Package ‘gwaRs’

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

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)
### 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

<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;SNP&quot;, &quot;CHR&quot;, &quot;BP&quot;, and &quot;P&quot; columns.</td>
</tr>
<tr>
<td>chromCol</td>
<td>A character vector indicating which colors to alternate for the chromosomes.</td>
</tr>
<tr>
<td>genomewideline</td>
<td>Where to draw the &quot;genome-wide significant&quot; line. Default -log10(5e-8). Set to FALSE or F to disable</td>
</tr>
<tr>
<td>suggestiveline</td>
<td>Where to draw the &quot;suggestive&quot; line. Default -log10(1e-5). Set to FALSE or F to disable.</td>
</tr>
<tr>
<td>chromosome</td>
<td>An integer indicating which chromosome to plot. Default is &quot;ALL&quot;.</td>
</tr>
<tr>
<td>annotatePval</td>
<td>If set, SNPs with p-value less than or equal to this p-value will be annotated on the plot.</td>
</tr>
<tr>
<td>annotateSNP</td>
<td>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.</td>
</tr>
<tr>
<td>annotateCol</td>
<td>A string denoting the color to use for the annotations.</td>
</tr>
<tr>
<td>highlight</td>
<td>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.</td>
</tr>
<tr>
<td>highlightCol</td>
<td>A string denoting the color to use to highlight the SNPs.</td>
</tr>
<tr>
<td>title</td>
<td>A string denoting the title to use for the plot. Default is 'Manhattan Plot'</td>
</tr>
</tbody>
</table>
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)

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

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

```
pcaData

genomewideline_color
  A character string denoting the color to be used for the "genome-wide signif-
  icant" 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

<table>
<thead>
<tr>
<th>pcaData</th>
<th>PCA results</th>
</tr>
</thead>
</table>

Description

Example PCA data.
Description

Creates a PCA plot.

Usage

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

Arguments

data
xComponent
yComponent
legendPos
soft
colPalette
title

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**

```r
cpa_plot(pcaData)
```

**Description**

Creates a Q-Q plot

**Usage**

```r
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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