Package ‘gwaRs’

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R topics documented:

  gwaRs ................................................................. 2
  gwasData ........................................................... 2
  highlightSNPS ....................................................... 2
  karyotype_plot .................................................... 3
  man_plot ............................................................ 4
### gwaRs

Create Manhattan, Q-Q, and PCA plots for GWAS data.

#### Description

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

#### Author(s)

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#### See Also

Useful links:

- [https://github.com/LindoNkambule/gwaRs](https://github.com/LindoNkambule/gwaRs)
- Report bugs at [https://github.com/LindoNkambule/gwaRs/issues](https://github.com/LindoNkambule/gwaRs/issues)

### gwasData

GWAS results

#### Description

Example GWAS data.

### highlightSNPS

Highlight SNPs

#### Description

A couple of SNPs to be annotated
Description

Creates a Karyotype plot

Usage

```r
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

```r
karyotype_plot(gwasData)
```
**Description**

Creates a Manhattan plot

**Usage**

```r
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**

```r
man_plot(gwasData)
```

---

**mirrored_man_plot**

*Mirrored Manhattan Plot*

**Description**

Creates a Mirrored Manhattan Plot for two traits

**Usage**

```r
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

data          A tab-delimited or data frame with the compulsory columns: "CHR", "SNP", "BP", "P", "Trait".

trait1        A character string of the trait1 as it appears in the input data.

trait2        A character string of the trait2 as it appears in the input data.

trait1_chromCols
A character vector indicating which colors to alternate for trait1 chromosomes.

trait2_chromCols
A character vector indicating which colors to alternate for trait2 chromosomes.

xlab          A character string to be used as the x-axis label.

title         A character string to be used as the plot title

annotate_trait1_pval
If set, trait1 SNPs with p-value less than or equal to this p-value will be annotated on the plot.

annotate_trait1_color
A character string indicating the color to be used for annotating trait1 SNPs by p-value

annotate_trait2_pval
If set, trait2 SNPs with p-value less than or equal to this p-value will be annotated on the plot.

annotate_trait2_color
A character string indicating the color to be used for annotating trait2 SNPs by p-value

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.

annotateSNPcolor
A character 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.

highlightcolor A character string denoting the color to use to highlight the SNPs.

genomewideline_trait1
Where to draw the "genome-wide significant" line for trait1

genomewideline_trait2
Where to draw the "genome-wide significant" line for trait2

genomewideline_type
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.
pcaData

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

---

**pcaData**

*PCA results*

**Description**
Example PCA data.
Description

Creates a PCA plot

Usage

```r
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
qq_plot

Examples

pca_plot(pcaData)

qq_plot(data)  

QQ Plot

Description

Creates a Q-Q plot

Usage

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>data</td>
<td>PLINK assoc output, tab-delimited, or a data.frame with &quot;P&quot; column.</td>
</tr>
<tr>
<td>point_col</td>
<td>A character vector indicating the color to use for the SNP p-values. Default is &quot;black&quot;.</td>
</tr>
<tr>
<td>diag_col</td>
<td>A character vector indicating the color to use for the diagonal line. Default is &quot;red&quot;.</td>
</tr>
<tr>
<td>diag_line</td>
<td>A character vector indicating the line type to use for the diagonal line. Default is &quot;solid&quot;.</td>
</tr>
<tr>
<td>title</td>
<td>A string denoting the title to use for the plot. Default is 'Q-Q Plot'</td>
</tr>
</tbody>
</table>

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)
Index

gwaRs, 2

`gwaRs-package (gwaRs), 2`
gwasData, 2

highlightSNPS, 2

karyotype_plot, 3

man_plot, 4
mirrored_man_plot, 5

pca_plot, 8
pcaData, 7

qq_plot, 9