

Package ‘pwrEWAS’

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

Version 1.16.0

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

Author Stefan Graw

Maintainer Stefan Graw <shgraw@uams.edu>

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

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()  
}
```

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