Package 'magpie'

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Type Package

Title MeRIP-Seq data Analysis for Genomic Power Investigation and Evaluation

Version 1.12.0

Description
This package aims to perform power analysis for the MeRIP-seq study. It calculates FDR, FDC, power, and precision under various study design parameters, including but not limited to sample size, sequencing depth, and testing method. It can also output results into .xlsx files or produce corresponding figures of choice.

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Contents

plotAll 2
plotAll_Strata 3
plotRes 4
plotStrata 4
power.test 5
powerEval 6
quickPower 7
writeToxlsx 8
writeToxlsx_strata 9

Index **11**

`plotAll` *All plots of power evaulation results under various scenarios.*

Description

This function plots all power measurements of a certain sequencing depth in a 2x2 panel. Power measurements to plot include "FDR", "FDC", "Power", and "Precision".

Usage

```
plotAll(Power.list, depth_factor = 1)
```

Arguments

`Power.list`	A list produced by `powerEval`.
`depth_factor`	A numerical value indicating which sequencing depth to plot. For example, 2 means doubling the original sequencing depth. Default is 1.

Value

It plots all power measurements of a certain sequencing depth in a 2x2 panel. Power measurements to plot include "FDR", "FDC", "Power", and "Precision".

Examples

```
library(magpie)
### Main function
power.test <- quickPower(dataset = "GSE46705", test_method = "TRESS")

### plot all in a panel under sequencing depth 1x
plotAll(power.test, depth_factor = 1)
```

`plotAll_Strata` *All plots of power evaulation results by strata.*

Description

This function plots all power measurements of the original sequencing depth by strata in a 2x2 panel. Power measurements to plot include "FDR", "FDC", "Power", and "Precision".

Usage

```
plotAll_Strata(Power.list)
```

Arguments

`Power.list`	A list produced by `powerEval`.

Value

It plots all power measurements of the original sequencing depth by strata in a 2x2 panel. Power measurements to plot include "FDR", "FDC", "Power", and "Precision".

Examples

```
library(magpie)
### Main function
power.test <- quickPower(dataset = "GSE55575", test_method = "TRESS")

### plot all strata results in a panel
plotAll_Strata(power.test)
```

plotRes *An individual Plot of power evaulation results under various scenarios.*

Description

This function plots a certain power measurement of a certain sequencing depth. Power measurements to plot include "FDR", "FDC", "Power", and "Precision".

Usage

```
plotRes(Power.list, depth_factor = 1, value_option = "FDR")
```

Arguments

Power.list	A list produced by powerEval.
depth_factor	A numerical value indicating which sequencing depth to plot. For example, 2 means doubling the original sequencing depth. Default is 1.
value_option	A character indicating which measurement to plot. Options include "FDR", "FDC", "Power", and "Precision".

Value

It plots a certain power measurement of a certain sequencing depth. Power measurements to plot include "FDR", "FDC", "Power", and "Precision".

Examples

```
library(magpie)
### Main function
power.test <- quickPower(dataset = "GSE46705", test_method = "TRESS")

### plot FDR under sequencing depth 1x
plotRes(power.test, depth_factor = 1, value_option = "FDR")
```

plotStrata *An individual plot of power evaulation results by strata.*

Description

This function plots a certain power measurement of the original sequencing depth by strata. Power measurements to plot include "FDR", "FDC", "Power", and "Precision".

Usage

```
plotStrata(Power.list, value_option = "FDR")
```

Arguments

Power.list	A list produced by powerEval.
value_option	A character indicating which measurement to plot. Options include "FDR", "FDC", "Power", and "Precision".

Value

It plots a certain power measurement of the original sequencing depth by strata. Power measurements to plot include "FDR", "FDC", "Power", and "Precision".

Examples

```
library(magpie)
### Main function
power.test <- quickPower(dataset = "GSE46705", test_method = "TRESS")

### plot a FDR strata result
plotStrata(power.test, value_option = "FDR")
```

---

power.test *Power calculation results for GSE46705*

Description

Human HeLa cell line: Two replicates of wild type (WT) and two replicates of knockdown (KD) of complex METTL3.

Usage

```
data(GSE46705_TRESS_res)
```

Format

A list object.

Examples

```
data(GSE46705_TRESS_res)
```

`powerEval` *Power evaluation for MeRIP-seq data under various study designs.*

Description

This function conducts simulations with various user-defined study design parameters, including but not limited to sample size, sequencing depth, and testing method. Users will need to provide either partial or whole-genome MeRIP-seq data for parameter estimation purposes.

Usage

```
powerEval(
  Input.file,
  IP.file,
  BamDir,
  annoDir,
  variable,
  bam_factor,
  nsim = 10,
  N.reps = c(2, 3, 5),
  depth_factor = c(1, 2, 5),
  thres = c(0.01, 0.05, 0.1, 0.2),
  Test_method = "TRESS"
)
```

Arguments

`Input.file`	A vector containing the name of BAM files of input samples.
`IP.file`	A vector containing the name of BAM files of IP samples.
`BamDir`	A character stating the directory path of all .BAM files.
`annoDir`	A character stating the directory path of the ".sqlite" file for annotation.
`variable`	A vector indicating the experimental conditions of all samples.
`bam_factor`	A numrical value indicating the ratio of provided data to the whole genome data. Default is 0.05.
`nsim`	An integer indicating the number of iterations to simulate under each scenario. Default is 10.
`N.reps`	A vector of integers indicating the numbers of replicates to simulate, in both groups. Default is c(2,3,5).
`depth_factor`	A vector of numerical values indicating how much sequencing depth of the provided data will be increased in simulations. For example, 2 means doubling the original sequencing depth. Default is c(1,2,5).
`thres`	A vector of numerical values indicating the p-value thresholds used in power calculation. Default is c(0.01, 0.05, 0.1, 0.2).
`Test_method`	A character indicating which DMR calling method to use. Options are "TRESS" and "exomePeak2". Default is "TRESS".

Value

A list of calculated power measurements that will be used as the input of functions writeToxlsx, writeToxlsx_strata, plotAll, plotRes, plotAll_Strata, and plotStrata. Measurements include:

FDR	The ratio of number of false positives to the number of positive discoveries.
FDC	The ratio of number of false positives to the number of true positives.
Power	Statistical power.
Precision	The ratio of number of true positives to the number of positive discoveries.

Examples

```
## Not run:
library(magpieData)
library(magpie)
### Get the example data
BAM_path <- getBAMpath()
### Call PowerEval()
power.test <- powerEval(
   Input.file = c("Ctrl1.chr15.input.bam", "Ctrl2.chr15.input.bam", "Case1.chr15.input.bam", "Case2.chr15.input.
   IP.file = c("Ctrl1.chr15.ip.bam", "Ctrl2.chr15.ip.bam", "Case1.chr15.ip.bam", "Case2.chr15.ip.bam"),
    BamDir = BAM_path,
    annoDir = paste0(BAM_path, "/hg18_chr15.sqlite"),
    variable = rep(c("Ctrl", "Trt"), each = 2),
    bam_factor = 0.03,
    nsim = 10,
    N.reps = c(2, 3, 5, 7),
    depth_factor = c(1, 2),
    thres = c(0.01, 0.05, 0.1),
    Test_method = "TRESS"
)

## End(Not run)
```

---

quickPower *Obtain pre-calculated results from four publicly available MeRIP-seq datasets*

Description

This function quickly outputs pre-calculated power evaluation results from four GEO MeRIP-seq datasets: (GSE46705, GSE55575, GSE115105, and GSE94613). The obtained results can be used to generate Excel files and various figures.

Usage

```
quickPower(dataset = "GSE46705", test_method = "TRESS")
```

Arguments

dataset	A character specifying the selected dataset. Default is 'GSE46705'. Options are 'GSE46705', 'GSE55575', 'GSE115105', and 'GSE94613'.
test_method	A character indicating which DMR calling method to use. Options are "TRESS" and "exomePeak2". Default is "TRESS".

Details

GSE46705: Human HeLa cell line: Two replicates of wild type (WT) and two replicates of knockdown (KD) of complex METTL3.
GSE55575: Mouse embryonic fibroblasts: Two replicates of wild type (WT) and four replicates of knockdown (KD) of WTAP.
GSE115105: Two sample types from WT and YTHDF1 KO mice. Each type has two replicates.
GSE94613: Human leukemia cell line: Four replicates of wild type (WT) and eight replicates of knockdown (KD) of complex METTL3.

Value

A list of calculated power measurements that will be used as the input of functions writeToxlsx, writeToxlsx_strata, plotAll, plotRes, plotAll_Strata, and plotStrata. Measurements include:

FDR	The ratio of number of false positives to the number of positive discoveries.
FDC	The ratio of number of false positives to the number of true positives.
Power	Statistical power.
Precision	The ratio of number of true positives to the number of positive discoveries.

Examples

```
library(magpie)
power.test <- quickPower(dataset = "GSE46705")
```

---

writeToxlsx *Write power evaulation results under all scenarios to a .xlsx file.*

Description

This function writes power evaulation results to a .xlsx file.

Usage

```
writeToxlsx(pl, file)
```

Arguments

pl	A list produced by powerEval.
file	A character indicating the name of the output .xlsx file.

Value

It outputs a .xlsx file including FDR, FDC, power, and precision under various sample sizes, sequencing depths, and adjusted p-value thresholds.

Examples

```
library(magpie)
### Main function
power.test <- quickPower(dataset = "GSE46705", test_method = "TRESS")

### write out .xlsx
writeToxlsx(power.test, file = "test_TRESS.xlsx")
```

---

writeToxlsx_strata *Write power evaulation results of four strata under all sample size scenarios to a .xlsx file.*

Description

This function writes power evaulation results of four strata to a .xlsx file. Only results from the original sequencing depth are saved. Here, strata are determined by mean input control levels of simulated data.

Usage

```
writeToxlsx_strata(pl, file)
```

Arguments

pl	A list produced by powerEval.
file	A character indicating the name of the output .xlsx file.

Value

It outputs a .xlsx file including FDR, FDC, power, and precision under the original sequencing depth and various sample sizes and input stratas.

Examples

```
library(magpie)
### Main function
power.test <- quickPower(dataset = "GSE46705", test_method = "TRESS")

### write out .xlsx
writeToxlsx_strata(power.test, file = "test_strata_TRESS.xlsx")
```

Index

∗ **datasets**
power.test, 5

plotAll, 2, *7, 8*
plotAll_Strata, 3, *7, 8*
plotRes, 4, *7, 8*
plotStrata, 4, *7, 8*
power.test, 5
powerEval, *2–5*, 6, *9*

quickPower, 7

writeToxlsx, *7, 8*, 8
writeToxlsx_strata, *7, 8*, 9