

# Package ‘powerEQTL’

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**Type** Package

**Title** Power and Sample Size Calculation for eQTL Analysis

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**Depends** R (>= 3.6.0)

**Imports** stats, nlme, GLMMadaptive, glmmTMB, parallel

**Description** Power and sample size calculation for eQTL analysis  
based on ANOVA or simple linear regression. It can also calculate power/sample size  
for testing the association of a SNP to a continuous type phenotype.

**License** GPL (>= 2)

**URL** <https://github.com/sterding/powerEQTL>

**LazyData** TRUE

**NeedsCompilation** no

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## R topics documented:

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powerEQTL.ANOVA	<i>Power Calculation for EQTL Analysis Based on Un-Balanced One-Way ANOVA</i>
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### Description

Power calculation for eQTL analysis that tests if a SNP is associated to a gene probe by using un-balanced one-way ANOVA. This function can be used to calculate one of the 3 parameters (power, sample size, and minimum allowable MAF) by setting the corresponding parameter as NULL and providing values for the other 2 parameters.

### Usage

```
powerEQTL.ANOVA(MAF,
                 deltaVec=c(-0.13, 0.13),
                 n=200,
                 power = NULL,
                 sigma = 0.13,
                 FWER = 0.05,
                 nTests = 200000,
                 n.lower = 4,
                 n.upper = 1e+30)
```

### Arguments

MAF	numeric. Minor allele frequency.
deltaVec	numeric. A vector having 2 elements. The first element is equal to $\mu_2 - \mu_1$ and the second element is equal to $\mu_3 - \mu_2$ , where $\mu_1$ is the mean gene expression level for the mutation homozygotes, $\mu_2$ is the mean gene expression level for the heterozygotes, and $\mu_3$ is the mean gene expression level for the wild-type gene expression level.
n	integer. Total number of subjects.
power	numeric. Power for testing if 3 genotypes have the same mean gene expression levels.
sigma	numeric. Standard deviation of the random error.
FWER	numeric. Family-wise Type I error rate.
nTests	integer. Number of tests (i.e., number of all (SNP, gene) pairs) in eQTL analysis.
n.lower	numeric. Lower bound of the total number of subjects. Only used when calculating total number of subjects.
n.upper	numeric. Upper bound of the total number of subjects. Only used when calculating total number of subjects.

## Details

If we would like to test potential non-linear relationship between genotype of a SNP and expression of a gene, we can use un-balanced one-way ANOVA. Actually, an article published by the GTEx Consortium in 2013 used this approach.

Suppose there are  $k = 3$  groups of subjects: (1) mutation homozygotes; (2) heterozygotes; and (3) wildtype homozygotes. We would like to test if the mean expression  $\mu_i$ ,  $i = 1, \dots, k$ , of the gene is the same among the  $k$  groups of subjects. We can use the following one-way ANOVA model to characterize the relationship between observed gene expression level  $y_{ij}$  and the population mean expression level  $\mu_i$ :

$$y_{ij} = \mu_i + \epsilon_{ij}, \quad \epsilon_{ij} \sim N(0, \sigma^2),$$

where  $i = 1, \dots, k$ ,  $j = 1, \dots, n_i$ ,  $y_{ij}$  is the observed gene expression level for the  $j$ -th subject in the  $i$ -th group,  $\mu_i$  is the mean gene expression level of the  $i$ -th group,  $\epsilon_{ij}$  is the random error,  $k$  is the number of groups,  $n_i$  is the number of subjects in the  $i$ -th group. Denote the total number of subjects as  $N = \sum_{i=1}^k n_i$ . That is, we have  $n_1$  mutation homozygotes,  $n_2$  heterozygotes, and  $n_3$  wildtype homozygotes.

We would like to test the null hypothesis  $H_0$  and alternative hypothesis  $H_1$ :

$$H_0 : \mu_1 = \mu_2 = \mu_3,$$

$$H_1 : \text{not all means are the same.}$$

According to O'Brien and Muller (1993), the power calculation formula for unbalanced one-way ANOVA is

$$\text{power} = Pr(F \geq F_{1-\alpha}(k-1, N-k) | F \sim F_{k-1, N-k, \lambda}),$$

where  $k = 3$  is the number of groups of subjects,  $N$  is the total number of subjects,  $F_{1-\alpha}(k-1, N-k)$  is the  $100(1-\alpha)$ -th percentile of central F distribution with degrees of freedoms  $k-1$  and  $N-k$ , and  $F_{k-1, N-k, \lambda}$  is the non-central F distribution with degrees of freedoms  $k-1$  and  $N-k$  and non-central parameter (ncp)  $\lambda$ . The ncp  $\lambda$  is equal to

$$\lambda = \frac{N}{\sigma^2} \sum_{i=1}^k w_i (\mu_i - \mu)^2,$$

where  $\mu_i$  is the mean gene expression level for the  $i$ -th group of subjects,  $w_i$  is the weight for the  $i$ -th group of subjects,  $\sigma^2$  is the variance of the random errors in ANOVA (assuming each group has equal variance), and  $\mu$  is the weighted mean gene expression level

$$\mu = \sum_{i=1}^k w_i \mu_i.$$

The weights  $w_i = n_i/N$  are the sample proportions for the 3 groups of subjects, where  $N = n_1 + n_2 + n_3$  is the total number of subjects. Hence,  $\sum_{i=1}^3 w_i = 1$ . Based on Hardy-Weinberg Equilibrium, we have  $w_1 = \theta^2$ ,  $w_2 = 2\theta(1-\theta)$ , and  $w_3 = (1-\theta)^2$ , where  $\theta$  is MAF.

Without loss of generality, we set  $\mu_1 = -\delta_1$ ,  $\mu_2 = 0$ , and  $\mu_3 = \delta_2$ .

We adopted the parameters from the GTEx cohort (see the "Power analysis" section of Nature Genetics, 2013; <https://www.nature.com/articles/ng.2653>), where they modeled the expression data as having a log-normal distribution with a log standard deviation of 0.13 within each genotype class (AA, AB, BB). This level of noise is based on estimates from initial GTEx data. In their power analysis, they assumed the across-genotype difference  $\delta = 0.13$  (i.e., equivalent to detecting a log expression change similar to the standard deviation within a single genotype class).

**Value**

power if the input parameter power = NULL.

sample size (total number of subjects) if the input parameter n = NULL;

minimum detectable slope if the input parameter slope = NULL.

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**References**

The GTEx Consortium. The Genotype-Tissue Expression (GTEx) project. *Nature Genetics*, 45:580-585, 2013.

O'Brien, RG and Muller, KE. Unified power analysis for t-tests through multivariate hypotheses. In LK Edwards, editor, *Applied Analysis of Variance in Behavioral Science*, pages 297-344. New York: Dekker, 1993.

Dong X, Li X, Chang T-W, Weiss ST, and Qiu W. powerEQTL: an R package and R shiny application for calculating sample size and power of bulk tissue and single-cell eQTL analysis. manuscript. (2020)

**Examples**

```
# calculate power
powerEQTL.ANOVA(MAF = 0.1,
                 deltaVec = c(-0.13, 0.13),
                 n = 282,
                 power = NULL,
                 sigma = 0.13,
                 FWER = 0.05,
                 nTests = 200000)

# calculate sample size (total number of subjects)
powerEQTL.ANOVA(MAF = 0.1,
                 deltaVec = c(-0.13, 0.13),
                 n = NULL,
                 power = 0.8,
                 sigma = 0.13,
                 FWER = 0.05,
                 nTests = 200000)

# calculate minimum allowable MAF
powerEQTL.ANOVA(MAF = NULL,
                 deltaVec = c(-0.13, 0.13),
                 n = 282,
                 power = 0.8,
                 sigma = 0.13,
```

```
FWER = 0.05,
nTests = 200000)
```

---

powerEQTL.scRNAseq      *Power Calculation for Association Between Genotype and Gene Expression Based on Single Cell RNAseq Data*

---

## Description

Power calculation for association between genotype and gene expression based on single cell RNAseq data. This function can be used to calculate one of the 4 parameters (power, sample size, minimum detectable slope, and minimum allowable MAF) by setting the corresponding parameter as NULL and providing values for the other 3 parameters.

## Usage

```
powerEQTL.scRNAseq(
  slope,
  n,
  m,
  power = NULL,
  sigma.y,
  MAF = 0.2,
  rho = 0.8,
  FWER = 0.05,
  nTests = 1,
  n.lower = 2.01,
  n.upper = 1e+30)
```

## Arguments

slope	numeric. Slope under alternative hypothesis.
n	integer. Total number of subjects.
m	integer. Number of cells per subject.
power	numeric. Power for testing if the slope is equal to zero.
sigma.y	numeric. Standard deviation of the gene expression.
MAF	numeric. Minor allele frequency (between 0 and 0.5).
rho	numeric. Intra-class correlation (i.e., correlation between $y_{ij}$ and $y_{ik}$ for the $j$ -th and $k$ -th cells of the $i$ -th subject).
FWER	numeric. Family-wise Type I error rate for one pair (SNP, gene).
nTests	integer. Number of tests (i.e., number of all (SNP, gene) pairs) in eQTL analysis.
n.lower	numeric. Lower bound of the total number of subjects. Only used when calculating total number of subjects.
n.upper	numeric. Upper bound of the total number of subjects. Only used when calculating total number of subjects.

### Details

We assume the following simple linear mixed effects model for each (SNP, gene) pair to characterize the association between genotype and gene expression:

$$y_{ij} = \beta_{0i} + \beta_1 * x_i + \epsilon_{ij},$$

where

$$\beta_{0i} \sim N(\beta_0, \sigma_\beta^2),$$

and

$$\epsilon_{ij} \sim N(0, \sigma^2),$$

$i = 1, \dots, n, j = 1, \dots, m, n$  is the number of subjects,  $m$  is the number of cells per subject,  $y_{ij}$  is the gene expression level for the  $j$ -th cell of the  $i$ -th subject,  $x_i$  is the genotype for the  $i$ -th subject using additive coding. That is,  $x_i = 0$  indicates the  $i$ -th subject is a wildtype homozygote,  $x_i = 1$  indicates the  $i$ -th subject is a heterozygote, and  $x_i = 2$  indicates the  $i$ -th subject is a mutation homozygote.

We would like to test the following hypotheses:

$$H_0 : \beta_1 = 0,$$

and

$$H_1 : \beta_1 = \delta,$$

where  $\delta \neq 0$ .

For a given SNP, we assume Hardy-Weinberg Equilibrium and denote the minor allele frequency of the SNP as  $\theta$ .

We can derive the power calculation formula is

$$power = 1 - \Phi(z_{\alpha^*/2} - a \times b) + \Phi(-z_{\alpha^*/2} - a \times b),$$

where

$$a = \frac{\sqrt{2\theta(1-\theta)}}{\sigma_y}$$

and

$$b = \frac{\delta \sqrt{m(n-1)}}{\sqrt{1 + (m-1)\rho}}$$

and  $z_{\alpha^*/2}$  is the upper  $100\alpha^*/2$  percentile of the standard normal distribution,  $\alpha^* = FWER/nTests$ ,  $nTests$  is the number of (SNP, gene) pairs,  $\sigma_y = \sqrt{\sigma_\beta^2 + \sigma^2}$ , and  $\rho = \sigma_\beta^2 / (\sigma_\beta^2 + \sigma^2)$  is the intra-class correlation.

### Value

power if the input parameter power = NULL.

sample size (total number of subjects) if the input parameter n = NULL;

minimum detectable slope if the input parameter slope = NULL;

minimum allowable MAF if the input parameter MAF = NULL.

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**References**

Dong X, Li X, Chang T-W, Weiss ST, and Qiu W. powerEQTL: an R package and R shiny application for calculating sample size and power of bulk tissue and single-cell eQTL analysis. manuscript. (2020)

**Examples**

```
n = 102
m = 227868

# calculate power
power = powerEQTL.scRNAseq(
  slope = 0.6,
  n = n,
  m = m,
  power = NULL,
  sigma.y = 0.29,
  MAF = 0.05,
  rho = 0.8,
  nTests = 1e+6)

print(power)

# calculate sample size (total number of subjects)
n = powerEQTL.scRNAseq(
  slope = 0.6,
  n = NULL,
  m = m,
  power = 0.9567288,
  sigma.y = 0.29,
  MAF = 0.05,
  rho = 0.8,
  nTests = 1e+6)

print(n)

# calculate slope
slope = powerEQTL.scRNAseq(
  slope = NULL,
  n = n,
  m = m,
  power = 0.9567288,
  sigma.y = 0.29,
  MAF = 0.05,
  rho = 0.8,
  nTests = 1e+6)
```

```

print(slope)

# calculate MAF
MAF = powerEQTL.scRNAseq(
  slope = 0.6,
  n = n,
  m = m,
  power = 0.9567288,
  sigma.y = 0.29,
  MAF = NULL,
  rho = 0.8,
  nTests = 1e+6)
print(MAF)

```

---

```
powerEQTL.scRNAseq.sim
```

*Power Calculation for Association Between Genotype and Gene Expression Based on Single Cell RNAseq Data via Simulation from ZINB Mixed Effects Regression Model*

---

## Description

Power calculation for association between genotype and gene expression based on single cell RNAseq data via simulation from ZINB mixed effects regression model. This function can be used to calculate one of the 4 parameters (power, sample size, minimum detectable slope, and minimum allowable MAF) by setting the corresponding parameter as NULL and providing values for the other 3 parameters.

## Usage

```

powerEQTL.scRNAseq.sim(slope,
  n,
  m,
  power = NULL,
  m.int = -1,
  sigma.int = 1,
  zero.p = 0.1,
  theta = 1,
  MAF = 0.2,
  FWER = 0.05,
  nTests = 1,
  nSim = 1000,
  estMethod = "GLMMadaptive",
  nCores = 1,
  n.lower = 2.01,
  n.upper = 1e+4,

```

```

        slope.lower = 1e-6,
        slope.upper = log(1.0e+6),
        MAF.lower = 0.05,
        MAF.upper = 0.49
    )

```

## Arguments

slope	numeric. Slope (see details).
n	integer. Total number of subjects.
m	integer. Number of cells per subject.
power	numeric. Power for testing if the slope is equal to zero.
m.int	numeric. Mean of random intercept (see details).
sigma.int	numeric. Standard deviation of random intercept (see details).
zero.p	numeric. Probability that an excess zero occurs.
theta	numeric. Dispersion parameter of negative binomial distribution. The smaller theta is, the larger variance of NB random variable is.
MAF	numeric. Minor allele frequency of the SNP.
FWER	numeric. Family-wise Type I error rate.
nTests	integer. Number of tests (i.e., number of all (SNP, gene) pairs) in eQTL analysis.
nSim	integer. Number of simulated datasets to be generated.
estMethod	character. Indicates which method would be used to fit zero inflated negative binomial mixed effects model. The possible choices are “GLMMadaptive” and “glmmTMB”.
nCores	integer. Number of computer cores used by mclapply for parallel computing. For Windows, nCores=1.
n.lower	numeric. Lower bound of the total number of subjects. Only used when calculating total number of subjects.
n.upper	numeric. Upper bound of the total number of subjects. Only used when calculating total number of subjects.
slope.lower	numeric. Lower bound of the slope. Only used when calculating minimum slope.
slope.upper	numeric. Upper bound of the slope Only used when calculating minimum slope.
MAF.lower	numeric. Lower bound of the MAF. Only used when calculating minimum MAF.
MAF.upper	numeric. Upper bound of the MAF Only used when calculating minimum MAF.

## Details

This function calculates the power for testing if genotypes of a SNP is associated with the expression of a gene via nSim datasets generated from zero-inflated negative binomial (ZINB) regression model.

Each dataset is generated from zero-inflated negative binomial mixed effects regression model with only one covariate: genotype. That is, the read counts of a gene follows a mixture of 2-component distributions. One component takes only one value: zero. The other component is negative binomial distribution, which takes non-negative values 0, 1, 2, .... The log mean of the negative binomial distribution is linear function of the genotype.

For each dataset, the p-value for testing if the slope for genotype is equal to zero will be calculated.

The proportion of p-values  $< \alpha$  is the estimated power, where  $\alpha = FWER/nTests$ .

Each simulated dataset contains gene expression levels of one gene and genotypes of one SNP for subjects with multiple cells. The gene expression levels (read counts) follow zero-inflated negative binomial distribution. Denote  $Y_{ij}$  as the read counts for the  $j$ -th cell of the  $i$ -th subject,  $i = 1, \dots, n$ ,  $j = 1, \dots, m$ ,  $n$  is the number of subjects, and  $m$  is the number of cells per subject. Denote  $p$  as the probability that  $Y_{ij} = 0$  is an excess zero. With probability  $1 - p$ ,  $Y_{ij}$  follows a negative binomial distribution  $NB(\mu, \theta)$ , where  $\mu$  is the mean (i.e.,  $\mu = E(Y_{ij})$ ) and  $\theta$  is the dispersion parameter. The variance of the NB distribution is  $\mu + \mu^2/\theta$ . The relationship between gene expression and genotype for the  $i$ -th subject is characterized by the equation

$$\mu_i = \exp(\beta_{0i} + \beta_1 x_i),$$

where  $\beta_{0i}$  is the random intercept following a normal distribution  $N(\beta_0, \sigma^2)$  to account for within-subject correlation of gene expression,  $\beta_0$  is the mean of the random intercept,  $\sigma$  is the standard deviation of the random intercept,  $\beta_1$  is the slope, and  $x_i$  is the additive-coded genotype for the SNP with minor allele frequency  $MAF$ .

We assume that the SNP satisfies the Hardy-Weinberg Equilibrium. That is, the probabilities of the 3 genotypes (0, 1, 2) are  $(1 - MAF)^2$ ,  $2MAF(1 - MAF)$ ,  $MAF^2$ , respectively.

For simplicity, we assume that excess zeros are caused by technical issues, hence are not related to genotypes.

## Value

power if the input parameter power = NULL.

sample size (total number of subjects) if the input parameter n = NULL;

minimum detectable slope if the input parameter slope = NULL;

minimum allowable MAF if the input parameter MAF = NULL.

## Note

The speed of simulation approach is slow. It is recommended to run the function `powerEQTL.scRNAseq.sim` in parallel computing environment (e.g., Unix/Linux) and set `nCores > 1`. Also, it is important to set appropriate ranges to search sample size, minimum detectable slope, or minimum allowable MAF. If the function (e.g., `glmmTMB`) to fit data returns an error message for a simulated dataset, then the function `powerEQTL.scRNAseq.sim` will try a few more runs with different simulated datasets. If all the runs failed, zero (for power estimation) or NA or NaN (for estimating slope, sample size, or MAF) would be output. It is recommended to set `nSim >= 1000` to get stable results.

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**Examples**

```
nSubj = 10
nCellPerSubj = 10

# calculate power
power = powerEQTL.scrNAseq.sim(
  slope = 1.62, # slope
  n = nSubj, # total number of subjects
  m = nCellPerSubj, # number of cells per subject
  power = NULL, # power to be estimated
  m.int = -1, # mean of random intercept
  sigma.int = 1, # SD of the random intercept
  zero.p = 0.01, # probability that an excess zero occurs
  theta = 1, # dispersion parameter of NB distribution NB(mu, theta)
  MAF = 0.45,
  FWER = 0.05,
  nTests = 1,
  nSim = 5, # number of simulations
  estMethod = "GLMMadaptive", # parameter estimation method for ZINB
  nCores = 1 # number of computer cores used by 'mclapply'
)

print(power)
```

---

powerEQTL.SLR

*Power Calculation for EQTL Analysis Based on Simple Linear Regression*

---

**Description**

Power calculation for eQTL analysis that tests if a SNP is associated to a gene probe by using simple linear regression. This function can be used to calculate one of the 4 parameters (power, sample size, minimum detectable slope, and minimum allowable MAF) by setting the corresponding parameter as NULL and providing values for the other 3 parameters.

**Usage**

```
powerEQTL.SLR(
  MAF,
  slope = 0.13,
```

```

n = 200,
power = NULL,
sigma.y = 0.13,
FWER = 0.05,
nTests = 2e+05,
n.lower = 2.01,
n.upper = 1e+30)

```

### Arguments

MAF	numeric. Minor allele frequency.
slope	numeric. Slope of the simple linear regression.
n	integer. Total number of subjects.
power	numeric. Power for testing if the slope is equal to zero.
sigma.y	numeric. Standard deviation of the outcome $y_i$ in simple linear regression.
FWER	numeric. Family-wise Type I error rate.
nTests	integer. Number of tests (i.e., number of all (SNP, gene) pairs) in eQTL analysis.
n.lower	numeric. Lower bound of the total number of subjects. Only used when calculating total number of subjects.
n.upper	numeric. Upper bound of the total number of subjects. Only used when calculating total number of subjects.

### Details

To test if a SNP is associated with a gene probe, we use the simple linear regression

$$y_i = \beta_0 + \beta_1 x_i + \epsilon_i,$$

where  $y_i$  is the gene expression level of the  $i$ -th subject,  $x_i$  is the genotype of the  $i$ -th subject, and  $\epsilon_i$  is the random error term with mean zero and standard deviation  $\sigma$ . Additive coding for genotype is used. That is,  $x_i = 0$  indicates wildtype homozygotes;  $x_i = 1$  indicates heterozygotes; and  $x_i = 2$  indicates mutation heterozygotes.

To test if the SNP is associated with the gene probe, we test the null hypothesis  $H_0 : \beta_1 = 0$  versus the alternative hypothesis  $H_1 : \beta_1 = \delta$ , where  $\delta \neq 0$ .

Denote  $\theta$  as the minor allele frequency (MAF) of the SNP. Under Hardy-Weinberg equilibrium, we can calculate the variance of genotype of the SNP:  $\sigma_x^2 = 2\theta(1 - \theta)$ , where  $\sigma_x^2$  is the variance of the predictor (i.e. the SNP)  $x_i$ .

The exact power calculation formula can be derived as

$$1 - T_{n-2,\lambda}(t_{n-2}(\alpha/2)) + T_{n-2,\lambda}(-t_{n-2}(\alpha/2)),$$

where  $T_{n-2,\lambda}(a)$  is the value at  $a$  of cumulative distribution function of non-central t distribution with  $n - 2$  degrees of freedom and non-centrality parameter  $\lambda = \delta/\sqrt{\sigma^2/[(n - 1)\bar{\sigma}_x^2]}$ . And  $\bar{\sigma}_x^2 = \sum_{i=1}^n (x_i - \bar{x})^2/(n - 1)$ .

Dupont and Plummer (1998) mentioned the following relationship:

$$\sigma^2 = \sigma_y^2 - \beta_1^2 \sigma_x^2.$$

So we can plug in the above equation to the power calculation formula.

Under Hardy-Weinberg equilibrium, we have  $\sigma_x^2 = 2\theta(1-\theta)$ , where  $\theta$  is the minor allele frequency (MAF).

Hence, the non-centrality parameter can be rewritten as

$$\lambda = \frac{\delta}{\sqrt{(\sigma_y^2 - \delta^2 2(1-\hat{\theta})\hat{\theta}) / [(n-1)2(1-\hat{\theta})\hat{\theta}]}}$$

We adopted the parameters from the GTEx cohort (see the "Power analysis" section of Nature Genetics, 2013; <https://www.nature.com/articles/ng.2653>), where they modeled the expression data as having a log-normal distribution with a log standard deviation of 0.13 within each genotype class (AA, AB, BB). This level of noise is based on estimates from initial GTEx data. In their power analysis, they assumed the across-genotype difference  $\delta = 0.13$  (i.e., equivalent to detecting a log expression change similar to the standard deviation within a single genotype class).

### Value

power if the input parameter power = NULL.

sample size (total number of subjects) if the input parameter n = NULL;

minimum detectable slope if the input parameter slope = NULL;

minimum allowable MAF if the input parameter MAF = NULL.

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### References

Dupont, W.D. and Plummer, W.D.. Power and Sample Size Calculations for Studies Involving Linear Regression. *Controlled Clinical Trials*. 1998;19:589-601.

Dong X, Li X, Chang T-W, Weiss ST, and Qiu W. powerEQTL: an R package and R shiny application for calculating sample size and power of bulk tissue and single-cell eQTL analysis. *manuscript*. (2020)

### Examples

```
# calculate power
powerEQTL.SLR(
  MAF = 0.1,
  slope = 0.13,
  n = 179,
  power = NULL,
  sigma.y = 0.13,
  FWER = 0.05,
  nTests = 2e+05)
```

```
# calculate sample size (total number of subjects)
powerEQL.SLR(
  MAF = 0.1,
  slope = 0.13,
  n = NULL,
  power = 0.8,
  sigma.y = 0.13,
  FWER = 0.05,
  nTests = 2e+05)

# calculate minimum detectable slope
powerEQL.SLR(
  MAF = 0.1,
  slope = NULL,
  n = 179,
  power = 0.8,
  sigma.y = 0.13,
  FWER = 0.05,
  nTests = 2e+05)

# calculate minimum allowable MAF
powerEQL.SLR(
  MAF = NULL,
  slope = 0.13,
  n = 179,
  power = 0.8,
  sigma.y = 0.13,
  FWER = 0.05,
  nTests = 2e+05)
```

---

powerLME

*Power Calculation for Simple Linear Mixed Effects Model*

---

## Description

Power calculation for simple linear mixed effects model. This function can be used to calculate one of the 3 parameters (power, sample size, and minimum detectable slope) by setting the corresponding parameter as NULL and providing values for the other 2 parameters.

## Usage

```
powerLME(
  slope,
  n,
  m,
  sigma.y,
  sigma.x,
```

```

power = NULL,
rho = 0.8,
FWER = 0.05,
nTests = 1,
n.lower = 2.01,
n.upper = 1e+30)

```

### Arguments

slope	numeric. Slope under alternative hypothesis.
n	integer. Total number of subjects.
m	integer. Number of observations per subject.
sigma.y	numeric. Standard deviation of the outcome y.
sigma.x	numeric. Standard deviation of the predictor x.
power	numeric. Desired power.
rho	numeric. Intra-class correlation (i.e., correlation between $y_{ij}$ and $y_{ik}$ for the $j$ -th and $k$ -th observations of the $i$ -th subject).
FWER	numeric. Family-wise Type I error rate.
nTests	integer. Number of tests (e.g., number of genes in differential expression analysis based on scRNAseq to compare gene expression between diseased subjects and healthy subjects).
n.lower	numeric. Lower bound of the total number of subjects. Only used when calculating total number of subjects.
n.upper	numeric. Upper bound of the total number of subjects. Only used when calculating total number of subjects.

### Details

We assume the following simple linear mixed effects model to characterize the association between the predictor x and the outcome y:

$$y_{ij} = \beta_{0i} + \beta_1 * x_i + \epsilon_{ij},$$

where

$$\beta_{0i} \sim N(\beta_0, \sigma_\beta^2),$$

and

$$\epsilon_{ij} \sim N(0, \sigma^2),$$

$i = 1, \dots, n$ ,  $j = 1, \dots, m$ ,  $n$  is the number of subjects,  $m$  is the number of observations per subject,  $y_{ij}$  is the outcome value for the  $j$ -th observation of the  $i$ -th subject,  $x_i$  is the predictor value for the  $i$ -th subject. For example,  $x_i$  is the binary variable indicating if the  $i$ -th subject is a diseased subject or not.

We would like to test the following hypotheses:

$$H_0 : \beta_1 = 0,$$

and

$$H_1 : \beta_1 = \delta,$$

where  $\delta \neq 0$ .

We can derive the power calculation formula is

$$power = 1 - \Phi(z_{\alpha^*/2} - a \times b) + \Phi(-z_{\alpha^*/2} - a \times b),$$

where

$$a = \frac{\hat{\sigma}_x}{\sigma_y}$$

and

$$b = \frac{\delta \sqrt{m(n-1)}}{\sqrt{1 + (m-1)\rho}}$$

and  $z_{\alpha^*/2}$  is the upper  $100\alpha^*/2$  percentile of the standard normal distribution,  $\alpha^* = \alpha/nTests$ ,  $nTests$  is the number of tests,  $\sigma_y = \sqrt{\sigma_\beta^2 + \sigma^2}$ ,  $\hat{\sigma}_x = \sqrt{\sum_{i=1}^n (x_i - \bar{x})^2 / (n-1)}$ , and  $\rho = \sigma_\beta^2 / (\sigma_\beta^2 + \sigma^2)$  is the intra-class correlation.

### Value

power if the input parameter power = NULL.

sample size (total number of subjects) if the input parameter n = NULL;

minimum detectable slope if the input parameter slope = NULL.

### Author(s)

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### References

Dong X, Li X, Chang T-W, Weiss ST, and Qiu W. powerEQTL: an R package and R shiny application for calculating sample size and power of bulk tissue and single-cell eQTL analysis. manuscript. (2020)

### Examples

```
n = 102
m = 227868

# calculate power
power = powerLME(
  slope = 0.6,
  n = n,
  m = m,
  sigma.y = 0.29,
  sigma.x = 0.308,
```

```
power = NULL,  
rho = 0.8,  
FWER = 0.05,  
nTests = 1e+6)  
  
print(power)  
  
# calculate sample size (total number of subjects)  
n = powerLME(  
  slope = 0.6,  
  n = NULL,  
  m = m,  
  sigma.y = 0.29,  
  sigma.x = 0.308,  
  power = 0.9562555,  
  rho = 0.8,  
  FWER = 0.05,  
  nTests = 1e+6)  
  
print(n)  
  
# calculate slope  
slope = powerLME(  
  slope = NULL,  
  n = n,  
  m = m,  
  sigma.y = 0.29,  
  sigma.x = 0.308,  
  power = 0.9562555,  
  rho = 0.8,  
  FWER = 0.05,  
  nTests = 1e+6)  
  
print(slope)
```

---

powerLMEnoCov

*Power Calculation for Simple Linear Mixed Effects Model Without Covariate*

---

### Description

Power calculation for simple linear mixed effects model without covariate. This function can be used to calculate one of the 3 parameters (power, sample size, and minimum detectable slope) by setting the corresponding parameter as NULL and providing values for the other 2 parameters.

**Usage**

```
powerLMEnoCov(
  slope,
  n,
  m,
  sigma.y,
  power = NULL,
  rho = 0.8,
  FWER = 0.05,
  nTests = 1,
  n.lower = 2.01,
  n.upper = 1e+30)
```

**Arguments**

slope	numeric. Slope under alternative hypothesis.
n	integer. Total number of subjects.
m	integer. Number of pairs of replicates per subject.
sigma.y	numeric. Standard deviation of the outcome y.
power	numeric. Desired power.
rho	numeric. Intra-class correlation (i.e., correlation between $y_{ij}$ and $y_{ik}$ for the $j$ -th and $k$ -th observations of the $i$ -th subject).
FWER	numeric. Family-wise Type I error rate.
nTests	integer. Number of tests (e.g., number of genes in differential expression analysis based on scRNAseq to compare gene expression before and after treatment).
n.lower	numeric. Lower bound of the total number of subjects. Only used when calculating total number of subjects.
n.upper	numeric. Upper bound of the total number of subjects. Only used when calculating total number of subjects.

**Details**

In an experiment, there are  $n$  samples. For each sample, we get  $m$  pairs of replicates. For each pair, one replicate will receive no treatment. The other replicate will receive treatment. The outcome is the expression of a gene. The overall goal of the experiment is to check if the treatment affects gene expression level or not. Or equivalently, the overall goal of the experiment is to test if the mean within-pair difference of gene expression is equal to zero or not. In the design stage, we would like to calculate the power/sample size of the experiment for testing if the mean within-pair difference of gene expression is equal to zero or not.

We assume the following linear mixed effects model to characterize the relationship between the within-pair difference of gene expression  $y_{ij}$  and the mean of the within-pair difference  $\beta_{0i}$ :

$$y_{ij} = \beta_{0i} + \epsilon_{ij},$$

where

$$\beta_{0i} \sim N(\beta_0, \sigma_\beta^2),$$

and

$$\epsilon_{ij} \sim N(0, \sigma^2),$$

$i = 1, \dots, n, j = 1, \dots, m$ ,  $n$  is the number of subjects,  $m$  is the number of pairs of replicates per subject,  $y_{ij}$  is the within-pair difference of outcome value for the  $j$ -th pair of the  $i$ -th subject.

We would like to test the following hypotheses:

$$H_0 : \beta_0 = 0,$$

and

$$H_1 : \beta_0 = \delta,$$

where  $\delta \neq 0$ . If we reject the null hypothesis  $H_0$  based on a sample, we then get evidence that the treatment affects the gene expression level.

We can derive the power calculation formula:

$$power = 1 - \Phi(z_{\alpha^*/2} - a \times b) + \Phi(-z_{\alpha^*/2} - a \times b),$$

where

$$a = \frac{1}{\sigma_y}$$

and

$$b = \frac{\delta \sqrt{mn}}{\sqrt{1 + (m-1)\rho}}$$

and  $z_{\alpha^*/2}$  is the upper  $100\alpha^*/2$  percentile of the standard normal distribution,  $\alpha^* = \alpha/nTests$ ,  $nTests$  is the number of tests,  $\sigma_y = \sqrt{\sigma_\beta^2 + \sigma^2}$  and  $\rho = \sigma_\beta^2 / (\sigma_\beta^2 + \sigma^2)$  is the intra-class correlation.

## Value

power if the input parameter power = NULL.

sample size (total number of subjects) if the input parameter n = NULL;

minimum detectable slope if the input parameter slope = NULL.

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## References

Dong X, Li X, Chang T-W, Weiss ST, and Qiu W. powerEQTL: an R package and R shiny application for calculating sample size and power of bulk tissue and single-cell eQTL analysis. manuscript. (2020)

**Examples**

```
n = 17
m = 5
sigma.y = 0.68
slope = 1.3*sigma.y
print(slope)

# estimate power
power = powerLMEnoCov(
  slope = slope,
  n = n,
  m = m,
  sigma.y = sigma.y,
  power = NULL,
  rho = 0.8,
  FWER = 0.05,
  nTests = 20345)

print(power)

# estimate sample size (total number of subjects)
n = powerLMEnoCov(
  slope = slope,
  n = NULL,
  m = m,
  sigma.y = sigma.y,
  power = 0.8721607,
  rho = 0.8,
  FWER = 0.05,
  nTests = 20345)

print(n)

# estimate slope
slope = powerLMEnoCov(
  slope = NULL,
  n = n,
  m = m,
  sigma.y = sigma.y,
  power = 0.8721607,
  rho = 0.8,
  FWER = 0.05,
  nTests = 20345)

print(slope)
```

---

simDat.eQTL.scRNAseq *Generate Gene Expression Levels Of One Gene And Genotypes Of One SNP For Subjects With Multiple Cells Based On ZINB Mixed Effects Regression Model*

---

## Description

Generate gene expression levels of one gene and genotypes of one SNP for subjects with multiple cells based on ZINB mixed effects regression model.

## Usage

```
simDat.eQTL.scRNAseq(nSubj = 50,
  nCellPerSubj = 100,
  zero.p = 0.01,
  m.int = 0,
  sigma.int = 1,
  slope = 1,
  theta = 1,
  MAF = 0.45)
```

## Arguments

nSubj	integer. Total number of subjects.
nCellPerSubj	integer. Number of cells per subject.
zero.p	numeric. Probability that an excess zero occurs.
m.int	numeric. Mean of random intercept (see details).
sigma.int	numeric. Standard deviation of random intercept (see details).
slope	numeric. Slope (see details).
theta	numeric. dispersion parameter of negative binomial distribution. The smaller theta is, the larger variance of NB random variable is.
MAF	numeric. Minor allele frequency of the SNP.

## Details

This function simulates gene expression levels of one gene and genotypes of one SNP for subjects with multiple cells based on zero-inflated negative binomial (ZINB) regression model with only one covariate: genotype. That is, the read counts of a gene follows a mixture of 2-component distributions. One component takes only one value: zero. The other component is negative binomial distribution, which takes non-negative values 0, 1, 2, .... The log mean of the negative binomial distribution is linear function of the genotype.

Denote  $Y_{ij}$  as the read counts for the  $j$ -th cell of the  $i$ -th subject,  $i = 1, \dots, n$ ,  $j = 1, \dots, m$ ,  $n$  is the number of subjects, and  $m$  is the number of cells per subject.

Denote  $p$  as the probability that  $Y_{ij} = 0$  is an excess zero. With probability  $1 - p$ ,  $Y_{ij}$  follows a negative binomial distribution  $NB(\mu, \theta)$ , where  $\mu$  is the mean (i.e.,  $\mu = E(Y_{ij})$ ) and  $\theta$  is the dispersion parameter. The variance of the NB distribution is  $\mu + \mu^2/\theta$ . The relationship between gene expression and genotype for the  $i$ -th subject is characterized by the equation

$$\mu_i = \exp(\beta_{0i} + \beta_1 x_i),$$

where  $\beta_{0i}$  is the random intercept following a normal distribution  $N(\beta_0, \sigma^2)$  to account for within-subject correlation of gene expression,  $\beta_0$  is the mean of the random intercept,  $\sigma$  is the standard

deviation of the random intercept,  $\beta_1$  is the slope, and  $x_i$  is the additive-coded genotype for the SNP with minor allele frequency  $MAF$ .

We assume that the SNP satisfies the Hardy-Weinberg Equilibrium. That is, the probabilities of the 3 genotypes (0, 1, 2) are  $(1 - MAF)^2$ ,  $2MAF(1 - MAF)$ ,  $MAF^2$ , respectively.

For simplicity, we assume that excess zeros are caused by technical issues, hence are not related to genotypes.

### Value

A data frame with 3 columns:

id	subject id
geno	additive-coded genotype of the SNP
counts	gene expression of the gene

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### Examples

```
frame = simDat.eQTL.scRNAseq(nSubj = 5,
  nCellPerSubj = 3,
  zero.p = 0.01,
  m.int = 0,
  sigma.int = 1,
  slope = 1,
  theta = 1,
  MAF = 0.45)
print(dim(frame))
print(frame[1:10,])
```

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