

# 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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**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	<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

<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 'targetDelta' or 'deltaSD' should be specified)
<code>deltaSD</code>	Standard deviation of simulated differences. (Either 'targetDelta' or 'deltaSD' 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)
```

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pwrEWAS\_deltaDensity *Density plot for simulated differences in mean methylation*

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### 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*

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### 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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