

# sizepower

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power.matched

*Power Calculations for Matched-Pairs Designs in Microarray Studies*

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## Description

This routine computes the individual power value for a matched-pairs design having  $n$  treatment units and  $n$  matched control units. This power value is the expected fraction of truly differentially expressed genes that will be correctly declared as differentially expressed by the tests.

## Usage

```
power.matched(ER0, G0, absMu1, sigmad, n)
```

## Arguments

ER0	mean number of false positives.
G0	anticipated number of genes in the experiment that are not differentially expressed.
absMu1	absolute mean difference in log-expression between treatment and control conditions as postulated under the alternative hypothesis H1.
sigmad	anticipated standard deviation of the difference in log-expression between matched treatment and control units. The relation between the standard deviation of the difference (sigmad) and the experimental error standard deviation (sigma) is $\text{sigmad} = \sqrt{2} / \text{sigma}$ .
n	the sample size for each group.

## Value

power	power.
psil	non-centrality parameter.

## Note

Examples and explanations can be found in <http://www.biostat.harvard.edu/people/faculty/mltlee/pdf/Web-power-matched050510.pdf>.

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**References**

Lee, M.-L. T. (2004). Analysis of Microarray Gene Expression Data. *Kluwer Academic Publishers*, ISBN 0-7923-7087-2.

Lee, M.-L. T., Whitmore, G. A. (2002). Power and sample size for DNA microarray studies. *Statistics in Medicine*, **21**:3543-3570.

**See Also**

[power.randomized](#), [power.multi](#), [sampleSize.randomized](#), [sampleSize.matched](#)

**Examples**

```
power.matched(ER0=2, G0=5000, absMu1=1, sigmad=0.4243, n=4)
```

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power.multi

*Power Calculations for Multiple Treatments Design with an Isolated Treatment Effect in Microarray Studies*

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**Description**

Assume numTrt treatment conditions are being studied in either a completely randomized or randomized block design. Under the alternative hypothesis H1, one treatment is distinguished from the other numTrt - 1 treatments by exhibiting differential expression for the gene. This computer routine calculates the individual power value for the design. This power value is the expected fraction of truly differentially expressed genes that will be correctly declared as differentially expressed by the tests.

**Usage**

```
power.multi(ER0, G0, numTrt, absMu1, sigma, n)
```

**Arguments**

ER0	mean number of false positives.
G0	anticipated number of genes in the experiment that are not differentially expressed.
numTrt	total number of treatment conditions.
absMu1	the absolute difference in expression between the distinguished treatment and the other treatments on the log-intensity scale.
sigma	anticipated experimental error standard deviation of the difference in log-expression between treatments.
n	the sample size for each group.

**Value**

power	power.
psi1	non-centrality parameter.

**Note**

Examples and explanations can be found in <http://www.biostat.harvard.edu/people/faculty/mltlee/pdf/Web-power-isolated050510.pdf>.

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**References**

Lee, M.-L. T. (2004). Analysis of Microarray Gene Expression Data. *Kluwer Academic Publishers, ISBN 0-7923-7087-2*.

Lee, M.-L. T., Whitmore, G. A. (2002). Power and sample size for DNA microarray studies. *Statistics in Medicine, 21:3543-3570*.

**See Also**

[power.randomized](#), [power.matched](#), [sampleSize.randomized](#), [sampleSize.matched](#)

**Examples**

```
power.multi(ER0=2, G0=10000, numTrt=6, absMu1=0.585, sigma=0.3, n=8)
```

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power.randomized    *Power Calculation for Completely Randomized Treatment-Control Designs in Microarray studies*

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**Description**

This routine computes the individual power value for a completely randomized design with  $n$  treatment units and  $n$  control units ( $2n$  units in total). This power value is the expected fraction of truly differentially expressed genes that will be correctly declared as differentially expressed by the tests.

**Usage**

```
power.randomized(ER0, G0, absMu1, sigmad, n)
```

**Arguments**

ER0	mean number of false positives.
G0	anticipated number of genes in the experiment that are not differentially expressed.
absMu1	absolute mean difference in log-expression between treatment and control conditions as postulated under the alternative hypothesis $H_1$ .

sigmad	anticipated standard deviation of the difference in log-expression between treatment and control conditions. The relation between the standard deviation of the difference (sigmad) and the experimental error standard deviation (sigma) is $\text{sigmad} = \sqrt{2} / \text{sigma}$ .
n	the sample size for each group.

**Value**

power	power.
psil	non-centrality parameter.

**Note**

Examples and explanations can be found in <http://www.biostat.harvard.edu/people/faculty/mltlee/pdf/Web-power-trt-cont050510.pdf>.

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**References**

- Lee, M.-L. T. (2004). Analysis of Microarray Gene Expression Data. *Kluwer Academic Publishers*, ISBN 0-7923-7087-2.
- Lee, M.-L. T., Whitmore, G. A. (2002). Power and sample size for DNA microarray studies. *Statistics in Medicine*, **21**:3543-3570.

**See Also**

[power.matched](#), [power.multi](#), [sampleSize.randomized](#), [sampleSize.matched](#)

**Examples**

```
power.randomized(ER0=2, G0=5000, absMu1=1, sigmad=0.5657, n=8)
```

---

sampleSize.matched *Sample Size Calculation for Matched-Pairs Designs in Microarray Studies*

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**Description**

This routine computes the sample size  $n$  required to achieve a specified power level for a matched-pairs design in which differential expression between  $n$  treatment units and  $n$  matched control units is of interest. The total number of experimental units for the study is  $2n$ .

**Usage**

```
sampleSize.matched(ER0, G0, power, absMu1, sigmad)
```

**Arguments**

ER0	mean number of false positives.
G0	anticipated number of genes in the experiment that are not differentially expressed.
power	specified power level for an individual gene, which represents the expected proportion of differentially expressed genes that will be declared as such by the tests.
absMul	absolute mean difference in log-expression between treatment and control units as postulated under the alternative hypothesis H1.
sigmad	anticipated standard deviation of the difference in log-expression between matched treatment and control units.

**Value**

n	sample size for each group.
d	statistical difference between treatment and control conditions under H1 (i.e. $d = \text{absMul} / \text{sigmad}$ ).

**Note**

Examples and explanations can be found in <http://www.biostat.harvard.edu/people/faculty/mltlee/pdf/Web-sampsize-matched050510.pdf>.

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- Lee, M.-L. T., Whitmore, G. A. (2002). Power and sample size for DNA microarray studies. *Statistics in Medicine, 21*:3543-3570.

**See Also**

[power.randomized](#), [power.matched](#) [power.multi](#), [sampleSize.randomized](#)

**Examples**

```
sampleSize.matched(ER0=1, G0=2000, power=0.9, absMul=1, sigmad=0.5)
```

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sampleSize.randomized

*Sample Size Calculation for Completely Randomized Treatment-Control Designs in Microarray Studies*

---

## Description

For any specified power, this routine computes the required sample size  $n$  for completely randomized designs in which differential expression between  $n$  treatment units and  $n$  control units is of interest. The total number of experimental units for the study is  $2n$ .

## Usage

```
sampleSize.randomized(ER0, G0, power, absMu1, sigmad)
```

## Arguments

ER0	mean number of false positives.
G0	anticipated number of genes in the experiment that are not differentially expressed.
power	specified power level for an individual gene, which represents the expected proportion of differentially expressed genes that will be declared as such by the tests.
absMu1	absolute mean difference in log-expression between treatment and control conditions as postulated under the alternative hypothesis H1.
sigmad	anticipated standard deviation of the difference in log-expression between treatment and control conditions. The relation between the standard deviation of the difference ( <code>sigmad</code> ) and the experimental error standard deviation ( <code>sigma</code> ) is $\text{sigmad} = \sqrt{2} / \text{sigma}$ .

## Value

<code>n</code>	sample size for each group.
<code>d</code>	statistical difference between treatment and control conditions under H1 (i.e. $d = \text{absMu1} / \text{sigmad}$ ).

## Note

Examples and explanations can be found in <http://www.biostat.harvard.edu/people/faculty/mltlee/pdf/Web-sampsize-trt-cont-050511r.pdf>.

## Author(s)

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Lee, M.-L. T., Whitmore, G. A. (2002). Power and sample size for DNA microarray studies. *Statistics in Medicine*, **21**:3543-3570.

## See Also

[power.randomized](#), [power.matched](#), [power.multi](#), [sampleSize.matched](#)

## Examples

```
sampleSize.randomized(ER0=1, G0=2000, power=0.9, absMu1=1, sigmad=0.566)
```

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