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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LazyData false

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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

`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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