Package: TrumpetPlots (via r-universe)

September 13, 2024

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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LazyData true

NeedsCompilation no

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`plot_trumpets` *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

`dataset`	Input text file with genetic association results. Columns required are rsID, freq, A1_beta, Analysis and Gene.
`rsID`	(required) Single Nucleotide Polymorphism (SNP) name.
`freq`	(required) allele frequency of effect SNP.
`A1_beta`	(required) risk allele effect size.
`Analysis`	(optional) adds colour to the type of analysis (e.g. GWAS, Sequencing).
`Gene`	(optional) Candidate gene name (can be empty).
`calculate_power`	(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.
`show_power_curves`	(TRUE/FALSE) Show power curves in plot
`exist_datapwr`	Existing dataframe containing columns: freq, pos.b.for.f, neg.b.for.f, powerline.

`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

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

`toy_data` *Toy dataset*

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

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