Package ‘ssize’

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Title Estimate Microarray Sample Size
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Description Functions for computing and displaying sample size information for gene expression arrays.
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Depends gdata, xtable
License LGPL
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NeedsCompilation no

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exp.sd Example baseline variability for gene expression experiment

Description

Example baseline variability for gene expression experiment

Usage
data(exp.sd)

Format

Vector of 12,625 standard deviations of gene expression data normalized via the RMA method (ie on log2 scale) with names from Affymetrix probe set IDs.
Examples

```r
data(exp.sd)

hist(exp.sd, prob=TRUE)
lines(density(exp.sd), col="red", lwd=2)
```

---

pow

*Compute and plot power, required sample-size, or detectible effect size for gene expression experiment*

Description

Compute and plot power, required sample-size, or detectible effect size for gene expression experiment

Usage

```r
pow(sd, n, delta, sig.level, alpha.correct = "Bonferonni")
power.plot(x, xlab = "Power", ylab = "Proportion of Genes with Power >= x",
           marks = c(0.7, 0.8, 0.9), ...)

ssize(sd, delta, sig.level, power, alpha.correct = "Bonferonni")
ssize.plot(x, xlab = "Sample Size (per group)",
           ylab = "Proportion of Genes Needing Sample Size <= n",
           marks = c(2, 3, 4, 5, 6, 8, 10, 20), ...)

delta(sd, n, power, sig.level, alpha.correct = "Bonferonni")
delta.plot (x, xlab = "Fold Change",
           ylab = "Proportion of Genes with Power >= 80% at Fold Change=delta",
           marks = c(1.5, 2, 2.5, 3, 4, 6, 10), ...)
```

Arguments

- **sd**: Vector of standard deviations for control samples, *on the log2 scale*
- **n**: Number of observations (per group)
- **delta**: Hypothetical True difference in expression, on the log2 scale.
- **sig.level**: Significance level (Type I error probability)
- **power**: Power
- **alpha.correct**: Type of correction for multiple comparison. One of "Bonferonni" or "None".
- **x**: Vector of powers generated by `pow`
- **xlab, ylab**: x and y axis labels
- **marks**: Powers at which percent of genes achieving the specified cutoff is annotated on the plot.
- **...**: Additional graphical parameters
The `pow` function computes power for each element of a gene expression experiment using an vector of estimated standard deviations. The power is computed separately for each gene, with an optional correction to the significance level for multiple comparison. The `power.plot` function generates a cumulative power plot illustrating the fraction and number of genes achieve a given power for the specified sample size, significance level, and delta. Periods are printed for every 10 calculations so that the user can see that the computation is proceeding.

**Value**

`pow` returns a vector containing the power for each standard deviation.

**Note**

This code was intended to be used with data are on the log2 scale, in which case the delta can be set to becomes log2(fold-change).

**Author(s)**

Gregory R. Warnes <greg@warnes.net>

**References**

Warnes GR and Fasheng Li, “Sample Size Selection for Microarray Experiments” submitted to *Biometrics*.


**See Also**

`ssize`, `ssize.plot`, `delta`, `delta.plot`

**Examples**

```r
library(gdata) # for nobs()

data(exp.sd)

# Histogram of the standard deviations

hist(exp.sd, n=20, col="cyan", border="blue", main="", xlab="Standard Deviation (for data on the log scale)"

dens <- density(exp.sd)

lines(dens$x, dens$y*par("usr")[4]/max(dens$y),col="red",lwd=2)

title("Histogram of Standard Deviations")

# 1) What is the power if using 6 patients 3 measurements assuming
#    Delta=1.0, Alpha=0.05 and Observed SDs?
#```
Description

Compute power of test, or determine parameters to obtain target power.
Usage

```r
power.t.test.FDR(sd=1, n=NULL, delta=NULL, 
               FDR.level=0.05, 
               pi0, 
               power=NULL, 
               type=c("two.sample", "one.sample", "paired"), 
               alternative=c("two.sided", "one.sided") )
```

Arguments

- `sd`: Standard deviation
- `n`: Number of observations (per group)
- `delta`: True difference in means
- `FDR.level`: False Discovery Rate (expected ratio of false discoveries among all discoveries)
- `pi0`: Proportion of true null hypotheses (fraction of tests that with no difference)
- `power`: Power of test (1 minus Type II error probability)
- `type`: Type of t test
- `alternative`: One- or two-sided test

Details

Exactly one of the parameters `n`, `delta`, `power`, `sd`, and `FDR.level` must be passed as NULL, and that parameter is determined from the others. Notice that the last two have non-NULL defaults so NULL must be explicitly passed if you want to compute them.

Value

Object of class "power.htest", a list of the arguments (including the computed one) augmented with `method` and `note` elements.

Note

`uniroot` is used to solve power equation for unknowns, so you may see errors from it, notably about inability to bracket the root when invalid arguments are given.

Author(s)

Peng Liu, based on `power.t.test` code by Peter Dalgaard, which in turn is based on previous work by Claus Ekström

See Also

- `t.test`, `uniroot`

Examples

```r
## Compute power given sd, n, delta, FDR & pi.0
power.t.test.FDR(sd=1, n=5, delta=2, FDR.level=0.05, pi0=0.95, 
                 power=NULL, type="two.sample", alternative="two.sided")
```

```r
## Compute power
```
power.t.test.FDR(n=20, delta=1, FDR=0.05, pi0=0.75)
power.t.test.FDR(n=29, delta=1, FDR=0.05, pi0=0.75)

## compute n
power.t.test.FDR(n=NULL, sd=1, power=.90, delta=1, FDR=0.05, pi0=0.975)
power.t.test.FDR(n=NULL, sd=1, power=.90, delta=1, FDR=0.05, pi0=0.975,
   alt="one.sided")

## compute sd
power.t.test.FDR(sd=NULL, n=29, power=.90, delta=1, FDR=0.05, pi0=0.975)

## compute FDR level
power.t.test.FDR(sd=1, n=29, power=.90, delta=1, FDR=NULL, pi0=0.975)
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