Package ‘TrumpetPlots’

June 13, 2023

Title Visualization of Genetic Association Studies

Version 0.0.1.1

Description Visualizes the relationship between allele frequency and effect size in genetic association studies. The input is a data frame containing association results. The output is a plot with the effect size of risk variants in the Y axis, and the allele frequency spectrum in the X axis. Corte et al (2023) <doi:10.1101/2023.04.21.23288923>.

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Encoding UTF-8

RoxygenNote 7.2.3

Depends R (>= 2.10), data.table, ggplot2, magrittr, stats, purrr (>= 1.0.1)

LazyData true

NeedsCompilation no

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Repository CRAN

Date/Publication 2023-06-13 08:50:13 UTC

R topics documented:

plot_trumpets .......................................................... 2
powerCurves .............................................................. 3
toy_data ................................................................. 4

Index 5
plot_trumpets

Description
This function generates trumpet plots

Usage
plot_trumpets(
  dataset = toy_data,
  rsID = "rsID",
  freq = "freq",
  A1_beta = "A1_beta",
  Analysis = "Analysis",
  Gene = "Gene",
  calculate_power = TRUE,
  show_power_curves = TRUE,
  exist_datapwr = NULL,
  threshold = c(0.7, 0.9),
  N = 1e+05,
  alpha = 5e-08,
  Nfreq = 500,
  power_color_palette = c("purple", "deeppink"),
  analysis_color_palette = c("#018571", "#a6611a")
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dataset</td>
<td>Input text file with genetic association results. Columns required are rsID, freq, A1_beta, Analysis and Gene.</td>
</tr>
<tr>
<td>rsID</td>
<td>(required) Single Nucleotide Polymorphism (SNP) name.</td>
</tr>
<tr>
<td>freq</td>
<td>(required) allele frequency of effect SNP.</td>
</tr>
<tr>
<td>A1_beta</td>
<td>(required) risk allele effect size.</td>
</tr>
<tr>
<td>Analysis</td>
<td>(optional) adds colour to the type of analysis (e.g. GWAS, Sequencing).</td>
</tr>
<tr>
<td>Gene</td>
<td>(optional) Candidate gene name (can be empty).</td>
</tr>
<tr>
<td>calculate_power</td>
<td>(TRUE/FALSE) Calculate power curves. Choose TRUE to add power curves for a given threshold, alpha, sample size N and number of allele frequencies. Choose FALSE if you already ran powerCurves() outside or do not want to show power curves.</td>
</tr>
<tr>
<td>show_power_curves</td>
<td>(TRUE/FALSE) Show power curves in plot</td>
</tr>
<tr>
<td>exist_datapwr</td>
<td>Existing dataframe containing columns: freq, pos.b.for.f, neg.b.for.f, powerline.</td>
</tr>
<tr>
<td>N</td>
<td>Sample size N</td>
</tr>
<tr>
<td>alpha</td>
<td>Significance level (alpha)</td>
</tr>
<tr>
<td>Nfreq</td>
<td>Number of allele frequencies</td>
</tr>
<tr>
<td>power_color_palette</td>
<td>Colour palette for power curves.</td>
</tr>
<tr>
<td>analysis_color_palette</td>
<td>Colour palette for analysis curves.</td>
</tr>
</tbody>
</table>
powerCurves

threshold  Required if power == TRUE. Can be a single number or a vector of statistical power thresholds.
N          (Required if calculate_power == TRUE). Sample size used to test the association.
alpha      (Required if calculate_power == TRUE).
Nfreq      (Required if calculate_power == TRUE). Number of allele frequency data points generated to calculate the power curves. We recommend Nfreq > 1000 for power curves with high resolution. Note that this will slow down the rendering of the plot.
power_color_palette
          A vector of colours for the power curves. Number of colors should match number of thresholds supplied.
analysis_color_palette
          A vector of colours for the analysis types.

Value

Creates a Trumpet plot with variant allele frequency (X axis, log10 scale) and effect size information (Y axis).

Examples

plot_trumpets(dataset = toy_data)

powerCurves  Power Curves for Trumpet Plots

Description

This function generates curves indicating statistical power in Trumpet plots

Usage

powerCurves(threshold = 0.8, N = 4e+05, alpha = 5e-08, Nfreq = 500)

Arguments

threshold    user-specified power level
N            sample size
alpha        significance threshold
Nfreq        Number of allele frequency data points generated to calculate the power curves

Value

A data frame with the power estimated for each allele frequency and effect size, given a: Statistical power threshold, significance threshold (alpha value), and sample size
Examples

toy_data

Examples

powerCurves(threshold = 0.8, N=400000, alpha = 5e-8)

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**Description**

A data frame with 9999 genetic associations

**Usage**

data(toy_data)

**Format**

A data frame with 9999 genetic associations

**Details**

- rsID. SNP name
- freq. allele frequency of effect SNP
- A1_beta. effect size
- Analysis. adds colour to the type of analysis (e.g. GWAS, Sequencing)
- Gene. Candidate gene name
- N.
- trait. ToyDataPheno
Index

* datasets
  toy_data, 4

plot_trumpets, 2
powerCurves, 3

toy_data, 4