Package 'ggpca'

October 28, 2024

Title Publication-Ready PCA, t-SNE, and UMAP Plots

Version 0.1.2

Description Provides tools for creating publication-ready dimensionality reduction plots, including Principal Component Analysis (PCA), t-Distributed Stochastic Neighbor Embedding (t-SNE), and Uniform Manifold Approximation and Projection (UMAP). This package helps visualize high-dimensional data with options for custom labels, density plots, and faceting, using the 'ggplot2' framework Wickham (2016) <doi:10.1007/978-3-319-24277-4>.

License GPL-3

Imports config (>= 0.3.2), golem (>= 0.4.1), shiny (>= 1.8.1.1), rlang, Rtsne, cowplot, dplyr, ggplot2, umap

Encoding UTF-8

RoxygenNote 7.3.2

Suggests knitr, tibble, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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ggpca   *Create publication-ready PCA, t-SNE, or UMAP plots*

Description

This function generates dimensionality reduction plots (PCA, t-SNE, UMAP) with options for custom labels, titles, density plots, and faceting. It allows users to visualize high-dimensional data using various dimensionality reduction techniques.

Usage

```
ggpca(
  data,
  metadata_cols,
  mode = c("pca", "tsne", "umap"),
  scale = TRUE,
  x_pc = "PC1",
  y_pc = "PC2",
  color_var = "Species",
  ellipse = TRUE,
  ellipse_level = 0.9,
  ellipse_type = "norm",
  ellipse_alpha = 0.9,
  point_size = 3,
  point_alpha = 0.6,
  facet_var = NULL,
  tsne_perplexity = 30,
  umap_n_neighbors = 15,
  density_plot = "none",
  color_palette = "Set1",
  xlab = NULL,
  ylab = NULL,
  title = NULL,
  subtitle = NULL,
  caption = NULL
)
```

Arguments

data	A data frame containing the data to be plotted. Must include both feature columns (numeric) and metadata columns (categorical).
metadata_cols	A character vector of column names or a numeric vector of column indices for the metadata columns. These columns are used for grouping and faceting.
mode	The dimensionality reduction method to use. One of "pca" (Principal Component Analysis), "tsne" (t-Distributed Stochastic Neighbor Embedding), or "umap" (Uniform Manifold Approximation and Projection).

scale	Logical indicating whether to scale features (default: TRUE for PCA). Not used for "tsne" or "umap".
x_pc	Name of the principal component or dimension to plot on the x-axis (default: "PC1" for PCA).
y_pc	Name of the principal component or dimension to plot on the y-axis (default: "PC2" for PCA).
color_var	Name of the column used to color points in the plot (default: "Species"). Should be a categorical variable in the data.
ellipse	Logical indicating whether to add confidence ellipses for groups (only supported for PCA; default: TRUE).
ellipse_level	Confidence level for ellipses (default: 0.9).
ellipse_type	Type of ellipse to plot, e.g., "norm" for normal distribution (default: "norm").
ellipse_alpha	Transparency level for ellipses, where 0 is fully transparent and 1 is fully opaque (default: 0.9).
point_size	Size of the points in the plot (default: 3).
point_alpha	Transparency level for the points, where 0 is fully transparent and 1 is fully opaque (default: 0.6).
facet_var	Formula for faceting the plot (e.g., Category ~ .), allowing users to split the plot by different groups.
tsne_perplexity	Perplexity parameter for t-SNE, which balances local and global aspects of the data (default: 30).
umap_n_neighbors	Number of neighbors for UMAP, which determines the local structure (default: 15).
density_plot	Controls whether to add density plots for the x, y, or both axes. Accepts one of "none", "x", "y", or "both" (default: "none").
color_palette	Name of the color palette to use for the plot. Supports "Set1", "Set2", etc. from RColorBrewer (default: "Set1").
xlab	Custom x-axis label (default: NULL, will be auto-generated based on the data).
ylab	Custom y-axis label (default: NULL, will be auto-generated based on the data).
title	Plot title (default: NULL).
subtitle	Plot subtitle (default: NULL).
caption	Plot caption (default: NULL).

Value

A ggplot2 object representing the dimensionality reduction plot, including scatter plots, optional density plots, and faceting options. The plot can be further customized using ggplot2 functions.

Examples

```
# Load dataset
pca_data <- read.csv(system.file("extdata", "example.csv", package = "ggpca"))

# PCA example
p_pca_y_group <- ggpca(
  pca_data,
  metadata_cols = c(1:6),
  mode = "pca",
  color_var = "group",
  ellipse = TRUE,
  density_plot = "y",
  title = "PCA with Y-axis Density Plot",
  subtitle = "Example dataset, colored by group",
  caption = "Data source: Example dataset"
)
print(p_pca_y_group)

# t-SNE example
p_tsne_time <- ggpca(
  pca_data,
  metadata_cols = c(1:6),
  mode = "tsne",
  color_var = "time",
  tsne_perplexity = 30,
  title = "t-SNE Plot of Example Dataset",
  subtitle = "Colored by time",
  caption = "Data source: Example dataset"
)
print(p_tsne_time)
```

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run_app   *Run the Shiny Application*

Description

This function launches the Shiny application with the specified user interface and server function. The function does not return a value but starts the Shiny app, allowing users to interact with it.

Usage

```
run_app(
  onStart = NULL,
  options = list(),
  enableBookmarking = NULL,
  uiPattern = "/",
  ...
)
```

Arguments

onStart   A function that will be called before the app is actually run. This is only needed for shinyAppObj, since in the shinyAppDir case, a global.R file can be used for this purpose.

options   Named options that should be passed to the runApp call (these can be any of the following: "port", "launch.browser", "host", "quiet", "display.mode" and "test.mode"). You can also specify width and height parameters which provide a hint to the embedding environment about the ideal height/width for the app.

enableBookmarking
                Can be one of "url", "server", or "disable". The default value, NULL, will respect the setting from any previous calls to enableBookmarking(). See enableBookmarking() for more information on bookmarking your app.

uiPattern   A regular expression that will be applied to each GET request to determine whether the ui should be used to handle the request. Note that the entire request path must match the regular expression in order for the match to be considered successful.

...   Arguments to pass to 'golem_opts'. See '?golem::get_golem_options' for more details.

Value

No return value, called for side effects.

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