Package ‘Methplot’
February 19, 2015

Type Package
Title Visualize the methylation patterns
Version 1.0
Date 2014-03-10
Author Xin Yang
Maintainer Xin Yang <xin.yang@cimr.cam.ac.uk>
Imports ggplot2, grid, reshape
Description It plots the output from Methpup (https://github.com/XinYang6699/Methpup)
License GPL (>= 2)
LazyData FALSE
NeedsCompilation no
Repository CRAN
Date/Publication 2014-04-03 12:04:00

R topics documented:

Methplot-package ......................................................... 1
getdata ........................................................................ 2
mydata ........................................................................ 2
plotdata ....................................................................... 3

Index

Methplot-package Methplot

Description

This package plots the output from Methpup in a 2-D barcode

Author(s)

Xin Yang <xin.yang@cimr.cam.ac.uk
getdata  This function read the output from Methpup into R

Description
This function read the output from Methpup into R

Usage
getdata(filelist, n, gene)

Arguments
- filelist  the directory where the output files are saved in
- gene    the region that you are interested to look at the methylation profile
- n        the number of CpG sites in the region that you specified in "gene".

Value
This function could yield a dataframe saying the read number detected in each methylation pattern in the given region in all samples under "filelist" directory.

Author(s)
Xin Yang <xin.yang@cimr.cam.ac.uk>

Examples
foxp3<-getdata(system.file("extdata", package="Methplot"), 10, "foxp3")

mydata  FOXP3 Methylation profiles of two samples

Description
This data set gives the read number detected in each methylation pattern in FOXP3 T-cell specific demthylation region using next generation bisulphite sequencing. Two samples names "P1_A1" and "P1_A2" are given.

Usage
mydata

Format
A matrix with 1024 rows and 2 columns where rows indicate how many reads detected in each methylation pattern and columns stand for two samples.
plotdata

This function visualizes the dataframe yielded by function "getdata".

Description

Prerequisites: You need to install packages: "ggplot2", "grid", and "reshape"

Usage

plotdata(x, x.title, condition, n, legendpos = "null")

Arguments

x  
the dataframe name that is in the format of "getdata" output

x.title  
the title of the output plot

condition  
a character vector that gives the sample list that you want to plot. These samples will be merged together by adding up the read numbers to yield one plot.

n  
the number of CpG sites in this region.

legendpos  
the position of the legend. Default: "null" ("left", "right", "bottom", "top", or two-element numeric vector)

Value

Output plot: Rows indicate reads and are presented in percentage (y axis), showing whether each of CpG sites (x axis) in the target region is methylated (light green) or demethylated (dark green). Reads are sorted so that those with no demethylated positions are at the bottom, and those with most demethylated positions are at the top.

Author(s)

Xin Yang <xin.yang@cimr.cam.ac.uk>

Examples

data(mydata)
plotdata(mydata, x.title="Methylation Plot", condition="P1_A1", n=10, legendpos="right")
Index

*Topic datasets
  mydata, 2
*Topic package
  Methplot-package, 1

gedata, 2

Methplot (Methplot-package), 1
Methplot-package, 1
mydata, 2

plotdata, 3