

Package ‘pwrEWAS’

May 10, 2023

Title A user-friendly tool for comprehensive power estimation for epigenome wide association studies (EWAS)

Version 1.14.0

Description pwrEWAS is a user-friendly tool to assists researchers in the design and planning of EWAS to help circumvent under- and overpowered studies.

Author Stefan Graw

Maintainer Stefan Graw <shgraw@uams.edu>

License Artistic-2.0

LazyData false

Imports doParallel, abind, truncnorm, CpGassoc, shiny, ggplot2, parallel, shinyWidgets, BiocManager, doSNOW, limma, genefilter, stats, grDevices, methods, utils, graphics, pwrEWAS.data

Depends shinyBS, foreach

Suggests knitr, RUnit, BiocGenerics, rmarkdown

biocViews DNAMethylation, Microarray, DifferentialMethylation, TissueMicroarray

Encoding UTF-8

RoxygenNote 6.1.1

VignetteBuilder knitr

git_url <https://git.bioconductor.org/packages/pwrEWAS>

git_branch RELEASE_3_17

git_last_commit 646c879

git_last_commit_date 2023-04-25

Date/Publication 2023-05-09

R topics documented:

pwrEWAS	2
pwrEWAS_deltaDensity	3
pwrEWAS_powerPlot	5
pwrEWAS_shiny	6

pwrEWAS	<i>pwrEWAS - A computationally efficient tool for comprehensive power estimation in EWAS</i>
---------	--

Description

pwrEWAS is a computationally efficient tool to estimate power in EWAS as a function of sample and effect size for two-group comparisons of DNAm (e.g., case vs control, exposed vs non-exposed, etc.). Detailed description of in-/outputs, instructions and an example, as well as interpretations of the example results are provided in the vignette: `vignette("pwrEWAS")`

Usage

```
pwrEWAS(minTotSampleSize, maxTotSampleSize, SampleSizeSteps, NcntPer,
  targetDelta = NULL, deltaSD = NULL, J = 1e+05, targetDmCpGs,
  tissueType = c("Adult (PBMC)", "Saliva", "Sperm", "Lymphoma",
  "Placenta", "Liver", "Colon", "Blood adult", "Blood 5 year olds",
  "Blood newborns", "Cord-blood (whole blood)", "Cord-blood (PBMC)"),
  detectionLimit = 0.01, DMmethod = c("limma", "t-test (unequal var)",
  "t-test (equal var)", "Wilcox rank sum", "CPGassoc"),
  FDRcritVal = 0.05, core = 1, sims = 50)
```

Arguments

<code>minTotSampleSize</code>	Minimum total sample size.
<code>maxTotSampleSize</code>	Maximum total sample size.
<code>SampleSizeSteps</code>	Sample size increments.
<code>NcntPer</code>	Percentage sample group 1 (control group) (<code>NcntPer = 0.5</code> indicates a balanced design).
<code>targetDelta</code>	Target maximum difference in mean DNAm. (Either <code>'targetDelta'</code> or <code>'deltaSD'</code> should be specified)
<code>deltaSD</code>	Standard deviation of simulated differences. (Either <code>'targetDelta'</code> or <code>'deltaSD'</code> should be specified)
<code>J</code>	Number of CpGs tested/simulated (default: 100000).
<code>targetDmCpGs</code>	Target number of DM CpGs.
<code>tissueType</code>	Select a tissue type from the list of most commonly used tissue types: "Adult (PBMC)" (default), "Saliva", "Sperm", "Lymphoma", "Placenta", "Liver", "Colon", "Blood adult", "Blood 5 year olds", "Blood newborns", "Cord-blood (whole blood)" or "Cord-blood (PBMC)".
<code>detectionLimit</code>	Smallest detectable difference in DNAm (default: 0.01).

DMmethod	Method of Differential Methylation analysis: "limma" (default), "t-test (unequal var)", "t-test (equal var)", "Wilcox rank sum", "CPGassoc".
FDRcritVal	FDRcritVal (default: 0.05).
core	Number of threads for multi-threading (default: 1).
sims	Number of simulated data sets (default: 50).

Value

pwrEWAS will return an object with the following four attributes: meanPower, powerArray, deltaArray, and metric, where metric contains marTypeI, classicalPower, FDR, and FDC

Examples

```
outDelta <- pwrEWAS(minTotSampleSize = 10,
  maxTotSampleSize = 20,
  SampleSizeSteps = 10,
  NcntPer = 0.5,
  targetDelta = c(0.2, 0.5),
  J = 1000,
  targetDmCpGs = 10,
  tissueType = "Adult (PBMC)",
  detectionLimit = 0.01,
  DMmethod = "limma",
  FDRcritVal = 0.05,
  core = 2,
  sims = 30)
```

```
outSD <- pwrEWAS(minTotSampleSize = 10,
  maxTotSampleSize = 20,
  SampleSizeSteps = 10,
  NcntPer = 0.5,
  deltaSD = c(0.02, 0.03),
  J = 1000,
  targetDmCpGs = 10,
  tissueType = "Adult (PBMC)",
  detectionLimit = 0.01,
  DMmethod = "limma",
  FDRcritVal = 0.05,
  core = 2,
  sims = 30)
```

pwrEWAS_deltaDensity *Density plot for simulated differences in mean methylation*

Description

pwrEWAS_deltaDensity create a density plot of the simulated differences in mean methylation for different effect sizes

Usage

```
pwrEWAS_deltaDensity(data, detectionLimit = 0.01, sd = FALSE)
```

Arguments

data "deltaArray" attribute within the pwrEWAS object create by pwrEWAS

detectionLimit Detection limit specified in pwrEWAS.

sd FALSE if targetDelta was specified in pwrEWAS, and TRUE if deltaSD was specified in pwrEWAS.

Value

pwrEWAS_deltaDensity return a figure displaying densities of simulated differences in mean methylation different effect sizes

Examples

```
outDelta <- pwrEWAS(minTotSampleSize = 10,
  maxTotSampleSize = 20,
  SampleSizeSteps = 10,
  NcntPer = 0.5,
  targetDelta = c(0.2, 0.5),
  J = 1000,
  targetDmCpGs = 10,
  tissueType = "Adult (PBMC)",
  detectionLimit = 0.01,
  DMmethod = "limma",
  FDRcritVal = 0.05,
  core = 2,
  sims = 30)
pwrEWAS_deltaDensity(data = outDelta$deltaArray, detectionLimit = 0.01, sd = FALSE)
outSD <- pwrEWAS(minTotSampleSize = 10,
  maxTotSampleSize = 20,
  SampleSizeSteps = 10,
  NcntPer = 0.5,
  deltaSD = c(0.02, 0.03),
  J = 1000,
  targetDmCpGs = 10,
  tissueType = "Adult (PBMC)",
  detectionLimit = 0.01,
  DMmethod = "limma",
  FDRcritVal = 0.05,
  core = 2,
  sims = 30)
pwrEWAS_deltaDensity(data = outSD$deltaArray, detectionLimit = 0.01, sd = TRUE)
```

pwrEWAS_powerPlot *Plot function to create a power plot*

Description

pwrEWAS_powerPlot create a figure with power (with 95-percentile interval (2.5

Usage

```
pwrEWAS_powerPlot(data, sd = FALSE)
```

Arguments

data	"powerArray" attribute within the pwrEWAS object create by pwrEWAS.
sd	FALSE if targetDelta was specified in pwrEWAS, and TRUE if deltaSD was specified in pwrEWAS.

Value

pwrEWAS_powerPlot return a figure displaying power as a function sample size for different effect sizes

Examples

```
outDelta <- pwrEWAS(minTotSampleSize = 10,
  maxTotSampleSize = 20,
  SampleSizeSteps = 10,
  NcntPer = 0.5,
  targetDelta = c(0.2, 0.5),
  J = 1000,
  targetDmCpGs = 10,
  tissueType = "Adult (PBMC)",
  detectionLimit = 0.01,
  DMmethod = "limma",
  FDRcritVal = 0.05,
  core = 2,
  sims = 30)
pwrEWAS_powerPlot(data = outDelta$powerArray, sd = FALSE)
outSD <- pwrEWAS(minTotSampleSize = 10,
  maxTotSampleSize = 20,
  SampleSizeSteps = 10,
  NcntPer = 0.5,
  deltaSD = c(0.02, 0.03),
  J = 1000,
  targetDmCpGs = 10,
  tissueType = "Adult (PBMC)",
  detectionLimit = 0.01,
  DMmethod = "limma",
  FDRcritVal = 0.05,
```

```
    core = 2,  
    sims = 30)  
pwrEWAS_powerPlot(data = outSD$powerArray, sd = TRUE)
```

pwrEWAS_shiny

Shiny pwrEWAS

Description

pwrEWAS_shiny provides a user-friendly point-and-click interface for pwrEWAS

Usage

```
pwrEWAS_shiny()
```

Value

pwrEWAS_shiny initializes pwrEWAS's user-interface

Examples

```
if(interactive()) {  
  pwrEWAS_shiny()  
}
```

Index

- * **DNAm**

 - pwrEWAS, [2](#)

 - pwrEWAS_shiny, [6](#)

- * **Shiny**

 - pwrEWAS_shiny, [6](#)

- * **microarray**

 - pwrEWAS, [2](#)

 - pwrEWAS_shiny, [6](#)

- * **power**

 - pwrEWAS, [2](#)

 - pwrEWAS_shiny, [6](#)

pwrEWAS, [2](#)

pwrEWAS_deltaDensity, [3](#)

pwrEWAS_powerPlot, [5](#)

pwrEWAS_shiny, [6](#)