leaf Morphology Using Image Analysis and Elliptic Fourier Descriptors. Breeding Science, 52(2), 89-94. doi:10.1270/jsbbs.52.89
- Yoshioka, Y., Iwata, H., Ohsawa, R., & Ninomiya, S. (2004). Analysis of petal shape variation of Primula sieboldii by elliptic fourier descriptors and principal component analysis. Annals of Botany, 94(5), 657-64. doi:10.1093/aob/mch190

See Also

rm_asym and rm_sym.

Examples

```
data(bot)
bot.f <- efourier(bot, 12)
res <- symmetry(bot.f)
hist(res[, 'sym'])
```

table *Cross-tabulates objects*

Description

Simply extends base table for a more convenient use on $fac slot.

Usage

```
table(...)

## Default S3 method:
table(...)

## S3 method for class 'Coo'
table(...)

## S3 method for class 'Coe'
table(...)

## S3 method for class 'PCA'
table(...)

## S3 method for class 'LDA'
table(...)
```

Arguments

...	a list of, first, a Momocs object (Coo, Coe, PCA, etc.), then, column names in the $fac slot. If not specified, returns a table on the entire $fac data.frame

Examples

```
data(bot)
table(bot)
data(olea)
table(olea, "var", "domes")
table(olea)
```

tfourier *Tangent angle Fourier transform*

Description

tfourier computes tangent angle Fourier analysis from a matrix or a list of coordinates.

Usage

```
tfourier(x, ...)

## Default S3 method:
tfourier(x, nb.h, smooth.it = 0, norm = FALSE,
  verbose = TRUE, ...)

## S3 method for class 'Out'
tfourier(x, nb.h = 40, smooth.it = 0, norm = TRUE,
  verbose = TRUE, ...)
```

Arguments

x	A list or matrix of coordinates or an Out
...	useless here
nb.h	integer. The number of harmonics to use. If missing 99pc harmonic power is used.
smooth.it	integer. The number of smoothing iterations to perform
norm	logical. Whether to scale and register new coordinates so that the first point used is sent on the origin.
verbose	logical. Whether to display diagnosis messages.

Value

A list with the following components:

- ao ao harmonic coefficient
- an vector of $a_{1->n}$ harmonic coefficients
- bn vector of $b_{1->n}$ harmonic coefficients
- phi vector of variation of the tangent angle
- t vector of distance along the perimeter expressed in radians
- perimeter numeric. The perimeter of the outline
- thetao numeric. The first tangent angle
- x1 The x-coordinate of the first point
- y1 The y-coordinate of the first point.

Note

Directly borrowed for Claude (2008), and called fourier2 there.

References

Zahn CT, Roskies RZ. 1972. Fourier Descriptors for Plane Closed Curves. *IEEE Transactions on Computers* **C-21**: 269-281.

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

See Also

Other tfourier: tfourier_i, tfourier_shape

Examples

```
data(bot)
coo <- bot[1]
coo_plot(coo)
tf  <- tfourier(coo, 12)
tf
tfi <- tfourier_i(tf)
coo_draw(tfi, border='red', col=NA) # the outline is not closed...
coo_draw(tfourier_i(tf, force2close=TRUE), border='blue', col=NA) # we force it to close.
```

---

tfourier_i *Inverse tangent angle Fourier transform*

Description

tfourier_i uses the inverse tangent angle Fourier transformation to calculate a shape, when given a list with Fourier coefficients, typically obtained computed with tfourier.

Usage

```
tfourier_i(tf, nb.h, nb.pts = 120, force2close = FALSE, rescale = TRUE,
  perim = 2 * pi, thetao = 0)
```

Arguments

tf	a list with ao, an and bn components, typically as returned by tfourier
nb.h	integer. The number of harmonics to calculate/use
nb.pts	integer. The number of points to calculate
force2close	logical. Whether to force the outlines calculated to close (see coo_force2close).
rescale	logical. Whether to rescale the points calculated so that their perimeter equals perim.
perim	The perimeter length to rescale shapes.
thetao	numeric. Radius angle to the reference (in radians)

Details

See tfourier for the mathematical background.

Value

A list with components:

x	vector of x-coordinates.
y	vector of y-coordinates.
phi	vector of interpolated changes on the tangent angle.
angle	vector of position on the perimeter (in radians).

Note

Directly borrowed for Claude (2008), and called ifourier2 there.

References

Zahn CT, Roskies RZ. 1972. Fourier Descriptors for Plane Closed Curves. *IEEE Transactions on Computers* **C-21**: 269-281.

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

See Also

Other tfourier: tfourier_shape, tfourier

Examples

```
data(bot)
tfourier(bot[1], 24)
tfourier_shape()
```

---

tfourier_shape *Calculates and draws 'tfourier' shapes.*

Description

tfourier_shape calculates a 'Fourier tangent angle shape' given Fourier coefficients (see Details) or can generate some 'tfourier' shapes.

Usage

```
tfourier_shape(an, bn, ao = 0, nb.h, nb.pts = 80, alpha = 2,
  plot = TRUE)
```

Arguments

an	numeric. The a_n Fourier coefficients on which to calculate a shape.
bn	numeric. The b_n Fourier coefficients on which to calculate a shape.
ao	ao Harmonic coefficient.
nb.h	integer. The number of harmonics to use.
nb.pts	integer. The number of points to calculate.
alpha	numeric. The power coefficient associated with the (usually decreasing) amplitude of the Fourier coefficients (see **Details**).
plot	logical. Whether to plot or not the shape.

Value

A matrix of (x; y) coordinates.

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

See Also

Other tfourier: tfourier_i, tfourier

Examples

```
data(bot)
tf <- tfourier(bot[1], 24)
tfourier_shape(tf$an, tf$bn) # equivalent to rfourier_i(rf)
tfourier_shape()
tfourier_shape(nb.h=6, alpha=0.4, nb.pts=500)
panel(Out(a2l(replicate(100,
coo_force2close(tfourier_shape(nb.h=6, alpha=2, nb.pts=200, plot=FALSE))))) # biological shapes
```

---

tie_jpg_txt *Binds .jpg outlines from .txt landmarks taken on them*

Description

Given a list of files (lf) that includes matching filenames with .jpg (black masks) and .txt (landmark positions on them as .txt), returns an Out with $ldk defined. Typically be useful if you use ImageJ to define landmarks on your outlines.

Usage

```
tie_jpg_txt(lf)
```

Arguments

lf	a list of filenames

Note

Not optimized (images are read twice). Please do not hesitate to contact me should you have a particular case or need something.

See Also

Other babel functions: bind_db, chc2Out, chc2pix, import_StereoMorph_curve1, import_jpg, import_tps, nef2Coe, ntsrow2Coo, pix2chc, tps2coo

---

tps2coo *Reads a single tps-like shape as lines*

Description

Internal function used in import_tps that may be useful for data import. When provided with lines (eg after readLines) from a tps-like description (with "LM", "CURVES", etc.) returns a list of coordinates, curves, etc.

Usage

```
tps2coo(tps, curves = TRUE)
```

Arguments

tps	lines, typically from readLines, describing a single shape in tps-like format
curves	logical whether to read curves, if any

Details

if curves are present add them to $coo (with the proper combination of do.call, rbind, then use def_slidings or define a slidings matrix (see Ldk).

Value

a list with components: coo a matrix of coordinates; cur a list of matrices; scale the scale as a numeric.

See Also

Other babel functions: bind_db, chc2Out, chc2pix, import_StereoMorph_curve1, import_jpg, import_tps, nef2Coe, ntsrow2Coo, pix2chc, tie_jpg_txt

Examples

```
## Not run:
# let's imagine this command works fine
coo <- import_tps(...)
# then you can
Ldk(coo)

## End(Not run)
```

---

tps2d *Thin Plate Splines for 2D data*

Description

tps2d is the core function for Thin Plate Splines. It is used internally for all TPS graphical functions.tps_apply is the very same function but with arguments properly named (I maintain tps2d as it is for historical reasons) when we want a apply a trasnformation grid.

Usage

```
tps2d(grid0, fr, to)

tps_apply(fr, to, new)
```

Arguments

grid0	a matrix of coordinates on which to calculate deformations
fr	the reference $(x; y)$ coordinates
to	the target $(x; y)$ coordinates
new	the target coordinates (again)

Value

a matrix of (x; y) coordinates with TPS-interpolated deformations

See Also

Other thin plate splines: tps_arr, tps_grid, tps_iso, tps_raw

tps_arr *Deformation 'vector field' using Thin Plate Splines*

Description

tps_arr(ows) calculates deformations between two configurations and illustrate them using arrows.

Usage

```
tps_arr(fr, to, amp = 1, grid = TRUE, over = 1.2, palette = col_summer,
  arr.nb = 200, arr.levels = 100, arr.len = 0.1, arr.ang = 20,
  arr.lwd = 0.75, arr.col = "grey50", poly = TRUE, shp = TRUE,
  shp.col = rep(NA, 2), shp.border = col_qual(2), shp.lwd = c(2, 2),
  shp.lty = c(1, 1), legend = TRUE, legend.text, ...)
```

Arguments

fr	the reference $(x; y)$ coordinates
to	the target $(x; y)$ coordinates
amp	an amplification factor of differences between fr and to
grid	whether to calculate and plot changes across the graphical window TRUE or just within the starting shape (FALSE)
over	numeric that indicates how much the thin plate splines extends over the shapes
palette	a color palette such those included in Momocs or produced with colorRamp-Palette
arr.nb	numeric The number of arrows to calculate
arr.levels	numeric. The number of levels for the color of arrows
arr.len	numeric for the length of arrows
arr.ang	numeric for the angle for arrows' heads
arr.lwd	numeric for the lwd for drawing arrows
arr.col	if palette is not used the color for arrows
poly	whether to draw polygons (for outlines) or points (for landmarks)
shp	logical. whether to draw shapes
shp.col	two colors for filling the shapes
shp.border	two colors for drawing the borders
shp.lwd	two lwd for drawing shapes
shp.lty	two lty fro drawing the shapes
legend	logical whether to plot a legend
legend.text	some text for the legend
...	additional arguments to feed coo_draw

Value

Nothing.

See Also

Other thin plate splines: tps2d, tps_grid, tps_iso, tps_raw

Examples

```
data(bot)
botF <- efourier(bot)
x <- mshapes(botF, 'type', nb.pts=80)$shp
fr <- x$beer
to <- x$whisky
tps_arr(fr, to, arr.nb=200, palette=col_sari, amp=3)
tps_arr(fr, to, arr.nb=200, palette=col_sari, amp=3, grid=FALSE)
```

---

tps_grid *Deformation grids using Thin Plate Splines*

Description

tps_grid calculates and plots deformation grids between two configurations.

Usage

```
tps_grid(fr, to, amp = 1, over = 1.2, grid.size = 15,
  grid.col = "grey80", poly = TRUE, shp = TRUE, shp.col = rep(NA, 2),
  shp.border = col_qual(2), shp.lwd = c(1, 1), shp.lty = c(1, 1),
  legend = TRUE, legend.text, ...)
```

Arguments

fr	the reference $(x; y)$ coordinates
to	the target $(x; y)$ coordinates
amp	an amplification factor of differences between fr and to
over	numeric that indicates how much the thin plate splines extends over the shapes
grid.size	numeric to specify the number of grid cells on the longer axis on the outlines
grid.col	color for drawing the grid
poly	whether to draw polygons (for outlines) or points (for landmarks)
shp	logical. Whether to draw shapes
shp.col	Two colors for filling the shapes
shp.border	Two colors for drawing the borders
shp.lwd	Two lwd for drawing shapes

shp.lty	Two lty fro drawing the shapes
legend	logical whether to plot a legend
legend.text	some text for the legend
...	additional arguments to feed coo_draw

Value

Nothing

See Also

Other thin plate splines: tps2d, tps_arr, tps_iso, tps_raw

Examples

```
data(bot)
botF <- efourier(bot)
x <- mshapes(botF, 'type', nb.pts=80)$shp
fr <- x$beer
to <- x$whisky
tps_grid(fr, to, amp=3, grid.size=10)
```

---

tps_iso *Deformation isolines using Thin Plate Splines.*

Description

tps_iso calculates deformations between two configurations and map them with or without isolines.

Usage

```
tps_iso(fr, to, amp = 1, grid = FALSE, over = 1.2, palette = col_spring,
  iso.nb = 1000, iso.levels = 12, cont = TRUE, cont.col = "black",
  poly = TRUE, shp = TRUE, shp.border = col_qual(2), shp.lwd = c(2, 2),
  shp.lty = c(1, 1), legend = TRUE, legend.text, ...)
```

Arguments

fr	The reference $(x; y)$ coordinates
to	The target $(x; y)$ coordinates
amp	An amplification factor of differences between fr and to
grid	whether to calculate and plot changes across the graphical window TRUE or just within the starting shape (FALSE)
over	A numeric that indicates how much the thin plate splines extends over the shapes

palette	A color palette such those included in Momocs or produced with colorRampPalette
iso.nb	A numeric. The number of points to use for the calculation of deformation
iso.levels	numeric. The number of levels for mapping the deformations
cont	logical. Whether to draw contour lines
cont.col	A color for drawing the contour lines
poly	whether to draw polygons (for outlines) or points (for landmarks)
shp	logical. Whether to draw shapes
shp.border	Two colors for drawing the borders
shp.lwd	Two lwd for drawing shapes
shp.lty	Two lty fro drawing the shapes
legend	logical whether to plot a legend
legend.text	some text for the legend
...	additional arguments to feed coo_draw

Value

No returned value

See Also

Other thin plate splines: tps2d, tps_arr, tps_grid, tps_raw

Examples

```
data(bot)
botF <- efourier(bot)
x <- mshapes(botF, 'type', nb.pts=80)$shp
fr <- x$beer
to <- x$whisky
tps_iso(fr, to, iso.nb=200, amp=3)
tps_iso(fr, to, iso.nb=200, amp=3, grid=TRUE)
```

---

tps_raw *Vanilla Thin Plate Splines*

Description

tps_raw calculates deformation grids and returns position of sampled points on it.

Usage

```
tps_raw(fr, to, amp = 1, over = 1.2, grid.size = 15)
```

Arguments

fr	the reference $(x; y)$ coordinates
to	the target $(x; y)$ coordinates
amp	an amplification factor of differences between fr and to
over	numeric that indicates how much the thin plate splines extends over the shapes
grid.size	numeric to specify the number of grid cells on the longer axis on the outlines

Value

a list with two components: grid the xy coordinates of sampled points along the grid; dim the dimension of the grid.

See Also

Other thin plate splines: tps2d, tps_arr, tps_grid, tps_iso

Examples

```
## Not run:
data(bot)
ms <- mshapes(efourier(bot, 10), "type")
b <- ms$shp$beer
w <- ms$shp$whisky
g <- tps_raw(b, w)
ldk_plot(g$grid)

# a wavy plot
ldk_plot(g$grid, pch=NA)
cols_ids <- 1:g$dim[1]
for (i in 1:g$dim[2]) lines(g$grid[cols_ids + (i-1)*g$dim[1], ])

## End(Not run)
```

TraCoe *Traditional morphometrics class*

Description

Defines the builder for traditional measurement class in Momocs. Is is intended to ease calculations, data handling and multivariate statistics just ad the other Momocs' classes

Usage

```
TraCoe(coe = matrix(), fac = data.frame())
```

Arguments

coe	a matrix of measurements
fac	a data.frame for covariates

Examples

```
data(iris)
# let's (more or less) rebuild the flower dataset
fl <- TraCoe(iris[, 1:4], data.frame(sp=iris$Species))
fl %>% PCA() %>% plot("sp")
```

---

transmute *Transmutes (ala dplyr) on Momocs objects*

Description

Add new variables to the $fac and drop existing ones. See examples and ?dplyr::transmute.

Usage

```
transmute(.data, ...)
```

Arguments

.data	a Coo, Coe, PCA object
...	comma separated list of unquoted expressions

Details

dplyr verbs are maintained.

Value

a Momocs object of the same class.

See Also

Other handling functions: arrange, at_least, chop, combine, dissolve, filter, mutate, rename, rm_uncomplete, rw_rule, sample_frac, sample_n, select, slice, subset.Coo

Examples

```
olea
transmute(olea, id=factor(1:length(olea)))
```

trilo *Data: Outline coordinates of cephalic outlines of trilobite*

Description

Data: Outline coordinates of cephalic outlines of trilobite

Format

A Out object 64 coordinates of 50 cephalic outlines from different ontogenetic stages of trilobite.

Source

Arranged from: http://folk.uio.no/ohammer/past/outlines.dat. The original data included 51 outlines and 5 ontogenetic stages, but one of them has just a single outline thas has been removed.

See Also

Other datasets: bot, chaff, charring, flower, hearts, molars, mosquito, oak, olea, shapes, wings

truss *Truss measurement*

Description

A method to calculate on shapes or on Coo truss measurements, which is all pairwise combinations of euclidean distances

Usage

```
truss(x)
```

Arguments

x	a shape or an Ldk object

Value

a named numeric or matrix

Note

Mainly implemented for historical/didactical reasons.

See Also

Other premodern: measure

Examples

```
# example on a single shape
data(shapes)
cat <- coo_sample(shapes[4], 6)
truss(cat)

# example on wings dataset
data(wings)
tx <- truss(wings)
dim(tx)
# we normalize and plot an heatmap
txn <- apply(tx$coe, 2, .normalize)
# heatmap(txn)

txp <- PCA(tx, scale. = TRUE, center=TRUE, fac=wings$fac)
plot(txp, 1)
```

---

validate *Validates Coo objects*

Description

No validation for S3 objects, so this method is a (cheap) attempt at checking Coo objects, Out, Opn and Ldk objects.

Usage

```
validate(Coo)
```

Arguments

Coo	any Coo object

Details

Implemented before all morphometric methods and handling verbs. To see what is checked, try eg `Momocs:::validate.Coo`

Value

a Coo object.

Examples

```
## Not run:
validate(bot)
bot[12] <- NA
validate(bot)

validate(hearts)
hearts$ldk[[4]] <- c(1, 2)
validate(hearts)

## End(Not run)
```

---

vecs_param *Some vector utilities.*

Description

Returns ratio of norms and signed angle between two vectors provided as four numeric.

Usage

```
vecs_param(r1, i1, r2, i2)
```

Arguments

r1	the 'real' part of the first vector, i.e. difference in x-coordinates.
i1	the 'imaginary' part of the first vector, i.e. difference in y-coordinates.
r2	the 'real' part of the second vector, i.e. difference in x-coordinates.
i2	the 'imaginary' part of the second vector, i.e. difference in y-coordinates.

Value

A list with two components: `r.norms` the ratio of (norm of vector 1)/(norm of vector 2) and `d.angle` the signed angle 'from' the first 'to' the second vector.

Examples

```
vecs_param(1, 0, 0, 2)
```

which_out *Remove outliers on Coe*

Description

First performs a PCA, then searches for outliers using dnorm

Usage

```
which_out(x, conf, nax, ...)
```

Arguments

x	object, either Coe or a numeric on which to search for outliers
conf	confidence for dnorm
nax	number of axes to retain (only for Coe), if <1 retain enough axes to retain this proportion of the variance
...	additional parameters to be passed to PCA (only for Coe)

Note

experimental. dnorm parameters used are `median(x), sd(x)`

Examples

```
x <- rnorm(10)
x[4] <- 99
which_out(x)
```

wings *Data: Landmarks coordinates of mosquito wings*

Description

Data: Landmarks coordinates of mosquito wings

Format

A Ldk object containing 18 (x; y) landmarks from 127 mosquito wings, from

Source

Rohlf and Slice 1990 and http://life.bio.sunysb.edu/morph/data/RohlfSlice1990Mosq.nts

See Also

Other datasets: bot, chaff, charring, flower, hearts, molars, mosquito, oak, olea, shapes, trilo

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