Package: gassocplot2 (via r-universe)

June 2, 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/gassocplot2,
https://mrcieu.r-universe.dev/gassocplot2

Depends R (>= 3.6.0)

Imports ggplot2, ggrepel, 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 05:30:56 UTC

RemoteUrl https://github.com/remlapmot/gassocplot2

RemoteRef fixes

RemoteSha 0fa99d1ae41d1fc3e9a9c8aed40cdce15ed1afbb

Contents

`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,
  build = 37,
  labels = NULL,
  sig.thres = NULL,
  point.padding = 0.15,
  nudge_x = 0,
  nudge_y = 0,
  ylim_prob1 = 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

`build`	genome build
`labels`	additional points to label
`sig.thres`	significance threshold
`point.padding`	point padding on labels
`nudge_x`	nudge x position on labels
`nudge_y`	nudge y position on labels
`ylim_prob1`	set upper y limit to 1 for probability plots

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,
  build = 37,
  labels = NULL,
  sig.thres = NULL,
  point.padding = 0.15,
  nudge_x = 0,
  nudge_y = 0,
  ylim_prob1 = 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

`build`	genome build
`labels`	additional points to label
`sig.thres`	significance threshold
`point.padding`	point padding on labels
`nudge_x`	nudge x position on labels
`nudge_y`	nudge y position on labels
`ylim_prob1`	set upper y limit to 1 for probability plots

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>

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