

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>

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Suggests testthat (>= 3.0.0), spelling

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NeedsCompilation no

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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

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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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