Package ‘relcircle’

July 23, 2025

Type Package

Title Draw Regulatory Relationships Between Genes

Version 1.0

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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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Contents

`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)
```

`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)
```

`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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