Package ‘omixVizR’

July 18, 2025

Title A Toolkit for Omics Data Visualization

Version 1.0.5

Description Provides a suite of tools for the comprehensive visualization of multi-omics data, including genomics, transcriptomics, and proteomics. Offers user-friendly functions to generate publication-quality plots, thereby facilitating the exploration and interpretation of complex biological datasets. Supports seamless integration with popular R visualization frameworks and is well-suited for both exploratory data analysis and the presentation of final results. Key formats and methods are presented in Huang, S., et al. (2024) ``The Born in Guangzhou Cohort Study enables generational genetic discoveries'' <doi:10.1038/s41586-023-06988-4>.

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URL `https://leslie-lu.github.io/`

Encoding UTF-8

Language en-US

RoxygenNote 7.3.2

Suggests testthat (>= 3.0.0), spelling

Config/testthat/edition 3

Imports data.table, ggbreak, ggplot2, ggrepel, ggtext, grid, magrittr, purrr, scales, showtext, sysfonts

NeedsCompilation no

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Repository CRAN

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Contents

`plot_qqman` *plot_qqman*

Description

Create GWAS QQ & Manhattan Plots.

Usage

```
plot_qqman(
  plink_assoc_file,
  pheno_name,
  maf_filter = NULL,
  output_graphics = "png",
  save_plot = TRUE
)
```

Arguments

`plink_assoc_file`	Path to the PLINK association file.
`pheno_name`	Phenotype name.
`maf_filter`	Minor allele frequency filter, Default: NULL
`output_graphics`	Output graphics format, Default: 'png'
`save_plot`	Logical, whether to save plots to files. If FALSE, plots are only displayed. Default: TRUE

Details

This function reads a PLINK association file and generates Manhattan and QQ plots for the GWAS results.

Value

A list containing the ggplot objects for the Manhattan and QQ plots.

Font Information

The MetroSans font included in this package is sourced from https://fontshub.pro/font/metro-sans-download#google_vignette. It is intended for academic research and non-commercial use only. For commercial use, please contact the font copyright holder.

The font files are included in the package's inst/extdata directory and are automatically loaded for plotting.

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See Also

lulab.utils

Examples

```
sample_file <- system.file("extdata", "sample_gwas.assoc.linear", package = "omixVizR")

# Check if the file exists before running the example
if (file.exists(sample_file)) {
  # Run the function with the sample data
  plots <- plot_qqman(
    plink_assoc_file = sample_file,
    pheno_name = "SamplePheno",
    save_plot = FALSE
  )
  # You can then access the plots like this:
  # print(plots$manhattan_plot)
  # print(plots$qq_plot)
} else {
  message("Sample file not found, skipping example.")
}
```

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