Package ‘omixVizR’

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Title A Toolkit for Omics Data Visualization

Version 1.1.3

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://github.com/Leslie-Lu/omixVizR`

BugReports `https://github.com/Leslie-Lu/omixVizR/issues`

Encoding UTF-8

Language en-US

RoxygenNote 7.3.2

Suggests testthat (>= 3.0.0), spelling

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NeedsCompilation no

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Contents

`plot_gwas_power` *Plot GWAS Statistical Power*

Description

Generates a statistical power analysis plot for GWAS studies. Supports binary (case-control) traits over a range of odds ratios and minor allele frequencies, and quantitative traits over a range of effect sizes and minor allele frequencies. This function uses the 'genpwr' package for calculations and creates a highly customized ggplot.

Usage

```
plot_gwas_power(
  trait_type = "bt",
  n_cases = NULL,
  n_controls = NULL,
  sd_trait = NULL,
  N = NULL,
  maf_levels = c(0.01, 0.02, 0.05, 0.1, 0.2, 0.5),
  or_range = seq(1.01, 2, 0.001),
  effect_size = seq(0.01, 0.3, 0.001),
  alpha = 5e-08,
  plot_title = NULL,
  save_plot = TRUE,
  output_graphics = "png",
  width = 17,
  height = 9,
  dpi = 600
)
```

Arguments

`trait_type`	Character string specifying trait type: "bt" for binary (case-control) or "qt" for quantitative traits. Default: `"bt"`.
`n_cases`	Number of cases in the study (required if `trait_type = "bt"`).
`n_controls`	Number of controls in the study (required if `trait_type = "bt"`).
`sd_trait`	Numeric, standard deviation of the quantitative trait (required if `trait_type = "qt"`).
`N`	Numeric, total sample size for quantitative traits (required if `trait_type = "qt"`).
`maf_levels`	A numeric vector of Minor Allele Frequencies (MAFs) to test. Default: `c(0.01, 0.02, 0.05, 0.10, 0.20, 0.50)`.
`or_range`	A numeric vector specifying the sequence of Odds Ratios (ORs) to test. Default: `seq(1.01, 2.00, 0.001)`. Used when `trait_type = "bt"`.
`effect_size`	A numeric vector specifying the sequence of effect sizes (beta) to test for quantitative traits. Default: `seq(0.01, 0.30, 0.001)`. Used when `trait_type = "qt"`.

`alpha`	The significance level (alpha) for the power calculation. Default: `5e-8`.
`plot_title`	A string for the plot title. Can include newlines (`\\n`). Default: A title generated from case/control numbers.
`save_plot`	Logical, whether to save the plot to a file. If `FALSE`, the plot object is only returned. Default: `TRUE`.
`output_graphics`	The file format for saving the plot. Currently supports "png" and "pdf". Default: "png".
`width`	The width of the saved plot in inches. Default: 17.
`height`	The height of the saved plot in inches. Default: 9.
`dpi`	The resolution of the saved plot in dots per inch. Default: 600.

Details

This function automates the process of calculating and visualizing GWAS power for both binary (case-control) and quantitative traits. For binary traits, it analyzes power across odds ratios, while for quantitative traits, it analyzes power across effect sizes. It highlights the minimum OR/effect size required to achieve 80% power for the lowest and third-lowest MAF levels, adding dashed lines and color-coded labels for clarity.

Value

A list containing two elements:

`plot`	The ggplot object for the power plot.
`power_data`	A data.table containing the full results from the power analysis.

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.

Author(s)

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Examples

```
# Binary trait example (case-control)
power_results_bt <- plot_gwas_power(
  trait_type = "bt",
  n_cases = 4324,
  n_controls = 93945,
  save_plot = FALSE
)
```

```
# Quantitative trait example
power_results_qt <- plot_gwas_power(
  trait_type = "qt",
  sd_trait = 0.09365788681305078,
  N = 10000,
  maf_levels = c(0.01, 0.02, 0.05, 0.10, 0.20, 0.50),
  effect_size = seq(0.01, 0.10, 0.001),
  save_plot = FALSE
)

# Access the ggplot object and data
# print(power_results_bt$plot)
# print(power_results_bt$power_data)
```

`plot_qqman` *Plot GWAS QQ and Manhattan Plots*

Description

Create GWAS QQ & Manhattan Plots.

Usage

```
plot_qqman(
  plink_assoc_file,
  pheno_name,
  maf_filter = NULL,
  output_graphics = "png",
  save_plot = TRUE,
  lambda1_qq_pos = c(2.1, -5.5),
  lambda2_qq_pos = c(1.565, -4)
)
```

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

`lambda1_qq_pos`	A numeric vector of length 2 specifying the `c(hjust, vjust)` for the lambda text in the QQ plot. Default: `c(2.1, -5.5)`.
`lambda2_qq_pos`	A numeric vector of length 2 specifying the `c(hjust, vjust)` for the SNP count (N) text in the QQ plot. Default: `c(1.565, -4.0)`.

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.

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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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