RnaSeqSampleSize: Sample size estimation based on real RNA-seq data

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Abstract

In this vignette, we demonstrated the application of RnaSeqSampleSize as an sample size estimation tool for RNA-seq data. A user friendly web interface is also provided at http://cqs.mc.vanderbilt.edu/shiny/RnaSeqSampleSize/ for researchers not familar with R.

RnaSeqSampleSize package provides the following features:

- Estimation of sample size or power by single read count and dispersion;
- Estimation of sample size or power by prior real data;
- Visualization of sample size and power by power curves;
- Optimization by power or sample size matrix;

Contents

1 Introduction

Sample size estimation is the most important issue in the design of RNA sequencing experiments. However, thousands of genes are quantified and tested for differential expression simultaneously in RNA-seq experiments. The false discovery rate for statistic tests should be controlled. At the same time, the thousands of genes have widely distributed read counts and dispersions, which were often estimated by experience or set at the most conservative values in previous sample size estimation methods. As a result, the estimated sample size will be inaccurate or over-estimated.

To solve these issues, we developed a sample size estimation method based on the distributions of gene read counts and dispersions from real data. Datasets from the user's preliminary experiments or the Cancer Genome Atlas (TCGA) can be used as reference. The read counts and their related dispersions will be selected randomly from the reference based on their distributions, and from that, the power and sample size will be estimated and summarized.

2 User friendly web interface

A user friendly web interface for RnaSeqSampleSize package is provided at http://cqs.mc.vanderbilt.edu/shiny/RnaSeqSampleSize/. Most of the functions in Examples section can be performed in this website.

3 Examples

First we will load the RnaSeqSampleSize package.

```
library(RnaSeqSampleSize)

## Loading required package:  RnaSeqSampleSizeData
## Loading required package:  edgeR
## Loading required package:  limma
```

3.1 Estimation of sample size or power by single read count and dispersion

3.1.1 Power estimation

For example, if we are estimating the power of finding significant genes for RNA-seq data with specified sample size, and we have the following parameters:

- Number of samples in each group: 63;
- Minimal fold change between two groups: 2;
- Minimal average read counts: 5;

- Maximal dispersion: 0.5;
- False discovery rate: 0.01;

As a result, the estimated power is 0.8 by *est_power* function. It means that we have 80% probability to find the significant genes with 63 samples in each group.

```
example(est_power)

##
## est_pw> n<-63;rho<-2;lambda0<-5;phi0<-0.5;f<-0.01
##
## est_pw> est_power(n=n, rho=rho, lambda0=lambda0, phi0=phi0,f=f)
## [1] 0.8
```

3.1.2   Sample size estimation

For example, if we are estimating the sample size for RNA-seq data to achieve desired power of finding significant genes, and we have the following parameters:

- Desired power of finding significant genes: 0.8;
- Minimal fold change between two groups: 2;
- Minimal average read counts: 5;
- Maximal dispersion: 0.5;
- False discovery rate: 0.01;

As a result, the estimated sample size is 63 by *sample_size* function. It means that if we want to have 80% probability to find the significant genes, we need 63 samples in each group.

```
example(sample_size)

##
## smpl_s> power<-0.8;rho<-2;lambda0<-5;phi0<-0.5;f<-0.01
##
## smpl_s> sample_size(power=power, f=f,rho=rho, lambda0=lambda0, phi0=phi0)
## [1] 63
```

3.2   Estimation of sample size or power by prior real data

3.2.1   Power estimation with datasets in RnaSeqSampleSizeData package

RnaSeqSampleSizeData package contains the read counts and dispersion distribution from some real datasets and can be used as prior data for sample size or power estimation. They can be called with following names:

```
##  [1] "TCGA_BLCA" "TCGA_BRCA" "TCGA_CESC" "TCGA_COAD" "TCGA_HNSC" "TCGA_KIRC" "TCGA_LGG"
##  [8] "TCGA_LUAD" "TCGA_LUSC" "TCGA_PRAD" "TCGA_READ" "TCGA_THCA" "TCGA_UCEC"
```

For example, if we are estimating the power of finding significant genes for RNA-seq data with specified sample size, and we have the following parameters:

- Number of samples in each group: 65;
- Minimal fold change between two groups: 2;
- Prior data: TCGA READ data, stored in RnaSeqSampleSizeData package, can be used with name TCGA_READ;
- False discovery rate: 0.01;

Here we demonstrated the power estimation by prior data in three different situations.

- If we are intesested in all genes, we can use repNumber parameter to specify random number of genes to perform power estimation;

```
est_power_distribtuion(n = 65, f = 0.01, rho = 2, distributionObject = "TCGA_READ", re
## [1] 0.8096763
```

Please note here the parameter repNumber was very small (5) to make the example code faster. We suggest repNumber should be at least set as 100 in real analysis.

- If we are only intesested in a list of genes, we can use selectedGenes parameter to specify the list of genes to perform power estimation;

```
# Power estimation based on some interested genes. We use storeProcess=TRUE to retur
# details for all selected genes.
selectedGenes <- names(TCGA_READ$pseudo.counts.mean)[c(1, 3, 5, 7, 9, 12:30)]
powerDistribution <- est_power_distribtuion(n = 65, f = 0.01, rho = 2, distributionObj
    selectedGenes = selectedGenes, minAveCount = 1, storeProcess = TRUE)
str(powerDistribution)
## List of 3
##  $ power     : num [1:24] 0.6753 0.6847 0.687 0.0272 0.9946 ...
##  $ count     : Named num [1:24] 55 27 2000 249 1365 ...
##   ..- attr(*, "names")= chr [1:24] "A1BG" "A2BP1" "A2M" "A4GALT" ...
##  $ dispersion: num [1:24] 0.7 2.7 0.3 0.5 0.2 1.1 6.4 0.6 0.2 0.2 ...
mean(powerDistribution$power)
## [1] 0.774561
```

- If we are only intesested a specified pathway, we can use pathway and species parameters to specify the genes in a pathway to perform power estimation.

```
powerDistribution <- est_power_distribtuion(n = 65, f = 0.01, rho = 2, distributionObj
    pathway = "00010", minAveCount = 1, storeProcess = TRUE)
mean(powerDistribution$power)
## [1] 0.7776358
```

As a result, we use *est_power_distribtuion* function and find the estimated power is 0.81 for random genes, 0.77 for specified gene list, and 0.77 for genes in Glycolysis and Gluconeogenesis (pathway 00010) pathway.

3.2.2 Sample size estimation with datasets in RnaSeqSampleSizeData package

For example, if we are estimating the sample size for RNA-seq data to achieve desired power of finding significant genes, and we have the following parameters:

- Desired power of finding significant genes: 0.8;
- Minimal fold change between two groups: 2;
- Prior data: TCGA READ data, stored in RnaSeqSampleSizeData package, can be used with name TCGA_READ;
- False discovery rate (FDR): 0.01;

As a result, we use *sample_size_distribution* function and find the estimated sample size is 65 for random genes.

```
sample_size_distribution(power = 0.8, f = 0.01, distributionObject = "TCGA_READ", repNumber
    showMessage = TRUE)

## [1] "x= 1   f(x)= -0.8"
## [1] "x= 33  f(x)= -0.272193328875705"
## [1] "x= 65  f(x)= 0.00149392491701938"
## [1] "x= 49  f(x)= -0.120384771506399"
## [1] "x= 57  f(x)= -0.0544219672787534"
## [1] "x= 61  f(x)= -0.0251251289997526"
## [1] "x= 63  f(x)= -0.0114954578587679"
## [1] "x= 64  f(x)= -0.00490859274826694"
## [1] 65
```

Please note here the parameter repNumber was very small (5) to make the example code faster. We suggest repNumber should be at least set as 100 in real analysis.

3.2.3 Sample size or power estimation with user's prior dataset

For example, if the user has a RNA-seq data with 10000 genes and 10 samples as prior dataset:

```
# Generate a 10000*10 RNA-seq data as prior dataset
set.seed(123)
dataMatrix <- matrix(sample(0:3000, 1e+05, replace = TRUE), nrow = 10000, ncol = 10)
colnames(dataMatrix) <- c(paste0("Control", 1:5), paste0("Treatment", 1:5))
row.names(dataMatrix) <- paste0("gene", 1:10000)
head(dataMatrix)

##        Control1 Control2 Control3 Control4 Control5 Treatment1 Treatment2 Treatment3
## gene1       863      932     2974      263      604        639       1270        561
## gene2      2365      973      906     2339     2935       1331       2357        503
## gene3      1227     2611     1301      843     1238        384       1806       1922
## gene4      2649      986      481     1649     1426       1434        245       2888
## gene5      2822      377     2469      584       53       2157        885       1991
```

```
## gene6      136     1069     624    1018    1104    2718    1016     919
##       Treatment4 Treatment5
## gene1      2056     2504
## gene2      1883     2146
## gene3      2294     1235
## gene4      2617     2889
## gene5       917     1676
## gene6      2343     1257
```

Then we are estimating the power of finding significant genes for RNA-seq data with specified sample size, and we have the following parameters:

- Number of samples in each group: 65;
- Minimal fold change between two groups: 2;
- Prior data: User's prior dataset with 10000 genes and 10 samples;
- False discovery rate: 0.01;

We will use *est_count_dispersion* to estitamete the gene read count and dispersion distribution of user's prior dataset. And then *est_power_distribtuion* function will be used to estimate power.

```
# Estitamete the gene read count and dispersion distribution
dataMatrixDistribution <- est_count_dispersion(dataMatrix, group = c(rep(0, 5), rep(1, 5)))
```

```
## Disp = 0.59734 , BCV = 0.7729
```

```
# Power estimation by read count and dispersion distribution
est_power_distribtuion(n = 65, f = 0.01, rho = 2, distributionObject = dataMatrixDistribut:
    repNumber = 5)
```

```
## [1] 0.9564837
```

As a result, we can find the estimated power is 0.82. Please note here the parameter repNumber was very small (5) to make the example code faster. We suggest repNumber should be at least set as 100 in real analysis.

3.3   Power curve visualization

For example, if we are going to compare the power of finding significant genes for different false discovery rate, and we have the following parameters:

- Number of samples in each group: 63;
- Minimal fold change between two groups: 2;
- Minimal average read counts: 5;
- Maximal dispersion: 0.5;
- False discovery rate: 0.01 and 0.05;

```
result1 <- est_power_curve(n = 63, f = 0.01, rho = 2, lambda0 = 5, phi0 = 0.5)
result2 <- est_power_curve(n = 63, f = 0.05, rho = 2, lambda0 = 5, phi0 = 0.5)
```

```
plot_power_curve(list(result1, result2))
```
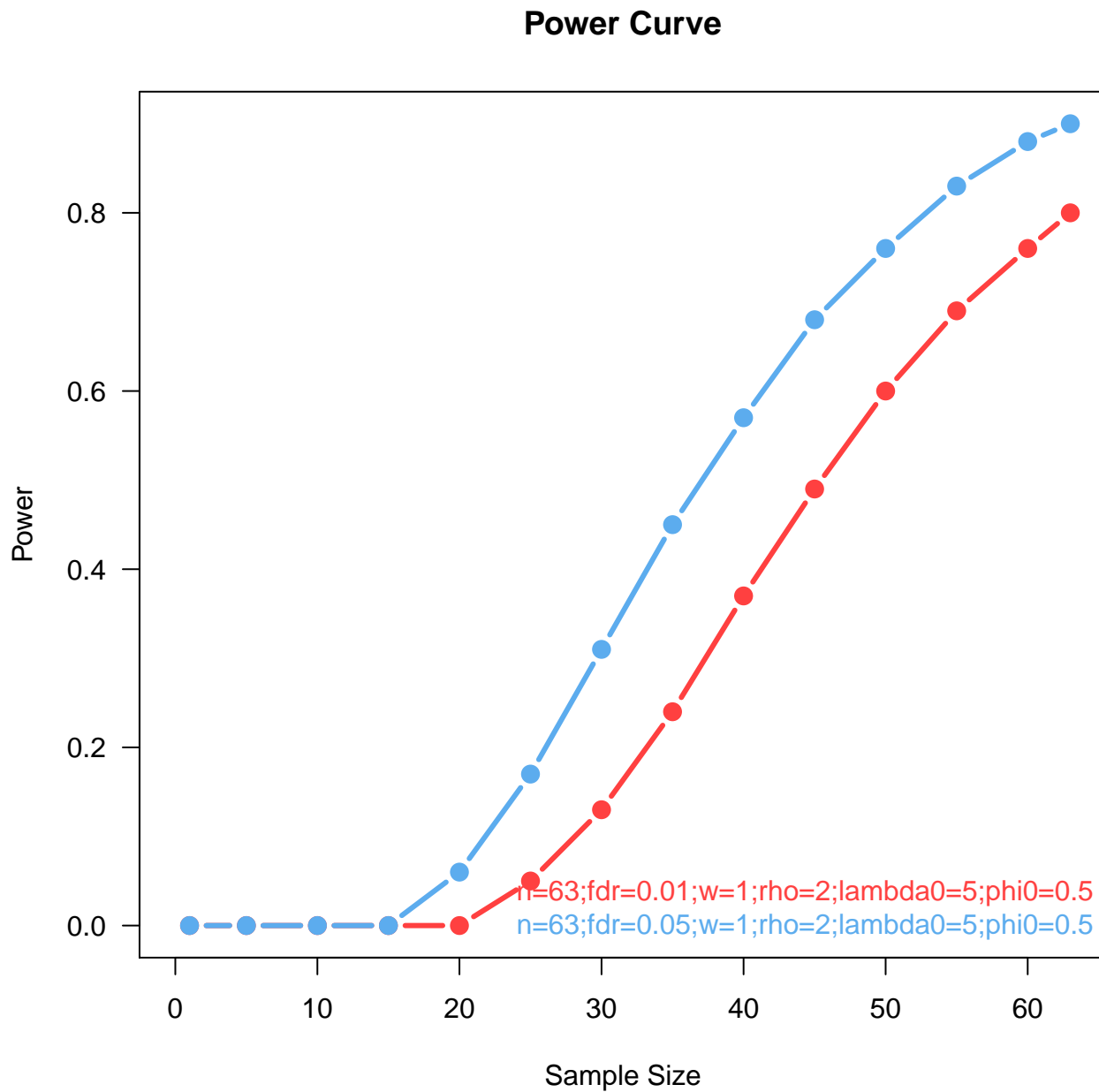
Power Curve

As a result, the relation between power and sample size can be estimated by *est_power_curve* function and the power curves can be generated by *plot_power_curve* function.

3.4 Optimization by power or sample size matrix

For example, if the budget is limited, we need to balance the number of replications and sequence depth. We can use the *optimize_parameter* function to find the relation between sample size, read counts, and estimated power. And then the optimized parameters can be determined.

```
result <- optimize_parameter(fun = est_power, opt1 = "n", opt2 = "lambda0", opt1Value = c(3,
    5, 10, 15, 20), opt2Value = c(1:5, 10, 20))
```
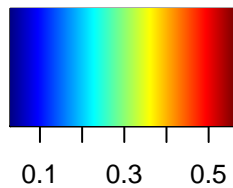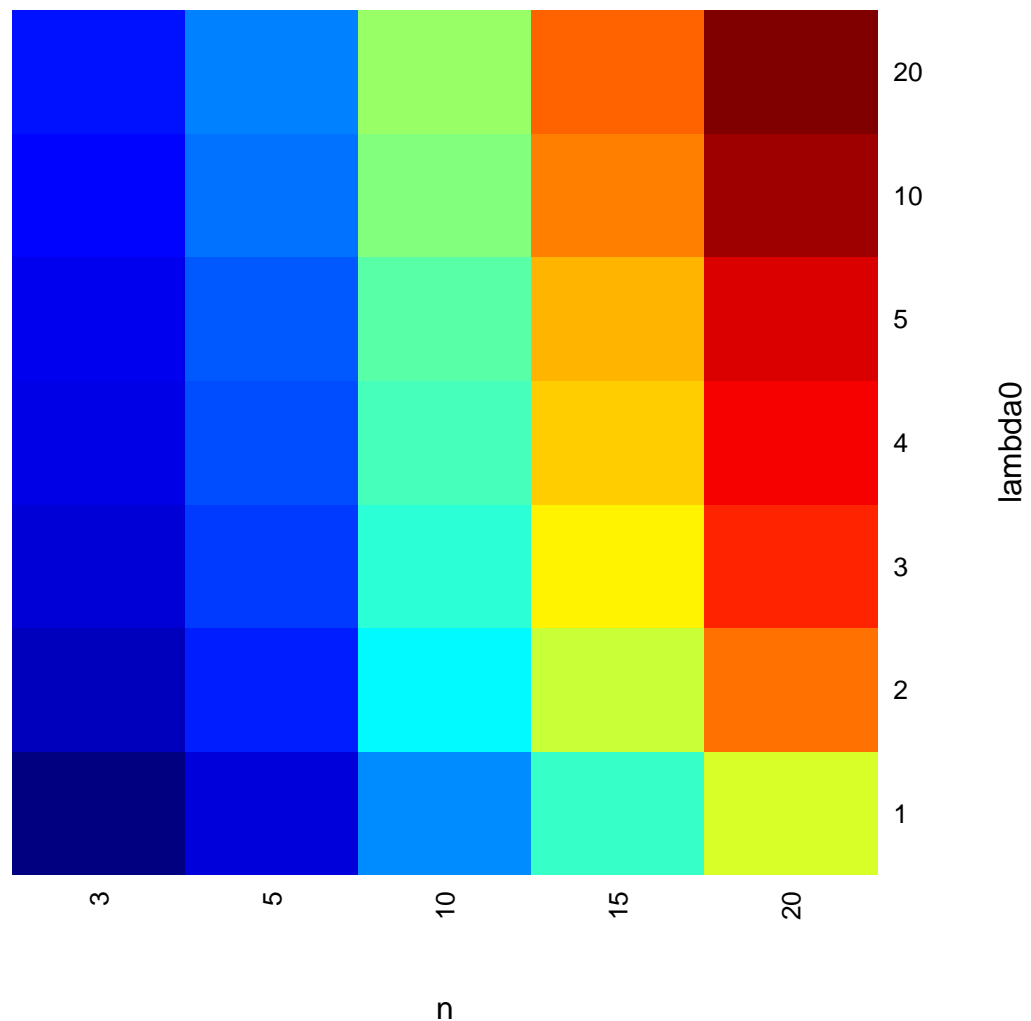

As a result, the estimated power distribution indicates that the number of replications plays a more

significant role in determining the power than the number of read counts.