

Package ‘genomeplot’

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Type Package

Title 'Plot genome wide values for all chromosomes'

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Description Plot values of markers(SNPs, expression, genes, RNA,...) for all chromosomes.

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Depends ggplot2

NeedsCompilation no

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genomeplot-package 'Plot genome wide values for all chromosomes'

Description

Plot values of markers(SNPs, expression, genes, RNA,...) for all chromosomes.

Details

the data to be read will contain four columns,which are cgID,chromosome number,the position,the values.

Author(s)

Jing Xu and Yongshuai Jiang

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References

2016 tutorial

See Also

[ggplot](#)

Examples

```
data(sample_data)
select <- 1
genomeplot(sample_data,select)
```

genomeplot

'Plot genome wide values for all chromosomes'

Description

Plot values of markers(SNPs, expression, genes, RNA,...) for all chromosomes.

Usage

```
genomeplot(data, select)
```

Arguments

data	The data are to be used. Each row of the table appears as one line of the file. If it does not contain an absolute path, the file name is relative to the current working directory, <code>getwd()</code> . Tilde-expansion is performed where supported. This can be a compressed file.
select	integer: the number of colour schemes which you will choose for the graphic.

Details

The data to be read will contain four columns, which are cgID, chromosome number, the position, the values.

Value

return the graphic.

Note

return the graphic.

Author(s)

Jing Xu and Yongshuai Jiang

References

2016 tutorial

See Also

[ggplot](#)

Examples

```
data(sample_data)
select <- 1
genomeplot(sample_data, select)
```

sample_data

'sample data'

Description

An example for the data input.

Usage

```
data("sample_data")
```

Format

A data frame with 22000 observations on the following 4 variables.

- V1 a factor with levels
- V2 a numeric vector
- V3 a numeric vector
- V4 a numeric vector

Details

The input data must be same as the sample data.

Source

nothing

References

2016 tutorial

Examples

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

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