Package: gassocplot (via r-universe)

October 30, 2026

Title Regional association plots

Version 0.0.2

Date 01-04-2024

Description This package is used plot regional association plots.

License GPL-3

URL https://github.com/jrs95/gassocplot,
https://mrcieu.r-universe.dev/gassocplot

Depends R (>= 3.6.0)

Imports ggplot2, grid, gridExtra, gtable

Suggests knitr

Encoding UTF-8

LazyData true

LazyDataCompression xz

RoxygenNote 7.3.2

Repository https://mrcieu.r-universe.dev

Date/Publication 2025-08-06 05:29:13 UTC

RemoteUrl https://github.com/remlapmot/gassocplot

RemoteRef suggestions

RemoteSha 1b873d152e0c09783d55426bc6a4071d7b5008be

Contents

assoc_plot 2
assoc_plot_save 3
stack_assoc_plot 3
stack_assoc_plot_save 4

Index **6**

assoc_plot *assoc_plot*

Description

assoc_plot plots a scatter graph of associations (e.g. log10 p-values)

Usage

```
assoc_plot(
  data,
  corr = NULL,
  corr.top = NULL,
  ylab = NULL,
  title = NULL,
  subtitle = NULL,
  type = "log10p",
  x.min = NULL,
  x.max = NULL,
  top.marker = NULL,
  legend = TRUE
)
```

Arguments

data	data.frame with markername (marker), chromosome (chr), position (pos) and either z-statistics (z) or probabilities (prob) columns
corr	correlation matrix between markers
corr.top	correlation statistics between the top marker and the rest of the markers
ylab	the y-axis label
title	title of the plot
subtitle	subtitle of the plot
type	the type of the plot either log10p or probabilities
x.min	start of region
x.max	end of region
top.marker	the top associated marker, i.e. the marker with the largest -log10p or probability
legend	add r2 legend

Author(s)

James R Staley <jrstaley95@gmail.com>

assoc_plot_save *assoc_plot_save*

Description

assoc_plot_save saves a png of the assoc_plot with the correct dimensions

Usage

```
assoc_plot_save(x, file, width = 9, height = 7, dpi = 500)
```

Arguments

x	the plot
file	the filepath
width	the width of the plot
height	the height of the plot
dpi	the resolution of the plot

Author(s)

James R Staley <jrstaley95@gmail.com>

stack_assoc_plot *stack_assoc_plot*

Description

stack_assoc_plot plots stacked regional association plots

Usage

```
stack_assoc_plot(
  markers,
  z,
  corr = NULL,
  corr.top = NULL,
  traits,
  ylab = NULL,
  type = "log10p",
  x.min = NULL,
  x.max = NULL,
  top.marker = NULL,
  legend = TRUE
)
```

Arguments

markers	data.frame of markers with markername (marker), chromosome (chr) and position (pos)
z	matrix of Z-scores or probabilities with one column for each trait
corr	matrix of correlation statistics between markers
corr.top	correlation statistics between the top marker and the rest of the markers
traits	trait names
ylab	the y-axis label
type	the type of the plot either log10p or probabilities
x.min	start of region
x.max	end of region
top.marker	the top associated marker, i.e. the marker with the largest -log10p or probability
legend	add r2 legend

Author(s)

James R Staley <jrstaley95@gmail.com>

---

stack_assoc_plot_save *stack_assoc_plot_save*

Description

stack_assoc_plot_save saves a png of the assoc_plot with the correct dimensions

Usage

```
stack_assoc_plot_save(
  x,
  file,
  n_traits,
  width = NULL,
  height = NULL,
  dpi = 500
)
```

Arguments

x	the plot
file	the filepath
n_traits	the filepath
width	the width of the plot
height	the height of the plot
dpi	the resolution of the plot

Author(s)

James R Staley <jrstaley95@gmail.com>

Index

assoc_plot, 2
assoc_plot_save, 3

stack_assoc_plot, 3
stack_assoc_plot_save, 4