

Package ‘gwaRs’

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Type Package

Title Manhattan, Q-Q, and PCA Plots using 'ggplot2'

Version 0.3.0

Description Generate Manhattan, Q-Q, and PCA plots from GWAS and PCA results using 'ggplot2'.

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LazyData true

Imports RColorBrewer (>= 1.1.2), ggplot2, ggrepel, dplyr, tidyr,
data.table, scales, stats, grDevices

RoxygenNote 7.1.1

Depends R (>= 2.10)

Suggests knitr, rmarkdown

VignetteBuilder knitr

URL <https://github.com/LindoNkambule/gwaRs>

BugReports <https://github.com/LindoNkambule/gwaRs/issues>

NeedsCompilation no

Author Lindokuhle Nkambule [aut, cre] (ORCID:
<<https://orcid.org/0000-0002-5682-2834>>)

Maintainer Lindokuhle Nkambule <lindonkambule116@gmail.com>

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gwaRs	<i>Create Manhattan, Q-Q, and PCA plots for GWAS data.</i>
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Description

A package for creating Manhattan, Q-Q, and PCA plots for GWAS data.

Author(s)

Lindokuhle Nkambule <lindonkambule116@gmail.com>

See Also

Useful links:

- <https://github.com/LindoNkambule/gwaRs>
- Report bugs at <https://github.com/LindoNkambule/gwaRs/issues>

gwasData	<i>GWAS results</i>
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Description

Example GWAS data.

highlightSNPS	<i>Highlight SNPs</i>
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Description

A couple of SNPs to be annotated

karyotype_plot	<i>Karyotype Plot</i>
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Description

Creates a Karyotype plot

Usage

```
karyotype_plot(  
  data,  
  density.col = c("darkgreen", "yellow", "red"),  
  window.size = 1e+06,  
  title = NULL  
)
```

Arguments

data	A data.frame with "CHR" and "BP" columns.
density.col	A character vector with colors to use for gradients.
window.size	A double precision numeric value indicating the window size.
title	A string denoting the title to use for the plot. Default is 'Manhattan Plot'

Details

Creates a SNP Karyotype or Density plot from an R dataframe with "CHR" and "BP" columns.

Value

A SNP Karyotype plot.

Author(s)

Lindokuhle Nkambule

Examples

```
karyotype_plot(gwasData)
```

 man_plot

Manhattan Plot

Description

Creates a Manhattan plot

Usage

```
man_plot(
  data,
  chromCol = c("gray44", "black"),
  genomewideline = -log10(5e-08),
  suggestiveline = -log10(1e-05),
  chromosome = "ALL",
  annotatePval = FALSE,
  annotateSNP = NULL,
  annotateCol = "red",
  highlight = NULL,
  highlightCol = "green3",
  title = NULL
)
```

Arguments

data	PLINK assoc output, tab-delimited, or a data.frame with "SNP", "CHR", "BP", and "P" columns.
chromCol	A character vector indicating which colors to alternate for the chromosomes.
genomewideline	Where to draw the "genome-wide significant" line. Default -log10(5e-8). Set to FALSE or F to disable
suggestiveline	Where to draw the "suggestive" line. Default -log10(1e-5). Set to FALSE or F to disable.
chromosome	An integer indicating which chromosome to plot. Default is "ALL".
annotatePval	If set, SNPs with p-value less than or equal to this p-value will be annotated on the plot.
annotateSNP	A character vector of SNPs in your dataset to annotate. If some of the SNPs are not in your dataset, gwaRs will throw a warning message.
annotateCol	A string denoting the color to use for the annotations.
highlight	A character vector of SNPs in the dataset to highlight. If some of the SNPs are not in your dataset, gwaRs will throw a warning message. Default is NULL.
highlightCol	A string denoting the color to use to highlight the SNPs.
title	A string denoting the title to use for the plot. Default is 'Manhattan Plot'

Details

Creates a Manhattan plot from PLINK assoc output (or any tab-delimited file or data frame with "SNP", "CHR", "BP", and "P" columns).

Value

A Manhattan plot.

Author(s)

Lindokuhle Nkambule

Examples

```
man_plot(gwasData)
```

mirrored_man_plot	<i>Mirrored Manhattan Plot</i>
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Description

Creates a Mirrored Manhattan Plot for two traits

Usage

```
mirrored_man_plot(  
  data,  
  trait1 = NULL,  
  trait2 = NULL,  
  trait1_chromCols = c("gray66", "grey36"),  
  trait2_chromCols = c("steelblue1", "steelblue4"),  
  xlab = "Genomic Position (chromosome)",  
  title = "Manhattan Plot",  
  annotate_trait1_pval = FALSE,  
  annotate_trait1_color = "red",  
  annotate_trait2_pval = FALSE,  
  annotate_trait2_color = "red",  
  annotateSNP = NULL,  
  annotateSNPcolor = "red",  
  highlight = NULL,  
  highlightcolor = "green3",  
  genomewideline_trait1 = NULL,  
  genomewideline_trait2 = NULL,  
  genomewideline_type = "dashed",  
  genomewideline_color = "red",  
  suggestiveline_trait1 = NULL,
```

```

    suggestiveline_trait2 = NULL,
    suggestiveline_type = "dashed",
    suggestiveline_color = "blue"
)

```

Arguments

<code>data</code>	A tab-delimited or data frame with the compulsory columns: "CHR", "SNP", "BP", "P", "Trait".
<code>trait1</code>	A character string of the trait1 as it appears in the input data.
<code>trait2</code>	A character string of the trait2 as it appears in the input data.
<code>trait1_chromCols</code>	A character vector indicating which colors to alternate for trait1 chromosomes.
<code>trait2_chromCols</code>	A character vector indicating which colors to alternate for trait2 chromosomes.
<code>xlab</code>	A character string to be used as the x-axis label.
<code>title</code>	A character string to be used as the plot title
<code>annotate_trait1_pval</code>	If set, trait1 SNPs with p-value less than or equal to this p-value will be annotated on the plot.
<code>annotate_trait1_color</code>	A character string indicating the color to be used for annotating trait1 SNPs by p-value
<code>annotate_trait2_pval</code>	If set, trait2 SNPs with p-value less than or equal to this p-value will be annotated on the plot.
<code>annotate_trait2_color</code>	A character string indicating the color to be used for annotating trait2 SNPs by p-value
<code>annotateSNP</code>	A character vector of SNPs in your dataset to annotate. If some of the SNPs are not in your dataset, gwaRs will throw a warning message.
<code>annotateSNPcolor</code>	A character string denoting the color to use for the annotations.
<code>highlight</code>	A character vector of SNPs in the dataset to highlight. If some of the SNPs are not in your dataset, gwaRs will throw a warning message. Default is NULL.
<code>highlightcolor</code>	A character string denoting the color to use to highlight the SNPs.
<code>genomewideline_trait1</code>	Where to draw the "genome-wide significant" line for trait1
<code>genomewideline_trait2</code>	Where to draw the "genome-wide significant" line for trait2
<code>genomewideline_type</code>	A character string denoting the type of line to be used for the "genome-wide significant" line. This is the same for both traits. Default is dashed.

`genomewideline_color`
A character string denoting the color to be used for the "genome-wide significant" line. This is the same for both traits. Default is red.

`suggestiveline_trait1`
Where to draw the "suggestive" line for trait1.

`suggestiveline_trait2`
Where to draw the "suggestive" line for trait2.

`suggestiveline_type`
A character string denoting the type of line to be used for the "suggestive" line. This is the same for both traits. Default is dashed

`suggestiveline_color`
A character string denoting the color to be used for the "suggestive" line. This is the same for both traits. Default is blue.

Details

Create a Mirrored Manhattan Plot from a tab-delimited file or data frame with the compulsory columns: "CHR", "SNP", "BP", "P", "Trait" .

Value

A Mirrored Manhattan plot for two traits.

Author(s)

Lindokuhle Nkambule

Examples

```
## Not run:  
mirrored_man_plot(inputData)  
  
## End(Not run)
```

pcaData

PCA results

Description

Example PCA data.

pca_plot	<i>PCA Plot</i>
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Description

Creates a PCA plot

Usage

```
pca_plot(  
  data,  
  xComponent = "PC1",  
  yComponent = "PC2",  
  legendPos = "right",  
  soft = "PLINK",  
  colPalette = "Accent",  
  title = NULL  
)
```

Arguments

data	PLINK pca or EIGENSTRAT smartpca output, (or any tab-delimited file or data.frame with the same format as PLINK pca or EIGENSTRAT smartpca output)
xComponent	A character vector indicating the principal component value to use for the x-axis. Default is "PC1"
yComponent	A character vector indicating the principal component value to use for the x-axis. Default is "PC2"
legendPos	A character vector indicating the legend position. Default is "right".
soft	A character vector indicating the software output format. Default is "PLINK". If you have a tab-delimited file or data.frame with the same format as EIGENSTRAT output, use "EIGENSTRAT"
colPalette	A character vector indicating the color palette to use. Default is "Accent".
title	A string denoting the title to use for the plot. Default is 'PCA Plot'

Details

Creates a PCA plot from PLINK pca output, EIGENSTRAT smartpca, (or any tab-delimited file or data.frame with the same format as PLINK pca or EIGENSTRAT smartpca output).

Value

A PCA plot.

Author(s)

Lindokuhle Nkambule

Examples

```
pca_plot(pcaData)
```

qq_plot

QQ Plot

Description

Creates a Q-Q plot

Usage

```
qq_plot(  
  data,  
  point_col = "black",  
  diag_col = "red",  
  diag_line = "solid",  
  title = NULL  
)
```

Arguments

data	PLINK assoc output, tab-delimited, or a data.frame with "P" column.
point_col	A character vector indicating the color to use for the SNP p-values. Default is "black".
diag_col	A character vector indicating the color to use for the diagonal line. Default is "red".
diag_line	A character vector indicating the line type to use for the diagonal line. Default is "solid".
title	A string denoting the title to use for the plot. Default is 'Q-Q Plot'

Details

Creates a Q-Q plot from PLINK assoc output (or any tab-delimited file or data frame with "P" column).

Value

A Q-Q plot.

Author(s)

Lindokuhle Nkambule

Examples

```
qq_plot(gwasData)
```

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