

Package ‘pwrEWAS’

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

Version 1.12.0

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

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pwrEWAS

*pwrEWAS - A computationally efficient tool for comprehensive power estimation in EWAS***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

minTotSampleSize	Minimum total sample size.
maxTotSampleSize	Maximum total sample size.
SampleSizeSteps	Sample size increments.
NcntPer	Percentage sample group 1 (control group) (NcntPer = 0.5 indicates a balanced design).
targetDelta	Target maximum difference in mean DNAm. (Either 'targetDelta' or 'deltaSD' should be specified)
deltaSD	Standard deviation of simulated differences. (Either 'targetDelta' or 'deltaSD' should be specified)
J	Number of CpGs tested/simulated (default: 100000).
targetDmCpGs	Target number of DM CpGs.
tissueType	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)".
detectionLimit	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

<code>data</code>	"deltaArray" attribute within the pwrEWAS object create by pwrEWAS
<code>detectionLimit</code>	Detection limit specified in pwrEWAS.
<code>sd</code>	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()  
}
```

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