

# Package ‘pwrEWAS’

April 15, 2020

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

**Version** 1.0.0

**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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**License** Artistic-2.0

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

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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**

<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).
<code>DMmethod</code>	Method of Differential Methylation analysis: "limma" (default), "t-test (unequal var)", "t-test (equal var)", "Wilcox rank sum", "CPGassoc".
<code>FDRcritVal</code>	FDRcritVal (default: 0.05).
<code>core</code>	Number of threads for multi-threading (default: 1).
<code>sims</code>	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)
```

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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)
```

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pwrEWAS\_shiny

*Shiny pwrEWAS*

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**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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