

Package: `geni.plots` (via `r-universe`)

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Title GENI plots

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Description GENI plots is designed to visualise results from genome-wide association studies.

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URL <https://github.com/jrs95/geni.plots>,
<https://jrs95.github.io/geni.plots/>

BugReports <https://github.com/jrs95/geni.plots/issues>

Depends R (>= 3.6.0)

Imports dplyr, tidyr, magrittr, ggplot2, ggiraph, ggrepel, ggnewscale, htmlwidgets, patchwork, zoo

Suggests knitr

Encoding UTF-8

ByteCompile true

LazyData true

RoxygenNote 7.2.3

VignetteBuilder knitr

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

RemoteUrl <https://github.com/jrs95/geni.plots>

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fig_manhattan	<i>Manhattan plot</i>
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Description

fig_manhattan creates a Manhattan plot for genomic markers from across the genome, e.g. results from genome-wide association studies.

Usage

```
fig_manhattan(
  data,
  colours = c("#7395D3", "#1D345D"),
  rank_pos = FALSE,
  thin_thresh = NULL,
  block_thresh = NULL,
  interactive = FALSE,
  interactive_n = NULL,
  thresh = c(1e-05, 5e-08),
  thresh_size = 0.5,
  thresh_colours = c("grey50", "red"),
  trunc = 1e-30,
  highlight_colours = NULL,
  point_size = 2,
  chr_dist = 1e+07,
  x_labels = TRUE,
  label_top = TRUE,
  label_thresh = 1e-05,
  label_size = 3,
  label_ylim = -log10(1e-05),
  label_nudge_y = 0,
  label_box = FALSE,
  title = NULL,
  title_size = NULL,
  title_center = FALSE,
  axis_text_size = NULL,
  axis_title_size = NULL,
  plot_width = 16,
  plot_height = 8,
```

```

    girafe = TRUE
  )

```

Arguments

data	<p>a data.frame containing the chromosome-position information and association statistics for each genomic marker (e.g., genetic variants) with the following columns:</p> <ul style="list-style-type: none"> • chr the chromosome for each genomic marker • pos the genomic position for each genomic marker • pvalue the association p-value for each genomic marker • highlight the optional highlight points variable, where 0 = point not highlighted, 1 = first highlight colour, 2 = second highlight colour, etc. • highlight_shape the optional highlight point shape variable, where 0 = standard circle, 1 = standard circle with border, 2 = standard rectangle, 3 = standard rectangle with border, 4 = standard diamond, 5 = standard diamond with border • label the optional point labelling variable (e.g. gene name), if label = "" for a point then no label is presented for that point • text the optional hover text variable for interactive plots to display further information, if text = "" for a point then no hover text is presented for that point
colours	a vector of colours used to differentiate chromosomes, these can either be a separate colour for each chromosome or a pair of colours (default: c("#7395D3", "#1D345D"))
rank_pos	a logical value whether genomic markers should be plotted by their rank position (default: FALSE)
thin_thresh	a numeric value representing the minimum p-value threshold for genomic markers to be displayed (default: NULL)
block_thresh	a numeric value for representing a p-value threshold, above which genomic markers are represented using blocks of colour (default: NULL)
interactive	a logical value indicating whether the plot should be interactive (default: FALSE)
interactive_n	a numeric value indicating the number of top associated points (max = 100,000) to present before using blocks of colour to minimise file size (default: NULL)
thresh	a numeric vector providing p-value thresholds to be plotted (default: c(1e-5, 5e-8))
thresh_size	a numeric value indicating the width of the lines indicating the p-value thresholds (default: 0.5)
thresh_colours	a character vector indicating the colours of the lines indicating the p-value thresholds (default: c("grey50", "red"))
trunc	a numeric value representing the maximum p-value for which results are displayed (default: 1e-30)
highlight_colours	a vector indicating the colours for the highlighted genomic markers (default: NULL)

<code>point_size</code>	a numeric value indicating the size of each point (default: 2)
<code>chr_dist</code>	a numeric value indicating the gap between different chromosomes (default: 10000000)
<code>x_labels</code>	a logical value whether the x-axis should be labelled (default: TRUE)
<code>label_top</code>	a logical value whether the top associated points should be labelled (default: TRUE)
<code>label_thresh</code>	a numeric value providing a p-value threshold for labelling points (default: 1e-5)
<code>label_size</code>	a numeric value indicating the size of each label (default: 3)
<code>label_ylim</code>	a numeric value indicating maximum y-axis value at which labels can be displayed (default: $-\log_{10}(1e-5)$)
<code>label_nudge_y</code>	a numeric value indicating the degree to which label placement on the y-axis should be adjusted (default: 0)
<code>label_box</code>	a logical value indicating whether labels should be surrounded by a box (default: FALSE)
<code>title</code>	a character string providing a title for the plot (default: NULL)
<code>title_size</code>	a numeric value indicating the size of the title text for the plot (default: NULL)
<code>title_center</code>	a numeric value indicating whether the plot title should be centered (default: FALSE)
<code>axis_text_size</code>	a numeric value indicating the size of the axis text for the plot (default: NULL)
<code>axis_title_size</code>	a numeric value indicating the size of the axis title text for the plot (default: NULL)
<code>plot_width</code>	a numeric value indicating the width of the plot (default: 16)
<code>plot_height</code>	a numeric value indicating the height of the plot (default: 8)
<code>girafe</code>	a logical value indicating whether an interactive plot should be turned into an interactive graphic using girafe() (default = TRUE)

Details

This plotting function plots a Manhattan plot for genomic markers from across the genome. The default is to truncate these results to p-value cut-off of $1e-30$.

Value

`fig_manhattan` returns a Manhattan plot for genomic markers from across the genome, e.g. results from genome-wide association studies.

Author(s)

James Staley jrstaley95@gmail.com

Examples

```
fig_manhattan(  
  data = geni.plots::geni_test_manhattan,  
  block_thresh = 1e-4,  
  label_box = TRUE  
)
```

`fig_phewas`*PheWAS plot*

Description

`fig_phewas` creates a plot visualising results from phenome-wide association studies (PheWAS).

Usage

```
fig_phewas(  
  data,  
  groups = NULL,  
  colours = NULL,  
  interactive = FALSE,  
  thresh = 1e-05,  
  thresh_size = 0.5,  
  trunc = 1e-30,  
  point_size = 2,  
  group_dist = 0.05,  
  x_labels = TRUE,  
  label_top = TRUE,  
  label_thresh = 1e-05,  
  label_n = NULL,  
  label_size = 3,  
  label_ymax = 1e-05,  
  label_box = FALSE,  
  label_nudge_x = 0,  
  label_nudge_y = 0,  
  title = NULL,  
  title_size = NULL,  
  title_center = FALSE,  
  axis_text_size = NULL,  
  axis_text_angle = -60,  
  axis_title_size = NULL,  
  legend = FALSE,  
  legend_title = "Group",  
  legend_text_size = NULL,  
  legend_title_size = NULL,  
  legend_point_size = NULL,
```

```

    legend_spacing_size = NULL,
    limit_padding = 20,
    plot_width = 9,
    plot_height = 6,
    girafe = TRUE
)

```

Arguments

data	a <code>data.frame</code> containing the association statistics for each phenotype with the following columns: <ul style="list-style-type: none"> • <code>pvalue</code> the association p-value for each phenotype • <code>sign</code> the direction of the association with the phenotype, where 0 = missing, 1 positive association, -1 negative association • <code>group</code> the phenotype group for each phenotype • <code>label</code> the optional point labelling variable (e.g. phenotype name), if <code>label = ""</code> for a point then no label is presented for that point • <code>text</code> the optional hover text variable for interactive plots to display further information, if <code>text = ""</code> for a point then no hover text is presented for that point
groups	a character vector of groups describing the grouping variable in data (default: NULL)
colours	a character vector of colours corresponding to defined groups (default: NULL)
interactive	a logical value indicating whether the plot should be interactive (default: FALSE)
thresh	a numeric value providing the p-value threshold to be plotted (default: NULL)
thresh_size	a numeric value indicating the width of the lines indicating the p-value thresholds (default: 0.5)
trunc	a numeric value representing the maximum p-value for which results are displayed (default: $1e-30$)
point_size	a numeric value indicating the size of each point (default: 2)
group_dist	a numeric value indicating the gap between different groups (default: 0.05)
x_labels	a logical value whether the x-axis should be labelled (default: TRUE)
label_top	a logical value whether the top associated points should be labelled (default: TRUE)
label_thresh	a numeric value providing a p-value threshold for labelling points (default: $1e-5$)
label_n	an integer value providing a limit on the number of top associations to label (default: NULL)
label_size	a numeric value indicating the size of each label (default: 3)
label_ymax	a numeric value indicating the p-value threshold for the maximum y-axis value at which labels can be displayed (default: $1e-5$)
label_box	a logical value indicating whether labels should be surrounded by a box (default: FALSE)

label_nudge_x	a numeric value indicating the degree to which label placement on the x-axis should be adjusted (default: 0)
label_nudge_y	a numeric value indicating the degree to which label placement on the y-axis should be adjusted (default: 0)
title	a character string providing a title for the plot (default: NULL)
title_size	a numeric value indicating the size of the title text for the plot (default: NULL)
title_center	a logical value indicating whether the plot title should be centered (default: FALSE)
axis_text_size	a numeric value indicating the size of the axis text for the plot (default: NULL)
axis_text_angle	a numeric value indicating the angle of the text on the x-axis of the plot (default: -60)
axis_title_size	a numeric value indicating the size of the axis title text for the plot (default: NULL)
legend	a logical value indicating whether a legend corresponding to the displayed groups should be included (default: FALSE)
legend_title	a character string providing a title for the legend (default: "Group")
legend_text_size	a numeric value indicating the size of the legend text (default: NULL)
legend_title_size	a numeric value indicating the size of the legend title (default: NULL)
legend_point_size	a numeric value indicating the size of each point within the legend (default: NULL)
legend_spacing_size	a numeric value indicating spacing of points present in the legend (default: NULL)
limit_padding	a numeric value indicating the relative distance of plotted points from x-axis extremes (default: 20)
plot_width	a numeric value indicating the width of the PheWAS plot (default: 9)
plot_height	a numeric value indicating the height of the PheWAS plot (default: 6)
girafe	a logical value indicating whether an interactive plot should be turned into an interactive graphic using <code>girafe()</code> (default = TRUE)

Details

This plotting function visualises results from phenome-wide association studies (PheWAS) in the form of a Manhattan style plot. Associations are grouped into phenotype categories. By default the results are truncated using a p-value cut-off of $1e-30$.

Value

`fig_phewas` returns a PheWAS plot for phenome-wide association studies.

Author(s)

James Staley jrstaley95@gmail.com

Examples

```
fig_phewas(  
  data = geni.plots::geni_test_phewas,  
  axis_text_angle = -85,  
  axis_text_size = 8  
)
```

fig_qq

QQ plot

Description

fig_qq creates a quantile-quantile (QQ) plot.

Usage

```
fig_qq(  
  pvalues = NULL,  
  group = NULL,  
  data = NULL,  
  groups = NULL,  
  colours = NULL,  
  interactive = FALSE,  
  thresh = NULL,  
  sample = FALSE,  
  sample_thresh = 0.1,  
  sample_prop = 0.1,  
  ci = TRUE,  
  ci_alpha = 0.05,  
  ci_print = FALSE,  
  inf_factor = FALSE,  
  point_size = 3,  
  label_top = FALSE,  
  label_thresh = 1e-05,  
  label_n = 10,  
  label_size = 3.25,  
  label_xlim = NULL,  
  label_box = FALSE,  
  title = NULL,  
  title_size = NULL,  
  title_center = FALSE,  
  axis_text_size = NULL,
```



```

axis_title_size = NULL,
legend = TRUE,
legend_title = "Group",
legend_text_size = NULL,
legend_title_size = NULL,
legend_point_size = NULL,
legend_spacing_size = NULL,
ymax = NULL,
plot_width = 6,
plot_height = 6,
girafe = TRUE
)

```

Arguments

pvalues	the association p-value for each marker (default: NULL)
group	a character vector determining the observation group for each marker (default: NULL)
data	a data.frame containing the association statistics for each marker with the following columns: <ul style="list-style-type: none"> • pvalue the association p-value for each marker • group the optional grouping variable for each marker • label the optional point labelling variable (e.g. genomic marker), if label = "" for a point then no label is presented for that point • text the optional hover text variable for interactive plots to display further information, if text = "" for a point then no hover text is presented for that point
groups	a character vector of groups describing the grouping variable in data (default: NULL)
colours	a character vector of colours corresponding to defined groups (default: NULL)
interactive	a logical value indicating whether the plot should be interactive (default: FALSE)
thresh	a numeric value providing the p-value threshold to be plotted (default: NULL)
sample	a logical value indicating whether a random subset of p-values above the plotting threshold should be plotted, the number of which is controlled by sample_prop (default = FALSE)
sample_thresh	a numeric value indicating the p-value threshold defining the sample from which additional observations are selected (default: 0.1)
sample_prop	a numeric value indicating the proportion of sampled observations to be plotted (default: 0.1)
ci	a logical value indicating whether confidence intervals should be displayed (default: TRUE)
ci_alpha	a numeric value providing the threshold defining the plotted confidence interval (default: 0.05)
ci_print	a logical value indicating whether the proportion of points contained within the confidence interval band should be printed (default: FALSE)

inf_factor	a logical value indicating whether the inflation factor should be added to the plot (default: FALSE)
point_size	a numeric value indicating the size of each point (default: 3)
label_top	a logical value whether the top associated points should be labelled (default: TRUE)
label_thresh	a numeric value providing a p-value threshold for labelling points (default: 1e-5)
label_n	an integer value providing a limit on the number of top associations to label (default: NULL)
label_size	a numeric value indicating the size of each label (default: 3)
label_xlim	a numeric value indicating maximum x-axis value at which labels can be displayed (default: NULL)
label_box	a logical value indicating whether labels should be surrounded by a box (default: FALSE)
title	a character string providing a title for the plot (default: NULL)
title_size	a numeric value indicating the size of the title text for the plot (default: NULL)
title_center	a logical value indicating whether the plot title should be centered (default: FALSE)
axis_text_size	a numeric value indicating the size of the axis text for the plot (default: NULL)
axis_title_size	a numeric value indicating the size of the axis title text for the plot (default: NULL)
legend	a logical value indicating whether a legend corresponding to the displayed groups should be included (default: FALSE)
legend_title	a character string providing a title for the legend (default: "Group")
legend_text_size	a numeric value indicating the size of the legend text (default: NULL)
legend_title_size	a numeric value indicating the size of the legend title (default: NULL)
legend_point_size	a numeric value indicating the size of each point within the legend (default: NULL)
legend_spacing_size	a numeric value indicating spacing of points present in the legend (default: NULL)
ymax	a numeric value defining the maximum value of the y-axis (default: NULL)
plot_width	a numeric value indicating the width of the plot (default: 6)
plot_height	a numeric value indicating the height of the plot (default: 6)
girafe	a logical value indicating whether an interactive plot should be turned into an interactive graphic using <code>girafe()</code> (default = TRUE)

Details

This plotting function plots a quantile-quantile plot of $-\log_{10}(\text{p-values})$. Observations can be divided into groups and can include corresponding confidence intervals. This plot is based on the [QQ plot](#) by Matthew Flickinger.

Value

fig_qq returns a quantile-quantile plot.

Author(s)

James Staley jrstaley95@gmail.com

Examples

```
fig_qq(  
  pvalues = geni.plots::geni_test_phewas$pvalue  
)  
  
fig_qq(  
  data = geni.plots::geni_test_phewas[, c("pvalue", "group", "label", "text")],  
  legend_title = "Category",  
  legend_title_size = 10,  
  legend_text_size = 8  
)
```

fig_region

Regional plot

Description

fig_region creates a regional plot, i.e. a scatter graph of genomic markers associations (e.g. $\log_{10}(\text{p-values})$) with a gene bar underneath.

Usage

```
fig_region(  
  data,  
  corr = NULL,  
  corr_top = NULL,  
  top_marker = NULL,  
  r2 = FALSE,  
  build = 38,  
  prob = FALSE,  
  interactive = FALSE,  
  thresh = NULL,  
  thresh_colour = "grey50",
```

```

x_min = NULL,
x_max = NULL,
y_title = NULL,
point_size = 3,
alpha = 1,
genebar = TRUE,
genebar_ntracks = NULL,
genebar_label_pos = 3.6,
genebar_label_size = 4,
genebar_line_size = 0.8,
label_size = 3.5,
highlights = NULL,
highlights_cat = NULL,
highlights_label = TRUE,
highlights_shape = 22,
highlights_nolabel_shape = 21,
highlights_sort = TRUE,
highlights_colours = NULL,
highlights_title = "Group",
title = NULL,
title_size = 16,
title_center = FALSE,
axis_text_size = 14,
axis_title_size = 16,
legend = TRUE,
legend_text_size = 12,
legend_title_size = 12,
point_padding = 0,
nudge_x = 0,
nudge_y = 0,
nudge_y_top = 0.06,
ylim_prob = 1,
assoc_plot_size = NULL,
genebar_plot_size = NULL,
legend_plot_dist = NULL,
plot_width = 9,
plot_height = 7,
girafe = TRUE
)

```

Arguments

data a data.frame containing the association statistics for each marker within a genomic region with the following columns:

- marker the genomic marker identifier (e.g. rsID)
- chr the chromosome for each genomic marker
- pos the genomic position for each genomic marker and one of the following:

	<ul style="list-style-type: none"> • pvalue the association p-value for each genomic marker • z the association z-statistic for each genomic marker • prob the association probability for each genomic marker
corr	a numeric matrix of correlation statistics between the markers (default: NULL)
corr_top	a numeric vector of correlation statistics between the top marker and the rest of the markers (default: NULL)
top_marker	a character value depicting the marker to plot the correlation statistics of the rest of the markers against (default: NULL)
r2	a logical value indicating whether the set of correlation statistics entered in corr or corr_top are squared (default: FALSE)
build	a numeric value indicating the genome build used to determine genomic position (default: 38 representing human assembly GRCh38)
prob	a logical value indicating whether probability statistics should be plotted instead of $-\log_{10}$ (p-values) (default: FALSE)
interactive	a logical value indicating whether the plot should be interactive (default: FALSE)
thresh	a numeric vector providing the p-value thresholds to be plotted (default: NULL)
thresh_colour	a character vector indicating the colours of the lines indicating the p-value thresholds (default: "grey50")
x_min	a numeric value depicting the minimum plotted x-axis value representing the start of the genomic region (default: NULL)
x_max	a numeric value depicting the maximum plotted x-axis value representing the end of the genomic region (default: NULL)
y_title	a character string defining the title of the y-axis (default: NULL)
point_size	a numeric value indicating the size of each point (default: 3)
alpha	a numeric value adjusting the opacity of colours representing the correlation statistics (default: 1)
genebar	a logical value indicating whether bars representing the genes should be included in the plot (default: TRUE)
genebar_ntracks	an integer value indicating the number of tracks to be included in the gene bar (default: NULL)
genebar_label_pos	a numeric value indicating the relative position of gene labels with respect to each gene bar (default: 3.6)
genebar_label_size	a numeric value defining the size of each gene label (default: 4.25)
genebar_line_size	a numeric value defining the line size of each gene bar (default: 0.8)
label_size	a numeric value indicating the size of each label (default: 3.5)
highlights	a character vector defining a set of markers to highlight in the plot (default: NULL)

<code>highlights_cat</code>	a character vector defining the category for each highlighted marker (default: NULL)
<code>highlights_label</code>	a logical value indicating whether highlighted points should be labelled (default: TRUE)
<code>highlights_shape</code>	a value defining the shape for highlighted points (default: 22)
<code>highlights_nolabel_shape</code>	a value defining the shape for points which are not highlighted (default: 21)
<code>highlights_sort</code>	a logical value indicating whether to sort highlight group label levels (default: TRUE)
<code>highlights_colours</code>	a character vector specifying colours for highlighted points (default: NULL)
<code>highlights_title</code>	a character string providing a title for the legend corresponding to the highlighted points (default: "Group")
<code>title</code>	a character string providing a title for the plot (default: NULL)
<code>title_size</code>	a numeric value indicating the size of the title text for the plot (default: NULL)
<code>title_center</code>	a logical value indicating whether the plot title should be centered (default: FALSE)
<code>axis_text_size</code>	a numeric value indicating the size of the axis text for the plot (default: 14)
<code>axis_title_size</code>	a numeric value indicating the size of the axis title text for the plot (default: 16)
<code>legend</code>	a logical value indicating whether a legend corresponding to the displayed groups should be included (default: TRUE)
<code>legend_text_size</code>	a numeric value indicating the size of the legend text (default: 12)
<code>legend_title_size</code>	a numeric value indicating the size of the legend title (default: 12)
<code>point_padding</code>	a numeric value indicating the relative distance of labels from plotted points (default: 0)
<code>nudge_x</code>	a numeric value indicating the degree to which label placement on the x-axis should be adjusted (default: 0)
<code>nudge_y</code>	a numeric value indicating the degree to which label placement on the y-axis should be adjusted (default: 0)
<code>nudge_y_top</code>	a numeric value indicating the degree to which the top marker should be adjusted on the y-axis by a proportion of the y-axis limit (default: 0.06)
<code>ylim_prob</code>	a numeric value defining the upper y-axis limit for probability plots (default: 1)
<code>assoc_plot_size</code>	a numeric value determining the size of the association plot (default: NULL)
<code>genebar_plot_size</code>	a numeric value determining the size of the gene bar plot (default: NULL)

legend_plot_dist	a numeric value defining the distance and size of the legend from the bottom of the regional plot (default = NULL)
plot_width	a numeric value indicating the width of the plot (default: 9)
plot_height	a numeric value indicating the height of the plot (default: 7)
girafe	a logical value indicating whether an interactive plot should be turned into an interactive graphic using <code>girafe()</code> (default = TRUE)

Value

fig_region returns a regional plot visualising associations of markers within a genomic region.

Author(s)

James Staley jrstaley95@gmail.com

Examples

```
fig_region(
  data = geni.plots::geni_test_region$assoc,
  corr = geni.plots::geni_test_region$corr,
  build = 37,
  axis_text_size = 11,
  axis_title_size = 12,
  genebar_label_size = 3.5,
  legend_text_size = 10,
  legend_title_size = 10
)

# Notes:
# (i) corr has to have the same markers as assoc in the same order
# (ii) by default fig_region assumes corr contains correlation
#       statistics that have not been squared
```

fig_region_save	<i>Regional plot save</i>
-----------------	---------------------------

Description

fig_region_save saves the regional plots to file.

Usage

```
fig_region_save(
  fig,
  file,
  ntraits = 1,
```

```

    interactive = FALSE,
    width = NULL,
    height = NULL,
    dpi = 500
  )

```

Arguments

fig	a regional plot object
file	a character string of the file path to save the plot
ntraits	an integer value of the number of traits plotted (default: 1)
interactive	a logical value indicating whether the plot is interactive (default: FALSE)
width	a numeric value indicating the width of the plot in inches (default: NULL)
height	a numeric value indicating the height of the plot in inches (default: NULL)
dpi	the resolution of the plot (default: 500)

Author(s)

James Staley jrstaley95@gmail.com

Examples

```

## Not run:
fig <- fig_region(
  data = geni.plots::geni_test_region$assoc,
  corr = geni.plots::geni_test_region$corr,
  build = 37
)
fig_region_save(fig, "test.png")

## End(Not run)

```

fig_region_stack	<i>Stacked regional plot</i>
------------------	------------------------------

Description

fig_region_stack creates a stacked regional association plot.

Usage

```

fig_region_stack(
  data,
  traits,
  corr = NULL,
  corr_top = NULL,

```



```
top_marker = NULL,  
r2 = FALSE,  
build = 38,  
prob = FALSE,  
interactive = FALSE,  
thresh = NULL,  
thresh_colour = "grey50",  
x_min = NULL,  
x_max = NULL,  
y_title = NULL,  
point_size = 3,  
alpha = 1,  
genebar = TRUE,  
genebar_ntracks = NULL,  
genebar_label_pos = 3.6,  
genebar_label_size = 4,  
genebar_line_size = 0.8,  
label_size = 3.5,  
highlights = NULL,  
highlights_cat = NULL,  
highlights_label = TRUE,  
highlights_shape = 22,  
highlights_nolabel_shape = 21,  
highlights_sort = TRUE,  
highlights_colours = NULL,  
highlights_title = "Group",  
title_size = 16,  
title_center = FALSE,  
axis_text_size = 14,  
axis_title_size = 16,  
legend = TRUE,  
legend_text_size = 12,  
legend_title_size = 12,  
point_padding = 0,  
nudge_x = 0,  
nudge_y = 0,  
nudge_y_top = 0.06,  
ylim_prob = 1,  
assoc_plot_size = NULL,  
genebar_plot_size = NULL,  
legend_plot_dist = NULL,  
plot_width = NULL,  
plot_height = NULL,  
girafe = TRUE  
)
```

Arguments

data	a data.frame containing the association statistics for each marker within a genomic region with the following columns: <ul style="list-style-type: none"> • marker the genomic marker identifier (e.g. rsID) • chr the chromosome for each genomic marker • pos the genomic position for each genomic marker and one of the following: <ul style="list-style-type: none"> • pvalue_1, pvalue_2, pvalue_3, etc. the association p-values for each genomic marker and trait • z_1, z_2, z_3, etc. the association z-statistics for each genomic marker and trait • prob_1, prob_2, prob_3, etc. the association probabilities for each genomic marker and trait
traits	a character vector of trait names
corr	a numeric matrix of correlation statistics between the markers (default: NULL)
corr_top	a numeric vector of correlation statistics between the top marker and the rest of the markers (default: NULL)
top_marker	a character value depicting the marker to plot the correlation statistics of the rest of the markers against (default: NULL)
r2	a logical value indicating whether the set of correlation statistics entered in corr or corr_top are squared (default: FALSE)
build	a numeric value indicating the genome build used to determine genomic position (default: 38 representing human assembly GRCh38)
prob	a logical value indicating whether probability statistics should be plotted instead of $-\log_{10}(\text{p-values})$ (default: FALSE)
interactive	a logical value indicating whether the plot should be interactive (default: FALSE)
thresh	a numeric vector providing the p-value thresholds to be plotted (default: NULL)
thresh_colour	a character vector indicating the colours of the lines indicating the p-value thresholds (default: "grey50")
x_min	a numeric value depicting the minimum plotted x-axis value representing the start of the genomic region (default: NULL)
x_max	a numeric value depicting the maximum plotted x-axis value representing the end of the genomic region (default: NULL)
y_title	a character string defining the title of the y-axis (default: NULL)
point_size	a numeric value indicating the size of each point (default: 3)
alpha	a numeric value adjusting the opacity of colours representing the correlation statistics (default: 1)
genebar	a logical value indicating whether bars representing the genes should be included in the plot (default: TRUE)
genebar_ntracks	an integer value indicating the number of tracks to be included in the gene bar (default: NULL)

genebar_label_pos	a numeric value indicating the relative position of gene labels with respect to each gene bar (default: 3.6)
genebar_label_size	a numeric value defining the size of each gene label (default: 4.25)
genebar_line_size	a numeric value defining the line size of each gene bar (default: 0.8)
label_size	a numeric value indicating the size of each label (default: 3.5)
highlights	a character vector defining a set of markers to highlight in the plot (default: NULL)
highlights_cat	a character vector defining the category for each highlighted marker (default: NULL)
highlights_label	a logical value indicating whether highlighted points should be labelled (default: TRUE)
highlights_shape	a value defining the shape for highlighted points (default: 22)
highlights_nolabel_shape	a value defining the shape for points which are not highlighted (default: 21)
highlights_sort	a logical value indicating whether to sort highlight group label levels (default: TRUE)
highlights_colours	a character vector specifying colours for highlighted points (default: NULL)
highlights_title	a character string providing a title for the legend corresponding to the highlighted points (default: "Group")
title_size	a numeric value indicating the size of the title text for the plot (default: NULL)
title_center	a logical value indicating whether the plot title should be centered (default: FALSE)
axis_text_size	a numeric value indicating the size of the axis text for the plot (default: 14)
axis_title_size	a numeric value indicating the size of the axis title text for the plot (default: 16)
legend	a logical value indicating whether a legend corresponding to the displayed groups should be included (default: TRUE)
legend_text_size	a numeric value indicating the size of the legend text (default: NULL)
legend_title_size	a numeric value indicating the size of the legend title (default: NULL)
point_padding	a numeric value indicating the relative distance of labels from plotted points (default: 0)
nudge_x	a numeric value indicating the degree to which label placement on the x-axis should be adjusted (default: 0)

nudge_y	a numeric value indicating the degree to which label placement on the y-axis should be adjusted (default: 0)
nudge_y_top	a numeric value indicating the degree to which the top marker should be adjusted on the y-axis by a proportion of the y-axis limit (default: 0.06)
ylim_prob	a numeric value defining the upper y-axis limit for probability plots (default: 1)
assoc_plot_size	a numeric value determining the size of the association plot (default: NULL)
genebar_plot_size	a numeric value determining the size of the gene bar plot (default: NULL)
legend_plot_dist	a numeric value defining the distance and size of the legend from the bottom of the regional plot (default = NULL)
plot_width	a numeric value indicating the width of the plot (default: NULL)
plot_height	a numeric value indicating the height of the plot (default: NULL)
girafe	a logical value indicating whether an interactive plot should be turned into an interactive graphic using girafe() (default = TRUE)

Value

fig_region_stack returns a stacked regional plot.

Author(s)

James Staley jrstaley95@gmail.com

Examples

```
fig <- fig_region_stack(
  data = geni.plots::geni_test_stack_region$assoc,
  traits = c("Interleukin-6 levels", "Interleukin-6 receptor levels"),
  corr = geni.plots::geni_test_stack_region$corr,
  build = 37,
  highlights = "rs11265611",
  title_center = TRUE
)

# Notes:
# (i) corr has to have the same markers as assoc in the same order
# (ii) by default fig_region_stack assumes corr contains correlation
# statistics that have not been squared
```

geni_test_manhattan *GENI plots test data for the Manhattan plot*

Description

An R object containing formatted results from a genome-wide association study (GWAS) of interleukin-6 levels with p -values $< 1e-3$ ([GCST90274815](#)).

Usage

```
geni_test_manhattan
```

Format

A data.frame containing the variables necessary for constructing a static Manhattan plot. Specifically, this includes the following information:

- chr the chromosome for each genomic marker
- pos the genomic position (GRCh37) for each genomic marker
- pvalue the association p-value for each genomic marker
- highlight an indicator variable whether the genomic marker should be highlighted: 0 = point not highlighted, 1 = first highlight colour
- highlight_shape an indicator variable of the illustrated shape for the genomic markers: 0 = standard circle, 5 = standard diamond with border
- label the name of the nearest gene for each sentinel genome-wide associated genetic variant, the labels for non-sentinel genetic variants are omitted

Author(s)

James Staley jrstaley95@gmail.com

Wes Spiller

Examples

```
head(geni_test_manhattan)
```

geni_test_phewas	<i>GENI plots test data for the PheWAS plot</i>
------------------	---

Description

An R object containing formatted data from a phenome-wide association study (PheWAS) of rs2228145 (1:154426970-A-C) from FinnGen r9.

Usage

```
geni_test_phewas
```

Format

A data.frame containing the variables necessary for constructing an interactive PheWAS plot. Specifically, this includes the following information:

- pvalue the association p-value for each phenotype
- sign the direction of the association with the phenotype, where 0 = missing, 1 positive association, -1 negative association
- group the phenotype group for each phenotype
- label the phenotype name
- text the hover text containing further information on the association including: phenotype, phenotypic category, genetic variant ID, direction of association, association p-value, number of cases and number of controls

Author(s)

James Staley jrstaley95@gmail.com

Wes Spiller

Examples

```
head(geni_test_phewas)
```

geni_test_region	<i>GENI plots test data for the regional plot</i>
------------------	---

Description

An R object containing formatted results from a genome-wide association study (GWAS) of interleukin-6 levels ([GCST90274815](#)) and linkage disequilibrium statistics from [1000 Genomes Phase 3](#) for the region 1:154301970-154551970.

Usage

```
geni_test_region
```

Format

A list containing 2 objects with the information necessary for constructing an interactive regional plot. Specifically, this includes the following information:

- `assoc` a `data.frame` with genetic association results for interleukin-6 levels from [GCST90274815](#) for the region 1:154301970-154551970
- `corr` a matrix of Pearson correlation statistics (not squared) from the European samples of [1000 Genomes Phase 3](#) for the region 1:154301970-154551970, this matrix has the same markers in the same order as `assoc`

Details

`assoc` is a `data.frame` with the following columns:

- `marker` the genomic marker identifier (i.e. rsID or chromosome-position)
- `chr` the chromosome for each genomic marker
- `pos` the genomic position (GRCh37) for each genomic marker
- `pvalue` the association p-value for each genomic marker

Author(s)

James Staley jrstaley95@gmail.com

Wes Spiller

Examples

```
head(geni_test_region$assoc)
head(geni_test_region$corr)
```

`geni_test_stack_region`*GENI plots test data for the stacked regional plot*

Description

An R object containing formatted results from genome-wide association studies (GWAS) of interleukin-6 levels ([GCST90274815](#)) and interleukin-6 receptor levels ([GCST90088597](#)) and linkage disequilibrium statistics from [1000 Genomes Phase 3](#) for the region 1:154301970-154551970.

Usage

```
geni_test_stack_region
```

Format

A list containing 2 objects with the information necessary for constructing an interactive stacked regional plot. Specifically, this includes the following information:

- `assoc` a `data.frame` with genetic association results for interleukin-6 levels from [GCST90274815](#) and for interleukin-6 receptor levels [GCST90088597](#) for the region 1:154301970-154551970
- `corr` a matrix of Pearson correlation statistics (not squared) from the European samples of [1000 Genomes Phase 3](#) for the region 1:154301970-154551970, this matrix has the same markers in the same order as `assoc`

Details

`assoc` is a `data.frame` with the following columns:

- `marker` the genomic marker identifier (i.e. rsID or chromosome-position)
- `chr` the chromosome for each genomic marker
- `pos` the genomic position (GRCh37) for each genomic marker
- `pvalue_1` the association p-value for interleukin-6 levels for each genomic marker
- `pvalue_2` the association p-value for interleukin-6 receptor levels for each genomic marker

Author(s)

James Staley jrstaley95@gmail.com

Wes Spiller

Examples

```
head(geni_test_stack_region$assoc)
head(geni_test_stack_region$corr)
```


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