

# Package ‘genomeplot’

October 13, 2022

**Type** Package

**Title** 'Plot genome wide values for all chromosomes'

**Version** 1.0

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**Author** Jing Xu and Yongshuai Jiang

**Maintainer** Jing Xu<xujingaddressee@foxmail.com>

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

**License** GPL (>= 3)

**Depends** ggplot2

**NeedsCompilation** no

**Repository** CRAN

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genomeplot-package	<i>'Plot genome wide values for all chromosomes'</i>
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## 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)
```

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genomeplot

*'Plot genome wide values for all chromosomes'*

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**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, getwd(). 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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