Package: ggtaxplot (via r-universe)

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Type Package

Title Create Plots to Visualize Taxonomy

Version 0.0.1

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Description Provides a comprehensive suite of functions for processing
and visualizing taxonomic data. It includes functionality to
clean and transform taxonomic data, categorize it into
hierarchical ranks (such as Phylum, Class, Order, Family, and
Genus), and calculate the relative abundance of each category.
The package also generates a color palette for visual
representation of the taxonomic data, allowing users to easily
identify and differentiate between various taxonomic groups.
Additionally, it features a river plot visualization to
effectively display the distribution of individuals across
different taxonomic ranks, facilitating insights into taxonomic
visualization.

License GPL-3

Imports ggplot2, dplyr, tidyr, tidyverse, scales, RColorBrewer,
cluster, vegan, ggalluvial, magrittr, rlang

Suggests knitr, rmarkdown, testthat, devtools

Encoding UTF-8

RoxygenNote 7.3.2

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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Config/pak/sysreqs libfontconfig1-dev libfreetype6-dev libfribidi-dev
make libharfbuzz-dev libicu-dev libjpeg-dev libpng-dev
libtiff-dev libxml2-dev libssl-dev libx11-dev zlib1g-dev

Contents

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ggtaxplot   *ggtaxplot Process and Plot Taxonomic Data*

Description

This function processes data and generates a taxonomic river plot.

Usage

```
ggtaxplot(
  data,
  ID_col = "ID",
  tax_col = "Taxonomy",
  rm_NA = FALSE,
  threshold = 2,
  custom_colors = NULL
)
```

Arguments

data	A data frame containing two columns: ID and Taxonomy.
ID_col	A column with ID values.
tax_col	A column with Taxonomy.
rm_NA	A logical value indicating whether to remove rows where the taxonomy column is 'Unknown' or NA. Default is FALSE.
threshold	A numeric threshold for filtering low-abundance taxa (Others).
custom_colors	Optional custom colors assigned to phyla.

Value

A ggplot object of the river plot.

Examples

```
# Example data frame
data <- data.frame(
 ID = c("ID1", "ID2", "ID3"),
 Taxonomy = c("d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;\
 o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia",
            "d__Bacteria;p__Actinobacteria;c__Actinobacteria;\
            o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium",
```

```
            "d__Bacteria;p__Firmicutes;c__Bacilli;\
            o__Bacillales;f__Bacillaceae;g__Bacillus")
            )
# Generate the river plot
plot <- ggtaxplot(data)
print(plot)
```

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lighten_color	*Lighten a Color*

Description

This function lightens a given color by a specified factor.

Usage

```
lighten_color(color, factor)
```

Arguments

color	A character string representing a color in any valid format (e.g., hex code, color name).
factor	A numeric value between 0 and 1 indicating the amount to lighten the color. A factor of 0 means no change, while a factor of 1 results in white.

Value

A character string representing the lightened color in RGB format.

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