Package: RNASeqPower (via r-universe)

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Title Sample size for RNAseq studies

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LazyLoad Yes

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`rnapower` *RNA-seq power computation*

Description

Sample size and power computation for RNA-seq studies

Usage

```
rnapower(depth, n, n2 = n, cv, cv2 = cv, effect, alpha, power)
```

Arguments

depth	average depth of coverage for the transcript or gene of interest. Common values are 5-20, any numeric value >0 is valid.
n	sample size in group 1 (or both)
n2	sample size in group 2
cv	biological coefficient of variation in group 1 (or both).
cv2	biological coefficient of variation in group 2
effect	target effect size
alpha	size of the test statistic (two sided), i.e., the false positive rate, a number between 0 and 1
power	power of the test, i.e., the fraction of true positives that will be detected, a number between 0 and 1

Details

The error in an RNA-seq study arises from two causes: the technical variability of the sequencing itself, and the within group biological variability of the specimens being compared. For human samples this latter will often be .4-1, for inbred animal lines values are commonly .1 or less. That is, we might see a 2-fold difference in mean expression between treated and untreated samples, and at the same time a 50% variation in expression between samples within the control or treatment group. This would correspond to an effect size of 2 and a CV of 0.5. As a general rule, sequencing depths of more than 5/CV^2 will lead to only minor gains in study efficiency and/or power, whereas addition of further samples is always efficatious.

Depth is a required argument; any one of the others may be left missing and the function will solve for it. An argument may be a vector, in which case a vector of values is returned. If multiple arguments are vectors a matrix or array of results is returned.

Common values for alpha and power would be .05 and .9. The effect parameter specifies the biological effect that, if it were true, the experimenter would want to be able to detect; values of 1.5 to 2 are commonly used. The statements that A has twice the expression of B and that B has half that of A are symmetric, likewise values of .5 and 2 for effect will yeild the same result. The estimated CV of expression within group may be the most difficult parameter to choose; see the vignette for an in depth discussion of this along with recommended values for diffrent types of data.

By default the samples sizes in the two groups are assumed to be equal (n2=n) if a second sample size is not given. Likewise the coefficients of variation in the two groups are assumed to be equal if cv2 is not specified.

Value

a vector, matrix, or array of values. If the function was used with all the arguments except n supplied then the result will be the needed samples size; if it were run with all arguments except power the result will contain power estimates, etc.

Author(s)

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References

Steven Hart, Terry Therneau, Yuji Zhang, Gregory Poland, and Jean-Pierre Kocher. Calculating sample size estimates for RNA sequencing data. J. Comp. Biology, 2013, in press.

Examples

```
# What would the power be for a study with 12 per group, to detect a
#  2-fold change, given deep (50x) coverage?
rnapower(50, cv=.6, effect=2, n=12, alpha=.05)

# Compute a sample size for several combinations of parameters
temp <- rnapower(10, cv=.5, effect=c(1.5, 2), alpha=c(.05, .01, .001),
                  power=c(.8, .9))
round(temp,1)
# Result is an array with dimensions of effect size, alpha, and power
# which contains the sample size per group for each combination.
```

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