Package 'tourr'

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Title Tour Methods for Multivariate Data Visualisation

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Description Implements geodesic interpolation and basis generation functions that allow you to create new tour methods from R.

Depends R (>= 4.1.0)

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Suggests aplpack, testthat, colorspace, ggplot2, gifski, knitr, rmarkdown, tidyr, covr, plotly

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Author Hadley Wickham [aut, ctb] (ORCID: <https://orcid.org/0000-0003-4757-117X>), Dianne Cook [aut, cre] (ORCID: <https://orcid.org/0000-0002-3813-7155>), Nick Spyrison [ctb] (ORCID: <https://orcid.org/0000-0002-8417-0212>), Ursula Laa [ctb] (ORCID: <https://orcid.org/0000-0002-0249-6439>), H. Sherry Zhang [ctb] (ORCID: <https://orcid.org/0000-0002-7122-1463>), Stuart Lee [ctb] (ORCID: <https://orcid.org/0000-0003-1179-8436>)

Maintainer Dianne Cook <dicook@monash.edu>

Repository CRAN

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Contents

`anchored_orthogonal_distance`

Calculate orthogonal distances

Description

For each datapoint this function calculates the orthogonal distance from the anchored projection plane.

Usage

```
anchored_orthogonal_distance(plane, data, anchor = NULL)
```

Arguments

plane	matrix specifying the projection plane
data	data frame or matrix
anchor	A vector specifying the reference point to anchor the plane If NULL (default) the slice will be anchored at the origin.

Value

distance vector

---

andrews *Compute Andrews' curves*

Description

This function takes a numeric vector of input, and returns a function which allows you to compute the value of the Andrew's curve at every point along its path from -pi to pi.

Usage

```
andrews(x)
```

Arguments

x	input a new parameter

Value

a function with single argument, theta

Examples

```
a <- andrews(1:2)
a(0)
a(-pi)
grid <- seq(-pi, pi, length = 50)
a(grid)

plot(grid, andrews(1:2)(grid), type = "l")
plot(grid, andrews(runif(5))(grid), type = "l")
```

angular_breaks *Returns n equidistant bins between -pi and pi*

Description

Returns n equidistant bins between -pi and pi

Usage

```
angular_breaks(n)
```

Arguments

n	number of bins

animate *Animate a tour path.*

Description

This is the function that powers all of the tour animations. If you want to write your own tour animation method, the best place to start is by looking at the code for animation methods that have already implemented in the package.

Usage

```
animate(
  data,
  tour_path = grand_tour(),
  display = display_xy(),
  start = NULL,
  aps = 1,
  fps = 10,
  max_frames = Inf,
  rescale = FALSE,
  sphere = FALSE,
  ...
)
```

Arguments

data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour
display	takes the display that is suppose to be used, defaults to the xy display
start	projection to start at, if not specified, uses default associated with tour path

aps	target angular velocity (in radians per second)
fps	target frames per second (defaults to 15, to accommodate RStudio graphics device)
max_frames	the maximum number of bases to generate. Defaults to Inf for interactive use (must use Ctrl + C to terminate), and 1 for non-interactive use.
rescale	Default FALSE. If TRUE, rescale all variables to range [0,1]?
sphere	if true, sphere all variables
...	ignored

Details

See render to render animations to disk.

Value

an (invisible) list of bases visited during this tour

Examples

```
f <- flea[, 1:6]
animate(f, grand_tour(), display_xy())
# or in short
animate(f)
animate(f, max_frames = 30)

animate(f, max_frames = 10, fps = 1, aps = 0.1)
```

---

anomaly_index *Anomaly index.*

Description

Calculates an index that looks for the best projection of observations that are outside a pre-determined p-D ellipse.

Usage

```
anomaly_index()
```

areColors *Test if all entries are colors*

Description

Test if all entries are colors

Usage

```
areColors(x)
```

Arguments

x	vector

center *Center a numeric vector by subtracting off its mean.*

Description

Center a numeric vector by subtracting off its mean.

Usage

```
center(x)
```

Arguments

x	numeric vector

cmass *Central mass index.*

Description

Calculates the central mass index. See Cook and Swayne (2007) Interactive and Dynamic Graphics for Data Analysis for equations.

Usage

```
cmass()
```

dcor2d *Distance correlation index.*

Description

Computes the distance correlation based index on 2D projections of the data. `dcor2d_2` uses the faster implementation of the distance correlation for bivariate data, see `energy::dcor2d`.

Usage

```
dcor2d()

dcor2d_2()
```

dependence_tour *A dependence tour path.*

Description

The dependence tour combines a set of independent 1d tours to produce a nd tour. For the special case of 2d, this is known as a correlation tour. This tour corresponds to the multivariate method known as generalised canonical correlation, and is used to investigate dependence between groups of variables.

Usage

```
dependence_tour(pos)
```

Arguments

`pos`	a numeric vector describing which variables are mapped to which dimensions: 1 corresponds to first, 2 to second etc.

Details

Usually, you will not call this function directly, but will pass it to a method that works with tour paths like `animate`, `save_history` or `render`.

Examples

```
animate_xy(flea[, 1:3], dependence_tour(c(1, 2, 2)))
animate_xy(flea[, 1:4], dependence_tour(c(1, 2, 1, 2)))
animate_pcp(flea[, 1:6], dependence_tour(c(1, 2, 3, 2, 1, 3)))
```

display_andrews *Andrews' curves tour path animation.*

Description

Animate a nD tour path with Andrews' curves. For more details about Andrew's curves, see andrews

Usage

```
display_andrews(col = "black", palette = "Zissou 1", ...)

animate_andrews(data, tour_path = grand_tour(3), col = "black", ...)
```

Arguments

col	color to be plotted. Defaults to "black"
palette	name of color palette for point colour, used by hcl.colors, default "Zissou 1"
...	other arguments passed on to animate
data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour

See Also

animate for options that apply to all animations

Examples

```
animate_andrews(flea[, 1:6])
animate_andrews(flea[, 1:6], grand_tour(d = 3))
animate_andrews(flea[, 1:6], grand_tour(d = 6))

# It's easy to experiment with different tour paths:
animate_andrews(flea[, 1:6], guided_tour(cmass()))
```

display_density2d *Display tour path with a density and scatterplot*

Description

Animate a 2D tour path with density contour(s) and a scatterplot.

Usage

```
display_density2d(
  center = TRUE,
  axes = "center",
  half_range = NULL,
  col = "black",
  pch = 20,
  cex = 1,
  contour_quartile = c(0.25, 0.5, 0.75),
  edges = NULL,
  palette = "Zissou 1",
  axislablong = FALSE,
  ...
)

animate_density2d(data, tour_path = grand_tour(), ...)
```

Arguments

center	if TRUE, centers projected data to (0,0). This pins the center of data cloud and make it easier to focus on the changing shape rather than position.
axes	position of the axes: center, bottomleft or off
half_range	half range to use when calculating limits of projected. If not set, defaults to maximum distance from origin to each row of data.
col	color to use for points, can be a vector or hexcolors or a factor. Defaults to "black".
pch	shape of the point to be plotted. Defaults to 20.
cex	size of the point to be plotted. Defaults to 1.
contour_quartile	Vector of quartiles to plot the contours at. Defaults to 5.
edges	A two column integer matrix giving indices of ends of lines.
palette	name of color palette for point colour, used by hcl.colors, default "Zissou 1"
axislablong	text labels only for the long axes in a projection, default FALSE
...	other arguments passed on to animate and display_density2d
data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour

Examples

```
animate_density2d(flea[, 1:6])
animate(flea[, 1:6], tour_path = grand_tour(), display = display_density2d())
animate(flea[, 1:6],
  tour_path = grand_tour(),
  display = display_density2d(axes = "bottomleft")
)
```

```
animate(flea[, 1:6],
  tour_path = grand_tour(),
  display = display_density2d(half_range = 0.5)
)
animate_density2d(flea[, 1:6], tour_path = little_tour())

animate_density2d(flea[, 1:3], tour_path = guided_tour(holes()), sphere = TRUE)
animate_density2d(flea[, 1:6], center = FALSE)

# The default axes are centered, like a biplot, but there are other options
animate_density2d(flea[, 1:6], axes = "bottomleft")
animate_density2d(flea[, 1:6], axes = "off")
animate_density2d(flea[, 1:6], dependence_tour(c(1, 2, 1, 2, 1, 2)),
  axes = "bottomleft"
)

animate_density2d(flea[, -7], col = flea$species)

# You can also draw lines
edges <- matrix(c(1:5, 2:6), ncol = 2)
animate(
  flea[, 1:6], grand_tour(),
  display_density2d(axes = "bottomleft", edges = edges)
)
```

`display_depth` *Display 3d projection with depth cues*

Description

Suggestion to use gray background and colour saturation (instead of gray shading) by Graham Wills.

Usage

```
display_depth(center = TRUE, half_range = NULL, ...)

animate_depth(data, tour_path = grand_tour(3), ...)
```

Arguments

`center`	should projected data be centered to have mean zero (default: TRUE). This pins the centre of the data to the same place, and makes it easier to focus on the shape.
`half_range`	half range to use when calculating limits of projected. If not set, defaults to maximum distance from origin to each row of data.
`...`	other arguments passed on to `animate`
`data`	matrix, or data frame containing numeric columns
`tour_path`	tour path generator, defaults to 2d grand tour

See Also

animate for options that apply to all animations

Examples

```
animate_depth(flea[, 1:6])
```

---

display_dist *1d distribution tour path animation.*

Description

Animate a 1d tour path with a density plot or histogram.

Usage

```
display_dist(
  method = "density",
  center = TRUE,
  half_range = NULL,
  col = "black",
  rug = FALSE,
  palette = "Zissou 1",
  density_max = 3,
  bw = 0.2,
  scale_density = FALSE,
  ...
)

animate_dist(data, tour_path = grand_tour(1), ...)
```

Arguments

method	display method, histogram or density plot
center	should 1d projection be centered to have mean zero (default: TRUE). This pins the centre of distribution to the same place, and makes it easier to focus on the shape of the distribution.
half_range	half range to use when calculating limits of projected. If not set, defaults to maximum distance from origin to each row of data.
col	color to use for points, can be a vector or hexcolors or a factor. Defaults to "black".
rug	draw rug plot showing position of actual data points?
palette	name of color palette for point colour, used by hcl.colors, default "Zissou 1"
density_max	allow control of the y range for density plot
bw	binwidth for histogram and density, between 0-1, default 0.2

scale_density	Height of density is scaled at each projection, default FALSE
...	other arguments passed on to animate
data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour

See Also

animate for options that apply to all animations

Examples

```
animate_dist(flea[, 1:6])

# Change inputs, to color by group, fix y axis, change bin width
# and scale bar height or density at each projection
animate_dist(flea[, 1:6], col=flea$species, density_max=5)
animate_dist(flea[, 1:6], col=flea$species, density_max=5, bw=0.1)
animate_dist(flea[, 1:6], col=flea$species, scale_density=TRUE)

# When the distribution is not centred, it tends to wander around in a
# distracting manner
animate_dist(flea[, 1:6], center = FALSE)

# Alternatively, you can display the distribution with a histogram
animate_dist(flea[, 1:6], method = "hist")
```

---

display_faces *Chernoff faces tour path animation.*

Description

Animate a nD tour path with Chernoff's faces. Can display up to 18 dimensions.

Usage

```
display_faces(...)

animate_faces(data, tour_path = grand_tour(3), ...)
```

Arguments

...	other arguments passed on to animate
data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour

Details

This function requires the aplpack package to draw the Chernoff faces. See faces for more details.

See Also

animate for options that apply to all animations

Examples

```
# The drawing code is fairly slow, so this animation works best with a
# limited number of cases
flea_s <- rescale(flea[,1:6])
animate_faces(flea_s[19:24, 1:6])

animate_faces(flea_s[19:24, 1:6], grand_tour(5))
```

---

display_groupxy *Display 2D tour projections displayed separately by groups*

Description

This function is designed to allow comparisons across multiple groups, especially for examining things like two (or more) different models on the same data. The primary display is a scatterplot, with lines or contours overlaid.

Usage

```
display_groupxy(
  centr = TRUE,
  axes = "center",
  half_range = NULL,
  col = "black",
  pch = 20,
  cex = 1,
  edges = NULL,
  edges.col = "black",
  edges.width = 1,
  group_by = NULL,
  plot_xgp = TRUE,
  palette = "Zissou 1",
  shapeset = c(15:17, 23:25),
  axislablong = FALSE,
  ...
)

animate_groupxy(data, tour_path = grand_tour(), ...)
```

Arguments

centr	if TRUE, centers projected data to (0,0). This pins the center of data cloud and make it easier to focus on the changing shape rather than position.

axes	position of the axes: center, bottomleft or off
half_range	half range to use when calculating limits of projected. If not set, defaults to maximum distance from origin to each row of data.
col	color to use for points, can be a vector or hexcolors or a factor. Defaults to "black".
pch	shape of the point to be plotted. Defaults to 20.
cex	size of the point to be plotted. Defaults to 1.
edges	A two column integer matrix giving indices of ends of lines.
edges.col	colour of edges to be plotted, Defaults to "black"
edges.width	line width for edges, default 1
group_by	variable to group by. Must have less than 25 unique values.
plot_xgp	if TRUE, plots points from other groups in light grey
palette	name of color palette for point colour, used by hcl.colors, default "Zissou 1"
shapeset	numbers corresponding to shapes in base R points, to use for mapping categorical variable to shapes, default=c(15:17, 23:25)
axislablong	text labels only for the long axes in a projection, default FALSE
...	other arguments passed on to animate and display_groupxy
data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour

Examples

```
animate_groupxy(flea[, 1:6], col = flea$species,
  pch = flea$species, group_by = flea$species)
animate_groupxy(flea[, 1:6], col = flea$species,
  pch = flea$species, group_by = flea$species,
  plot_xgp = FALSE)
# Edges example
x <- data.frame(x1=runif(10, -1, 1), x2=runif(10, -1, 1), x3=runif(10, -1, 1))
x$cl <- factor(c(rep("A", 3), rep("B", 3), rep("C", 4)))
x.edges <- cbind(from=c(1,2, 4,5, 7,8,9), to=c(2,3, 5,6, 8,9,10))
x.edges.col <- factor(c(rep("A", 2), rep("B", 2), rep("C", 3)))
animate_groupxy(x[,1:3], col=x$cl, group_by=x$cl, edges=x.edges, edges.col=x.edges.col)
```

---

display_idx *Display a 1D linear aggregation index*

Description

Animate a 1D tour path for data where individuals are ranked by a multivariate index. Allows one to examine the sensitivity of the ranking on the linear combination. Variables should be scaled to be between 0-1. This is only designed to work with a local tour, or a radial tour.

Usage

```
display_idx(
  center = FALSE,
  half_range = NULL,
  abb_vars = TRUE,
  col = "red",
  cex = 3,
  panel_height_ratio = c(3, 2),
  label_x_pos = 0.7,
  label = NULL,
  label_cex = 1,
  label_col = "grey80",
  add_ref_line = TRUE,
  axis_bar_col = "#000000",
  axis_bar_lwd = 3,
  axis_label_cex_upper = 1,
  axis_label_cex_lower = 1,
  axis_bar_label_cex = 1,
  axis_bar_label_col = "#000000",
  axis_var_cex = 1,
  axis_var_col = "#000000",
  palette = "Zissou 1",
  ...
)

animate_idx(data, tour_path = grand_tour(1), ...)
```

Arguments

center	should 1d projection be centered to have mean zero (default: TRUE). This pins the centre of distribution to the same place, and makes it easier to focus on the shape of the distribution.
half_range	half range to use when calculating limits of projected. If not set, defaults to maximum distance from origin to each row of data.
abb_vars	logical, whether to abbreviate the variable name, if long
col	the color used for points, can be a vector or hexcolors or a factor, default to "red".
cex	the size used for points, default to 0.5
panel_height_ratio	input to the height argument in [graphics::layout()] for the height of data and axis panel.
label_x_pos	the x position of text label, currently labels are positioned at a fixed x value for each observation
label	the text label, a vector
label_cex	the size for text labels
label_col	the color for text labels

add_ref_line	whether to add a horizontal reference line for each observation, logical default to TRUE
axis_bar_col	the color of the axis bar
axis_bar_lwd	the width of the axis bar
axis_label_cex_upper	the size of the axis label in the upper panel
axis_label_cex_lower	the size of the axis label in the lower panel
axis_bar_label_cex	the size of the axis label
axis_bar_label_col	the color of the axis label
axis_var_cex	the size of the variable name to the right of the axis panel
axis_var_col	the color of the variable name to the right of the axis panel
palette	name of color palette for point colour, used by hcl.colors, default "Zissou 1"
...	ignored
data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour

Examples

```
data(places)
places_01 <- apply(places[1:10,1:9], 2, function(x) (x-min(x))/(max(x)-min(x)))
b <- matrix(rep(1/sqrt(9), 9), ncol=1)
places_init <- cbind(places_01, idx = as.vector(as.matrix(places_01) %*% b))
places_sorted <- places_init[order(places_init[,10]), 1:9]
animate_idx(places_sorted, tour_path = local_tour(b, angle=pi/8),
            label=as.character(places$stnum[1:9]),
            label_x_pos = 0)
```

---

display_image *Image tour path animation.*

Description

Animate a 1d tour path with an image plot. This animation requires a different input data structure, a 3d array. The first two dimensions are locations on a grid, and the 3rd dimension gives the observations to be mixed with the tour.

Usage

```
display_image(xs, ys, ...)

animate_image(data, tour_path = grand_tour(1), ...)
```

Arguments

xs	x limit that is used in making the size of the plot
ys	y limit that is used in making the size of the plot
...	other arguments passed on to animate
data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour

See Also

animate for options that apply to all animations

Examples

```
str(ozone)
animate_image(ozone)
```

---

display_pca *Display tour path with principal component scores with original axes*

Description

Animate a 2D tour path on data that has been transformed into principal components, and also show the original variable axes.

Usage

```
display_pca(
  center = TRUE,
  axes = "center",
  half_range = NULL,
  col = "black",
  pch = 20,
  cex = 1,
  pc_coefs = NULL,
  edges = NULL,
  edges.col = "black",
  palette = "Zissou 1",
  axislablong = FALSE,
  ...
)

animate_pca(data, tour_path = grand_tour(), rescale = FALSE, ...)
```

Arguments

center	if TRUE, centers projected data to (0,0). This pins the center of data cloud and make it easier to focus on the changing shape rather than position.
axes	position of the axes: center, bottomleft or off
half_range	half range to use when calculating limits of projected. If not set, defaults to maximum distance from origin to each row of data.
col	color to use for points, can be a vector or hexcolors or a factor. Defaults to "black".
pch	shape of the point to be plotted. Defaults to 20.
cex	size of the point to be plotted. Defaults to 1.
pc_coefs	coefficients relating the original variables to principal components. This is required.
edges	A two column integer matrix giving indices of ends of lines.
edges.col	colour of edges to be plotted, Defaults to "black.
palette	name of color palette for point colour, used by hcl.colors, default "Zissou 1"
axislablong	text labels only for the long axes in a projection, default FALSE
...	other arguments passed on to animate and display_slice
data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour
rescale	Default FALSE. If TRUE, rescale all variables to range [0,1].

Examples

```
flea_std <- apply(flea[,1:6], 2, function(x) (x-mean(x))/sd(x))
flea_pca <- prcomp(flea_std, center = FALSE, )
flea_coefs <- flea_pca$rotation[, 1:3]
flea_scores <- flea_pca$x[, 1:3]
animate_pca(flea_scores, pc_coefs = flea_coefs)
```

---

display_pcp *Parallel coordinates tour path animation.*

Description

Animate a nD tour path with a parallel coordinates plot.

Usage

```
display_pcp(...)

animate_pcp(data, tour_path = grand_tour(3), ...)
```

Arguments

...	other arguments passed on to animate
data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour

Details

The lines show the observations, and the points, the values of the projection matrix.

See Also

animate for options that apply to all animations

Examples

```
animate_pcp(flea[, 1:6], grand_tour(3))
animate_pcp(flea[, 1:6], grand_tour(5))
```

---

display_sage *Display tour path with a sage scatterplot*

Description

Animate a 2D tour path with a sage scatterplot that uses a radial transformation on the projected points to re-allocate the volume projected across the 2D plane.

Usage

```
display_sage(
  axes = "center",
  half_range = NULL,
  col = "black",
  pch = 20,
  gam = 1,
  R = NULL,
  palette = "Zissou 1",
  axislablong = FALSE,
  ...
)

animate_sage(data, tour_path = grand_tour(), ...)
```

Arguments

axes	position of the axes: center, bottomleft or off
half_range	half range to use when calculating limits of projected. If not set, defaults to maximum distance from origin to each row of data.
col	color to use for points, can be a vector or hexcolors or a factor. Defaults to "black".
pch	marker for points. Defaults to 20.
gam	scaling of the effective dimensionality for rescaling. Defaults to 1.
R	scale for the radial transformation. If not set, defaults to maximum distance from origin to each row of data.
palette	name of color palette for point colour, used by hcl.colors, default "Zissou 1"
axislablong	text labels only for the long axes in a projection, default FALSE
...	other arguments passed on to animate and display_sage
data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour

Examples

```
# Generate uniform samples in a 10d sphere using the geozoo package
sphere10 <- geozoo::sphere.solid.random(10)$points
# Columns need to be named before launching the tour
colnames(sphere10) <- paste0("x", 1:10)
# Standard grand tour display, points cluster near center
animate_xy(sphere10)
# Sage display, points are uniformly distributed across the disk
animate_sage(sphere10)
```

---

display_scatmat *Scatterplot matrix tour path animation.*

Description

Animate a nD tour path with a scatterplot matrix.

Usage

```
display_scatmat(...)

animate_scatmat(data, tour_path = grand_tour(3), ...)
```

Arguments

...	other arguments passed on to animate
data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour

Details

The lines show the observations, and the points, the values of the projection matrix.

See Also

`animate` for options that apply to all animations

Examples

```
animate_scatmat(flea[, 1:6], grand_tour(2))
animate_scatmat(flea[, 1:6], grand_tour(6))
```

---

display_slice *Display tour path with a sliced scatterplot*

Description

Animate a 2D tour path with a sliced scatterplot.

Usage

```
display_slice(
  center = TRUE,
  axes = "center",
  half_range = NULL,
  col = "black",
  pch_slice = 20,
  pch_other = 46,
  cex_slice = 2,
  cex_other = 1,
  v_rel = NULL,
  anchor = NULL,
  anchor_nav = "off",
  edges = NULL,
  edges.col = "black",
  palette = "Zissou 1",
  axislablong = FALSE,
  ...
)

animate_slice(data, tour_path = grand_tour(), rescale = FALSE, ...)
```

Arguments

center	if TRUE, centers projected data to (0,0). This pins the center of data cloud and make it easier to focus on the changing shape rather than position.
axes	position of the axes: center, bottomleft or off

half_range	half range to use when calculating limits of projected. If not set, defaults to maximum distance from origin to each row of data.
col	color to use for points, can be a vector or hexcolors or a factor. Defaults to "black".
pch_slice	marker for plotting points inside the slice. Defaults to 20.
pch_other	marker for plotting points outside the slice. Defaults to 46.
cex_slice	size of the points inside the slice. Defaults to 2.
cex_other	size if the points outside the slice. Defaults to 1.
v_rel	relative volume of the slice. If not set, suggested value is calculated and printed to the screen.
anchor	A vector specifying the reference point to anchor the slice. If NULL (default) the slice will be anchored at the data center.
anchor_nav	position of the anchor: center, topright or off
edges	A two column integer matrix giving indices of ends of lines.
edges.col	colour of edges to be plotted, Defaults to "black.
palette	name of color palette for point colour, used by hcl.colors, default "Zissou 1"
axislablong	text labels only for the long axes in a projection, default FALSE
...	other arguments passed on to animate and display_slice
data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour
rescale	Default FALSE. If TRUE, rescale all variables to range [0,1].

Examples

```
# Generate samples on a 3d and 5d hollow sphere using the geozoo package
sphere3 <- geozoo::sphere.hollow(3)$points
sphere5 <- geozoo::sphere.hollow(5)$points

# Columns need to be named before launching the tour
colnames(sphere3) <- c("x1", "x2", "x3")
colnames(sphere5) <- c("x1", "x2", "x3", "x4", "x5")

# Animate with the slice display using the default parameters
animate_slice(sphere3)
animate_slice(sphere5)

# Animate with off-center anchoring
anchor3 <- matrix(rep(0.7, 3), ncol=3)
anchor5 <- matrix(rep(0.3, 5), ncol=5)
animate_slice(sphere3, anchor = anchor3)
# Animate with thicker slice to capture more points in each view
animate_slice(sphere5, anchor = anchor5, v_rel = 0.02)
```

`display_stars` *Star glyph tour path animation.*

Description

Animate a nD tour path with star glyphs.

Usage

```
display_stars(...)

animate_stars(data, tour_path = grand_tour(3), ...)
```

Arguments

`...`	other arguments passed on to `stars`
`data`	matrix, or data frame containing numeric columns
`tour_path`	tour path generator, defaults to 2d grand tour

Details

Currently, scaling doesn't seem to be computed absolutely correctly, as centres move around as well as outside points.

See Also

`animate` for options that apply to all animations

Examples

```
animate_stars(flea[1:10, 1:6])
animate_stars(flea[1:10, 1:6], grand_tour(5))
animate_stars(flea[, 1:6], grand_tour(5))
animate_stars(flea[1:10, 1:6], grand_tour(5),
  col.stars = rep("grey50", 10), radius = FALSE
)
```

display_stereo *Anaglpyh tour path animation.*

Description

Uses red-blue anaglyphs to display a 3d tour path. You'll need some red- blue glasses to get much out of this displays!

Usage

```
display_stereo(blue, red, cex = 1, ...)

animate_stereo(
  data,
  tour_path = grand_tour(3),
  blue = rgb(0, 0.91, 0.89),
  red = rgb(0.98, 0.052, 0),
  ...
)
```

Arguments

blue	blue colour (for right eye)
red	red colour (for left eye)
cex	size of the point to be plotted. Defaults to 1.
...	other arguments passed on to animate
data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour

Examples

```
animate_stereo(flea[, 1:6])
```

display_trails *Display tour path with trails*

Description

Animate a 2D tour path with a point trails

Usage

```
display_trails(
  center = TRUE,
  axes = "center",
  half_range = NULL,
  col = "black",
  pch = 20,
  cex = 1,
  past = 3,
  axislablong = FALSE,
  ...
)

animate_trails(data, tour_path = grand_tour(), ...)
```

Arguments

center	if TRUE, centers projected data to (0,0). This pins the center of data cloud and make it easier to focus on the changing shape rather than position.
axes	position of the axes: center, bottomleft or off
half_range	half range to use when calculating limits of projected. If not set, defaults to maximum distance from origin to each row of data.
col	color to be plotted. Defaults to "black"
pch	shape of the point to be plotted. Defaults to 20.
cex	magnification of plotting text relative to default. Defaults to 1.
past	draw line between current projection and projection `past` steps ago
axislablong	text labels only for the long axes in a projection, default FALSE
...	other arguments passed on to `animate` and `display_xy`
data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour

Examples

```
animate_trails(flea[,1:6], col=flea$species)
```

---

display_xy *Display tour path with a scatterplot*

Description

Animate a 2D tour path with a scatterplot.

Usage

```
display_xy(
  center = TRUE,
  axes = "center",
  half_range = NULL,
  col = "black",
  pch = 20,
  cex = 1,
  edges = NULL,
  edges.col = "black",
  edges.width = 1,
  obs_labels = NULL,
  ellipse = NULL,
  ellc = NULL,
  ellmu = NULL,
  ellmarks = TRUE,
  palette = "Zissou 1",
  shapeset = c(15:17, 23:25),
  axislablong = FALSE,
  ...
)

animate_xy(data, tour_path = grand_tour(), ...)
```

Arguments

center	if TRUE, centers projected data to (0,0). This pins the center of data cloud and make it easier to focus on the changing shape rather than position.
axes	position of the axes: center, bottomleft or off
half_range	half range to use when calculating limits of projected. If not set, defaults to maximum distance from origin to each row of data.
col	color to use for points, can be a vector or hexcolors or a factor. Defaults to "black".
pch	shape of the point to be plotted, can be a factor or integer. Defaults to 20.
cex	size of the point to be plotted. Defaults to 1.
edges	A two column integer matrix giving indices of ends of lines.
edges.col	colour of edges to be plotted, Defaults to "black"
edges.width	line width for edges, default 1
obs_labels	vector of text labels to display
ellipse	pxp variance-covariance matrix defining ellipse, default NULL. Useful for comparing data with some null hypothesis
ellc	This can be considered the equivalent of a critical value, used to scale the ellipse larger or smaller to capture more or fewer anomalies. Default 3.
ellmu	This is the centre of the ellipse corresponding to the mean of the normal population. Default vector of 0's

ellmarks	mark the extreme points with red crosses, default TRUE
palette	name of color palette for point colour, used by hcl.colors, default "Zissou 1"
shapeset	numbers corresponding to shapes in base R points, to use for mapping categorical variable to shapes, default=c(15:17, 23:25)
axislablong	text labels only for the long axes in a projection, default FALSE
...	other arguments passed on to animate and display_xy
data	matrix, or data frame containing numeric columns
tour_path	tour path generator, defaults to 2d grand tour

Examples

```
animate_xy(flea[, 1:6])
animate(flea[, 1:6], tour_path = grand_tour(), display = display_xy())
# This won't do anything because the flea data is standardised
# but use rescale option to force scaling before displaying
animate(flea[, 1:6],
  tour_path = grand_tour(),
  display = display_xy(),
  rescale = TRUE
)
animate(flea[, 1:6],
  tour_path = grand_tour(),
  display = display_xy(half_range = 0.5)
)
animate_xy(flea[, 1:6], tour_path = little_tour())
animate_xy(flea[, 1:3], tour_path = guided_tour(holes()), sphere = TRUE)
animate_xy(flea[, 1:6], center = FALSE)

# The default axes are centered, like a biplot, but there are other options
animate_xy(flea[, 1:6], axes = "bottomleft")
animate_xy(flea[, 1:6], axes = "off")
animate_xy(flea[, 1:6], dependence_tour(c(1, 2, 1, 2, 1, 2)),
  axes = "bottomleft"
)

animate_xy(flea[, -7], col = flea$species)
animate_xy(flea[, -7], col = flea$species,
             pch = flea$species)

animate_xy(flea[, -7], col = flea$species,
  obs_labels=as.character(1:nrow(flea)), axes="off")

# You can also draw lines
edges <- matrix(c(1:5, 2:6), ncol = 2)
animate(
  flea[, 1:6], grand_tour(),
  display_xy(axes = "bottomleft", edges = edges)
)
# An ellipse can be drawn on the data using a specified var-cov
animate_xy(flea[, 1:6], axes = "off", ellipse=cov(flea[,1:6]))
```

draw_tour_axes *Draw tour axes on the projected data with base graphics*

Description

Draw tour axes on the projected data with base graphics

Usage

```
draw_tour_axes(
  proj,
  labels,
  limits = 1,
  position = "center",
  axis.col = "grey50",
  axis.lwd = 1,
  axis.text.col = "grey50",
  longlabels = FALSE,
  ...
)
```

Arguments

proj	matrix of projection coefficients
labels	variable names for the axes, of length the same as the number of rows of proj
limits	value setting the lower and upper limits of projected data, default 1
position	position of the axes: center (default), bottomleft or off
axis.col	colour of axes, default "grey50"
axis.lwd	linewidth of axes, default 1
axis.text.col	colour of axes text, default "grey50"
longlabels	text labels only for the long axes in a projection, default FALSE
...	other arguments passed

Examples

```
data(flea)
flea_std <- apply(flea[,1:6], 2, function(x) (x-mean(x))/sd(x))
prj <- basis_random(ncol(flea[,1:6]), 2)
flea_prj <- as.data.frame(as.matrix(flea_std) %*% prj)
par(pty = "s", mar = rep(0.1, 4))
plot(flea_prj$V1, flea_prj$V2,
     xlim = c(-3, 3), ylim = c(-3, 3),
     xlab="P1", ylab="P2")
draw_tour_axes(prj, colnames(flea)[1:6], limits=3)
```

```
plot(flea_prj$V1, flea_prj$V2,
     xlim = c(-3, 3), ylim = c(-3, 3),
     xlab="P1", ylab="P2")
draw_tour_axes(prj, colnames(flea)[1:6], limits=3, position="bottomleft")
draw_tour_axes(prj, colnames(flea)[1:6], longlabels=TRUE)
```

`estimate_eps` *Estimate cutoff eps for section pursuit.*

Description

Estimate cutoff eps for section pursuit.

Usage

```
estimate_eps(N, p, res, K, K_theta, r_breaks)
```

Arguments

`N`	total number of points in the input data.
`p`	number of dimensions of the input data.
`res`	resolution, (slice radius)/(data radius)
`K`	total number of bins
`K_theta`	number of angular bins
`r_breaks`	boundaries of the radial bins

`Flea measurements` *Flea beatle measurements*

Description

This data is from a paper by A. A. Lubischew, "On the Use of Discriminant Functions in Taxonomy", Biometrics, Dec 1962, pp.455-477. Data is standardized, and original units are in flea_raw.

Usage

```
flea
```

Format

A 74 x 7 numeric array

Details

- tars1, width of the first joint of the first tarsus in microns (the sum of measurements for both tarsi)
- tars2, the same for the second joint
- head, the maximal width of the head between the external edges of the eyes in 0.01 mm
- ade1, the maximal width of the aedeagus in the fore-part in microns
- ade2, the front angle of the aedeagus (1 unit = 7.5 degrees)
- ade3, the aedeagus width from the side in microns
- species, which species is being examined - concinna, heptapotamica, heikertingeri

Examples

```
head(flea)
animate_xy(flea[, -7])
animate_xy(flea[, -7], col = flea[, 7])
```

`frozen_guided_tour` *The frozen guided tour*

Description

The frozen guided tour

Usage

```
frozen_guided_tour(frozen, index_f, d = 2, max.tries = 25)
```

Arguments

`frozen`	matrix of frozen variables, as described in `freeze`
`index_f`	the index function to optimise.
`d`	target dimensionality
`max.tries`	the maximum number of unsuccessful attempts to find a better projection before giving up

See Also

`cmass`, `holes` and `lda_pp` for examples of index functions. The function should take a numeric matrix and return a single number, preferrably between 0 and 1.

Examples

```
frozen <- matrix(NA, nrow = 4, ncol = 2)
frozen[3, ] <- .5
animate_xy(flea[, 1:4], frozen_guided_tour(frozen, holes()))
```

`frozen_tour` *A frozen tour path.*

Description

A frozen tour fixes some of the values of the orthonormal projection matrix and allows the others to vary freely according to any of the other tour methods. This frozen tour is a frozen grand tour. See `frozen_guided_tour` for a frozen guided tour.

Usage

```
frozen_tour(d = 2, frozen)
```

Arguments

`d`	target dimensionality
`frozen`	matrix of frozen variables, as described in `freeze`

Details

Usually, you will not call this function directly, but will pass it to a method that works with tour paths like `animate`, `save_history` or `render`.

Examples

```
frozen <- matrix(NA, nrow = 4, ncol = 2)
frozen[3, ] <- .5
animate_xy(flea[, 1:4], frozen_tour(2, frozen))

frozen <- matrix(NA, nrow = 4, ncol = 2)
frozen[1, 1] <- 0.5
animate_xy(flea[, 1:4], frozen_tour(2, frozen))

# Doesn't work - a bug?
frozen <- matrix(NA, nrow = 4, ncol = 2)
frozen[1:2, 1] <- 1 / 4
animate_xy(flea[, 1:4], frozen_tour(2, frozen))

## Not run:
# This freezes one entire direction which causes a problem,
# and is caught by error handling.
# If you want to do this it would be best with a dependence
# tour, with one variable set one axis, eg 3rd variable to
# x axis would be indicated from the code below
frozen <- matrix(NA, nrow = 4, ncol = 2)
frozen[3, ] <- c(0, 1)
animate_xy(flea[, 1:4], frozen_tour(2, frozen))

## End(Not run)
```

```
# Two frozen variables in five.
frozen <- matrix(NA, nrow = 5, ncol = 2)
frozen[3, ] <- .5
frozen[4, ] <- c(-.2, .2)
animate_xy(flea[, 1:5], frozen_tour(2, frozen))
```

---

grand_tour *A grand tour path.*

Description

This method generates target bases by randomly sampling on the space of all d-dimensional planes in p-space.

Usage

```
grand_tour(d = 2, ...)
```

Arguments

d	target dimensionality
...	arguments sent to the generator

Details

Usually, you will not call this function directly, but will pass it to a method that works with tour paths like animate, save_history or render.

Examples

```
# All animation methods use the grand tour path by default
animate_dist(flea[, 1:6])
animate_xy(flea[, 1:6])
animate_pcp(flea[, 1:6])
animate_pcp(flea[, 1:6], grand_tour(4))

# The grand tour is a function:
tour2d <- grand_tour(2)
is.function(tour2d)

# with two parameters, the previous projection and the data set
args(tour2d)
# if the previous projection is null, it will generate a starting
# basis, otherwise the argument is ignored
tour2d(NULL, mtcars)
# the data argument is just used to determine the correct dimensionality
# of the output matrix
tour2d(NULL, mtcars[, 1:2])
```

`guided_anomaly_tour` *A guided anomaly tour path.*

Description

The guided anomaly tour is a variation of the guided tour that is using an ellipse to determine anomalies on which to select target planes.

Usage

```
guided_anomaly_tour(
  index_f,
  d = 2,
  alpha = 0.5,
  cooling = 0.99,
  max.tries = 25,
  max.i = Inf,
  ellipse,
  ellc = NULL,
  ellmu = NULL,
  search_f = search_geodesic,
  ...
)
```

Arguments

`index_f`	the section pursuit index function to optimise. The function needs to take two arguments, the projected data, indexes of anomalies.
`d`	target dimensionality
`alpha`	the initial size of the search window, in radians
`cooling`	the amount the size of the search window should be adjusted by after each step
`max.tries`	the maximum number of unsuccessful attempts to find a better projection before giving up
`max.i`	the maximum index value, stop search if a larger value is found
`ellipse`	pxp variance-covariance matrix defining ellipse, default NULL. Useful for comparing data with some hypothesized null.
`ellc`	This can be considered the equivalent of a critical value, used to scale the ellipse larger or smaller to capture more or fewer anomalies. Default 3.
`ellmu`	This is the centre of the ellipse corresponding to the mean of the normal population. Default vector of 0's
`search_f`	the search strategy to use
`...`	arguments sent to the search_f

Details

Usually, you will not call this function directly, but will pass it to a method that works with tour paths like animate_xy, save_history or render.

See Also

slice_index for an example of an index functions. search_geodesic, search_better, search_better_random for different search strategies

Examples

```
animate_xy(flea[, 1:6], guided_anomaly_tour(anomaly_index(),
  ellipse=cov(flea[,1:6])), ellipse=cov(flea[,1:6]), axes="off")
```

---

guided_section_tour *A guided section tour path.*

Description

The guided section tour is a variation of the guided tour that is using a section pursuit index for the selection of target planes.

Usage

```
guided_section_tour(
  index_f,
  d = 2,
  alpha = 0.5,
  cooling = 0.99,
  max.tries = 25,
  max.i = Inf,
  v_rel = NULL,
  anchor = NULL,
  search_f = search_geodesic,
  ...
)
```

Arguments

index_f	the section pursuit index function to optimise. The function needs to take three arguments, the projected data, the vector of distances from the current projection plane, and the slice thickness h.
d	target dimensionality
alpha	the initial size of the search window, in radians
cooling	the amount the size of the search window should be adjusted by after each step

max.tries	the maximum number of unsuccessful attempts to find a better projection before giving up
max.i	the maximum index value, stop search if a larger value is found
v_rel	relative volume of the slice. If not set, suggested value is calculated and printed to the screen.
anchor	A vector specifying the reference point to anchor the slice. If NULL (default) the slice will be anchored at the data center.
search_f	the search strategy to use
...	arguments sent to the search_f

Details

Usually, you will not call this function directly, but will pass it to a method that works with tour paths like animate_slice, save_history or render.

See Also

slice_index for an example of an index functions. search_geodesic, search_better, search_better_random for different search strategies

Examples

```
# Generate samples on a 3d hollow sphere using the geozoo package
set.seed(12345)
sphere3 <- geozoo::sphere.hollow(3)$points
# Columns need to be named before launching the tour
colnames(sphere3) <- c("x1", "x2", "x3")
# Off-center anchoring
anchor3 <- matrix(rep(0.75, 3), ncol=3)
# Index setup
r_breaks <- linear_breaks(5, 0, 1)
a_breaks <- angular_breaks(10)
eps <- estimate_eps(nrow(sphere3), ncol(sphere3), 0.1 / 1, 5 * 10, 10, r_breaks)
idx <- slice_index(r_breaks, a_breaks, eps, bintype = "polar", power = 1, reweight = TRUE, p = 3)
# Running the guided section tour select sections showing a big hole in the center
animate_slice(sphere3, guided_section_tour(idx, v_rel = 0.1, anchor = anchor3, max.tries = 5),
  v_rel = 0.1, anchor = anchor3
)
```

---

guided_tour *A guided tour path.*

Description

Instead of choosing new projections at random like the grand tour, the guided tour always tries to find a projection that is more interesting than the current projection.

Usage

```
guided_tour(
  index_f,
  d = 2,
  cooling = 0.99,
  max.tries = 25,
  max.i = Inf,
  search_f = search_geodesic,
  n_jellies = 30,
  n_sample = 100,
  alpha = 0.5,
  ...
)
```

Arguments

index_f	the index function to optimise.
d	target dimensionality
cooling	the amount the size of the search window should be adjusted by after each step
max.tries	the maximum number of unsuccessful attempts to find a better projection before giving up
max.i	the maximum index value, stop search if a larger value is found
search_f	the search strategy to use: search_geodesic, search_better, search_better_random, search_polish. Default is search_geodesic.
n_jellies	only used for search_jellyfish, the number of jellyfish to use
n_sample	number of samples to generate if search_f is search_polish
alpha	the initial size of the search window, in radians
...	arguments sent to the search_f

Details

Currently the index functions only work in 2d.

Usually, you will not call this function directly, but will pass it to a method that works with tour paths like animate, save_history or render.

See Also

cmass, holes and lda_pp for examples of index functions. The function should take a numeric matrix and return a single number, preferably between 0 and 1. search_geodesic, search_better, search_better_random for different search strategies

Examples

```
flea_std <- apply(flea[,1:6], 2, function(x) (x-mean(x))/sd(x))
animate_xy(flea_std, guided_tour(holes()), sphere = TRUE)
```

```
animate_xy(flea_std, guided_tour(holes(), search_f = search_better_random), sphere = TRUE)
animate_dist(flea_std, guided_tour(holes(), 1), sphere = TRUE)
animate_xy(flea_std, guided_tour(lda_pp(flea$species)), sphere = TRUE, col = flea$species)

# save_history is particularly useful in conjunction with the
# guided tour as it allows us to look at the tour path in many different
# ways
f <- flea_std[, 1:3]
tries <- replicate(5, save_history(f, guided_tour(holes())), simplify = FALSE)
```

---

holes *Holes index.*

Description

Calculates the holes index. See Cook and Swayne (2007) Interactive and Dynamic Graphics for Data Analysis for equations.

Usage

```
holes()
```

---

interpolate *Interpolate geodesically between bases.*

Description

This function takes a set of bases and produces a tour by geodesically interpolating between each basis

Usage

```
interpolate(basis_set, angle = 0.05, cycle = FALSE)
```

Arguments

basis_set	input basis set
angle	target distance (in radians) between bases
cycle	For planned_tour cycle through continuously (TRUE) or stop after first pass (FALSE)

Examples

```
t1 <- save_history(flea[, 1:6], grand_tour(1), max = 3)
dim(t1)
dim(interpolate(t1, 0.01))
dim(interpolate(t1, 0.05))
dim(interpolate(t1, 0.1))
t2 <- save_history(flea[, 1:6], grand_tour(2), max = 2)
dim(interpolate(t2, 0.05))
```

Laser measurements *Turnable laser measurements from Bellcore*

Description

This data came from an investigation of an experimental laser at Bellcore. It was a tunable laser, in the sense that both its wavelength and power output were controllable.

Format

A 64 x 4 numeric array

Details

Rotation helped the experimental physicists to characterize the laser, which turned out not to be a very good one, due to its unstable operating region.

This data initially came to the statistics research group when Janette Cooper asked Paul Tukey to help her analyze the data she had collected to describe the laser.

- ifront, current applied to the front of the laser
- iback, current applied to the back of the laser
- power, output power
- lambda, output wavelength

Examples

```
head(laser)
animate_xy(laser[, -4])
```

lda_pp *LDA projection pursuit index.*

Description

Calculate the LDA projection pursuit index. See Cook and Swayne (2007) Interactive and Dynamic Graphics for Data Analysis for equations.

Usage

```
lda_pp(cl)
```

Arguments

cl	class to be used. Such as "color"

linear_breaks *Returns n equidistant bins between a and b*

Description

Returns n equidistant bins between a and b

Usage

```
linear_breaks(n, a, b)
```

Arguments

n	number of bins
a	lower bound
b	upper bound

little_tour *A little tour path.*

Description

The little tour is a planned tour that travels between all axis parallel projections. (John McDonald named this type of tour.)

Usage

```
little_tour(d = 2)
```

Arguments

d	target dimensionality

Details

Usually, you will not call this function directly, but will pass it to a method that works with tour paths like `animate`, `save_history` or `render`.

Examples

```
animate_xy(flea[, 1:6], little_tour())
animate_pcp(flea[, 1:6], little_tour(3))
animate_scatmat(flea[, 1:6], little_tour(3))
animate_pcp(flea[, 1:6], little_tour(4))
```

local_tour *A local tour path.*

Description

The local tour alternates between the starting position and a nearby random projection.

Usage

```
local_tour(start, angle = pi/4)
```

Arguments

start	initial projection matrix
angle	distance in radians to stay within

Details

Usually, you will not call this function directly, but will pass it to a method that works with tour paths like `animate`, `save_history` or `render`.

Examples

```
animate_xy(flea[, 1:3], local_tour(basis_init(3, 2)))
animate_xy(flea[, 1:3], local_tour(basis_init(3, 2), 0.2))
animate_xy(flea[, 1:3], local_tour(basis_random(3, 2), 0.2))
```

---

mahal_dist *Calculate the Mahalanobis distance between points and center.*

Description

Computes the Mahalanobis distance using a provided variance-covariance matrix of observations from 0.

Usage

```
mahal_dist(x, vc)
```

Arguments

x	matrix of data
vc	pre-determined variance-covariance matrix

---

manual_slice *Manually slice along a variable axis.*

Description

The manual slice tour takes the current projection, with display_slice, and changes the slice center.

Usage

```
manual_slice(
  data,
  proj,
  var = 1,
  nsteps = 20,
  v_rel = 0.01,
  rescale = FALSE,
  sphere = FALSE,
  col = "black",
```

```
  half_range = NULL,
  anchor_nav = "topright",
  palette = "Zissou 1",
  ...
)
```

Arguments

data	numeric matrix, with n rows and p columns
proj	projection from which slices are constructed
var	variable axis to run the center along: 1, ..., p
nsteps	number of changes in center to make
v_rel	relative volume of the slice. If not set, suggested value is calculated and printed to the screen.
rescale	Default FALSE. If TRUE, rescale all variables to range [0,1]?
sphere	if true, sphere all variables
col	color to use for points, can be a vector or hexcolors or a factor. Defaults to "black".
half_range	half range to use when calculating limits of projected. If not set, defaults to maximum distance from origin to each row of data.
anchor_nav	position of the anchor: center, topright or off
palette	name of color palette for point colour, used by hcl.colors, default "Zissou 1"
...	other options passed to output device

Examples

```
# Note that you might need to use the quartz()
# on OSX to see the animation
sphere5 <- data.frame(geozoo::sphere.hollow(5)$points)
proj <- basis_random(5, 2)
manual_slice(sphere5, proj, var=3, nsteps=10, rescale=TRUE, half_range=1.5)
```

---

mapColors *Map vector of factors to color*

Description

Map vector of factors to color

Usage

```
mapColors(x, palette)
```

Arguments

x	vector
palette	name of color palette for point colour, used by hcl.colors, default "Zissou 1"

mapShapes *Map vector of factors to pch*

Description

Map vector of factors to pch

Usage

```
mapShapes(x, shapeset)
```

Arguments

x	vector
shapeset	vector of integers indicating point shapes

MIC *Maximum and total information coefficient index.*

Description

Compute the maximum and total information coefficient indexes, see `minerva::mine`.

Usage

```
MIC()

TIC()
```

norm_bin *Normality index.*

Description

Compares the similarity between the projected distribution and a normal distribution.

- norm_bin: compares the count in 100 histogram bins
- norm_kol: compares the cdf based on the Kolmogorov–Smirnov test (KS test)

Usage

```
norm_bin(nr)

norm_kol(nr)
```

Arguments

nr	The number of rows in the target matrix

Examples

```
# manually compute the norm_kol index
# create the index function
set.seed(123)
index <- norm_kol(nrow(flea[, 1:3]))
# create the projection
proj <- matrix(c(1, 0, 0), nrow = 3)
# pre-process the example data
flea_s <- sphere_data(flea[, 1:3])
# produce the index value
index(flea_s %*% proj)
```

Olive oil measurements

Olive oil samples from Italy

Description

This data is from a paper by Forina, Armanino, Lanteri, Tiscornia (1983) Classification of Olive Oils from their Fatty Acid Composition, in Martens and Russwurm (ed) Food Research and Data Anlysis. We thank Prof. Michele Forina, University of Genova, Italy for making this dataset available.

Format

A 572 x 10 numeric array

Details

- region Three super-classes of Italy: North, South and the island of Sardinia
- area Nine collection areas: three from North, four from South and 2 from Sardinia
- palmitic, palmitoleic, stearic, oleic, linoleic, linolenic, arachidic, eicosenoic fatty acids percent x 100

Examples

```
head(olive)
animate_xy(olive[, c(7, 9, 10)])
animate_xy(olive[, c(7, 9, 10)], col = olive[, 1])
```

Ozone measurements *Monthly ozone measurements over Central America*

Description

This data set is a subset of the data from the 2006 ASA Data expo challenge. The data are monthly ozone averages on a very coarse 24 by 24 grid covering Central America, from Jan 1995 to Dec 2000. The data is stored in a 3d area with the first two dimensions representing latitude and longitude, and the third representing time.

Format

A 24 x 24 x 72 numeric array

Examples

```
example(display_image)
```

path_curves *Draw the path that the geodesics took.*

Description

This computes the projected values of each observation at each step, and allows you to recreate static views of the animated plots.

Usage

```
path_curves(history, data = attr(history, "data"))
```

Arguments

history	list of bases produced by save_history (or otherwise)
data	dataset to be projected on to bases

Examples

```
path1d <- save_history(flea[, 1:6], grand_tour(1), 3)
path2d <- save_history(flea[, 1:6], grand_tour(2), 3)

if (require("ggplot2")) {
  plot(path_curves(path1d))
  plot(path_curves(interpolate(path1d)))

  plot(path_curves(path2d))
  plot(path_curves(interpolate(path2d)))
```

```
  # Instead of relying on the built in plot method, you might want to
  # generate your own.  Here are few examples of alternative displays:

  df <- path_curves(path2d)
  ggplot(data = df, aes(x = step, y = value, group = obs:var, colour = var)) +
    geom_line() +
    facet_wrap(~obs)

  library(tidyr)
  ggplot(
    data = pivot_wider(df,
      id_cols = c(obs, step),
      names_from = var, names_prefix = "Var",
      values_from = value
    ),
    aes(x = Var1, y = Var2)
  ) +
    geom_point() +
    facet_wrap(~step) +
    coord_equal()
}
```

---

path_dist *Compute distance matrix from bases.*

Description

Compute distance matrix from bases.

Usage

```
path_dist(history)
```

Arguments

history	history of the plots

Examples

```
# This code is to be used as an example but you should increase
# the max from 2 to 50, say, to check tour coverage.
flea_std <- apply(flea[,1:6], 2, function(x) (x-mean(x))/sd(x))
grand <- interpolate(save_history(flea_std, max = 2), 0.2)
# The grand tour  ----------------------------
# Look at the tour path in a tour, how well does it cover a sphere
# Using MDS to summarise the high-d space of projections
# Last basis is a duplicate, needs removing
d <- path_dist(grand[,,-dim(grand)[[3]]])
ord <- as.data.frame(MASS::isoMDS(d)$points)
```

```
require(ggplot2)
ggplot(data = ord, aes(x=V1, y=V2)) +
  geom_path() +
  coord_equal() +
  labs(x = NULL, y = NULL)

# Compare five guided tours  ----------------------------
holes1d <- guided_tour(holes(), 1)
tour_reps <- replicate(5, save_history(flea_std, holes1d, max = 2),
  simplify = FALSE
)
tour_reps2 <- lapply(tour_reps, interpolate, 0.2)

bases <- unlist(lapply(tour_reps2, as.list), recursive = FALSE)
class(bases) <- "history_list"
index_values <- paths_index(tour_reps2, holes())
index_values$step <- index_values$step.1
d <- path_dist(bases)
ord <- as.data.frame(cmdscale(d, 2))

info <- cbind(ord, index_values)
ggplot(data = info, aes(x = step, y = value, group = try)) +
  geom_line()
##ggplot(data = info, aes(x = V1, y = V2, group = try)) +
##  geom_path() +
##  geom_point(aes(size = value)) +
##  coord_equal()
##last_plot() + facet_wrap(~try)
```

---

path_index *Compute index values for a tour history.*

Description

Compute index values for a tour history.

Usage

```
path_index(history, index_f, data = attr(history, "data"))
```

Arguments

history	list of bases produced by save_history (or otherwise)
index_f	index function to apply to each basis
data	dataset to be projected on to bases

See Also

save_history for options to save history

Examples

```
fl_holes <- save_history(flea[, 1:6], guided_tour(holes()), sphere = TRUE)
path_index(fl_holes, holes())
## path_index(fl_holes, cmass())

plot(path_index(fl_holes, holes()), type = "l")
## plot(path_index(fl_holes, cmass()), type = "l")


# Use interpolate to show all intermediate bases as well
hi <- path_index(interpolate(fl_holes), holes())
hi
plot(hi)
```

---

pda_pp *PDA projection pursuit index.*

Description

Calculate the PDA projection pursuit index. See Lee and Cook (2009) A Projection Pursuit Index for Large p, Small n Data

Usage

```
pda_pp(cl, lambda = 0.2)
```

Arguments

cl	class to be used. Such as "color"
lambda	shrinkage parameter (0 = no shrinkage, 1 = full shrinkage)

Places Ratings *Ratings of different locations across North America*

Description

The "places data" were distributed to interested ASA members a few years ago so that they could apply contemporary data analytic methods to describe these data and then present results in a poster session at the ASA annual conference. Latitude and longitude have been added by Paul Tukey.

Format

A 329 x 14 numeric array

Details

The first dataset is taken from the Places Rated Almanac, by Richard Boyer and David Savageau, copyrighted and published by Rand McNally. This book order (SBN) number is 0-528-88008-X, and it retails for $14.95 . The data are reproduced on disk by kind permission of the publisher, and with the request that the copyright notice of Rand McNally, and the names of the authors appear in any paper or presentation using these data.

The nine rating criteria used by Places Rated Almanac are: Climate and Terrain Housing Health Care and Environment Crime Transportation Education The Arts Recreation Economics

For all but two of the above criteria, the higher the score, the better. For Housing and Crime, the lower the score the better.

The scores are computed using the following component statistics for each criterion (see the Places Rated Almanac for details):

Climate and Terrain: very hot and very cold months, seasonal temperature variation, heating- and cooling-degree days, freezing days, zero-degree days, ninety-degree days.

Housing: utility bills, property taxes, mortgage payments.

Health Care and Environment: per capita physicians, teaching hospitals, medical schools, cardiac rehabilitation centers, comprehensive cancer treatment centers, hospices, insurance/hospitalization costs index, flouridation of drinking water, air pollution.

Crime: violent crime rate, property crime rate.

Transportation: daily commute, public transportation, Interstate highways, air service, passenger rail service.

Education: pupil/teacher ratio in the public K-12 system, effort index in K-12, accademic options in higher education.

The Arts: museums, fine arts and public radio stations, public television stations, universities offering a degree or degrees in the arts, symphony orchestras, theatres, opera companies, dance companies, public libraries.

Recreation: good restaurants, public golf courses, certified lanes for tenpin bowling, movie theatres, zoos, aquariums, family theme parks, sanctioned automobile race tracks, pari-mutuel betting attractions, major- and minor- league professional sports teams, NCAA Division I football and basketball teams, miles of ocean or Great Lakes coastline, inland water, national forests, national parks, or national wildlife refuges, Consolidated Metropolitan Statistical Area access.

Economics: average household income adjusted for taxes and living costs, income growth, job growth.

Examples

```
head(places)
animate_xy(places[, 1:9])
```

`planned_tour` *A planned tour path.*

Description

The planned tour takes you from one basis to the next in a set order. Once you have visited all the planned bases, you either stop or start from the beginning once more (if `cycle = TRUE`).

Usage

```
planned_tour(basis_set, cycle = FALSE)

planned2_tour(basis_set)
```

Arguments

`basis_set`	the set of bases as a list of projection matrices or a 3d array
`cycle`	cycle through continuously (`TRUE`) or stop after first pass (`FALSE`)

Details

Usually, you will not call this function directly, but will pass it to a method that works with tour paths like `animate`, `save_history` or `render`.

See Also

The `little_tour`, a special type of planned tour which cycles between all axis parallel projections.

Examples

```
twod <- save_history(flea[, 1:3], max = 5)
str(twod)
animate_xy(flea[, 1:3], planned_tour(twod))
animate_xy(flea[, 1:3], planned_tour(twod, TRUE))

oned <- save_history(flea[, 1:6], grand_tour(1), max = 3)
animate_dist(flea[, 1:6], planned_tour(oned))
```

proj_dist *Calculate the distance between two bases.*

Description

Computes the Frobenius norm between two bases, in radians. This is equals to the Euclidean norm of the vector of principal angles between the two subspaces.

Usage

```
proj_dist(x, y)
```

Arguments

x	projection matrix a
y	projection matrix b

radial_tour *A radial tour path.*

Description

The radial tour rotates a chosen variable axis out of the current projection.

Usage

```
radial_tour(start, mvar = 1, ...)
```

Arguments

start	initial projection matrix
mvar	variable(s) chosen to rotate out
...	additional arguments for drawing

Details

Usually, you will not call this function directly, but will pass it to a method that works with tour paths like animate, save_history or render.

Examples

```
animate_xy(flea[, 1:6], radial_tour(basis_random(6, 2), mvar = 4), rescale=TRUE)
animate_xy(flea[, 1:6], radial_tour(basis_random(6, 2), mvar = c(3,4)), rescale=TRUE)
animate_dist(flea[, 1:6], radial_tour(basis_random(6, 1), mvar = 4), rescale=TRUE)
animate_scatmat(flea[, 1:6], radial_tour(basis_random(6, 3), mvar = 4), rescale=TRUE)
```

`Rat CNS` *Rat CNS Gene Expression*

Description

Columns:

Format

A 112 x 11 numeric array

Details

e11 e13 e15 e18 e21 p0 p7 p14 a class1 class2

- e11, an ebryonic timepoint from the original data with the number corresponding to the day
- e13, an ebryonic timepoint from the original data with the number corresponding to the day
- e15, an ebryonic timepoint from the original data with the number corresponding to the day
- e18, an ebryonic timepoint from the original data with the number corresponding to the day
- e21, an ebryonic timepoint from the original data with the number corresponding to the day
- p0, a postnatal timpoint from the original data with the number corresponding to the day
- p7, a postnatal timpoint from the original data with the number corresponding to the day
- p14, a postnatal timpoint from the original data with the number corresponding to the day
- a, a postnatal timpoint from the original data. It is equivalent to p90.
- class1, is the high-level class: its range is 1:4
- class2, breaks down the high-level classes, so its range is 1:14

Rows: Each case is a gene (or gene family?) And each cell is the gene expression level for that gene at time t, averaging a few measured values and normalizing using the maximum expression value for that gene.

Reference (available on the web at pnas.org): Large-scale temporal gene expression mapping of central nervous system development by X. Wen, S. Fuhrman, G. S. Michaels, D. B. Carr, S. Smith, J. L. Barker, R. Somogyi in the Proceedings of the National Academy of Science, Vol 95, pp. 334-339, January 1998

References

https://www.pnas.org

Examples

```
head(ratcns)
animate_xy(ratcns[, 1:8], col = ratcns[, 10])
```

render *Render frames of animation to disk*

Description

Render frames of animation to disk

Usage

```
render(
  data,
  tour_path,
  display,
  dev,
  ...,
  apf = 1/10,
  frames = 50,
  rescale = FALSE,
  sphere = FALSE,
  start = NULL
)
```

Arguments

data	matrix, or data frame containing numeric columns
tour_path	tour path generator
display	the method used to render the projected data, e.g. display_xy, display_pcp
dev	name of output device to use (e.g. png, pdf)
...	other options passed to output device
apf	angle (in radians) per frame
frames	number of frames in output
rescale	default FALSE. If TRUE, rescale all variables to range [0,1]
sphere	if true, sphere all variables
start	starting projection. If NULL, uses path default.

Examples

```
tmp_path <- tempdir()
render(flea[, 1:6], grand_tour(), display_xy(), "pdf",
  frames = 3,
  file.path(tmp_path, "test.pdf")
)
render(flea[, 1:6], grand_tour(), display_xy(), "png",
  frames = 3,
  file.path(tmp_path, "test-%03d.png")
)
```

render_anim *Render a set of animation frames*

Description

This function takes a set of frames as produced by save_history(), and creates the projected data and axes in for format needed to create the animation using plotly. It will be useful for showing a tour where mouseover can be used to identify points. Note that for now this only works for 2D projections.

Usage

```
render_anim(
  data,
  vars = NULL,
  frames,
  edges = NULL,
  axis_labels = NULL,
  obs_labels = NULL,
  limits = 1,
  position = "center"
)
```

Arguments

data	matrix, or data frame containing numeric columns, should be standardised to have mean 0, sd 1
vars	numeric columns of data to be projected, as a vector, eg 1:4
frames	array of projection matrices, should be interpolated already
edges	to and from of row id's to connect with an line
axis_labels	labels of the axes to be displayed
obs_labels	labels of the observations to be available for interactive mouseover
limits	value setting the lower and upper limits of projected data, default 1
position	position of the axes: center (default), left of data or off

Value

list containing indexed projected data, edges, circle and segments for axes

Examples

```
data(flea)
flea_std <- apply(flea[,1:6], 2, function(x) (x-mean(x))/sd(x))
t1 <- save_history(flea_std, max=2)
t1i <- tourr::interpolate(t1, 0.1)
p <- render_anim(data=flea_std, frames=t1i)
```

```
if (require(ggplot2)) {
  pg <- ggplot() +
    geom_path(data=p$circle, aes(x=c1, y=c2, frame=frame)) +
    geom_segment(data=p$axes, aes(x=x1, y=y1, xend=x2, yend=y2, frame=frame)) +
    geom_text(data=p$axes, aes(x=x2, y=y2, frame=frame, label=axis_labels)) +
    geom_point(data=p$frames, aes(x=P1, y=P2, frame=frame, label=obs_labels)) +
    coord_equal() +
    theme_bw() +
    theme(axis.text=element_blank(),
        axis.title=element_blank(),
        axis.ticks=element_blank(),
        panel.grid=element_blank())
  if (interactive()) {
    require(plotly)
    ggplotly(pg, width=500, height=500) |>
      animation_button(label="Go") |>
      animation_slider(len=0.8, x=0.5, xanchor="center") |>
      animation_opts(easing="linear", transition=0, redraw=FALSE)
  }
}
```

`render_gif` *Render frames of animation to a gif file*

Description

Render frames of animation to a gif file

Usage

```
render_gif(
  data,
  tour_path,
  display,
  gif_file = "animation.gif",
  ...,
  apf = 1/10,
  frames = 50,
  rescale = FALSE,
  sphere = FALSE,
  start = NULL,
  loop = TRUE
)
```

Arguments

`data`	matrix, or data frame containing numeric columns
`tour_path`	tour path generator

display	the method used to render the projected data, e.g. display_xy, display_pcp
gif_file	Name of gif file (default = "animation.gif")
...	other options passed to png
apf	angle (in radians) per frame
frames	number of frames in output
rescale	default FALSE. If TRUE, rescale all variables to range [0,1]
sphere	if true, sphere all variables
start	starting projection. If NULL, uses path default.
loop	Logical for gifski to loop or not, default=TRUE

Examples

```
## Not run:
# gifski needs to be installed to render a gif
if (requireNamespace("gifski", quietly = TRUE)) {
  gif_file <- file.path(tempdir(), "test.gif")
  render_gif(flea[, 1:6], grand_tour(), display_xy(), gif_file)
  utils::browseURL(gif_file)
  unlink(gif_file)
}

## End(Not run)
```

---

render_proj *Render plotly animation frame*

Description

This function takes a projection matrix as produced by save_history(), and draws it on the projected data like a biplot. This will product the data objects needed in order for the user to plot with base or ggplot2. Note that for now this only works for 2D projections.

Usage

```
render_proj(
  data,
  prj,
  axis_labels = NULL,
  obs_labels = NULL,
  limits = 1,
  position = "center"
)
```

Arguments

data	matrix, or data frame containing numeric columns, should be standardised to have mean 0, sd 1
prj	projection matrix
axis_labels	of the axes to be displayed
obs_labels	labels of the observations to be available for interactive mouseover
limits	value setting the lower and upper limits of projected data, default 1
position	position of the axes: center (default), bottomleft or off

Value

list containing projected data, circle and segments for axes

Examples

```
data(flea)
flea_std <- apply(flea[,1:6], 2, function(x) (x-mean(x))/sd(x))
prj <- basis_random(ncol(flea[,1:6]), 2)
p <- render_proj(flea_std, prj)
if (require("ggplot2")) {
  ggplot() +
    geom_path(data=p$circle, aes(x=c1, y=c2)) +
    geom_segment(data=p$axes, aes(x=x1, y=y1, xend=x2, yend=y2)) +
    geom_text(data=p$axes, aes(x=x2, y=y2, label=rownames(p$axes))) +
    geom_point(data=p$data_prj, aes(x=P1, y=P2)) +
    xlim(-1,1) + ylim(-1, 1) +
    theme_bw() +
    theme(aspect.ratio=1,
       axis.text=element_blank(),
       axis.title=element_blank(),
       axis.ticks=element_blank(),
       panel.grid=element_blank())
}
```

---

rescale *Rescale a matrix or data frame*

Description

Standardise each column to have range [0, 1]

Usage

```
rescale(df)
```

Arguments

df	data frame or matrix

save_history *Save tour history.*

Description

Save a tour path so it can later be displayed in many different ways.

Usage

```
save_history(
  data,
  tour_path = grand_tour(),
  max_bases = 100,
  start = NULL,
  rescale = FALSE,
  sphere = FALSE,
  step_size = Inf,
  ...
)
```

Arguments

data	matrix, or data frame containing numeric columns
tour_path	tour path generator
max_bases	maximum number of new bases to generate. Some tour paths (like the guided tour) may generate less than the maximum.
start	starting projection, if you want to specify one
rescale	Default FALSE. If TRUE, rescale all variables to range [0,1]?
sphere	if true, sphere all variables
step_size	distance between each step - defaults to Inf which forces new basis generation at each step.
...	additional arguments passed to tour path

Examples

```
# You can use a saved history to replay tours with different visualisations

t1 <- save_history(flea[, 1:6], max = 3)
animate_xy(flea[, 1:6], planned_tour(t1))
## andrews_history(t1)
## andrews_history(interpolate(t1))

## t1 <- save_history(flea[, 1:6], grand_tour(4), max = 3)
## animate_pcp(flea[, 1:6], planned_tour(t1))
## animate_scatmat(flea[, 1:6], planned_tour(t1))
```

```
## t1 <- save_history(flea[, 1:6], grand_tour(1), max = 3)
## animate_dist(flea[, 1:6], planned_tour(t1))

testdata <- matrix(rnorm(100 * 3), ncol = 3)
testdata[1:50, 1] <- testdata[1:50, 1] + 10
testdata <- sphere_data(testdata)
t2 <- save_history(testdata, guided_tour(holes()),
  max = 5
)
animate_xy(testdata, planned_tour(t2))

# Or you can use saved histories to visualise the path that the tour took.
plot(path_index(interpolate(t2), holes()))

# And you can plot any individual frame using
best_prj <- matrix(t2[,,3], ncol=2)
p <- render_proj(testdata, best_prj)
# which creates a data frame with the elements
# to make the plot, see render_proj() for plotting code
# OR see draw_tour_axes() for similar code in base graphics
```

`search_better` *Search for a better projection near the current projection.*

Description

Search for a better projection near the current projection.

Usage

```
search_better(
  current,
  alpha = 0.5,
  index,
  tries,
  max.tries = Inf,
  ...,
  method = "linear",
  cur_index = NA
)
```

Arguments

`current`	starting projection
`alpha`	the angle used to search the target basis from the current basis
`index`	index function
`tries`	the counter of the outer loop of the opotimiser
`max.tries`	maximum number of iteration before giving up

...	other arguments being passed into the search_better()
method	whether the nearby bases are found by a linear/ geodesic formulation
cur_index	the index value of the current basis

Examples

```
animate_xy(flea[, 1:6], guided_tour(holes(), search_f = search_better))
```

---

search_better_random *Search for a better projection using simulated annealing*

Description

Given an initial $t0$, the cooling scheme updates temperature at

$$T = t0/\log(i+1)$$

The candidate basis is sampled via

$$B_j = (1-\alpha) * B_i + \alpha * B$$

where alpha defines the neighbourhood, B_i is the current basis, B is a randomly generated basis The acceptance probability is calculated as

$$prob = \exp -abs(I(B_i) - I(B_j))/T$$

For more information, see https://projecteuclid.org/download/pdf_1/euclid.ss/1177011077

Usage

```
search_better_random(
  current,
  alpha = 0.5,
  index,
  tries,
  max.tries = Inf,
  method = "linear",
  cur_index = NA,
  t0 = 0.01,
  ...
)
```

Arguments

current	starting projection
alpha	the angle used to search the target basis from the current basis
index	index function

tries	the counter of the outer loop of the opotimiser
max.tries	maximum number of iteration before giving up
method	whether the nearby bases are found by a linear/ geodesic formulation
cur_index	the index value of the current basis
t0	initial decrease in temperature
...	other arguments being passed into the search_better_random()

Examples

```
animate_xy(flea[, 1:6], guided_tour(holes(), search_f = search_better_random))
```

---

search_geodesic *A pseudo-derivative, line search algorithm.*

Description

This is a novel method for finding more interesting projections for the guided tour. It works by first taking a small step in n random directions, and then picking the direction that looks most promising (based on the height of the index function), which is effectively a gradient search. Then it performs a linear search along the geodesic in that direction, traveling up to half way around the sphere.

Usage

```
search_geodesic(
  current,
  alpha = 1,
  index,
  tries,
  max.tries = 5,
  ...,
  n = 5,
  delta = 0.01,
  cur_index = NA
)
```

Arguments

current	starting projection
alpha	maximum distance to travel (currently ignored)
index	interestingness index function
tries	the counter of the outer loop of the opotimiser
max.tries	maximum number of failed attempts before giving up
...	other arguments being passed into the search_geodesic()
n	number of random steps to take to find best direction
delta	step size for evaluation of best direction
cur_index	index value for starting projection, set NA if it needs to be calculated

Details

You should not to have call this function directly, but should supply it to the guided_tour as a search strategy.

Examples

```
animate_xy(flea[, 1:6], guided_tour(holes(), search_f = search_geodesic))
```

`search_jellyfish` *A jellyfish optimiser for projection pursuit guided tour*

Description

A jellyfish optimiser for projection pursuit guided tour

Usage

```
search_jellyfish(current, index, tries, max.tries = 50, verbose = FALSE, ...)

check_dup(bases, min_dist)
```

Arguments

`current`	starting projection, a list of basis of class "multi-bases"
`index`	index function
`tries`	the counter of the outer loop of the opotimiser
`max.tries`	the maximum number of iteration before giving up
`verbose`	whether to print out the progress messages
`...`	other arguments being passed into the `search_jellyfish()`
`bases`	a list of bases extracted from the data collection object, see examples
`min_dist`	the minimum distance between two bases

Examples

```
library(dplyr)
res <- animate_xy(flea[, 1:6], guided_tour(lda_pp(cl = flea$species),
search_f = search_jellyfish))
bases <- res |> filter(loop == 1) |> pull(basis) |> check_dup(0.1)
animate_xy(data = flea[,1:6], tour_path = planned_tour(bases), col = flea$species)
```

`search_polish` *Search very locally to find slightly better projections to polish a broader search.*

Description

Search very locally to find slightly better projections to polish a broader search.

Usage

```
search_polish(
  current,
  alpha = 0.5,
  index,
  tries,
  polish_max_tries = 30,
  cur_index = NA,
  n_sample = 100,
  polish_cooling = 1,
  ...
)
```

Arguments

`current`	the current projection basis
`alpha`	the angle used to search the target basis from the current basis
`index`	index function
`tries`	the counter of the outer loop of the opotimiser
`polish_max_tries`	maximum number of iteration before giving up
`cur_index`	the index value of the current basis
`n_sample`	number of samples to generate
`polish_cooling`	percentage of reduction in polish_alpha when no better basis is found
`...`	other arguments being passed into the `search_polish()`

Examples

```
data(t1)
best_proj <- t1[, , dim(t1)[3]]
attr(best_proj, "data") <- NULL
best_proj <- unclass(drop(best_proj))
animate_xy(
  flea[, 1:6],
  guided_tour(holes()),
    search_f = search_polish(
         polish_max_tries = 5),
```

```
  start = best_proj
)
```

`search_posse` *Search for a better projection based on Poss, 1995*

Description

Search for a better projection based on Poss, 1995

Usage

```
search_posse(
  current,
  alpha = 0.5,
  index,
  tries,
  max.tries = 300,
  cur_index = NA,
  ...
)
```

Arguments

`current`	starting projection
`alpha`	the angle used to search the target basis from the current basis
`index`	index function
`tries`	the counter of the outer loop of the opotimiser
`max.tries`	maximum number of iteration before giving up
`cur_index`	the index value of the current basis
`...`	other arguments being passed into the `search_better()`

`skewness` *Skewness index.*

Description

Calculates the skewness index. See Cook, Buja and Cabrera (1993) Projection pursuit indexes based on orthonormal function expansions for equations.

Usage

```
skewness()
```

slice_index *Section pursuit index.*

Description

Calculates a section pursuit index that compares the distribution inside and outside a slice.

Usage

```
slice_index(
  breaks_x,
  breaks_y,
  eps,
  bintype = "polar",
  power = 1,
  flip = 1,
  reweight = FALSE,
  p = 4
)
```

Arguments

breaks_x	binning on the first variable (x or radius).
breaks_y	binning on the second variable (y or angle).
eps	cutoff values to suppress summing up small differences. Vector with one entry for each bin, can be estimated using estimate_eps.
bintype	select polar (default) or square binning.
power	exponent q used in the index compuatation.
flip	sign of the index computation, select +1 when searching for low densities and -1 when searching for high densities.
reweight	if TRUE will reweight according to the expected distribution in a uniform hypersphere (default is FALSE).
p	number of variables in the data (needed for accurate reweighting, default is 4).

sphere_data *Sphere a matrix (or data frame) by transforming variables to principal components.*

Description

Sphering is often useful in conjunction with the guided tour, as it removes simpler patterns that may conceal more interesting findings.

Usage

```
sphere_data(df)
```

Arguments

df	data frame or matrix

---

splines2d *Spline/loess based index.*

Description

Compares the variance in residuals of a fitted spline/loess model to the overall variance to find functional dependence in 2D projections of the data.

Usage

```
splines2d()

loess2d()
```

---

stringy *Scagnostic indexes.*

Description

Compute the scagnostic measures from the cassowaryr package

Usage

```
stringy()
```

---

t1 *Saved history of guided tour with holes*

Description

This data was generated from the following code: set.seed(2020) t1 <- save_history(flea[, 1:6], guided_tour(holes()), max = 100) attr(t1, "class") <- NULL And used as an example for search_polish() to start optimising from the best projection from search_geodesic. t1 is a 3D array or 2D projections.

`Tropical Atmosphere Ocean`

Tropical Atmosphere Ocean data

Description

This is a subset of data taken from the NOAA web site https://www.pmel.noaa.gov/tao/. The data is generated from recording instruments on a grid of buoys laid out over the Pacific Ocean. The grid was setup to monitor El Nino and La Nina events. This subset contains measurements from 5 locations (0deg/110W, 2S/110W, 0deg/95W,2S/95W,5S/95W) and two time points Nov-Jan 1993 (normal), 1997 (El Nino). There are missing values in this data set, which need to be removed, or imputed before running a tour.

Format

A 736 x 8 numeric array

References

https://www.pmel.noaa.gov/tao/

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