Package 'VoronoiBiomedPlot'

June 6, 2025

Type Package

Title Projection Visualization Plots for Dimensionally Reduced Data

Version 0.1.0

Description Creates visualization plots for 2D projected data including ellipse plots, Voronoi diagram plots, and combined ellipse-Voronoi plots. Designed to visualize class separation in dimensionally reduced data from techniques like principal component analysis (PCA), partial least squares discriminant analysis (PLS-DA) or others. For more details see Lötsch and Ultsch (2024) <doi:10.1016/j.imu.2024.101573>.

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Encoding UTF-8

Depends R (>= 3.5.0)

Imports ggplot2, ggrepel, deldir

RoxygenNote 7.2.0

NeedsCompilation no

Author Jorn Lotsch [aut, cre]

Maintainer Jorn Lotsch <j.lotsch@em.uni-frankfurt.de>

Repository CRAN

Date/Publication 2025-06-06 12:50:01 UTC

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`VoronoiBiomedPlot-package` *Projection Visualization Plots for Dimensionally Reduced Data*

Description

Creates visualization plots for 2D projected data including ellipse plots, Voronoi diagram plots, and combined ellipse-Voronoi plots. Designed to visualize class separation in dimensionally reduced data from techniques like principal component analysis (PCA), partial least squares discriminant analysis (PLS-DA) or others. For more details see Lötsch and Ultsch (2024) <doi:10.1016/j.imu.2024.101573>.

Details

The VoronoiBiomedPlot package provides functions for creating visualization plots of 2D projected data, particularly useful for biomedical data analysis and dimensionality reduction results.

The package includes two main functions:

- `create_projection_plots`: Creates three types of plots (ellipse, Voronoi, and combined)
- `create_voronoi_plot`: Creates standalone Voronoi tessellation plots

These functions are designed to visualize class separation in dimensionally reduced data from techniques like PCA, PLS-DA, t-SNE, or other projection methods commonly used in biomedical research.

Voronoi tessellation divides the plot space into regions based on proximity to data points, providing an intuitive visualization of class boundaries and decision regions. Confidence ellipses show the distribution spread and correlation structure within each class.

Author(s)

Jorn Lotsch <j.lotsch@em.uni-frankfurt.de>

References

Lötsch, J. and A. Ultsch (2024). Comparative assessment of projection and clustering method combinations in the analysis of biomedical data. Informatics in Medicine Unlocked 50: 101573. https://www.sciencedirect.com/science/article/pii/S2352914824001291

See Also

- https://github.com/JornLotsch/voronoi_projection_plot
- Report bugs at https://github.com/JornLotsch/voronoi_projection_plot/issues

Examples

```
# Load the iris dataset
data <- iris[, c("Sepal.Length", "Petal.Length", "Species")]

# Create comprehensive projection plots
plots <- create_projection_plots(
  data = data,
  class_column = "Species",
  legend_position = "bottom",
  add_grid_lines = FALSE
)

# Access individual plots
# plots$ellipse_plot
# plots$voronoi_plot
# plots$voronoi_plot_plus_ellipse

# Create standalone Voronoi plot
voronoi_plot <- create_voronoi_plot(
  data = data,
  class_column = "Species",
  legend_position = "bottom",
  add_grid_lines = FALSE
)
```

`create_projection_plots`

Create Projection Visualization Plots

Description

Creates three types of visualization plots for 2D projected data: ellipse plots, Voronoi diagram plots, and combined ellipse-Voronoi plots. The function is designed to visualize class separation in dimensionally reduced data.

Usage

```
create_projection_plots(
  data,
  class_column = NULL,
  alternative_class_column = NULL,
  coordinate_columns = NULL,
  case_labels = NULL,
  coord_names = c("Dim1", "Dim2"),
  title = NULL,
  show_labels = FALSE,
  ellipse_alpha = 0.1,
  voronoi_alpha = 0.3,
```

```
  point_size = 2,
  legend_position = "bottom",
  color_palette = NULL,
  add_grid_lines = FALSE,
  color_points = "primary",
  fill_voronoi = "primary"
)
```

Arguments

data	A data frame containing projected data. Must have at least 2 numeric columns. If more than 2 columns are provided, the first 2 are used as coordinates.
class_column	Character string specifying the column name containing class labels, or a vector of class labels. If NULL, all observations are treated as a single class. Default: NULL.
alternative_class_column	Character string specifying the column name containing alternative class labels, or a vector of alternative class labels. If NULL, uses class_column. Default: NULL.
coordinate_columns	Character vector of length 2 specifying the column names to use as coordinates. If NULL, uses the first two numeric columns. Default: NULL.
case_labels	Character vector of case labels for individual observations. If NULL, row numbers are used. Default: NULL.
coord_names	Character vector of length 2 specifying names for the coordinate axes. Default: c("Dim1", "Dim2").
title	Character string for plot title. If NULL, no title is added. Default: NULL.
show_labels	Logical indicating whether to show case labels on plots. Default: FALSE.
ellipse_alpha	Numeric value (0-1) for ellipse transparency. Default: 0.1.
voronoi_alpha	Numeric value (0-1) for Voronoi polygon transparency. Default: 0.3.
point_size	Numeric value for point size. Default: 2.
legend_position	Character string or numeric vector specifying legend position. Default: "bottom".
color_palette	Function or character vector for color palette. If NULL, uses ggplot2 default colors. Default: NULL.
add_grid_lines	Logical indicating whether to add dashed grid lines at origin. Default: FALSE.
color_points	Character string specifying which classification to use for point colors. Either "primary" (uses class_column) or "alternative" (uses alternative_class_column). Default: "primary".
fill_voronoi	Character string specifying which classification to use for Voronoi fill. Either "primary" (uses class_column) or "alternative" (uses alternative_class_column). Default: "primary".

Details

The function creates visualizations for 2D projected data, particularly useful for displaying results from dimensionality reduction techniques like PCA, PLS-DA, or t-SNE.

Voronoi tessellation divides the plot space into regions based on proximity to data points, providing an intuitive visualization of class boundaries and decision regions.

Confidence ellipses show the distribution spread and correlation structure within each class.

Value

A list containing three ggplot objects:

`ellipse_plot` Plot with confidence ellipses for each class

`voronoi_plot` Plot with Voronoi tessellation regions

`voronoi_plot_plus_ellipse`
Combined plot with both Voronoi regions and ellipses

Examples

```
# Basic usage with iris dataset
data <- iris[, c("Sepal.Length", "Petal.Length", "Species")]
plots <- create_projection_plots(
  data = data,
  class_column = "Species",
  legend_position = "bottom",
  add_grid_lines = FALSE
)
```

`create_voronoi_plot` *Create Voronoi Projection Visualization Plot*

Description

Creates a Voronoi tessellation visualization for 2D projected data, showing class separation through proximity-based regions.

Usage

```
create_voronoi_plot(
  data,
  class_column = NULL,
  alternative_class_column = NULL,
  coordinate_columns = NULL,
  case_labels = NULL,
  coord_names = c("Dim1", "Dim2"),
  title = NULL,
  show_labels = FALSE,
```

```
  voronoi_alpha = 0.3,
  point_size = 2,
  legend_position = "bottom",
  color_palette = NULL,
  add_grid_lines = FALSE,
  color_points = "primary",
  fill_voronoi = "primary"
)
```

Arguments

data	A data frame containing projected data. Must have at least 2 numeric columns. If more than 2 columns are provided, the first 2 are used as coordinates.
class_column	Character string specifying the column name containing class labels, or a vector of class labels. If NULL, all observations are treated as a single class. Default: NULL.
alternative_class_column	Character string specifying the column name containing alternative class labels, or a vector of alternative class labels. If NULL, uses class_column. Default: NULL.
coordinate_columns	Character vector of length 2 specifying the column names to use as coordinates. If NULL, uses the first two numeric columns. Default: NULL.
case_labels	Character vector of case labels for individual observations. If NULL, row numbers are used. Default: NULL.
coord_names	Character vector of length 2 specifying names for the coordinate axes. Default: c("Dim1", "Dim2").
title	Character string for plot title. If NULL, no title is added. Default: NULL.
show_labels	Logical indicating whether to show case labels on plots. Default: FALSE.
voronoi_alpha	Numeric value (0-1) for Voronoi polygon transparency. Default: 0.3.
point_size	Numeric value for point size. Default: 2.
legend_position	Character string or numeric vector specifying legend position. Default: "bottom".
color_palette	Function or character vector for color palette. If NULL, uses ggplot2 default colors. Default: NULL.
add_grid_lines	Logical indicating whether to add dashed grid lines at origin. Default: TRUE.
color_points	Character string specifying which classification to use for point colors. Either "primary" (uses class_column) or "alternative" (uses alternative_class_column). Default: "primary".
fill_voronoi	Character string specifying which classification to use for Voronoi fill. Either "primary" (uses class_column) or "alternative" (uses alternative_class_column). Default: "primary".

Details

The function creates a Voronoi tessellation visualization for 2D projected data, particularly useful for displaying results from dimensionality reduction techniques. Voronoi tessellation divides the plot space into regions based on proximity to data points, providing an intuitive visualization of class boundaries and decision regions.

Value

A ggplot object showing the Voronoi tessellation plot.

Examples

```
# Basic usage with iris dataset
data <- iris[, c("Sepal.Length", "Petal.Length", "Species")]
plot <- create_voronoi_plot(
  data = data,
  class_column = "Species",
  legend_position = "bottom",
  add_grid_lines = FALSE
)
```

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