Package: relcircle (via r-universe)

September 11, 2024

Type Package

Title Draw Regulatory Relationships Between Genes

Version 1.0

Date 2024-04-07

Description According to the order of the loci on the chromosome, the
loci can be connected according to the interrelationship
between them and classified according to different locus types.

License GPL (>= 3)

Depends R (>= 3.5.0)

NeedsCompilation no

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Date/Publication 2024-04-12 15:20:05 UTC

Repository https://lin429.r-universe.dev

RemoteUrl https://github.com/cran/relcircle

RemoteRef HEAD

RemoteSha 008eab46cca9bf70bdbbc05b59e38c33e19a05aa

Contents

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relcircle-package   *Draw Regulatory Relationships Between Genes*

Description

Connect relevant sites and label their relationships.

Details

Relationship table, needs to include "rs","rs.CHR","rs.gene","rs.POS","cg","cg.CHR","cg.gene","cg.POS".

Author(s)

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References

2016 tutorial

See Also

plot

Examples

```
data(sampledata)
relacircle(sampledata)
```

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relacircle   *Draw Regulatory Relationships Between Genes*

Description

Connect relevant sites and label their relationships.

Usage

```
relacircle(table, type1 = FALSE, type2 = FALSE, line.col = FALSE,
pch = 1, pch.col = "blue", lty = FALSE)
```

Arguments

table	Relationship table, needs to include "rs","rs.CHR","rs.gene","rs.POS","cg","cg.CHR","cg.gene","cg.POS
type1	Classification of corresponding relationships, displayed by different colors, optional, default gray.
type2	The second classification is displayed according to different line types, which can be left blank and defaults to solid lines.
line.col	The color, vector, and length of the line connecting the points need to be consistent with the number of types in type1. If type1 is not set, enter one, and default to gray.
pch	The type of annotation site on the chromosome, default to a hollow circle.
pch.col	The color of the upper chromosomal site, default to blue.
lty	The type, array, and length of the line connecting the points need to be consistent with the number of types in type2. If type2 is not set, enter one. The default is a solid line.

Details

Relationship table, needs to include "rs","rs.CHR","rs.gene","rs.POS","cg","cg.CHR","cg.gene","cg.POS".

Value

return the graphic.

Note

return the graphic.

Author(s)

Ruilin Li

References

2016 tutorial

See Also

plot

Examples

```
data(sampledata)
relacircle(sampledata)
```

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sampledata   *Sample Data*

Description

An example for the data input.

Usage

```
data("sampledata")
```

Format

A data frame with 74 observations on the following 10 variables.

sig_type a character vector

qtl_type a character vector

cg a character vector

rs a character vector

rs.CHR a character vector

rs.POS a numeric vector

rs.gene a character vector

cg.CHR a numeric vector

cg.POS a numeric vector

cg.gene a character vector

Details

The input data must contain cols that sampledata has

Source

nothing

References

2016 tutorial

Examples

```
data(sampledata)
## maybe str(sampledata) ; plot(sampledata) ...
```

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