Package ‘spinifex’

January 29, 2024

Title Manual Tours, Manual Control of Dynamic Projections of Numeric Multivariate Data

Version 0.3.7.0

Description Data visualization tours animates linear projection of multivariate data as its basis (ie. orientation) changes. The ‘spinifex’ packages generates paths for manual tours by manipulating the contribution of a single variable at a time Cook & Buja (1997) <doi:10.1080/10618600.1997.10474754>. Other types of tours, such as grand (random walk) and guided (optimizing some objective function) are available in the ‘tourn’ package Wickham et al. <doi:10.18637/jss.v040.i02>.

’spinifex’ builds on ‘tourn’ and can render tours with ‘gganimate’ and ‘plotly’ graphics, and allows for exporting as an .html widget and as an .gif, respectively. This work is fully discussed in Spyrison & Cook (2020) <doi:10.32614/RJ-2020-027>.

Depends R (>= 3.5.0), tourr

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URL https://github.com/nsprison/spinifex/

BugReports https://github.com/nsprison/spinifex/issues

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.bind_elements2df

Binds replicated elements of a list as columns of a data frame.

Description

Internal function. To be applied to aes_args replicates elements to the length of the data and bind as a column.

Usage

.bind_elements2df(list, df)

Arguments

list A list of arguments such as those passed in aes_args and identity_args.
df A data.frame to column bind the elements of list to.

See Also

Other Internal utility: .init4proto, .lapply_rep_len()

Examples

## This function is not meant for external use
### `.init4proto`

*Initialize common obj from `.global ggtour()` objects & test their existence*

**Description**

Internal expression. Creates local .objects to be commonly consumed by spinifex proto_* functions.

**Usage**

`.init4proto`

**Format**

An object of class expression of length 1.

**See Also**

Other Internal utility: `.bind_elements2df()`, `.lapply_rep_len()`

**Examples**

```r
## This expression. is not meant for external use.
```

---

### `.lapply_rep_len`

*Replicate all vector elements of a list*

**Description**

Internal function. To be applied to aes_args and identity_args, replicates vectors of length data to length of data*frames for animation.

**Usage**

`.lapply_rep_len(list, to_length, expected_length)`

**Arguments**

- **list**: A list of arguments such as those passed in aes_args and identity_args.
- **to_length**: Scalar number, length of the output vector; the number of rows in the data frames to replicate to.
- **expected_length**: Scalar number, the expected length of the each element of list.

**See Also**

Other Internal utility: `.bind_elements2df()`, `.init4proto`
animate_gganimate

Examples

```r
## This function is not meant for external use
```n

---

### animate_gganimate

*Animate a ggtour as a .gif via gganimate*

#### Description

Animates the ggplot return of `ggtour()` and added `proto_*()` functions as a .gif without interaction, through use of `gganimate`.

#### Usage

```r
animate_gganimate(
  ggtour,  
  fps = 8,  
  rewind = FALSE,  
  start_pause = 1,  
  end_pause = 1,  
  ...
)
```

#### Arguments

- `ggtour` A grammar of graphics tour with appended protos added. A return from `ggtour()` + `proto_*()`.
- `fps` Number of Frames Per Second, the speed resulting animation.
- `rewind` Whether or not the animation should play backwards, in reverse order once reaching the end. Defaults to FALSE.
- `start_pause` The duration in seconds to wait before starting the animation. Defaults to 1 second.
- `end_pause` The duration in seconds to wait after ending the animation, before it restarts from the first frame. Defaults to 1 second.
- `...` Other arguments passed to `gganimate::animate`.

#### See Also

`gganimate::animate`

Other ggtour animator: `animate_plotly()`,
`filmstrip()`
Examples

```r
library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species
bas <- basis_pca(dat)
mv <- manip_var_of(bas)
mt_path <- manual_tour(bas, manip_var = mv)

ggt <- ggtour(mt_path, dat, angle = .3) +
  proto_default(aes_args = list(color = clas, shape = clas),
               identity_args = list(size = 1.5, alpha = .7))

## Not run:
## Default .gif rendering
animate_gganimate(ggt)

if(FALSE){
## Don't accidentally save file
## Option arguments, rendering to default .gif
  anim <- animate_gganimate(ggt, fps = 10, rewind = TRUE,
                           start_pause = 1, end_pause = 2,
                           height = 10, width = 15, units = "cm",
                           res = 200)

## Save rendered animation
  gganimate::anim_save("my_tour.gif",
                      animation = anim,
                      path = ".\figures")

## Alternative renderer saving directly to .mp4
  animate_gganimate(ggt, fps = 5,
                    height = 4, width = 6, units = "in",
                    res = 200)
}
```

## End(Not run)

---

**animate_plotly**

_Aimate a ggtour as an HTML widget via {plotly}_.

### Description

Animates the static ggtour() and added proto_*() functions as a {plotly} animation, an .html widget with slider and hover tooltip showing the row number.

### Usage

```r
animate_plotly(ggtour, fps = 8, ...)
```
Arguments

- `ggtour` A grammar of graphics tour with appended protos added. A return from `ggtour()` + proto_*().
- `fps` Number of Frames Per Second, the speed resulting animation.
- `...` Other arguments passed to `plotly::ggplotly`.

See Also

Other ggtour animator: `animate_gganimate()`, `filmstrip()`

Examples

```r
library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species
bas <- basis_pca(dat)
mv <- manip_var_of(bas)
mt_path <- manual_tour(bas, manip_var = mv)

ggt <- ggtour(mt_path, dat, angle = .3) +
  proto_origin() +
  proto_basis() +
  proto_point(aes_args = list(color = clas, shape = clas),
              identity_args = list(size = 1.5, alpha = .7))

animate_plotly(ggt, width = 700, height = 450) ## pixels only, no resolution argument

## Example saving to a .html widget, may require additional setup.
if(FALSE){
  anim <- animate_plotly(ggt, fps = 10,
                          width = 700, height = 450) ## in pixels

  htmlwidgets::saveWidget(widget = anim,
                          file = "./figures/my_tour.html",
                          selfcontained = TRUE)}
```

Description

 Adds/overwrites the y of the projected data. Useful for 1D projections and appending information related to, but independent from the projection; model predictions or residuals for instance. Wants to be called early so that the following proto calls adopt the changes.

Usage

```
append_fixed_y(fixed_y)
```
Arguments

fixed_y Vector of length of the data, values to fix vertical height. Typically related to but not an explanatory variable, for instance, predicted Y, or residuals.

See Also

Other ggtour proto functions: facet_wrap_tour(), ggtour(), proto_basis(), proto_default(), proto_density(), proto_density2d(), proto_hex(), proto_highlight(), proto_hline0(), proto_origin(), proto_point(), proto_text()

Examples

library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species
bas <- basis_pca(dat)
mv <- manip_var_of(bas)
mt_path <- manual_tour(bas, manip_var = mv)

# Fixed y height with related information, independent of a 1D tour
# _eg_ predictions or residuals.
message("don't forget to scale your fixed_y.")
dummy_y <- scale_sd(as.integer(clas) + rnorm(nrow(dat), 0, .5))
gt_path <- save_history(dat, grand_tour(d = 1), max_bases = 5)

message("append_fixed_y wants to be called early so other proto's adopt the fixed_y.")
gt <- ggtour(gt_path, dat, angle = .3) +
append_fixed_y(fixed_y = dummy_y) + ## insert/overwrites vertical values.
proto_point(list(fill = clas, color = clas)) +
proto_basis1d() +
proto_origin()

animate_plotly(gt)

array2df

Turns a tour path array into a long data frame.

Description

Internal function, many end users will not need this. Takes the result of manual_tour() or tourr::save_history(). Restructures the array of interpolated bases into a long data frame for use in ggplots.

Usage

array2df(
basis_array,
data = NULL,
basis_label = NULL,
basis_guided

```r

data_label = rownames(data),
do_center_frame = TRUE
)
```

**Arguments**

- **basis_array** A full \((p, d, n\_frames)\) interpolated basis array of a tour, the output of manual_tour or save_history(*_tour()).
- **data** Optional, \((n, p)\) dataset to project, consisting of numeric variables.
- **basis_label** Labels for basis display, a character vector with length equal to the number of variables. Defaults to NULL; 3 character abbreviation from colnames of data or rownames of basis.
- **data_label** Labels for plotly tooltip display. Defaults to the rownames of data. If null, initializes to 1:nrow(data).
- **do_center_frame** Whether or not to center the mean within each animation frame. Defaults to TRUE.

**Examples**

```r
## !!This function is not meant for external use!!
dat <- scale_sd(wine[, 2:6])
class <- wine$Type
bas <- basis_pca(dat)
mv <- manip_var_of(bas)

## Radial tour array to long df, as used in play_manual_tour()
mt_array <- manual_tour(basis = bas, manip_var = mv)
ls_df_frames <- array2df(basis_array = mt_array, data = dat, basis_label = paste0("MyLabs", 1:nrow(bas)))
str(ls_df_frames)

## tourr::save_history tour array to long df, as used in play_tour_path()
gt_array <- tourr::save_history(data = dat, max_bases = 10)
ls_df_frames2 <- array2df(basis_array = gt_array, data = dat)
str(ls_df_frames2)
```

**Description**

Solve for the last basis of a guided tour.

Performs simulated annealing on the index function, solving for it’s local extrema. Returns only the last identified basis of the optimization. A truncated, muted extension of tourr::save_history(guided_tour()).

**Usage**

```r
basis_guided(data, index_f = tourr::holes(), d = 2, ...)
```
basis_half_circle

Arguments

- data: Numeric matrix or data.frame of the observations.
- index_f: The index function to optimize. \{tourr\} exports holes(), cmass(), and lda_pp(class).
- d: Number of dimensions in the projection space.
- ...: Optional, other arguments to pass to \texttt{tourr::guided_tour}.

Value

Numeric matrix of the last basis of a guided tour.

See Also

\texttt{tourr::guided_tour} for annealing arguments.

Other basis producing functions: \texttt{basis_half_circle()}, \texttt{basis_odp()}, \texttt{basis_olda()}, \texttt{basis_onpp()}, \texttt{basis_pca()}

Examples

```r
dat <- scale_sd(wine[, 2:6])
basis_guided(data = dat, index_f = tourr::holes())

basis_guided(data = dat, index_f = tourr::cmass(),
             alpha = .4, cooling = .9, max.tries = 10, n_sample = 4)
```

---

**basis_half_circle**

Create a basis that gives uniform contribution in a circle

Description

Orthonormalizes uniform variable contributions on a unit circle. This serves as a NULL basis, one that is variable agnostic while spacing the variables to have minimize variable dependence.

Usage

```r
basis_half_circle(data)
```

Arguments

- data: The data to create a basis for.

See Also

Other basis producing functions: \texttt{basis_guided()}, \texttt{basis_odp()}, \texttt{basis_olda()}, \texttt{basis_onpp()}, \texttt{basis_pca()}

Examples

```r
dat <- scale_sd(wine[, 2:6])
bas <- basis_half_circle(dat)
```
The basis of Orthogonal Discriminant Projection (ODP)

Description

Orthogonal Discriminant Projection (ODP) is a linear dimension reduction method with class supervision. It maximizes weighted difference between local and non-local scatter while local information is also preserved by constructing a neighborhood graph.

Usage

basis_odp(data, class, d = 2, type = c("proportion", 0.1), ...)

Arguments

data: Numeric matrix or data.frame of the observations, coerced to matrix.
class: The class for each observation, coerced to a factor.
d: Number of dimensions in the projection space. of class.
type: A vector specifying the neighborhood graph construction. Expects; c("knn", k), c("enn", radius), or c("proportion", ratio). Defaults to c("knn", sqrt(nrow(data))), nearest neighbors equal to the square root of observations.

References


See Also

Rdimtools::do.odp for locality preservation arguments.
Rdimtools::aux.graphnbd for details on type.

Other basis producing functions: basis_guided(), basis_half_circle(), basis_olda(), basis_onpp(), basis_pca()

Examples

dat <- scale_sd(wine[, 2:6])
clas <- wine$Type
basis_odp(data = dat, class = clas)
The basis of Orthogonal Linear Discriminant Analysis (OLDA)

Description

Orthogonal LDA (OLDA) is an extension of classical LDA where the discriminant vectors are orthogonal to each other.

Usage

```
basis_olda(data, class, d = 2)
```

Arguments

- `data`: Numeric matrix or data.frame of the observations, coerced to matrix.
- `class`: The class for each observation, coerced to a factor.
- `d`: Number of dimensions in the projection space.

Value

A numeric matrix, an orthogonal basis that best distinguishes the group means of `class`.

References


See Also

- `Rdimtools::do.olda`
- Other basis producing functions: `basis_guided()`, `basis_half_circle()`, `basis_odp()`, `basis_onpp()`, `basis_pca()`

Examples

```
dat <- scale_sd(wine[, 2:6])
clas <- wine$Type
basis_olda(data = dat, class = clas)
```
The basis of Orthogonal Neighborhood Preserving Projection (OLPP)

Description
Orthogonal Neighborhood Preserving Projection (ONPP) is an unsupervised linear dimension reduction method. It constructs a weighted data graph from LLE method. Also, it develops LPP method by preserving the structure of local neighborhoods. For the more details on type see `Rdimtools::aux.graphnbd()`.

Usage
basis_onpp(data, d = 2, type = c("knn", sqrt(nrow(data))))

Arguments
data Numeric matrix or data.frame of the observations, coerced to matrix.
d Number of dimensions in the projection space.
type A vector specifying the neighborhood graph construction. Expects; c("knn", k), c("enn", radius), or c("proportion", ratio). Defaults to c("knn", sqrt(nrow(data))), nearest neighbors equal to the square root of observations.

Value
Orthogonal matrix basis that distinguishes the levels of class based on local and non-local variation as weighted against the neighborhood graph.

References

See Also
`Rdimtools::do.onpp`
`Rdimtools::aux.graphnbd` for details on type.

Other basis producing functions: `basis_guided()`, `basis_half_circle()`, `basis_odp()`, `basis_olda()`, `basis_pca()`

Examples
dat <- scale_sd(wine[, 2:6])
basis_onpp(data = dat)
b

\textit{The basis of Principal Component Analysis (PCA)}

\textbf{Description}

The orthogonal linear components of the variables in the next largest direction of variance.

\textbf{Usage}

\begin{verbatim}
basis_pca(data, d = 2)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{data} Numeric matrix or data.frame of the observations.
  \item \texttt{d} Number of dimensions in the projection space.
\end{itemize}

\textbf{See Also}

\begin{itemize}
  \item \texttt{Rdimtools::do.pca}
  \item Other basis producing functions: \texttt{basis_guided()}, \texttt{basis_half_circle()}, \texttt{basis_odp()}, \texttt{basis_olda()}, \texttt{basis_onpp()}
\end{itemize}

\textbf{Examples}

\begin{verbatim}
dat <- scale_sd(wine[, 2:6])
basis_pca(data = dat)
\end{verbatim}

\textit{Wisconsin Breast Cancer Database}

\textbf{Description}

The objective is to identify each of a number of benign or malignant classes. Samples arrive periodically as Dr. Wolberg reports his clinical cases. The database therefore reflects this chronological grouping of the data. This grouping information appears immediately below, having been removed from the data itself. Each variable except for the first was converted into 11 primitive numerical attributes with values ranging from 0 through 10. Rows with missing attribute values and duplicate rows removed.

\textbf{Usage}

\begin{verbatim}
BreastCancer_na.rm
\end{verbatim}
Format

A data frame with 675 observations of 8 numeric variables and target factor Class.

- Id, Sample code number
- Cl.thickness, Clump thickness
- Cell.size, Uniformity of cell size
- Cell.shape, Uniformity of cell shape
- Marg.adhesion, Marginal adhesion
- Epith.c.size, Single Epithelial cell size
- Bare.nuclei, Bare nuclei
- Bl.cromatin, Bland chromatin
- Normal.nucleoli, Normal Nucleoli
- Mitoses, Mitoses
- Class, Class of cancer, either "benign" or "malignant"

Details

This is a cleaned subset of mlbench's BreastCancer. See help(BreastCancer, package = "mlbench") for the original.

Replicating this dataset:

```r
require("mlbench")
data(BreastCancer)

raw <- BreastCancer
## rownumber index of 8 duplicate 16 incomplete rows
idx <- !duplicated(raw) & complete.cases(raw)
d <- raw[idx, 3:10]
d <- apply(d, 2L, as.integer)
d <- data.frame(d, Class = as.factor(raw$Class[idx]))
BreastCancer_na.rm <- d
## save(BreastCancer_na.rm, file = "/data/BreastCancer_na.rm.rda")
```

Source


create_manip_space

Create a manipulation space to rotate the manipulation variable in.

Description

Typically called by manual_tour(). Creates a \((p, d)\) orthonormal matrix, the manipulation space from the given basis right concatenated with a zero vector, with \text{manip\_var} set to 1.

Usage

\[
\text{create\_manip\_space}(\text{basis}, \text{manip\_var} = \text{manip\_var\_of}(\text{basis}))
\]

Arguments

- **basis**: A \((p, d)\) orthonormal numeric matrix, the linear combination the original variables contribute to projection frame. Required, no default.
- **manip\_var**: The number of the variable/column to rotate. Defaults to \text{manip\_var\_of}(\text{basis}), the variable with the largest contribution in the basis.

Value

A \((p, d + 1)\) orthonormal matrix, the manipulation space to manipulate the projection in.

See Also

Other manual tour adjacent functions: \text{interpolate\_manual\_tour()}, \text{manip\_var\_of()}, \text{manual\_tour()}, \text{rotate\_manip\_space()}

Examples

```r
library(spinifex)
str(BreastCancer_na.rm)
dat <- scale_sd(BreastCancer_na.rm[, 1:8])
clas <- BreastCancer_na.rm$Class

bas <- basis_pca(dat)
mv <- manip_var_of(bas)
mt <- manual_tour(bas, mv)

ggt <- ggtour(mt, dat, angle = .2) +
    proto_default(aes_args = list(color = clas, shape = clas))
animate_plotly(ggt)
```
Examples

```r
library(spinifex)
dat <- scale_sd(wine[, 2:6])
bas <- basis_pca(dat)
mv <- manip_var_of(bas)
create_manip_space(basis = bas, manip_var = mv)

## d = 1 case
bas1d <- basis_pca(dat, d = 1)
mv <- manip_var_of(bas1d)
create_manip_space(bas1d, mv)
```

Description

Send a message if the 4th chunk of the package version is 9000.

Usage

```r
devMessage(text)
```

Arguments

text A character string to message() if package version is _9000.

Description

Additively draws a basis on a static ggplot. Not a geom or proto. Expects

Usage

```r
draw_basis(basis,
map_to = data.frame(x = c(0, 1), y = c(0, 1)),
position = c("left", "center", "right", "bottomleft", "topright", "off"),
mapi
col = "blue",
line_size = 0.6,
text_size = 4,
basis_label = abbreviate(gsub("[[:alnum:]=]","", rownames(basis), 3L))
)`
```
**Arguments**

- **basis**: A \((p \times d)\) basis to draw. Draws the first two components. If `facet` is used `cbind` the facet variable to a specific facet level (2nd example), otherwise the basis prints on all facet levels.

- **map_to**: A `data.frame` to scale the basis to. Defaults to a unitbox; `data.frame(x = c(0,1), y = c(0,1))`.

- **position**: The position, to place the basis axes relative to the centered data. _basis_ expects one of c("left", "center", "right", "bottomleft", "topright", "off"), defaults to "left".

- **manip_col**: The color to highlight the manipulation variable with. Not applied if the tour isn’t a manual tour. Defaults to "blue".

- **line_size**: (2D bases only) the thickness of the lines used to make the axes and unit circle. Defaults to 0.6.

- **text_size**: Size of the text label of the variables. Defaults to 4.

- **basis_label**: The text labels of the data variables. Defaults to the 3 character abbreviation of the rownames of the basis.

**Examples**

```r
library(spinifex)
library(ggplot2)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species
bas <- basis_pca(dat)
proj <- as.data.frame(dat %*% bas)

ggplot() + geom_point(aes(PC1, PC2), proj) + draw_basis(bas, proj, "left") + coord_fixed()
```

```
## Aesthetics and basis on specific facet levels
proj <- cbind(proj, clas = penguins_na.rm$species)
bas <- cbind(as.data.frame(bas), clas = levels(clas)[2])

ggplot() + facet_wrap(vars(clas)) + geom_point(aes(PC1, PC2, color = clas, shape = clas), proj) + draw_basis(bas, proj, "left") + theme_spinifex()

## To repeat basis in all facet levels don’t cbind a facet variable.
```
**facet_wrap_tour**

**Description**

Create and wrap a 1d ribbon of panels in 2d. Because of the side effects of ggtour and facet_wrap_tour this wants to be applied after ggtour and before any proto_* functions. plotly may not display well with with faceting.

**Usage**

```r
facet_wrap_tour(facet_var, nrow = NULL, ncol = NULL, dir = "h")
```

**Arguments**

- **facet_var** Expects a single variable to facet the levels of. Should be a vector, not a formula (~cyl) or ggplot2::vars() call.
- **nrow** Number of rows. Defaults to NULL; set by display dim.
- **ncol** Number of columns. Defaults to NULL; set by display dim.
- **dir** Direction of wrapping: either "h" horizontal by rows, or "v", for vertical by columns. Defaults to "h".

**See Also**

Other ggtour proto functions: append_fixed_y(), ggtour(), proto_basis(), proto_default(), proto_density(), proto_density2d(), proto_hex(), proto_highlight(), proto_hline0(), proto_origin(), proto_point(), proto_text()

**Examples**

```r
library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species
bas <- basis_pca(dat)
mv <- manip_var_of(bas)
mt_path <- manual_tour(bas, manip_var = mv)
## d = 2 case
message("facet_wrap_tour wants be called early, so that other proto's adopt the facet_var.")
ggt <- ggtour(mt_path, dat, angle = .3) +
    facet_wrap_tour(facet_var = clas, ncol = 2, nrow = 2) +
    proto_default(aes_args = list(color = clas, shape = clas),
                   identity_args = list(size = 1.5))
## Not run:
animate_gganimate(ggt) ## May not always play well with plotly
## End(Not run)
```
Create a “filmstrip” of the frames of a ggtour.

Description

Appends facet_wrap(vars(frame_number)) & minor themes to the ggtour. If the number of frames is more than desired, try increasing the angle argument on the tour. Is very demanding on the plots pane, works better with ggsave().

Usage

filmstrip(ggtour, ...)

Arguments

ggtour A grammar of graphics tour with appended protos added. A return from ggtour() + proto_*(
... optionally pass arguments to ggplot2::facet_wrap, such as nrow = 3, ncol = 2, scales = "free".

See Also

Other ggtour animator: animate_gganimate(), animate_plotly()

Examples

library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species
bas <- basis_pca(dat)
mv <- manip_var_of(bas)

## d = 2 case
mt_path <- manual_tour(bas, manip_var = mv)
ggt <- ggtour(mt_path, dat, angle = .3) +
    proto_point(list(color = clas, shape = clas),
        list(size = 1.5)) +
    proto_basis()
filmstrip(ggt)

## d = 1 case & specify facet dim
bas1d <- basis_pca(dat, d = 1)
mt_path1d <- manual_tour(basis = bas1d, manip_var = mv)
ggt1d <- ggtour(mt_path1d, dat, angle = 99) +
    proto_default1d(aes_args = list(fill = clas, color = clas))
filmstrip(ggt1d, nrow = 12, ncol = 3)
ggtour

Prepare a new grammar of graphics tour

Description

ggtour() initializes a ggplot object for a tour. proto_* functions are added to the tour, analogous to ggplot() + geom_* . The final tour object is then animated with animate_plotly() or animate_ggtour(), or passed to filmstrip() for static plot faceting on frames.

Usage

ggtour(
    basis_array,
    data = NULL,
    angle = 0.05,
    basis_label = NULL,
    data_label = NULL,
    do_center_frame = TRUE
)

Arguments

- **basis_array**: An array of projection bases for the tour, as produced with manual_tour() or tour::save_history(), or a single basis.
- **data**: Numeric data to project. If left NULL, will check if it data is stored as an attribute of the the basis_array.
- **angle**: Target angle (radians) for interpolation frames between frames of the basis_array. Defaults to .05. To opt out of interpolation set to NA or 0.
- **basis_label**: Labels for basis display, a character vector with length equal to the number of variables. Defaults to NULL; 3 character abbreviation from colnames of data or rownames of basis.
- **data_label**: Labels for plotly tooltip display. Defaults to the NULL, rownames and/or numbers of data.
- **do_center_frame**: Whether or not to center the mean within each animation frame. Defaults to TRUE.

See Also

Other ggtour proto functions: append_fixed_y(), facet_wrap_tour(), proto_basis(), proto_default(), proto_density(), proto_density2d(), proto_hex(), proto_highlight(), proto_hline0(), proto_origin(), proto_point(), proto_text()
Examples

```r
library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species
bas <- basis_pca(dat)
mv <- manip_var_of(bas)
mt_path <- manual_tour(bas, manip_var = mv)

## d = 2 case

ggt <- ggtour(basis_array = mt_path, data = dat, angle = .3) +
  proto_default(aes_args = list(color = clas, shape = clas),
               identity_args = list(size = 1.5, alpha = .8))

animate_plotly(ggt)

## Finer control calling individual proto_* functions

ggt <- ggtour(basis_array = mt_path, data = dat, angle = .3) +
  proto_point(aes_args = list(color = clas, shape = clas),
              identity_args = list(size = 1.5, alpha = .8),
              row_index = which(clas == levels(clas)[1])) +
  proto_basis(position = "right",
              manip_col = "red",
              text_size = 7L) +
  proto_origin()

animate_plotly(ggt)

## d = 1 case

bas1d <- basis_pca(dat, d = 1)
mt_path1d <- manual_tour(basis = bas1d, manip_var = mv)

ggt1d <- ggtour(basis_array = mt_path1d, data = dat, angle = .3) +
  proto_default1d(aes_args = list(fill = clas, color = clas))

animate_plotly(ggt1d)

## Single basis

ggt <- ggtour(basis_array = bas, data = dat) +
  proto_default(aes_args = list(fill = clas, color = clas))

## ggtour() returns a static ggplot2 plot

ggt

### or as html widget with tooltips

animate_plotly(ggt)
```
interpolate_manual_tour

Interpolates a manual tour

Description

Internal function. Interpolates a manual tour over the stored theta, and phi specifications. Returns an interpolated basis_array to be consumed by array2df.

Usage

interpolate_manual_tour(basis_array, angle = 0.05)

Arguments

basis_array array, of the target bases, the extrema of the walk/segments.
angle The step size between interpolated frames, in radians.

See Also

Other manual tour adjacent functions: create_manip_space(), manip_var_of(), manual_tour(), rotate_manip_space()

Examples

## This function is not meant for external use
dat <- scale_sd(wine[, 2:6])
clas <- wine$Type
bas <- basis_pca(dat)
mv <- manip_var_of(bas)
mt <- manual_tour(bas, mv)

tinterp <- spinifex:::interpolate_manual_tour(basis_array = mt, angle = .1)
dim(interp)
str(interp)

is_any_layer_class

Check ggplot layers for use of a specific geom

Description

Checks if any of the layers of a ggplot contain a specific class.

Usage

is_any_layer_class(ggplot, class_nm = "GeomDensity")
\section*{is_orthonormal}

\textbf{Orthonormality of a matrix}

Test if a numeric matrix is orthonormal, that is, each column is orthogonal, at a right angle with the others, and each column has a norm length of 1. This must be true for a projection to be linear.

\subsection*{Usage}

\begin{verbatim}
is_orthonormal(x, tol = 0.001)
\end{verbatim}

\subsection*{Arguments}

\begin{itemize}
  \item \texttt{x} \hspace{1cm} Numeric matrix to test the orthonormality of.
  \item \texttt{tol} \hspace{1cm} Max tolerance of floating point differences of the element-wise distance of t(x) \%*% x from the identity matrix.
\end{itemize}

\subsection*{Value}

Single logical, whether or not the matrix is orthonormal.

\subsection*{Examples}

\begin{verbatim}
spinifex::is_orthonormal(tourr::basis_random(n = 6))
spinifex::is_orthonormal(matrix(1:12, ncol = 2), tol = 0.01)
\end{verbatim}
**manip_var_of**

* Suggest a manipulation variable.

**Description**

Find the column number of the variable with the rank-i th largest contribution of the basis. Useful for identifying a variable to change the contribution of in a manual tour, it's `manip_var` argument.

**Usage**

```r
manip_var_of(basis, rank = 1)
```

**Arguments**

- **basis**: Numeric matrix (p x d), orthogonal linear combinations of the variables.
- **rank**: The number, specifying the variable with the rank-th largest contribution. Defaults to 1.

**Value**

Numeric scalar, the column number of a variable.

**See Also**

Other manual tour adjacent functions: `create_manip_space()`, `interpolate_manual_tour()`, `manual_tour()`, `rotate_manip_space()`

**Examples**

```r
dat <- scale_sd(wine[, 2:6])
bas <- basis_pca(dat)

manip_var_of(basis = bas)  ## Variable with the largest contribution
manip_var_of(basis = bas, rank = 5)  ## Variable with 5th-largest contribution
```

---

**manual_tour**

* Produc the series of projection bases to rotate a variable into and out of a projection.

**Description**

Typically called by `array2af()`. An array of projections, the radial tour of the `manip_var`, which is rotated from phi's starting position to phi_max, to phi_min, and back to the start position.
Usage

```r
manual_tour(
  basis,
  manip_var,
  theta = NULL,
  phi_min = 0,
  phi_max = pi/2,
  data = NULL
)
```

Arguments

- **basis**: A (p, d) orthonormal numeric matrix. The linear combination the original variables contribute to projection space. Defaults to NULL, generating a random basis.
- **manip_var**: Integer column number or string exact column name of the variable to manipulate. Required, no default.
- **theta**: Angle in radians of "in-plane" rotation, on the xy plane of the reference frame. Defaults to theta of the basis for a radial tour.
- **phi_min**: Minimum value phi should move to. Phi is angle in radians of the "out-of-plane" rotation, the z-axis of the reference frame. Required, defaults to 0.
- **phi_max**: Maximum value phi should move to. Phi is angle in radians of the "out-of-plane" rotation, the z-axis of the reference frame. Required, defaults to pi/2.
- **data**: Optionally attach data to the basis path.

Value

A (p, d, 4) history_array of the radial tour. The bases set for phi_start, phi_min, phi_max, and back to phi_start.

See Also

Other manual tour adjacent functions: `create_manip_space()`, `interpolate_manual_tour()`, `manip_var_of()`, `rotate_manip_space()`

Examples

```r
library(spinifex)
dat <- scale_sd(wine[, 2:6])
clas <- wine$Type
bas <- basis_pca(dat)
mv <- manip_var_of(bas)
manual_tour(basis = bas, manip_var = mv)

## All arguments
manual_tour(basis = bas, manip_var = mv,
  theta = pi / 2, phi_min = pi / 16, phi_max = pi)
```
## Animating with ggtour() & proto_* (d = 2 case)

```r
t <- manual_tour(basis = bas, manip_var = mv)
g <- ggtour(mt, dat, angle = .2) +
    proto_origin() +
    proto_point(list(color = clas, shape = clas)) +
    proto_basis()
animate_plotly(g)
```

## d = 1 case

## basis could be 1- or 2D; protos_* only use 1st column

```r
mv <- manip_var_of(bas)
t <- manual_tour(basis = bas, manip_var = mv)
g <- ggtour(mt, dat, angle = .3) +
    proto_density(aes_args = list(color = clas, fill = clas)) +
    proto_basis1d() +
    proto_origin1d()
animate_plotly(g)
```

## Bring your own basis

```r
bas <- matrix(rnorm(2 * ncol(dat)), ncol = 2)
bas <- orthonormalise(bas) ## manual_tour warns if basis isn’t orthonormal
t <- manual_tour(basis = bas, manip_var = 1)
g <- ggtour(mt, dat, angle = .2) +
    proto_default(aes_args = list(color = clas, shape = clas))
animate_plotly(g)
```

---

**map_absolute**

*Manually offset and scale the first 2 columns of a matrix or data.frame.*

### Description

A manual variant of `map_relative()`. Can be used as the `axes` argument to manually set the size and locations of the axes.

### Usage

```r
map_absolute(x, offset = c(0, 0), scale = c(1, 1))
```

### Arguments

- **x**: Numeric data object with 2 columns to scale and offset. Defaults to NULL, passing arguments to `scale_axes` for use internally.
- **offset**: 2 Numeric values to offset/pan the first 2 dimensions of `x`.
- **scale**: 2 Numeric values to scale/zoom to the first 2 dimensions of `x`. 

map_relative

Value

Scaled and offset x.

See Also

scale_axes for preset choices.

Other linear mapping functions: map_relative()

Examples

bas <- tourr::basis_random(4, 2)

map_absolute(bas, offset = c(-2, 0), scale = c(2/3, 2/3))

map_relative

Returns the axis scale and position.

Description

Internal function. Typically called by other functions to scale the position of the axes data.frame or another data.frame to plot relative to the data.

Usage

map_relative(
  x,
  position = c("center", "left", "right", "bottomleft", "topright", "off", "top1d",
               "floor1d", "bottom1d", "full", "facetleft", "facettight", "facetbottom", "facetbottom"),
  to = NULL
)

Arguments

x

Numeric matrix or data.frame, first 2 columns and scaled and offset the to object.

position

Text specifying the position the axes should go to. Defaults to "center" expects one of: c("center", "left", "right", "bottomleft", "topright", "off", "full", "top1d",
               "floor1d", "bottom1d", "full", "facetleft", "facettight", "facetbottom", "facetbottom").

to

Data.frame to scale to. Based on the min/max of the first 2 columns. If left NULL defaults to data.frame(x = c(0, 1), y = c(0, 1)).

Value

Transformed values of x, dimension and class unchanged.
**See Also**

map_absolute for more manual control.

Other linear mapping functions: map_absolute()

**Examples**

```r
## !!This function is not meant for external use!!
rb <- tourr::basis_random(4, 2)

map_relative(x = rb, position = "bottomleft")
map_relative(x = rb, position = "right", to = wine[, 2:3])
```

---

**penguins_na.rm**  
Size measurements for adult foraging penguins near Palmer Station, Antarctica

**Description**

Includes measurements for penguin species, island in Palmer Archipelago, size (flipper length, body mass, bill dimensions), and sex.

**Usage**

penguins_na.rm

**Format**

A data frame with 333 rows and 4 numeric variables and 3 factor variables

- **bill_length_mm** a number denoting bill length (millimeters)
- **bill_depth_mm** a number denoting bill depth (millimeters)
- **flipper_length_mm** an integer denoting flipper length (millimeters)
- **body_mass_g** an integer denoting body mass (grams)
- **species** a factor denoting penguin species (Adelie, Chinstrap and Gentoo)
- **sex** a factor denoting penguin sex (female, male)
- **island** a factor denoting island in Palmer Archipelago, Antarctica (Biscoe, Dream or Torgersen)

**Details**

This is a cleaned subset of palmerpenguins::penguins.

Replicating this dataset:

```r
require(palmerpenguins)
d <- palmerpenguins::penguins
d <- d[complete.cases(d), ]  # Remove missing, 2 obs of numeric and several in sex
d <- d[, c(3:6, 1, 7, 2)]    # Numeric to front, group factors, remove year
penguins_na.rm <- as.data.frame(d)  # Remove {tibble} dependency
# save(penguins_na.rm, file = "/data/penguins_na.rm.rda")
```
Source


Examples

library(spinifex)
str(penguins_na.rm)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas1 <- penguins_na.rm$species
clas2 <- penguins_na.rm$sex
bas <- basis_pca(dat)
mv <- manip_var_of(bas)
mt <- manual_tour(bas, mv)
ggt <- ggtour(mt, dat, angle = .2) +
  proto_default(aes_args = list(color = clas1, shape = clas2))
animate_plotly(ggt)

PimaIndiansDiabetes_long

Pima Indians Diabetes Dataset, long

Description

The data set PimaIndiansDiabetes2 contains a corrected version of the original data set. While the UCI repository index claims that there are no missing values, closer inspection of the data shows several physical impossibilities, e.g., blood pressure or body mass index of 0. In PimaIndiansDiabetes2, all zero values of glucose, pressure, triceps, insulin and mass have been set to NA, see also Wahba et al (1995) and Ripley (1996).
Usage

PimaIndiansDiabetes_long

Format

A data frame with 724 observations of 6 numeric variables, and target factor diabetes.

- pregnant, Number of times pregnant
- glucose, Plasma glucose concentration (glucose tolerance test)
- pressure, Diastolic blood pressure (mm Hg)
- mass, Body mass index (weight in kg/(height in m, squared))
- pedigree, Diabetes pedigree function
- age, Age (years)
- diabetes, Class variable (test for diabetes), either "pos" or "neg"

Details

This is a cleaned subset of mlbench’s PimaIndiansDiabetes2. See help(PimaIndiansDiabetes2, package = "mlbench").

Replicating this dataset:

```r
require("mlbench")
data(PimaIndiansDiabetes2)
d <- PimaIndiansDiabetes2
d <- d[, c(1:3, 6:9)] # Remove 2 columns with the most NAs
d <- d[complete.cases(d), ] # Remove ~44 row-wise incomplete rows
PimaIndiansDiabetes_long <- d
# save(PimaIndiansDiabetes_long, file = "/data/PimaIndiansDiabetes_long.rda")
```

Source


Examples

```r
library(spinifex)
str(PimaIndiansDiabetes_long)
dat <- scale_sd(PimaIndiansDiabetes_long[, 1:6])
clas <- PimaIndiansDiabetes_long$diabetes

bas <- basis_pca(dat)
mv <- manip_var_of(bas)
```
mt <- manual_tour(bas, mv)

ggt <- ggtour(mt, dat, angle = .2) +
    proto_default(aes_args = list(color = clas, shape = clas))

animate_plotly(ggt)

PimaIndiansDiabetes_wide

Description

The data set PimaIndiansDiabetes2 contains a corrected version of the original data set. While the UCI repository index claims that there are no missing values, closer inspection of the data shows several physical impossibilities, e.g., blood pressure or body mass index of 0. In PimaIndiansDiabetes2, all zero values of glucose, pressure, triceps, insulin and mass have been set to NA, see also Wahba et al (1995) and Ripley (1996).

Usage

PimaIndiansDiabetes_wide

Format

A data frame with 392 observations of 8 numeric variables, and target factor diabetes.

- pregnant, Number of times pregnant
- glucose, Plasma glucose concentration (glucose tolerance test)
- pressure, Diastolic blood pressure (mm Hg)
- triceps, Triceps skin fold thickness (mm)
- insulin, 2-Hour serum insulin (mu U/ml)
- mass, Body mass index (weight in kg/(height in m, squared))
- pedigree, Diabetes pedigree function
- age, Age (years)
- diabetes, Class variable (test for diabetes), either "pos" or "neg"

Details

This is a cleaned subset of mlbench’s PimaIndiansDiabetes2. See help(PimaIndiansDiabetes2, package = "mlbench").

Replicating this dataset:
require("mlbench")
data(PimaIndiansDiabetes2)

d <- PimaIndiansDiabetes2
d <- d[complete.cases(d),]  ## Remove ~350 row-wise incomplete rows
PimaIndiansDiabetes_wide <- d
## save(PimaIndiansDiabetes_wide, file = "./data/PimaIndiansDiabetes_wide.rda"

Examples

library(spinifex)
str(PimaIndiansDiabetes_wide)
dat <- scale_sd(PimaIndiansDiabetes_wide[, 1:8])
clas <- PimaIndiansDiabetes_wide$diabetes

bas <- basis_pca(dat)
mv <- manip_var_of(bas)
mt <- manual_tour(bas, mv)

ggt <- ggtour(mt, dat, angle = .2) +
    proto_default(aes_args = list(color = clas, shape = clas))

animate_plotly(ggt)

Description

[Superseded], see ggtour. Performs the a manual tour and returns an animation of render_type.
For use with tourr::save_history() tour paths see play_tour_path().

Usage

play_manual_tour(
basis = NULL,
data,
manip_var,
theta = NULL,
phi_min = 0,
phi_max = 0.5 * pi,
angle = 0.05,
render_type = render_plotly,
...)

Arguments

- **basis**: A \((p, d)\) orthonormal numeric matrix. The linear combination the original variables contribute to projection space. Defaults to NULL, generating a random basis.
- **data**: \((n, p)\) dataset to project, consisting of numeric variables.
- **manip_var**: Integer column number or string exact column name of the variable to manipulate. Required, no default.
- **theta**: Angle in radians of "in-plane" rotation, on the xy plane of the reference frame. Defaults to theta of the basis for a radial tour.
- **phi_min**: Minimum value phi should move to. Phi is angle in radians of the "out-of-plane" rotation, the z-axis of the reference frame. Required, defaults to 0.
- **phi_max**: Maximum value phi should move to. Phi is angle in radians of the "out-of-plane" rotation, the z-axis of the reference frame. Required, defaults to \(\pi/2\).
- **angle**: Target distance (in radians) between steps. Defaults to .05.
- **render_type**: Which graphics to render to. Defaults to render_plotly, ...

Value

An animation of a radial tour.

See Also

- **render_** For arguments to pass into . . . .

Examples

```r
library(spinifex)
message("It's suggested to switch to the proto api, see `?ggtour` to get started.")

## Setup
dat_std <- scale_sd(wine[, 2:6])
class <- wine$Type
bas <- basis_pca(dat_std)
mv <- manip_var_of(bas)

## Not run:
suppressWarnings(
  play_manual_tour(basis = bas, data = dat_std, manip_var = mv)
)

suppressWarnings(
  play_manual_tour(
    basis = bas, data = dat_std, manip_var = mv,
    theta = .5 * pi, axes = "right", fps = 5,
    angle = .08, phi_min = 0, phi_max = 2 * pi,
    aes_args = list(color = class, shape = clas),
    identity_args = list(size = 1.5, alpha = .7),
)
play_tour_path

Animates the provided tour path.

Description

[Superseded], see ggtour. Takes the result of tourr::save_history() or manual_tour(). interpolates over the path and renders into a specified render_type.

Usage

play_tour_path(
  tour_path,
  data = NULL,
  angle = 0.05,
  render_type = render_plotly,
  ...)

Arguments

tour_path The result of tourr::save_history() or manual_tour().
data Optional, number of columns must match that of tour_path.
angle Target distance (in radians) between steps. Defaults to .05.
render_type Graphics to render to. Defaults to render_plotly, alternative use render_gganimate.
... Optionally pass additional arguments to render_ and the function used in render_type.

See Also

render_ For arguments to pass into ....
Examples

library(spinifex)
message("It's suggested to switch to the proto api, see '\?ggtour' to get started.")

dat_std <- scale_sd(wine[, 2:6])
clas <- wine$Type
bas <- basis_pca(dat_std)
gt_path <- save_history(dat_std, tour_path = tourr::grand_tour(), max = 5)

## Not run:
suppressWarnings(
    play_tour_path(tour_path = gt_path, data = dat_std)
)
suppressWarnings(
    play_tour_path(tour_path = gt_path, data = dat_std,
        axes = "bottomleft", angle = .08, fps = 8,
        aes_args = list(color = clas, shape = clas),
        identity_args = list(size = 1.5, alpha = .7),
        ggproto =
            list(ggplot2::theme_void(), ggplot2::ggtitle("My title")),
        render_type = render_gganimate)
)

## Saving a .gif (may require additional setup)
if(FALSE){ ## Don't accidentally save file
    ## Export plotly .html widget
    play_tour_path(tour_path = gt_path, data = dat_std,
        render_type = render_plotly,
        html_filename = "myRadialTour.html")

    ## Export gganimate .gif
    play_tour_path(tour_path = gt_path, data = dat_std,
        render_type = render_gganimate,
        gif_path = "myOutput", gif_filename = "myRadialTour.gif")
}

## End(Not run)

proto_basis

Tour proto for a 2D and 1D basis axes respectively

Description

Adds basis axes to the animation, the direction and magnitude of contributions of the variables to the projection space inscribed in a unit circle for 2D or rectangle of unit width for 1D.
proto_basis

Usage

proto_basis(
  position = c("left", "center", "right", "bottomleft", "topright", "full", "off"),
  manip_col = "blue",
  line_size = 0.6,
  text_size = 4
)

proto_basis1d(
  position = c("bottom1d", "floor1d", "top1d", "full", "off"),
  manip_col = "blue",
  segment_size = 2,
  text_size = 4,
  text_offset = -1.15
)

Arguments

position The position, to place the basis axes relative to the data. proto_basis expects one of c("left", "center", "right", "bottomleft", "topright", "off"), defaults to "left". proto_basis1d expects one of c("bottom1d", "floor1d", "top1d", "off"). Defaults to "bottom1d".

manip_col The color to highlight the manipulation variable with. Not applied if the tour isn't a manual tour. Defaults to "blue".

line_size (2D bases only) the thickness of the lines used to make the axes and unit circle. Defaults to 0.6.

text_size Size of the text label of the variables. Defaults to 4.

segment_size (1D bases only) the width thickness of the rectangle bar showing variable magnitude on the axes. Defaults to 2.

text_offset The horizontal offset of the text labels relative to the variable contributions in the basis between (-1, 1). Defaults to -1.15.

See Also

Other ggtour proto functions: append_fixed_y(), facet_wrap_tour(), ggtour(), proto_default(), proto_density(), proto_density2d(), proto_hex(), proto_highlight(), proto_hline0(), proto_origin(), proto_point(), proto_text()

Examples

library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species
bas <- basis_pca(dat)
mv <- manip_var_of(bas)

## 2D case:
mt_path <- manual_tour(bas, manip_var = mv)
proto_default

Wrapper function for default 2D/1D tours respectively.

Description

An easier way to get to default 2D tour settings. Returns a list of proto_origin(), proto_point(...), proto_basis() for 2D. Returns a list of proto_origin1d(), proto_density(...), proto_basis1d() for 1D.

Usage

proto_default()
position = c("left", "center", "right", "bottomleft", "topright", "off"),
...)

proto_default1d(position = c("bottom1d", "floor1d", "top1d", "off"), ...)

Arguments

position The position, to place the basis axes relative to the data. proto_basis expects
one of c("left", "center", "right", "bottomleft", "topright", "off"), defaults to
"left". proto_basis1d expects one of c("bottom1d", "floor1d", "top1d", "off").
Defaults to "bottom1d".

... Optionally pass additional arguments to proto_point or proto_density.

See Also

Other ggtour proto functions: append_fixed_y(), facet_wrap_tour(), ggtour(), proto_basis(),
proto_density(), proto_density2d(), proto_hex(), proto_highlight(), proto_hline0(),
proto_origin(), proto_point(), proto_text()

Examples

library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species

## 2D case:
bas <- basis_pca(dat)
mv <- manip_var_of(bas)
mt_path <- manual_tour(bas, mv)

ggt <- ggtour(mt_path, dat) +
proto_default(aes_args = list(color = clas, shape = clas))

animate_plotly(ggt)

library(spinifex)

## 1D case:
gt_path <- save_history(dat, grand_tour(d = 1), max_bases = 3)

ggt <- ggtour(gt_path, dat) +
proto_default1d(aes_args = list(fill = clas, color = clas))

animate_plotly(ggt)
proto_density

Description

Adds geom_density() and geom_rug() of the projected data. Density position = "stack" does not work with animate_plotly(), GH issue is open.

Usage

proto_density(
    aes_args = list(),
    identity_args = list(alpha = 0.7),
    row_index = NULL,
    density_position = c("identity", "stack", "fill"),
    rug_shape = c(3, 142, 124, NULL)
)

Arguments

 absolutes A list of arguments to call inside of aes(). aesthetic mapping of the primary geom. For example, geom_point(aes(color = my_fct, shape = my_fct)) becomes aes_args = list(color = my_fct, shape = my_fct).

identity_args A list of static, identity arguments passed into the primary geom. For instance, geom_point(size = 2, alpha = .7) becomes identity_args = list(size = 2, alpha = .7). Also passes more foundational arguments such as stat and position, though these have been tested less.

row_index A numeric or logical index of rows to subset to. Defaults to NULL, all observations.

density_position The ggplot2 position of geom_density(). Either c("identity", "stack"), defaults to "identity". Warning: "stack" does not work with animate_plotly() at the moment.

rug_shape Numeric, the number of the shape to make rug marks. Expects either 3 142, 124 or NULL, '+', '|' (plotly), '|' (ggplot2) respectively. Defaults to 3.

See Also

Other ggtour proto functions: append_fixed_y(), facet_wrap_tour(), ggtour(), proto_basis(), proto_default(), proto_density2d(), proto_hex(), proto_highlight(), proto_hline0(), proto_origin(), proto_point(), proto_text()

Examples

library(spinifex)
dat <- scale_sd(penguins_na[, 1:4])
clas <- penguins_na$species
proto_density2d

## Manual tour
bas <- basis_olda(dat, clas)
mt <- manual_tour(bas, manip_var = 2)
ggt <- ggtour(mt, dat, angle = .3) +
  proto_density(aes_args = list(color = clas, fill = clas)) +
  proto_basis1d() +
  proto_origin1d()

animate_plotly(ggt)

## Grand tour
gt_path <- save_history(dat, grand_tour(), max = 3)
ggt <- ggtour(gt_path, dat, angle = .3) +
  proto_density(aes_args = list(color = clas, fill = clas)) +
  proto_basis1d() +
  proto_origin1d()

animate_plotly(ggt)

---

### proto_density2d

**Tour proto for data, 1D density, with rug marks**

#### Description

Adds geom_density_2d() of the projected data.

#### Usage

```r
proto_density2d(
  aes_args = list(),
  identity_args = list(bins = 4),
  row_index = NULL
)
```

#### Arguments

- **aes_args**
  A list of arguments to call inside of aes(). aesthetic mapping of the primary geom. For example, geom_point(aes(color = my_fct, shape = my_fct)) becomes aes_args = list(color = my_fct, shape = my_fct).

- **identity_args**
  A list of static, identity arguments passed into the primary geom. For instance, geom_point(size = 2, alpha = .7) becomes identity_args = list(size = 2, alpha = .7). Also passes more foundational arguments such as stat and position, though these have been tested less.

- **row_index**
  A numeric or logical index of rows to subset to. Defaults to NULL, all observations.
See Also

Other ggtour proto functions: `append_fixed_y()`, `facet_wrap_tour()`, `ggtour()`, `proto_basis()`, `proto_default()`, `proto_density()`, `proto_hex()`, `proto_highlight()`, `proto_hline0()`, `proto_origin()`, `proto_point()`, `proto_text()`

Examples

```r
library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species
gt_path <- save_history(dat, grand_tour(), max = 3)

## geom_density_2d args can be passed in identity_args (bins, binwidth, breaks)
ggt <- ggtour(gt_path, dat, angle = .3) +
    proto_density2d(aes_args = list(color = clas, fill = clas),
                    identity_args = list(binwidth = .3)) +
    proto_point(aes_args = list(color = clas, shape = clas),
                identity_args = list(alpha = .2)) +
    proto_basis()
animate_plotly(ggt)
```

---

**proto_frame_cor2**

Tour proto for frames square correlation

Description

Adds text to the animation, the frame and its specified correlation.

Usage

```r
proto_frame_cor2(
  text_size = 4,
  row_index = TRUE,
  xy_position = c(0.7, -0.1),
  ...)
```

Arguments

- `text_size`  
  Size of the text. Defaults to 4.
- `row_index`  
  A numeric or logical index of rows to subset to. Defaults to NULL, all observations.
- `xy_position`  
  Vector of the x and y position, the fraction of the range of the data in each direction. The projection data is contained in (0, 1) in each direction. Defaults to `c(0.7, -0.1)`, in the bottom right.
- `...`  
  Optionally, pass additional arguments to `stats::cor`, specifying the type of within frame correlation.
proto_hex

See Also

stats::cor

Examples

library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species
gt_path <- save_history(dat, grand_tour(), max_bases = 5)

ggt <- ggtour(gt_path, dat, angle = .3) +
  proto_default(aes_args = list(color = clas, shape = clas)) +
  proto_frame_cor2(xy_position = c(.5, 1.1))

animate_plotly(ggt)

proto_hex

Tour proto for data, hexagonal heatmap

Description

Adds geom_hex() of the projected data. Does not display hexagons in plotly animations; will not work with animate_plotly().

Usage

proto_hex(
  aes_args = list(),
  identity_args = list(),
  row_index = NULL,
  bins = 30
)

Arguments

- **aes_args**: A list of arguments to call inside of aes(). aesthetic mapping of the primary geom. For example, geom_point(aes(color = my_fct, shape = my_fct)) becomes aes_args = list(color = my_fct, shape = my_fct).
- **identity_args**: A list of static, identity arguments passed into the primary geom. For instance, geom_point(size = 2, alpha = .7) becomes identity_args = list(size = 2, alpha = .7). Also passes more foundational arguments such as stat and position, though these have been tested less.
- **row_index**: A numeric or logical index of rows to subset to. Defaults to NULL, all observations.
- **bins**: Numeric vector giving number of bins in both vertical and horizontal directions. Defaults to 30.
See Also

Other ggtour proto functions: `append_fixed_y()`, `facet_wrap_tour()`, `ggtour()`, `proto_basis()`, `proto_default()`, `proto_density()`, `proto_density2d()`, `proto_highlight()`, `proto_hline0()`, `proto_origin()`, `proto_point()`, `proto_text()`

Examples

```r
library(spinifex)
raw  <- ggplot2::diamonds
dat  <- scale_sd(raw[1:10000, c(1, 5:6, 8:10)])
gt_path <- save_history(dat, grand_tour(), max = 3)

## 10000 rows is quite heavy to animate.
## Increase performance by aggregating many points into few hexagons
ggp <- ggtour(gt_path, dat) +
  proto_basis() +
  proto_hex(bins = 20)

## Hexagons don't show up in plotly animation.
## Not run:
animate_gganimate(ggp)

## End(Not run)
```

### proto_highlight

**Tour proto highlighting specified points**

**Description**

A `geom_point` or `geom_segment` (1d case) call to draw attention to a subset of points. This is mostly redundant with the implementation of the `row_index` argument on data protos, still helpful in the 1d case and for `mark_initial`, does not use `bkg_row_color`

**Usage**

```r
proto_highlight(
  aes_args = list(),
  identity_args = list(color = "red", size = 5, shape = 8),
  row_index = 1,
  mark_initial = FALSE
)
```

```r
proto_highlight1d(
  aes_args = list(),
  identity_args = list(color = "red", linetype = 2, alpha = 0.9),
  row_index = 1,
  mark_initial = FALSE
)
```
Arguments

aes_args  A list of arguments to call inside of aes(). aesthetic mapping of the primary geom. For example, geom_point(aes(color = my_fct, shape = my_fct)) becomes aes_args = list(color = my_fct, shape = my_fct).

identity_args  A list of static, identity arguments passed into geom_point(), but outside of aes(), for instance geom_point(aes(...), size = 2, alpha = .7) becomes identity_args = list(size = 2, alpha = .7). Typically a single numeric for point size, alpha, or similar.

row_index  A numeric or logical index of rows to subset to. Defaults to 1, highlighting the first row.

mark_initial  Logical, whether or not to leave a fainter mark at the subset’s initial position. Defaults to FALSE.

See Also

Other ggtour proto functions: append_fixed_y(), facet_wrap_tour(), ggtour(), proto_basis(), proto_default(), proto_density(), proto_density2d(), proto_hex(), proto_hline0(), proto_origin(), proto_point(), proto_text()

Examples

library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species
gt_path <- save_history(dat, grand_tour(), max_bases = 5)

## d = 2 case

ggt <- ggtour(gt_path, dat, angle = .3) +
  proto_default(aes_args = list(color = clas, shape = clas)) +
  proto_highlight(row_index = 5)
animate_plotly(ggt)

## Highlight multiple observations

ggt2 <- ggtour(gt_path, dat, angle = .3) +
  proto_default(aes_args = list(color = clas, shape = clas)) +
  proto_highlight(row_index = c(2, 6, 19),
                   identity_args = list(color = "blue", size = 4, shape = 4))
animate_plotly(ggt2)

## 1D case:

gt_path1d <- save_history(dat, grand_tour(d = 1), max_bases = 3)

ggt <- ggtour(gt_path1d, dat, angle = .3) +
  proto_default1d(aes_args = list(fill = clas, color = clas)) +
  proto_highlight1d(row_index = 7)
animate_plotly(ggt)
## Highlight multiple observations, mark_initial defaults to off

```r
gt2 <- ggtour(gt_path1d, dat, angle = .3) +
    proto_default1d(aes_args = list(fill = clas, color = clas)) +
    proto_highlight1d(row_index = c(2, 6, 7),
                       identity_args = list(color = "green", linetype = 1))
```

animate_plotly(ggt2)

---

**proto_hline0**  
**Tour proto adding a vertical/horizontal line**

### Description

Adds a vertical/horizontal line with an intercept of 0, scaled to the data frame.

### Usage

```r
proto_hline0(identity_args = list(color = "grey80", size = 0.5, alpha = 0.9))
```

### Arguments

**identity_args**  
A list of static, identity arguments passed into the primary geom. For instance, `geom_point(size = 2, alpha = .7)` becomes `identity_args = list(size = 2, alpha = .7)`. Also passes more foundational arguments such as stat and position, though these have been tested less.

### See Also

Other `ggtour` proto functions: `append_fixed_y()`, `facet_wrap_tour()`, `ggtour()`, `proto_basis()`, `proto_default()`, `proto_density()`, `proto_density2d()`, `proto_hex()`, `proto_highlight()`, `proto_origin()`, `proto_point()`, `proto_text()`

### Examples

```r
library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species

## 2D case:
gt_path <- save_history(dat, grand_tour(), max_bases = 5)
gt <- ggtour(gt_path, dat, angle = .1) +
    proto_point(list(color = clas, shape = clas)) +
    proto_hline0() + ## horizontal line at 0
    proto_vline0() ## vertical line at 0
```
proto_origin

animate_plotly(ggt)

---

proto_origin | Tour proto for data origin zero mark

Description

Adds a zero mark showing the location of the origin for the central data area.

Usage

```r
proto_origin(
    identity_args = list(color = "grey60", size = 0.5, alpha = 0.9),
    tail_size = 0.05
)
```

```r
proto_origin1d(identity_args = list(color = "grey60", size = 0.5, alpha = 0.9))
```

Arguments

- `identity_args` A list of static, identity arguments passed into the primary geom. For instance, `geom_point(size = 2, alpha = .7)` becomes `identity_args = list(size = 2, alpha = .7)`. Also passes more foundational arguments such as `stat` and `position`, though these have been tested less.

- `tail_size` How long the origin mark should extended relative to the observations. Defaults to .05, 5% of the projection space.

See Also

Other ggtour proto functions: `append_fixed_y()`, `facet_wrap_tour()`, `ggtour()`, `proto_basis()`, `proto_default()`, `proto_density()`, `proto_density2d()`, `proto_hex()`, `proto_highlight()`, `proto_hline0()`, `proto_point()`, `proto_text()`

Examples

```r
library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species

## 2D case:
gt_path <- save_history(dat, grand_tour(), max_bases = 5)
ggt <- ggtour(gt_path, dat, angle = .1) +
  proto_point(list(color = clas, shape = clas)) +
  proto_origin() ## `+` in center

animate_plotly(ggt)
```
## 1D case:

gt_path1d <- save_history(dat, grand_tour(d = 1), max_bases = 5)

ggt <- ggtour(gt_path1d, dat) +
  proto_density(list(fill = clas, color = clas)) +
  proto_origin1d() ## Adds line at 0.

animate_plotly(ggt)

---

**proto_point**

### Tour proto for data point

**Description**

Adds geom_point() of the projected data.

**Usage**

```r
proto_point(
  aes_args = list(),
  identity_args = list(alpha = 0.9),
  row_index = NULL,
  bkg_color = "grey80"
)
```

**Arguments**

- **aes_args**
  A list of arguments to call inside of aes(). aesthetic mapping of the primary geom. For example, `geom_point(aes(color = my_fct, shape = my_fct))` becomes `aes_args = list(color = my_fct, shape = my_fct)`.

- **identity_args**
  A list of static, identity arguments passed into the primary geom. For instance, `geom_point(size = 2, alpha = .7)` becomes `identity_args = list(size = 2, alpha = .7)`.

- **row_index**
  A numeric or logical index of rows to subset to. Defaults to NULL, all observations.

- **bkg_color**
  The character color by name or hexadecimal to display background observations, those not in the `row_index`. Defaults to "grey80". Use FALSE or NULL to skip rendering background points. Other aesthetic values such as shape and alpha are set adopted from `aes_args` and `identity_args`.

**See Also**

Other ggtour proto functions: `append_fixed_y()`, `facet_wrap_tour()`, `ggtour()`, `proto_basis()`, `proto_default()`, `proto_density()`, `proto_density2d()`, `proto_hex()`, `proto_highlight()`, `proto_hline0()`, `proto_origin()`, `proto_text()`
Examples

```r
library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species
gt_path <- save_history(dat, grand_tour(), max_bases = 5)

ggt <- ggtour(gt_path, dat, angle = .3) +
  proto_point(aes_args = list(color = clas, shape = clas),
              identity_args = list(size = 2, alpha = .7))
animate_plotly(ggt)

## Select/highlight observations with `row_index`

ggt <- ggtour(gt_path, dat, angle = .3) +
  proto_point(aes_args = list(color = clas, shape = clas),
              identity_args = list(size = 2, alpha = .7),
              row_index = which(clas == levels(clas)[1]),
              bkg_color = "grey80") ## FALSE or NULL to skip plotting background

animate_plotly(ggt)
```

---

**proto_text**  
*Tour proto for data, text labels*

**Description**

Adds `geom_text()` of the projected data.

**Usage**

```r
proto_text(
  aes_args = list(vjust = "outward", hjust = "outward"),
  identity_args = list(nudge_x = 0.05),
  row_index = TRUE
)
```

**Arguments**

- `aes_args`  
  A list of arguments to call inside of `aes()`. aesthetic mapping of the primary geom. For example, `geom_point(aes(color = my_fct, shape = my_fct))` becomes `aes_args = list(color = my_fct, shape = my_fct)

- `identity_args`  
  A list of static, identity arguments passed into the primary geom. For instance, `geom_point(size = 2, alpha = .7)` becomes `identity_args = list(size = 2, alpha = .7)`. Also passes more foundational arguments such as `stat` and `position`, though these have been tested less.

- `row_index`  
  A numeric or logical index of rows to subset to. Defaults to NULL, all observations.
See Also

Other ggtour proto functions: `append_fixed_y()`, `facet_wrap_tour()`, `ggtour()`, `proto_basis()`, `proto_default()`, `proto_density()`, `proto_density2d()`, `proto_hex()`, `proto_highlight()`, `proto_hline0()`, `proto_origin()`, `proto_point()`

Examples

```r
library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
clas <- penguins_na.rm$species
bas <- basis_pca(dat)
mv <- manip_var_of(bas)
gt_path <- save_history(dat, grand_tour(), max_bases = 5)

gt <- ggtour(gt_path, dat, angle = .2) +
    proto_text(list(color = clas))

animate_plotly(gt)

## Custom labels, subset of points

gt2 <- ggtour(gt_path, dat) +
    proto_text(list(color = clas, size = as.integer(clas)),
               list(alpha = .7),
               row_index = 1:15)

animate_plotly(gt2)
```

Description

[Superseded], see `ggtour`. Typically called by `render_plotly()` or `render_gganimate()`. Takes the result of `array2df()`, and renders them into a ggplot2 object.

Usage

```r
render_(
    frames,
    axes = "center",
    manip_col = "blue",
    line_size = 0.6,
    text_size = 4,
    aes_args = list(),
    identity_args = list(),
    ggproto = list(theme_spinifex())
)
```
Arguments

frames
The result of array2df(), a long df of the projected frames.

axes
Position of the axes, expects one of: "center", "left", "right", "bottomleft", "topright", "off", or a map_absolute() call. Defaults to "center".

manip_col
String of the color to highlight the manip_var, if used. Defaults to "blue".

line_size
The size of the lines of the unit circle and variable contributions of the basis. Defaults to .6.

text_size
The size of the text labels of the variable contributions of the basis. Defaults to 4.

aes_args
A list of aesthetic arguments to passed to geom_point(aes(X)). Any mapping of the data to an aesthetic, for example, geom_point(aes(color = myCol, shape = myCol)) becomes aes_args = list(color = myCol, shape = myCol).

identity_args
A list of static, identity arguments passed into geom_point(), but outside of aes(); geom_point(aes(), X). Typically a single numeric for point size, alpha, or similar. For example, geom_point(aes(), size = 2, alpha = .7) becomes identity_args = list(size = 2, alpha = .7).

ggproto
A list of ggplot2 function calls. Anything that would be "added" to ggplot(); in the case of applying a theme, ggplot() + theme_bw() becomes ggproto = list(theme_bw()). Intended for aesthetic ggplot2 functions (not geom_* family).

Examples

library(spinifex)
message("It's suggested to switch to the proto api, see '?ggtour' to get started.")

## Setup
dat_std <- scale_sd(wine[, 2:6])
clas <- wine$Type
bas <- basis_pca(dat_std)
mv <- manip_var_of(bas)

mt_array <- manual_tour(basis = bas, manip_var = mv)
mt_df_ls <- array2df(basis_array = mt_array, data = dat_std)

## Required arguments
render_(frames = mt_df_ls)

## Full arguments
require("ggplot2")
render_(frames = mt_df_ls, axes = "left", manip_col = "purple",
aes_args = list(color = clas, shape = clas),
identity_args = list(size = 1.5, alpha = .7),
ggproto = list(theme_minimal(),
ggtitle("My title"),
scale_color_brewer(palette = "Set2"))"
render_gganimate

Render the frames as a gganimate animation.

Description

[Superseded], see ggtour. Takes the result of array2df() and renders them into a gganimate animation.

Usage

render_gganimate(
  fps = 8,
  rewind = FALSE,
  start_pause = 0.5,
  end_pause = 1,
  gif_filename = NULL,
  gif_path = NULL,
  gganimate_args = list(),
  ...
)

Arguments

fps Frames animated per second. Defaults to 8.

rewind Logical, should the animation play backwards after reaching the end? Default to FALSE.

start_pause Number of seconds to pause on the first frame for. Defaults to .5.

dead_pause Number of seconds to pause on the last frame for. Defaults to 1.

gif_filename Optional, saves the animation as a GIF to this string (without the directory path). Defaults to NULL (no GIF saved). For more output control, call gganimate::anim_save() on a return object of render_gganimate().

gif_path Optional, A string of the directory path (without the filename) to save a GIF to. Defaults to NULL (current work directory).

gganimate_args A list of arguments assigned to a vector passe outside of an aes() call. Anything that would be put in geom_point(aes(), X). Typically a single numeric for point size, alpha, or similar For example, geom_point(aes(), size = 2, alpha = .7) becomes identity_args = list(size = 2, alpha = .7).

... Passes arguments to render_(...).

See Also

render_ for ... arguments.

gganimate::anim_save for more control of .gif output.
Examples

library(spinifex)
message("It's suggested to switch to the proto api, see \`?ggtour\` to get started.")

## Setup
dat_std <- scale_sd(wine[, 2:6])
clas <- wine$Type
bas <- basis_pca(dat_std)
mv <- manip_var_of(bas)
mt <- manual_tour(basis = bas, manip_var = mv)
mt_df_ls <- array2df(basis_array = mt, data = dat_std)

## Not run:
render_gganimate(frames = mt_df_ls)

require("ggplot2")
render_gganimate(
  frames = mt_df_ls, axes = "bottomleft",
  fps = 10, rewind = TRUE, start_pause = 1, end_pause = 1.5,
  aes_args = list(color = clas, shape = clas),
  identity_args = list(size = 2, alpha = .7),
  ggproto = list(theme_void(),
                  ggtitle("My title"),
                  scale_color_brewer(palette = "Set2")))

## Saving a .gif(may require additional setup)
if(FALSE) ## Don't run by mistake
  render_gganimate(frames = mt_df_ls, axes = "bottomleft",
                   gif_filename = "myRadialTour.gif", gif_path = "/output")

## End(Not run)

render_plotly

Animation the frames as a HTML widget.

Description

[Superseded], see ggtour. Takes the result of array2df() and animations them via {plotly} into a self-contained HTML widget.

Usage

render_plotly(fps = 8, html_filename = NULL, save_widget_args = list(), ...)

Arguments

fps Frames animated per second. Defaults to 8.
html_filename Optional, saves the plotly object as an HTML widget to this string (without the directory path). Defaults to NULL (not saved). For more output control use save_widget_args or call htmlwidgets::saveWidget() on a return object of render_plotly().
save_widget_args
A list of arguments to be called in htmlwidgets::saveWidget() when used with a html_filename.

... 
Passes arguments to render_.

See Also
render_ for ... arguments.
ggplotly for source documentation of tooltip.
saveWidget for more control of .html output.

Examples
library(spinifex)
message("It's suggested to switch to the proto api, see '?ggtour' to get started.")

## Setup
dat_std <- scale_sd(wine[, 2:6])
clas <- wine$Type
bas <- basis_pca(dat_std)
mv <- manip_var_of(bas)
mt_array <- manual_tour(basis = bas, manip_var = mv)
mt_df_ls <- array2df(basis_array = mt_array, data = dat_std)

render_plotly(frames = mt_df_ls)

require("ggplot2")
render_plotly(
  frames = mt_df_ls, axes = "bottomleft", fps = 10,
aes_args = list(color = clas, shape = clas),
identity_args = list(size = 1.5, alpha = .7),
gproto = list(theme_bw(), scale_color_brewer(palette = "Set2")))

## Saving a .gif, may require additional setup
if(FALSE) ## Don't accidentally save file
  render_plotly(frames = mt_df_ls, axes = "bottomleft", fps = 10,
              html_filename = "myRadialTour.html")

---

rotate_manip_space
Performs a rotation on the manipulation space of the given manip var.

Description
A specific R3 rotation of the manipulation space for a 2D tour. Typically called by manual_tour().
The first 2 columns are x and y in the projection plane. The 3rd column extends "in the z-direction" orthogonal to the projection plane.
**Usage**

rotate_manip_space(manip_space, theta, phi)

**Arguments**

- **manip_space**: A \((p, d+1)\) dim matrix (manipulation space) to be rotated.
- **theta**: Angle (radians) of "in-projection-plane" rotation (ie. on xy- of the projection). Typically set by the `manip_type` argument in `proj_data()`.
- **phi**: Angle (radians) of "out-of-projection-plane" rotation (ie. into the z-direction of the manipulation space. Effectively changes the norm of the `manip_var` in the projection plane.

**Value**

A \((p, d+1)\) orthonormal matrix of the rotated (manipulation) space. The first 2 columns are x and y in the projection plane. The 3rd column extends "in the z-direction" orthogonal to the projection plane.

**See Also**

Other manual tour adjacent functions: `create_manip_space()`, `interpolate_manual_tour()`, `manip_var_of()`, `manual_tour()`

**Examples**

```r
library(spinifex)
dat <- scale_sd(wine[, 2:6])
bas <- basis_pca(dat)
mv <- manip_var_of(bas)
msp <- create_manip_space(basis = bas, manip_var = mv)
rotate_manip_space(msp, theta = runif(1, max = 2 * pi), phi = runif(1, max = 2 * pi))

## d = 1 case
bas1d <- basis_pca(dat, d = 1)
mv <- manip_var_of(bas1d)
msp <- create_manip_space(bas1d, mv)
rotate_manip_space(msp, theta = 0, phi = runif(1, max = 2 * pi))
```

---

**Description**

Runs a local shiny app that demonstrates manual tour and comparable traditional techniques for static projections of multivariate data sets.
Usage

run_app(app_nm = "radial_tour", ...)

Arguments

app_nm  name of the shiny app to run. Expects "manual_tour".
...
Other arguments passed into shiny::runApp(). Such as display.mode = "showcase".

Value

Runs a locally hosted shiny app.

Examples

## Not run:
run_app("radial_tour")
run_app(app_nm = "radial_tour", display.mode = "showcase")
## End(Not run)

---

save_history  Save a tour basis array.

Description

Save a tour path so it can later be displayed in many different ways. A wrapper function can mute the noisy text side effects of tourr::save_history. Changes a few argument defaults differ: doesn’t scale data columns to (0, 1), max_bases = 10, appends the start basis if tour_path is grand, it isn’t already there, and has correct dim.

Usage

save_history(
  data,
  tour_path = tourr::grand_tour(),
  max_bases = 10,
  start = NULL,
  rescale = FALSE,
  sphere = FALSE,
  step_size = Inf,
  verbose = getOption("verbose"),
  ...
)
Arguments

data Matrix, or data frame containing complete numeric columns
tour_path Tour path generator. Defaults to `tourr::grand_tour`.
max_bases The maximum number of new bases to generate. Some tour paths (like the
guided tour) may generate less than the maximum. Defaults to 10.
start First basis, is appended as first frame grand tour if possible.
rescale Whether or not to rescale all variables to range (0,1). Defaults to FALSE.
sphere Whether or not to sphere (whiten) covariance matrix to the identity matrix. De-
defaults to FALSE.
step_size Distance (in radians) between target frames (not interpolated frames). Defaults
to Inf, forcing new basis generation at each step.
verbose Whether or not to suppress the text output side effects from `tourr::save_history`.
Defaults to FALSE.
... Additional arguments passed to `tourr::new_tour`.

See Also

`tourr::save_history` `tourr::new_tour` `tourr::grand_tour`

Examples

```r
library(spinifex)
dat <- scale_sd(penguins_na.rm[, 1:4])
## A grand tour path
gt_path <- save_history(data = dat, tour_path = grand_tour(), max_bases = 10)
dim(gt_path)

## A 1d grand tour path
gt1d_path <- save_history(dat, grand_tour(d = 1), 10)
dim(gt1d_path)

## A holes guided tour path
holes_path <- save_history(dat, guided_tour(holes(), max.tries = 10))
dim(holes_path)

## These are basis_arrays to be used in ?spinifex::ggtour()
```

scale_colour_discrete Set default color & fill for discrete variables

Description

Masks ggplot2’s default color/fill color palette for discrete variables.
Usage

scale_colour_discrete(...)  
scale_fill_discrete(...)

Arguments

...  

Passes arguments to ggplot2::scale_colour/fill_brewer.

scale_sd  

Preprocess numeric variables

Description

Centers and scales each column by standard deviation (sd) or to the interval (0, 1).

Usage

scale_sd(data)

scale_01(data)

Arguments

data  

Numeric matrix or data.frame of the observations.

Examples

scale_sd(data = wine[, 2:6])
scale_01(data = wine[, 2:6])

---

spinifex  

spinifex

Description

spinifex is a package that extends the package tourr. It builds the functionality for manual tours and allows other tours to be rendered by plotly or gganimate. Tours are a class of dynamic linear (orthogonal) projections of numeric multivariate data from p down to d dimensions that are viewed as an animation as p-space is rotated. Manual tours manipulate a selected variable, exploring how they contribute to the sensitivity of the structure in the projection. This is particularly useful after finding an interesting basis, perhaps via a guided tour optimizing the projection for some objective function.
theme_spinifex

Details

GitHub: https://github.com/nspyris/spinifex

Author(s)

Maintainer: Nicholas Spyrison <spyrison@gmail.com> (ORCID)
Authors:
  • Dianne Cook (ORCID) [thesis advisor]

See Also

  manual_tour() ggtour() proto_default()

theme_spinifex      Theme spinifex

Description

A ggplot2 theme suggested for linear projections with spinifex. The default theme in spinifex functions.

Usage

theme_spinifex(...)  

Arguments

...  

Optionally pass arguments to ggplot2::theme().

See Also

  ggplot2::theme for all theme options.

Examples

  theme_spinifex()

    require("ggplot2")
    ggplot(mtcars, aes(wt, mpg, color = as.factor(cyl))) +
    geom_point() + theme_spinifex()
view_frame

Plot a single frame of a manual tour.

Description

[Superseded], see ggtour. Projects the specified rotation as a 2D ggplot object. One static frame of manual tour. Useful for providing user-guided interaction.

Usage

view_frame(
basis = NULL,
data = NULL,
manip_var = NULL,
theta = 0,
phi = 0,
basis_label = abbreviate(row.names(basis), 3),
rescale_data = FALSE,
...
)

Arguments

basis A (p, d) dim orthonormal numeric matrix. Defaults to NULL, giving a random basis.
data A (n, p) dataset to project, consisting of numeric variables.
manip_var Optional, number of the variable to rotate. If NULL, theta and phi must be 0 as is no manip space to rotate.
theta Angle in radians of "in-projection plane" rotation, on the xy plane of the reference frame. Defaults to 0, no rotation.
phi Angle in radians of the "out-of-projection plane" rotation, into the z-direction of the axes. Defaults to 0, no rotation.
basis_label Optional, character vector of p length, add name to the axes in the frame, defaults to 3 letter abbreviation of the original variable names.
rescale_data When TRUE scales the data to between 0 and 1. Defaults to FALSE.
... Optionally pass additional arguments to the proto_default for projection point aesthetics;

Value

A ggplot object of the rotated projection.

See Also

proto_default For arguments to pass into . . .
view_manip_space

Examples

library(spinifex)
message("It's suggested to switch to the proto api, see \`ggtour\` to get started.")

## Setup

dat_std <- scale_sd(wine[, 2:6])
clas <- wine$Type
bas <- basis_pca(dat_std)
mv <- manip_var.of(bas)

## Minimal example

suppressWarnings(
  view_frame(basis = bas)
)

## Typical example

suppressWarnings(
  view_frame(basis = bas, data = dat_std, manip_var = mv, axes = "left")
)

## Full example

rtheta <- runif(1, 0, 2 * pi)
rphi <- runif(1, 0, 2 * pi)
suppressWarnings(
  view_frame(
    basis = bas, data = dat_std, manip_var = mv,
    theta = rtheta, phi = rphi, basis_label = paste0("MyNm", 1:ncol(dat_std)),
    aes_args = list(color = clas, shape = clas),
    identity_args = list(size = 1.5, alpha = .7))
)

view_manip_space  Plot 2D projection frame and return the axes table.

Description

Uses base graphics to plot the circle with axes representing the projection frame. Returns the corresponding table. Only works for 2d manual tours.

Usage

view_manip_space(
  basis,
  manip_var,
  tilt = 0.1 * pi,
  basis_label = abbreviate(row.names(basis), 3),
  manip_col = "blue",
)
manip_sp_col = "red",
line_size = 0.6,
text_size = 4
)

Arguments

basis A (p, d) orthonormal numeric matrix. The linear combination the original variables contribute to projection space. Required, no default.
manip_var Number of the column/dimension to rotate.
tilt angle in radians to rotate the projection plane. Defaults to .1 * pi.
basis_label Optional, character vector of p length, add name to the axes in the frame, defaults to 3 letter abbreviation of the orginal variable names.
manip_col String of the color to highlight the manip_var.
manip_sp_col Color to illustrate the z direction, orthogonal to the projection plane.
line_size The size of the lines of the unit circle and variable contributions of the basis. Defaults to 1.
text_size The size of the text labels of the variable contributions of the basis. Defaults to 5.

Value
ggplot object of the basis.

Examples

library(spinifex)
dat_std <- scale_sd(wine[, 2:6])
bas <- basis_pca(dat_std)
mv <- manip_var_of(bas)

view_manip_space(basis = bas, manip_var = mv)

view_manip_space(basis = bas, manip_var = mv,
tilt = 2/12 * pi, basis_label = paste0("MyNm", 1:ncol(dat.std)),
manip_col = "purple", manip_sp_col = "orange")

weather Sample dataset of daily weather observations from Canberra airport in Australia.

Description

One year of daily weather observations collected from the Canberra airport in Australia was obtained from the Australian Commonwealth Bureau of Meteorology and processed to create this sample dataset for illustrating data mining using R and Rattle.
Usage

weather_na.rm

Format

A data frame of 354 observations of 20 variables. One year of daily observations of weather variables at Canberra airport in Australia between November 1, 2007 and October 31, 2008.

- Date, The date of observation (Date class).
- MinTemp, The minimum temperature in degrees Celsius.
- MaxTemp, The maximum temperature in degrees Celsius.
- Rainfall, The amount of rainfall recorded for the day in mm.
- Evaporation, The "Class A pan evaporation" (mm) in the 24 hours to 9am.
- WindSpeed3pm, Wind speed (km/hr) averaged over 10 minutes prior to 3pm.
- Humid9am, Relative humidity (percent) at 9am.
- Humid3pm, Relative humidity (percent) at 3pm.
- Pressure9am, Atmospheric pressure (hpa) reduced to mean sea level at 9am.
- Pressure3pm, Atmospheric pressure (hpa) reduced to mean sea level at 3pm.
- Cloud9am, Fraction of sky obscured by cloud at 9am. This is measured in "oktas", which are a unit of eighths. It records how many eighths of the sky are obscured by cloud. A 0 measure indicates completely clear sky whilst an 8 indicates that it is completely overcast.
- Cloud3pm, Fraction of sky obscured by cloud (in "oktas": eighths) at 3pm. See Cloud9am for a description of the values.
- Temp9am, Temperature (degrees C) at 9am.
- Temp3pm, Temperature (degrees C) at 3pm.
- RISK_MM, The amount of rain. A kind of measure of the "risk".
- RainToday, Factor: "yes" if precipitation (mm) in the 24 hours to 9am exceeds 1mm, otherwise 0.
- RainTomorrow, Factor: "yes" if it rained the following day, the target variable.


Details

The data has been processed to provide a target variable RainTomorrow (whether there is rain on the following day - No/Yes) and a risk variable RISK_MM (how much rain recorded in millimeters). Various transformations were performed on the source data. The dataset is quite small and is useful only for repeatable demonstration of various data science operations.

This is a cleaned subset of rattle::weather.

Replicating this dataset:
require("rattle")
d <- rattle::weather[, c(1, 3:7, 9, 12:21, 23, 22, 24)]
d <- d[complete.cases(d), ] ## Remove ~12 row-wise incomplete rows
d <- as.data.frame(d) ## Remove tibble dependency
weather_na.rm <- d
## save(weather_na.rm, file = "./data/weather_na.rm.rda")

Source

rattle, R package. G. Williams, 2020. rattle: Graphical User Interface for Data Science in R
https://CRAN.R-project.org/package=rattle

Examples

library(spinifex)
str(weather_na.rm)
dat <- scale_sd(weather_na.rm[, 2:18])
clas <- weather_na.rm$RainTomorrow
bas <- basis_pca(dat)
mv <- manip_var_of(bas)
mt <- manual_tour(bas, mv)
ggt <- ggtour(mt, dat, angle = .2) +
    proto_default(aes_args = list(color = clas, shape = clas))
animate_plotly(ggt)

wine

The wine dataset from the UCI Machine Learning Repository.

Description

The wine dataset contains the results of a chemical analysis of wines grown in a specific area of Italy.
Three types of wine are represented in the 178 samples, with the results of 13 chemical analyses recorded for each sample. The Type variable has been transformed into a categorical variable.

Usage

wine

Format

A data frame of 178 observations of target class Type and 12 numeric variables:

- Type, The type of wine, the target factor, 1 (59 obs), 2 (71 obs), and 3 (48 obs).
• Alcohol, Alcohol
• Malic, Malic acid
• Ash, Ash
• Alcalinity, Alcalinity of ash
• Magnesium, Magnesium
• Phenols, Total phenols
• Flavanoids, Flavanoids
• Nonflavanoids, Nonflavanoid phenols
• Proanthocyanins, Proanthocyanins
• Color, Color intensity
• Hue, Hue
• Dilution, D280/OD315 of diluted wines
• Proline, Proline

Details

The data contains no missing values and consist of only numeric data, with a three class target variable (Type) for classification.

Replicating this dataset:

```r
require("rattle")
str(rattle::wine)
## save(wine, file = ".//data/wine.rda")
```

Source

rattle, R package. G. Williams, 2020. rattle: Graphical User Interface for Data Science in R
https://CRAN.R-project.org/package=rattle


Examples

```r
library(spinifex)
str(wine)
dat <- scale_sd(wine[, 2:6])
clas <- wine$Type

bas <- basis_pca(dat)
mv <- manip_var_of(bas)
mt <- manual_tour(bas, mv)

ggt <- ggtour(mt, dat, angle = .2) +
    proto_default(aes_args = list(color = clas, shape = clas))

animate_plotly(ggt)
```
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