sizepower

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R topics documented:

`power.matched` *Power Calculations for Matched-Pairs Designs in Microarray Studies*

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`	absoulte 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 `sigmad=sqrt(2)/sigma`.
`n`	the sample size for each group.

Value

power	power.
psi1	non-centrality parameter.

Note

Examples and explainations 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*

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 explainations can be found in http://www.biostat.harvard.edu/people/faculty/mltlee/pdf/Web-power-isolated050510.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, sampleSize.randomized, sampleSize.matched

Examples

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

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

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 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 (`sigmad`) and the experimental error standard deviation (`sigma`) is `sigmad=sqrt(2)/sigma`.
`n`	the sample size for each group.

Value

`power`	power.
`psi1`	non-centrality parameter.

Note

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

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References

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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.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*

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.
absMu1	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=absMu1/sigmad).

Note

Examples and explainations 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, absMu1=1, sigmad=0.5)
```

---

sampleSize.randomized

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

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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 (`sigmad`) and the experimental error standard deviation (`sigma`) is `sigmad=sqrt(2)/sigma`.

Value

`n`	sample size for each group.
`d`	statistical difference between treatment and control conditions under H1 (i.e. `d=absMu1/sigmad`).

Note

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

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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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