

# ssize

April 20, 2011

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exp.sd

*Example baseline variability for gene expression experiment*

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## 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

```
data(exp.sd)

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

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power.t.test.FDR

*Power calculations for one and two sample t tests using FDR correction*

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## Description

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

## Usage

```
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**

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

**See Also**

[t.test](#), [uniroot](#)

**Examples**

```
## 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")

## 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)
```

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

```
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

## Details

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  $\log_2$  scale, in which case the delta can be set to becomes  $\log_2(\text{fold-change})$ .

## Author(s)

Gregory R. Warnes <[greg@random-technologies-llc.com](mailto:greg@random-technologies-llc.com)>

## References

Warnes GR and Fasheng Li Warnes GR and Liu P, "Sample Size Selection for Microarray Experiments" submitted to *Biometrics*.

Warnes GR and Fasheng Li, "Sample Size Selection for Microarray based Gene Expression Studies," Talk, "2003 FDA/Industry Statistics Workshop: From Theory to Regulatory Acceptance", American Statistical Association, Bethesda, MD, Sept 18-19, 2003. <http://www.warnes.net/Research/PresentationFolder/SampleSize.pdf>

## See Also

[ssize](#), [ssize.plot](#), [delta](#), [delta.plot](#)

## Examples

```
library(gdata) # for nobis()

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?
#
```

```

n=6; fold.change=2.0; power=0.8; sig.level=0.05;
#
all.power <- pow(sd=exp.sd, n=n, delta=log2(fold.change),
                sig.level=sig.level)

power.plot(all.power, lwd=2, col="blue")
xmax <- par("usr")[2]-0.05; ymax <- par("usr")[4]-0.05
legend(x=xmax, y=ymax,
       legend= strsplit( paste("n=",n,"",
                                "fold change=",fold.change,"",
                                "alpha=", sig.level, "",
                                "# genes=", nobs(sd), sep=''), ", " )[[1]],
       xjust=1, yjust=1, cex=1.0)
title("Power to Detect 2-Fold Change")

# 2) What is necessary sample size for 80% power using 3 measurements/patient
#     assuming Delta=1.0, Alpha=0.05 and Observed SDs?
#
all.size <- ssize(sd=exp.sd, delta=log2(fold.change),
                 sig.level=sig.level, power=power)
ssize.plot(all.size, lwd=2, col="magenta", xlim=c(1,20))
xmax <- par("usr")[2]-1; ymin <- par("usr")[3] + 0.05
legend(x=xmax, y=ymin,
       legend= strsplit( paste("fold change=",fold.change,"",
                                "alpha=", sig.level, "",
                                "power=",power,"",
                                "# genes=", nobs(sd), sep=''), ", " )[[1]],
       xjust=1, yjust=0, cex=1.0)
title("Sample Size to Detect 2-Fold Change")

# 3) What is necessary fold change to achieve 80% power using 3
#     measurements/patient assuming n=6, Delta=1.0, Alpha=0.05 and Observed
#     SDs?
#
all.delta <- delta(sd=exp.sd, power=power, n=n,
                 sig.level=sig.level)
delta.plot(all.delta, lwd=2, col="magenta", xlim=c(1,10))
xmax <- par("usr")[2]-1; ymin <- par("usr")[3] + 0.05
legend(x=xmax, y=ymin,
       legend= strsplit( paste("n=",n,"",
                                "alpha=", sig.level, "",
                                "power=",power,"",
                                "# genes=", nobs(sd), sep=''), ", " )[[1]],
       xjust=1, yjust=0, cex=1.0)
title("Fold Change to Achieve 80% Power")

```

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