

Introduction to scPower

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scPower is a R package for design and power analysis of single cell transcriptomics experiments for differential expression and eQTL analysis. A detection of cell-type specific DE and eQTL genes is possible with the help of single cell RNA-seq. It enables the user to calculate the power for a given experimental setup and to choose for a restricted budget the optimal combination of experimental parameters which maximizes the power. Necessary experimental priors, e.g. effect sizes and expression distributions, can be taken from example data sets, saved in the package, or estimated from new data sets.

The tool was evaluated with data from different tissues and single cell technologies, based on UMI counts and read counts.

A detailed description of all methods and citation of all used tools and data sets can be found in the associated paper “Design and power analysis for multi-sample single cell genomics experiments”. An explanation how the plots in the paper were generated can be found in the second vignette “reproduce-paper-plots”.

In the first part of this tutorial, the estimation of power and optimal design with the example priors of `scPower` is shown, in the second part, the fitting of new priors using own data is described. Additionally, in the third part, the power to detect a sufficient number of cells of a specific cell type is explained.

We will show the analysis for an eQTL study, for a DE study it works completely analogously.

```
library(scPower)
library(reshape2)
library(ggplot2)
```

Part 1: Power estimation and experimental design selection with example data sets

In the package, there exist two versions of power estimation, one for droplet based methods using UMI counts, such as 10X Genomics and drop-seq, and one for read based methods, such as Smart-seq2. They differ in the modelling of experimental costs and of multiplet rates (overloading possible for 10X Genomics). Furthermore, the UMI based methods need an additional layer of modelling between reads and UMI counts.

Power estimation

We model the overall detection power as the product of the expression probability of a gene and the eQTL power of a gene. Both are influenced by the three main experimental parameters:

- number of measured samples
- number of measured cells per sample
- read depth

Exemplarily, we want to see the power, which can be reached for a specific combination of the three parameters, when we want to analyze eQTLs in the cell type Monocyte. The experimental parameters are a sample size of 100, 1,500 cells per sample and a read depth to 25,000.

The expected effect sizes and the expression ranks of the eQTL genes have a large influence on the power. To get realistic cell type specific estimates, we use the results of eQTL studies performed with FACS sorted bulk RNA-seq. In this example calculation, a reference study of `scPower` is used, containing data from the Blueprint project, which estimated eQTLs in FACS sorted Monocytes.

Another important influence on the detection power is how many genes are found in the data set in general. Single cell RNA-seq is typically sparser than bulk RNA-seq and a fraction of eQTL genes can be already missed because no counts are detected for them. So in total, the overall detection power depends on the eQTL power and the expression probability of the genes.

For the expression probability, it needs to be defined, how often the target cells appear in the sample, i.e. the cell type frequency, and how the expression distribution of the genes in this cell type looks like. We assume a cell type frequency of 20%. Expression distribution fits from an example PBMC data set are available in the package, including one for “CD14+ Monocytes”, our cell type of interest. The expression distribution fits describe the mean and dispersion parameters of all genes in the cell type. The mean distribution is modelled as a mixed distribution of with a zero component and two left censored gamma components parameterized over the UMI counts, for which the data frame `gamma.mixed.fits` is necessary. The relationship between gene expression means and dispersion is modelled using DESeq fits, an example fit is available in the data frame `disp.fun.param`.

To estimate the mean number of UMI counts for a given read depth, the relationship between read depth and UMI counts is modelled logarithmic. Example fit for different data sets are available in the data frame `read.umi.fit`, we choose here the one called “10X_PBMC_1”, which was generated by fitting data from our

own PBMC study. Additionally, the mapping efficiency of the reads is important, we assume a efficiency of 80%.

The definition of expression can be set user-specific to be above a specific count threshold in a certain fraction of all samples. We will set the definition of an expressed gene to have more than 3 counts in more than 50% of the samples.

The significance threshold used for the power calculation can be set user-specific and different multiple testing adjustments are possible. We recommend ‘FDR’ for DE analyses and ‘Bonferroni’ for eQTL analyses.

In the following, different example scenarios for different single cell technologies are shown.

Case 1: Droplet-based method with flexible overloading For droplet-based methods, the so called overloading is possible. Loading more cells on a lane than recommended increases the multiplet rate, but reduces the cost.

We modelled the multiplet rate linear increasing with the number of cells loaded per lane, using data from the 10X Genomics user guide V3. A doublet gets on average more reads than a singlet, for this, a model of Satija lab is used (<https://satijalab.org/costpercell>). The multiplet factor describes the ratio of reads in multiplets compared to reads in singlets.

In this model, we permit overloading of the lane, setting only the number of samples per lane to a specific number.

```
power<-power.general.withDoublets(nSamples=100,nCells=1500,readDepth=25000,
  ct.freq=0.2,type="eqtl",
  ref.study=scPower::eqtl.ref.study,
  ref.study.name="Blueprint (Monocytes)",
  samplesPerLane=4,
  read.umi.fit = scPower::read.umi.fit[
    read.umi.fit$type=="10X_PBMC_1",],
  gamma.mixed.fits = scPower::gamma.mixed.fits,
  ct="CD14+ Monocytes",
  disp.fun.param=scPower::disp.fun.param,
  mappingEfficiency = 0.8,
  min.UMI.counts = 3,
  perc.indiv.expr = 0.5,
  sign.threshold = 0.05,
  MTmethod="Bonferroni")

#> Loading required package: pwr

print(power)
#>           name powerDetect exp.probs      power sampleSize totalCells
#> 1 Blueprint (Monocytes)  0.2857611 0.5556629 0.3542051      100      1500
#>   usableCells multipletFraction ctCells readDepth readDepthSinglet
#> 1          1431          0.04602    286    25000          24091.28
#>   mappedReadDepth expressedGenes
#> 1          19273.02          8094
```

The output shows an overall detection power for this parameter combination of 35.0%, which is the product of the expression probability of 55.6% and the eQTL power of 63.5%. Of in total 1,500 cells, 1,431 are “usable”, which means that they are singlets (estimating a multiplet fraction of 5%). Of this, 286 cells are estimated to be cells of the correct cell type “CD14+ Monocytes”. The read depth declines with more multiplets, resulting in an average read depth of 24,091 for a singlet and an average mapped read depths of 19,273. 8094 genes are estimated to be expressed, i.e. to have more than 3 counts in more than 50% of the 100 samples.

Case 2: Droplet-based method with restricted overloading We implemented a second variant of the power function, where instead of the number of samples per lane the number of cells per lane is set. This restricts the overloading and gives the possibility to set the multiplet rate. For example, setting the cells per lane to 20,000 results in a multiplet rate of 15%.

```
power<-power.general.restrictedDoublets(nSamples=100,nCells=1500,readDepth=25000,
                                         ct.freq=0.2,type="eqtl",
                                         ref.study=scPower::eqtl.ref.study,
                                         ref.study.name="Blueprint (Monocytes)",
                                         cellsPerLane=20000,
                                         read.umi.fit = scPower::read.umi.fit[
                                           read.umi.fit$type=="10X_PBM1",],
                                         gamma.mixed.fits = scPower::gamma.mixed.fits,
                                         ct="CD14+ Monocytes",
                                         disp.fun.param=scPower::disp.fun.param,
                                         mappingEfficiency = 0.8,
                                         min.UMI.counts = 3,
                                         perc.indiv.expr = 0.5,
                                         sign.threshold = 0.05,
                                         MTmethod="Bonferroni")

print(power)
#>               name powerDetect exp.probs      power sampleSize totalCells
#> 1 Blueprint (Monocytes)  0.2751464 0.534071 0.3446039      100      1500
#>   usableCells multipletFraction ctCells readDepth readDepthSinglet
#> 1         1276          0.149565   255    25000      22272.64
#>   mappedReadDepth expressedGenes
#> 1         17818.11          7774
```

In this case, the power decreases slightly compared to case 1, but the overall experimental cost is lower.

Experimental cost calculation The experimental costs are the sum of the library preparation cost and the sequencing costs. They depend on the three main experimental parameters (sample size, cells per sample and read depth). The library preparation costs for 10X are determined by the cost of a 10X kit, the sequencing cost by the cost of a flow cell and the reads that can be sequenced with a flow cell. Example values are chosen for all three to calculate the experimental costs for case 1 and case 2.

```
costKit<-5600
costFlowCell<-14032
readsPerFlowcell<-4100*10^6

#Experimental cost for case 1
cost<-budgetCalculation(nSamples=100,nCells=1500,readDepth=25000,
                        costKit=costKit,samplesPerLane=4,
                        costFlowCell=costFlowCell,readsPerFlowcell = readsPerFlowcell)
print(paste("Costs for case 1:",round(cost)))
#> [1] "Costs for case 1: 36167"

#Experimental cost for case 2
cost<-budgetCalculation.restrictedDoublets(nSamples=100,nCells=1500,readDepth=25000,
                                           costKit=costKit,cellsPerLane=20000,
                                           costFlowCell=costFlowCell,
                                           readsPerFlowcell = readsPerFlowcell)
print(paste("Costs for case 2:",round(cost)))
```

```
#> [1] "Costs for case 2: 20014"
```

Case 3: Droplet-based method with constant multiplet rate If data is missing to model the overloading of the lane, a constant multiplet rate can be used instead. This is influenced by the parameter `multipletRateGrowth`, which is either “linear” (for a linear increase with cells per lane during overloading) or “constant”. The parameter `multipletRate` will be interpreted correspondingly.

```
power<-power.general.restrictedDoublets(nSamples=100,nCells=1500,readDepth=25000,
                                         ct.freq=0.2,type="eqtl",
                                         ref.study=scPower::eqtl.ref.study,
                                         ref.study.name="Blueprint (Monocytes)",
                                         cellsPerLane=8000,
                                         read.umi.fit = scPower::read.umi.fit[
                                           read.umi.fit$type=="10X_PBMC_1",],
                                         gamma.mixed.fits = scPower::gamma.mixed.fits,
                                         ct="CD14+ Monocytes",
                                         disp.fun.param=scPower::disp.fun.param,
                                         mappingEfficiency = 0.8,
                                         min.UMI.counts = 3,
                                         perc.indiv.expr = 0.5,
                                         multipletRateGrowth = "constant",
                                         multipletRate=0.05,
                                         sign.threshold = 0.05,
                                         MTmethod="Bonferroni")

print(power)
#>               name powerDetect exp.probs      power sampleSize totalCells
#> 1 Blueprint (Monocytes)  0.2854917  0.555008  0.3538619      100      1500
#>   usableCells multipletFraction ctCells readDepth readDepthSinglet
#> 1          1425             0.05    285    25000      24015.37
#>   mappedReadDepth expressedGenes
#> 1          19212.3          8084
```

Case 4: Smart-seq2 Read based technologies, such as Smart-seq2, need to be modelled slightly differently. The fit between reads and UMI is not required, as the gamma mixed curves are directly parameterized over the read depth. Instead, specific gene curve fits with Smart-seq data are used. As an additional prior, the gene length of the eQTL/DE genes is taken here, which can also be gained from the FACS sorted bulk eQTL/DE studies. As example case, a pancreas Smart-seq data set is used here together with a DE study performed in pancreas tissue.

```
power<-power.smartseq(nSamples=100,nCells=1500,readDepth=25000,
                      ct.freq=0.2,type="de",
                      ref.study=scPower::de.ref.study,
                      ref.study.name="Pancreas_alphabeta",
                      gamma.mixed.fits = scPower::gamma.mixed.fits.smart,
                      ct="alpha",
                      disp.linear.fit = scPower::disp.fun.param.smart,
                      mappingEfficiency = 0.8,
                      min.norm.count = 3,
                      perc.indiv.expr = 0.5,
                      sign.threshold = 0.05,
                      MTmethod="FDR")

#> Loading required package: MKmisc
```

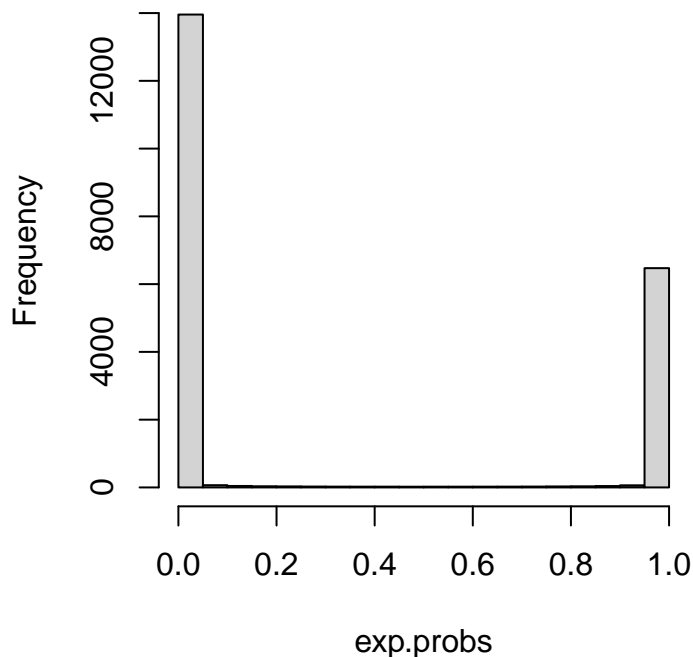
```
print(power)
#>               name powerDetect exp.probs      power sampleSize totalCells
#> 1 Pancreas_alpha 0.5475028 0.547559 0.7024558      100      1500
#>   usableCells multipletFraction ctCells readDepth readDepthSinglet
#> 1      1500              0      300      25000      25000
#>   mappedReadDepth expressedGenes
#> 1      20000      12232
```

Expression probabilities As mentioned before, the detection power is the product of the expression probabilities and the power. The expression probabilities can also be calculated independently, using the function `estimate.exp.prob.param`. However, in this function doublets and cell type frequencies are not taken into account, but instead directly the number of cells per cell type and individual need to be entered.

```
exp.probs<-scPower::estimate.exp.prob.param(nSamples=100,readDepth=25000,nCellsCt=150,
      read.umi.fit = scPower::read.umi.fit[
        read.umi.fit$type=="10X_PBM1",],
      gamma.mixed.fits = scPower::gamma.mixed.fits,
      ct="CD14+ Monocytes",
      disp.fun.param=scPower::disp.fun.param,
      min.counts = 3,
      perc.indiv = 0.5)

hist(exp.probs,main="Histogram of expression probabilities")
```

Histogram of expression probabilities



```
print(paste("Expected number of expressed genes:",round(sum(exp.probs))))
#> [1] "Expected number of expressed genes: 6754"
```

Selection of optimal parameter combination for a restricted budget

scPower gives the user the opportunity to select the best parameter combination for a restricted budget. In the following example, we optimize the experimental design for a budget of 100,000. For two of the three parameters, sample size, cells per individual and read depth, vectors with potential values are required, the third variable is determined uniquely given the other two and the overall budget. Which of the variables is left out, can be freely chosen. In this example we set the number of cells per individual and read depths in the parameters readDepthRange and cellPersRange, and leave out the sample size, which will be determined by the algorithm

To calculate the budget, again costs per 10X kit and flow cells and reads per flow cell need to be defined. The other parameters are the ones that were already necessary for the power calculation in the section before, such as gamma and dispersion fits.

There are two options to speed up power calculation, which make the power calculation itself less accurate, but have only very little effect on the overall detection power, which determines the best parameter calculation. Option 1 is not to use simulated power for eQTL genes with small mean (which is in general recommend as analytic power calculations overestimate eQTL power for small mean values). Option 2 is to not calculate the power for genes with little expression probability at all, as these genes will have an overall detection power close to zero anyway (this option is called speedPowerCalc). In the example below, the calculation is sped up by option 1 (using no simulated power), but not by option 2.

```
opt.design<-optimize.constant.budget(totalBudget=100000,type="eqtl",
                                     ct="CD14+ Monocytes",ct.freq=0.2,
                                     costKit=5600,
                                     costFlowCell=14032,
                                     readsPerFlowcell = 4100*10^6,
                                     ref.study=scPower::eqtl.ref.study,
                                     ref.study.name="Blueprint (Monocytes)",
                                     samplesPerLane=4,
                                     read.umi.fit = scPower::read.umi.fit[
                                       read.umi.fit$type=="10X_PBMC_1",],
                                     gamma.mixed.fits = scPower::gamma.mixed.fits,
                                     disp.fun.param=scPower::disp.fun.param,
                                     nSamplesRange=NULL,
                                     nCellsRange=seq(1000,10000,by=1000),
                                     readDepthRange=seq(10000,50000,by=5000),
                                     mappingEfficiency = 0.8,
                                     sign.threshold = 0.05,
                                     MTmethod="Bonferroni",
                                     useSimulatedPower = FALSE,
                                     speedPowerCalc = FALSE)

#First lines of result data frame
head(opt.design)
#>           name powerDetect exp.probs      power sampleSize totalCells
#> 1 Blueprint (Monocytes)  0.4360902 0.4374897 0.9968654      372      1000
#> 2 Blueprint (Monocytes)  0.5421126 0.5470747 0.9907958      330      2000
#> 3 Blueprint (Monocytes)  0.5873511 0.5991505 0.9800617      296      3000
#> 4 Blueprint (Monocytes)  0.6145879 0.6361099 0.9655698      270      4000
#> 5 Blueprint (Monocytes)  0.6254030 0.6612685 0.9449349      246      5000
#> 6 Blueprint (Monocytes)  0.6257946 0.6787536 0.9204830      226      6000
#>   usableCells multipletFraction ctCells readDepth readDepthSinglet
#> 1          969          0.03068     194     10000          9752.102
#> 2         1877          0.06136     375     10000          9519.911
```

```

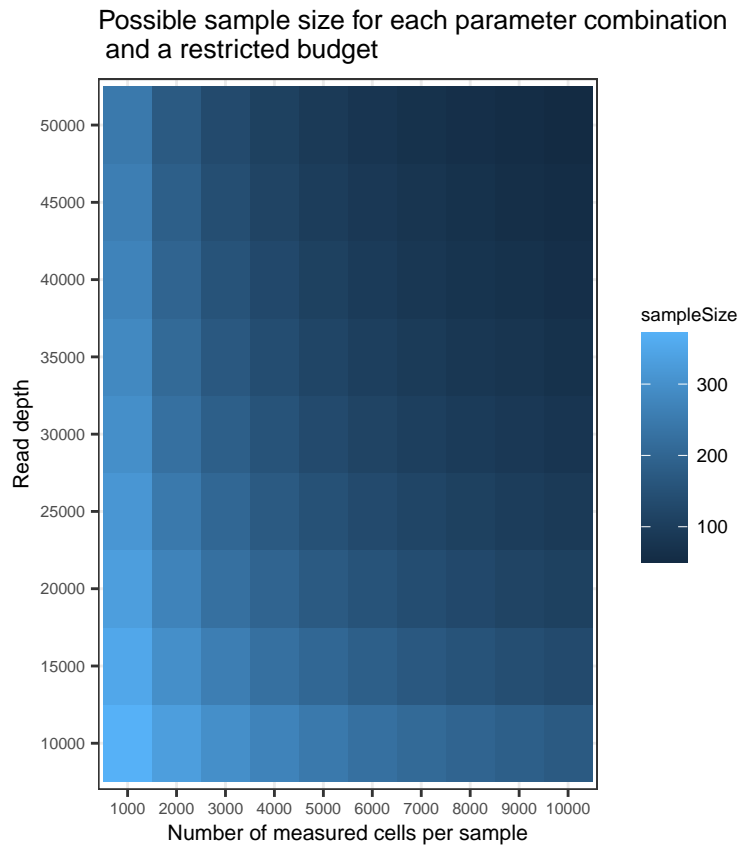
#> 3      2724      0.09204      545      10000      9298.520
#> 4      3509      0.12272      702      10000      9085.499
#> 5      4233      0.15340      847      10000      8882.667
#> 6      4896      0.18408      979      10000      8689.003
#> mappedReadDepth expressedGenes
#> 1      7801.681      6444
#> 2      7615.929      7958
#> 3      7438.816      8749
#> 4      7268.399      9251
#> 5      7106.134      9606
#> 6      6951.203      9867

#Optimal experimental design combination
print(opt.design[which.max(opt.design$powerDetect),])
#>           name powerDetect exp.probs   power sampleSize totalCells
#> 6 Blueprint (Monocytes)  0.6257946 0.6787536 0.920483      226      6000
#> usableCells multipletFraction ctCells readDepth readDepthSinglet
#> 6      4896      0.18408      979      10000      8689.003
#> mappedReadDepth expressedGenes
#> 6      6951.203      9867

#Plot relation between the three parameters
opt.design$totalCells<-as.factor(opt.design$totalCells)
opt.design$readDepth<-as.factor(opt.design$readDepth)
g<-ggplot(opt.design,aes(x=totalCells,y=readDepth,fill=sampleSize))+
  geom_tile()+
  xlab("Number of measured cells per sample")+ylab("Read depth")+
  ggtitle("Possible sample size for each parameter combination \n and a restricted budget")+
  theme_bw()+
  theme(plot.title = element_text(size=10),
        axis.title=element_text(size=8),
        axis.text=element_text(size=6),
        legend.title=element_text(size=7),
        legend.text=element_text(size=7))

print(g)

```

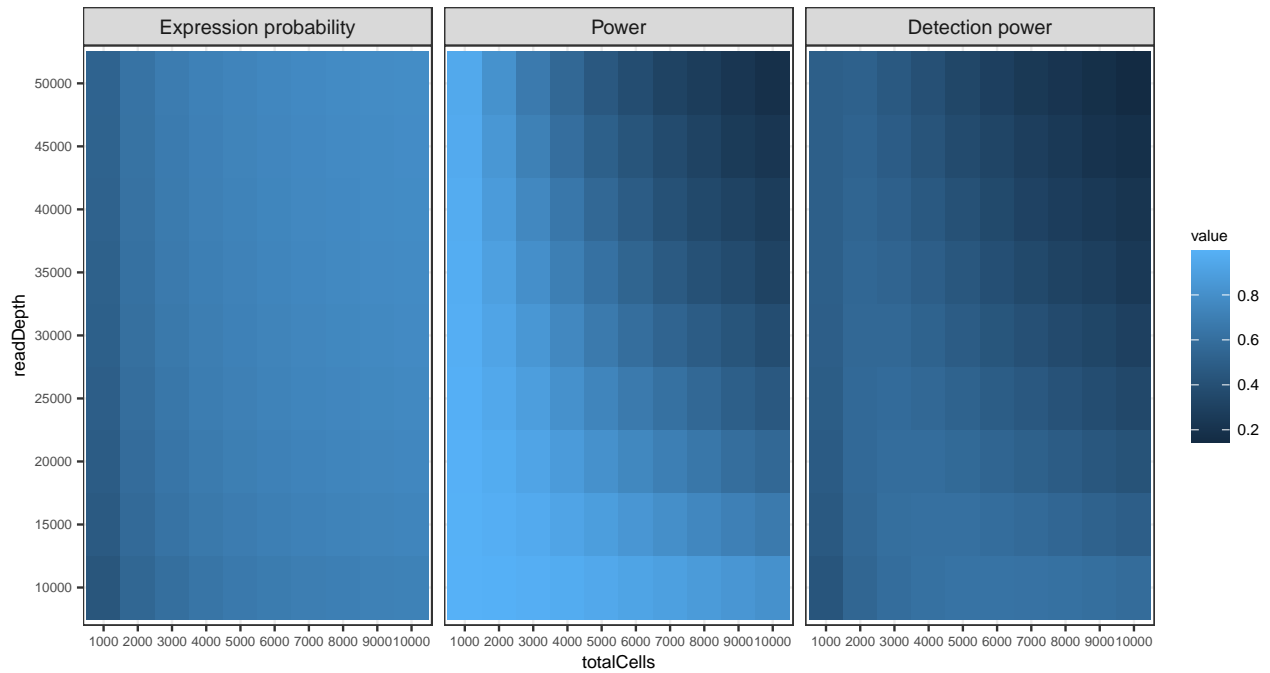
Visualization of all power values as a grid of two variable axes is possible with the function `visualize.power.grid`. It returns a ggplot object, which can further be formatted, as shown below.

```
g<-visualize.power.grid(opt.design,var.axis1 ="totalCells",var.axis2="readDepth")

#Add figure title and change text size
g<-g+ggtitle("Possible power for each parameter combination and a restricted budget")+
  theme(plot.title = element_text(size=10),
        axis.title=element_text(size=8),
        axis.text=element_text(size=6),
        legend.title=element_text(size=7),
        legend.text=element_text(size=7))

print(g)
```

Possible power for each parameter combination and a restricted budget



The function returns for each combination of read depth and cells per individual, how many samples can be measured with the given budget and which detection power can be reached. The combination in the data frame with the maximal detection power is the optimal experimental design.

Instead of the sample size, the flexible parameter can also be the number of cells per individual or the read depth. We set here the sample size to values between 50 and 300 and leave one of the other two parameters out.

```
#Infer cells per sample
opt.design<-optimize.constant.budget(totalBudget=100000,type="eqtl",
  ct="CD14+ Monocytes",ct.freq=0.2,
  costKit=5600,
  costFlowCell=14032,
  readsPerFlowcell = 4100*10^6,
  ref.study=scPower::eqtl.ref.study,
  ref.study.name="Blueprint (Monocytes)",
  samplesPerLane=4,
  read.umi.fit = scPower::read.umi.fit[
    read.umi.fit$type=="10X_PBMC_1",],
  gamma.mixed.fits = scPower::gamma.mixed.fits,
  disp.fun.param=scPower::disp.fun.param,
  nSamplesRange=seq(100,300,by=25),
  nCellsRange=NULL,
  readDepthRange=seq(10000,50000,by=5000),
  mappingEfficiency = 0.8,
  sign.threshold = 0.05,
  MTmethod="Bonferroni",
  useSimulatedPower = FALSE,
  speedPowerCalc = FALSE)

#Optimal experimental design combination
print(opt.design[which.max(opt.design$powerDetect),])
```

```

#>           name powerDetect exp.probs      power sampleSize totalCells
#> 6 Blueprint (Monocytes) 0.6274373 0.681604 0.9189894      225      6168
#>   usableCells multipletFraction ctCells readDepth readDepthSinglet
#> 6          5001          0.1892342    1000    10000      8656.915
#>   mappedReadDepth expressedGenes
#> 6          6925.532          9910

#Infer read depth
opt.design<-optimize.constant.budget(totalBudget=100000,type="eqtl",
                                     ct="CD14+ Monocytes",ct.freq=0.2,
                                     costKit=5600,
                                     costFlowCell=14032,
                                     readsPerFlowcell = 4100*10^6,
                                     ref.study=scPower::eqtl.ref.study,
                                     ref.study.name="Blueprint (Monocytes)",
                                     samplesPerLane=4,
                                     read.umi.fit = scPower::read.umi.fit[
                                       read.umi.fit$type=="10X_PBMC_1",],
                                     gamma.mixed.fits = scPower::gamma.mixed.fits,
                                     disp.fun.param=scPower::disp.fun.param,
                                     nSamplesRange=seq(100,300,by=25),
                                     nCellsRange=seq(1000,10000,by=1000),
                                     readDepthRange=NULL,
                                     mappingEfficiency = 0.8,
                                     sign.threshold = 0.05,
                                     MTmethod="Bonferroni",
                                     useSimulatedPower = FALSE,
                                     speedPowerCalc = FALSE)

#Optimal experimental design combination
print(opt.design[which.max(opt.design$powerDetect),])
#>           name powerDetect exp.probs      power sampleSize totalCells
#> 70 Blueprint (Monocytes) 0.6370081 0.6708074 0.9486616      250      8000
#>   usableCells multipletFraction ctCells readDepth readDepthSinglet
#> 70          6036          0.24544    1207    6087      5066.969
#>   mappedReadDepth expressedGenes
#> 70          4053.575          9744

```

Similar to the power calculation, variants of the function exist to model a restricted number of cells per lane (`optimize.constant.budget.restrictedDoublets`) and to model Smart-seq data (`optimize.constant.budget.smartseq`). Furthermore, there is the option to calculate the library preparation cost per cell instead of per kit (`optimize.constant.budget.libPrepCell`).

Selecting expression thresholds

Both the individual level expression threshold “min.UMI.counts”/“min.counts” and the population level expression threshold “perc.indiv.expr” can be flexibly chosen by the user. As a rule of thumb, lower more lenient thresholds increase the number of expressed genes and so in many cases also the power, while higher more conservative thresholds select more likely only accurately quantified genes and reduce so the number of false positives.

If the users are interested in optimizing the threshold to reach the maximal possible power in their setting, `scPower` provides a function for that called “select.cutoffs”. As a higher number of expressed genes is increasing also the multiple testing burden, thresholds of zero are here necessarily always the optimal choice. The range

of thresholds that should be considered can be specified both for the individual level threshold (`umi_range`) and the population level threshold (`pop_range`). The optimal thresholds in the example below are an UMI threshold of 3 and population threshold of 0.

```
optimal_cutoffs<-select.cutoffs(umi_range=c(0,3,5),
  pop_range=c(0,0.2,0.5),
  nSamples=100,nCells=1500,readDepth=25000,
  ct.freq=0.2,type="eqtl",
  ref.study=scPower::eqtl.ref.study,
  ref.study.name="Blueprint (Monocytes)",
  cellsPerLane=20000,
  read.umi.fit = scPower::read.umi.fit[
    read.umi.fit$type=="10X_PBMC_1",],
  gamma.mixed.fits = scPower::gamma.mixed.fits,
  ct="CD14+ Monocytes",
  disp.fun.param=scPower::disp.fun.param,
  mappingEfficiency = 0.8,
  sign.threshold = 0.05,
  MTmethod="Bonferroni")

optimal_cutoffs
#>               name powerDetect exp.probs      power sampleSize totalCells
#> 1 Blueprint (Monocytes)  0.3300945 0.7996696 0.3316349      100      1500
#>   usableCells multipletFraction ctCells readDepth readDepthSinglet
#> 1          1276          0.149565      255      25000      22272.64
#>   mappedReadDepth expressedGenes umiThreshold popThreshold
#> 1          17818.11          11890           3           0
```

Part 2: Generation of new priors from a data set

Additionally to the priors given by the package, `scPower` offers the option to generate new priors from your own data set. Two types of priors are necessary:

- the cell type specific expression distribution of all genes for the expression probability curves, which can be fitted from single cell RNA-seq data of the same technology (e.g. data from a pilot study). The distribution include the read-UMI fit to estimate the UMI counts per cell, the gamma mixed fits for the mean values of each gene and the mean-dispersion fits for the dispersion values of each gene.
- effect sizes and expression ranks of the DE/eQTL genes, which can be taken from any kind of study or simulated. We recommend studies with FACS sorted bulk RNA-seq to get a realistic cell type specific estimations of the priors.

Generating new cell type specific expression priors (droplet-based methods)

The cell type specific expression priors differ dependent whether they should be used for droplet-based methods or plate-based methods. In the following, the approach for generating priors for droplet-based methods, such as 10X Genomics or Drop-Seq, is explained, the adaptations for plate-based methods are further discussed in the downstream section “Generating new cell type specific expression priors (plate-based methods)”.

A small toy data set with a UMI count matrix is provided in the package to show the fitting of the expression priors for droplet-based methods (sampled from GSE185714). It contains data of one cell type, as each cell type needs to be fitted separately. The data set is a list of four raw count matrices, the first one is the original count matrix and 3 subsampled matrices to evaluate the effect of the read depth. The subsampling was performed on the reads using the tool `fastq-sample` from `fastq-tools` version 0.8 and then the mapping was repeated with `cellranger`.

Additionally, an annotation data frame is necessary, which defines for each cell the cell type and the

donor/sample. This information is typically saved in the meta data of the single cell objects (e.g. for Scanpy or Seurat objects). Importantly, the rows of the annotation data frame must match the columns in the count matrix, including the same ordering of the cells. In this example, the dataset comprises cells from 14 different donors (S1-S14) and one cell type called “default_ct”.

```
#Load example count matrices (list with count matrix and 3 subsampled versions of it)
data(countMatrixExample)

#Dimensions of the three count matrices
sapply(count.matrix.example,dim)
#>      complete subsampled75 subsampled50 subsampled25
#> [1,]      32738          32738          32738          32738
#> [2,]         410           410           410           409

#Load the associated annotation data frame with the necessary meta data columns
#for cell type and donor information
data(annotDfExample)
head(annot.df)
#>      cell cell_type individual
#> 1 AAACGGGCATGGTTGT-1 default_ct      S2
#> 2 AAAGTAGAGTCGTACT-1 default_ct      S13
#> 3 AAAGTAGGTCTTGCGG-1 default_ct      S3
#> 4 AAATGCCGTTCTCCA-1 default_ct      S5
#> 5 AAATGCCCTCGTTACGA-1 default_ct      S4
#> 6 AACACGTAGAAGCCCA-1 default_ct      S5

#Make sure that the annotation data frame is order the same way as the count matrix
all(colnames(count.matrix.example[["complete"]]) == annot.df$cell)
#> [1] TRUE
```

Counting observed expressed genes The number of expressed genes in the data set can be estimated by reformatting the 2d count matrix into a 3d pseudobulk matrix, using the function “create.pseudobulk”. The rows of the annotation data frame must match the columns in the count matrix in this step (same ordering of cells). After the pseudobulk matrix is created, the expressed genes are extracted using the function “calculate.gene.counts”. Here, we use a threshold of more than 3 counts in more 50% of the individuals.

```
expressed.genes.df<-NULL

#Assign rownames to annot dataframe for easier filtering later
rownames(annot.df)<-annot.df$cell

#Iterate over each count matrix
for(name in names(count.matrix.example)){

  count.matrix<-count.matrix.example[[name]]

  #Filter the annotation data frame to be ordered in the same way as the count matrix
  annot.df<-annot.df[colnames(count.matrix),]

  #Reformat count matrix into pseudobulk matrix
  pseudo.bulk<-create.pseudobulk(count.matrix,annot.df,colName="cell_type")
  #Calculate expressed genes in the pseudobulk matrix
  expressed.genes<-calculate.gene.counts(pseudo.bulk,min.counts=3, perc.indiv=0.5)
  #Get the number of expressed genes
```

```

num.expressed.genes<-nrow(expressed.genes)

#Save expressed genes
expressed.genes.df<-rbind(expressed.genes.df,
                           data.frame(matrix=name,
                                       num.cells=ncol(count.matrix),
                                       expressed.genes=num.expressed.genes))
}

print(expressed.genes.df)
#>      matrix num.cells expressed.genes
#> 1   complete      410          2063
#> 2 subsampled75      410          1945
#> 3 subsampled50      410          1753
#> 4 subsampled25      409          1346

```

As expected, the subsampling of the count matrix leads to an reduction of the number of expressed genes.

Estimation of negative binomial paramters for each gene As a first step for fitting the expression distribution, the negative binomial fit for each gene, i.e. the mean and disperion parameter, is estimated with “nbinom.estimation”. The function uses DESeq for library normalization and parameter estimation. For the normalization, the standard normalization of DESeq can be used or a variant of it called poscounts. It can be set in the parameter “sizeFactorMethod” of the function. Default is “standard”, but for very sparse data, “poscounts” might be the better option. For too sparse data, “standard” is not working and will give an error message.

The function returns a list with three elements: the normalized mean values, the dispersion values and the parameters of the mean-dispersion function fitted from DESeq. We will save the mean values and the parameters of the mean-dispersion function for further processing.

```

norm.mean.values<-NULL
disp.param<-NULL
for(name in names(count.matrix.example)){
  temp<-nbinom.estimation(count.matrix.example[[name]])

  #Save the normalized mean values
  norm.mean.values.temp<-temp[[1]]
  norm.mean.values.temp$matrix<-name
  norm.mean.values<-rbind(norm.mean.values,norm.mean.values.temp)

  #Save the parameter of the mean-dispersion function
  disp.param.temp<-temp[[3]]
  disp.param.temp$matrix<-name
  disp.param<-rbind(disp.param,disp.param.temp)
}

#First rows of the data frame with normalized mean values
head(norm.mean.values)
#>      gene      mean  matrix
#> 1 ENSG00000243485 0.00000000 complete
#> 2 ENSG00000237613 0.00000000 complete
#> 3 ENSG00000186092 0.00000000 complete
#> 4 ENSG00000238009 0.00343702 complete
#> 5 ENSG00000239945 0.00000000 complete

```

```
#> 6 ENSG00000237683 0.00323091 complete

#Parameter of the mean - dispersion function
print(disparam)
#>   asymptDisp extraPois      matrix
#> 1 0.07182929 0.1783764    complete
#> 2 0.07198079 0.1753460 subsampled75
#> 3 0.06526182 0.1785742 subsampled50
#> 4 0.05327572 0.1784178 subsampled25
```

Estimation of a gamma mixed distribution over all means A mixed distribution of a zero component and two left zensored gamma components is fitted for each mean value vector (one fit per count matrix). The count matrix contains often a large number of genes with a mean of zero. To reduce the matrix size and facilitate so the fit, the parameter of “num.genes.kept” regulates the number of mean values for the fit (it removes only genes with a mean of zero). The number should however never be smaller than the number of positive means values. As a fraction of the zero values can be expressed genes below the detection threshold of the experiment, the gamma distributions are modelled as left censored. If no censoring point is set in the variable “censoredPoint”, the smallest positive value in the data set is taken as the censoring point. For our models, we use $1/\text{num_cells_celltype}$ as the censoring point.

```
gamma.fits<-NULL
for(name in names(count.matrix.example)){

  #Number of cells per cell type as censoring point
  censoredPoint<- 1 / ncol(count.matrix.example[[name]])

  norm.mean.values.temp<-norm.mean.values[norm.mean.values$matrix==name,]
  gamma.fit.temp<-mixed.gamma.estimation(norm.mean.values.temp$mean,
                                          num.genes.kept = 21000,
                                          censoredPoint = censoredPoint)

  gamma.fit.temp$matrix<-name
  gamma.fits<-rbind(gamma.fits,gamma.fit.temp)
}

#> Warning in em(mean.vals, ncomp = 3, prop = c(zero.prop, 1 - (zero.prop + :
#> Problem in the EM algorithm: likelihood is decreasing!

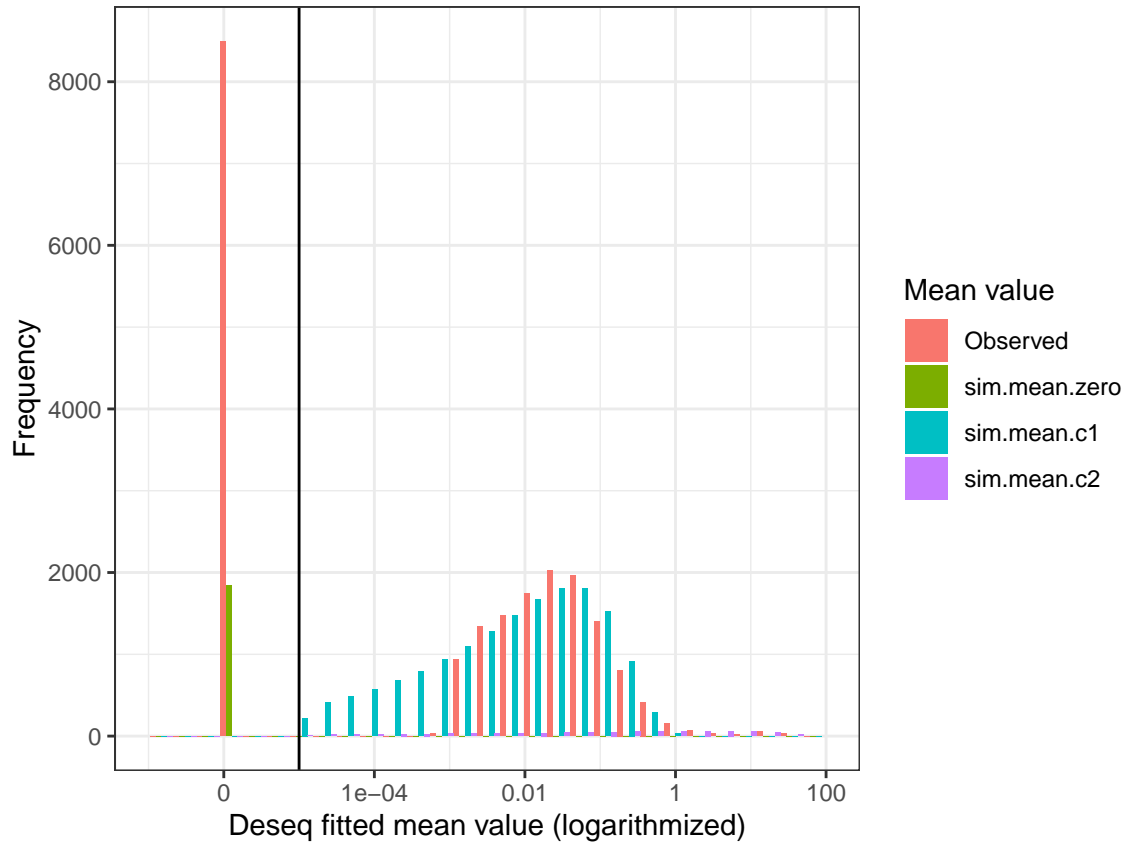
#> Warning in em(mean.vals, ncomp = 3, prop = c(zero.prop, 1 - (zero.prop + :
#> Problem in the EM algorithm: likelihood is decreasing!

print(gamma.fits)
#>           p1      p2      s1      s2      r1      r2
#> shape 0.08758546 0.8613671 0.2287536 0.1121582 5.531980 0.04097829
#> shape1 0.09048839 0.8584937 0.2274075 0.1128169 5.870218 0.04351160
#> shape2 0.09407477 0.8549064 0.2251922 0.1130537 6.510165 0.04830043
#> shape3 0.10216490 0.8468297 0.2223828 0.1121208 8.458974 0.06295549
#>           matrix
#> shape      complete
#> shape1 subsampled75
#> shape2 subsampled50
#> shape3 subsampled25
```

Comparison of gamma mixed fits with original means The fit can be evaluated by simulating mean values using this gamma distribution. This is done here inside the plotting function visualize.gamma.fits. In gen-

eral, the package provides two options for the sampling the values, either random (`sample.mean.values.random`) or using the quantiles of the gamma mixed distribution (`sample.mean.values.quantiles`).

```
g<-visualize.gamma.fits(norm.mean.values$mean[norm.mean.values$matrix=="complete"],
  gamma.fits[gamma.fits$matrix=="complete",],
  nGenes=21000)
print(g)
#> Warning: Removed 5 rows containing missing values (`geom_bar()`).
```



Parameterization of the parameters of the gamma fits by the mean UMI counts per cell The gamma fits over all matrices are parameterized by the mean UMI counts per cell. The mean UMI counts are calculated from the original count matrices using the function “`meanUMI.calculation`”. For the fits, the parameterization of the mixtures need to be converted from rate-shape parameters to mean-standard deviation parameters by “`convert.gamma.parameters`”.

```
#Estimate the mean umi values per cell for each matrix
umi.values<-NULL
for(name in names(count.matrix.example)){
  mean.umi<-meanUMI.calculation(count.matrix.example[[name]])
  umi.values<-rbind(umi.values,data.frame(mean.umi,matrix=name))
}

print(umi.values)
#>   mean.umi      matrix
#> 1 3922.559    complete
#> 2 3707.690 subsampled75
#> 3 3340.644 subsampled50
```

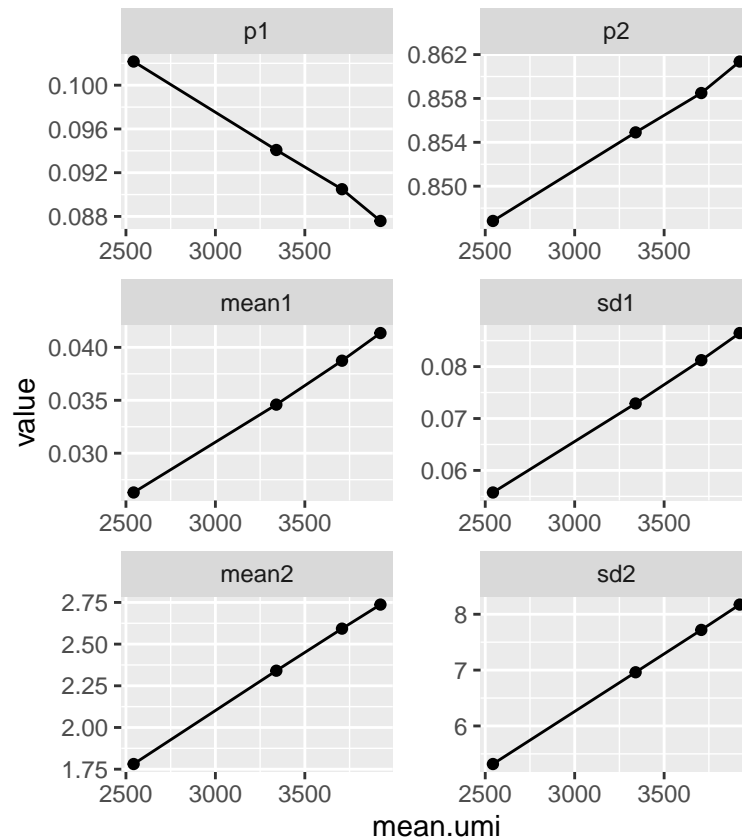


```
#> 4 2543.046 subsampled25

gamma.fits<-merge(gamma.fits,umi.values,by="matrix")

#Convert the gamma fits from the shape-rate parametrization to the mean-sd parametrization
gamma.fits<-convert.gamma.parameters(gamma.fits)

#Visualize the linear relationship between gamma parameters and UMI values in plots
plot.values<-melt(gamma.fits,id.vars=c("matrix","mean.umi"))
plot.values<-plot.values[plot.values$variable %in% c("mean1","mean2","sd1","sd2","p1","p2"),]
ggplot(plot.values,aes(x=mean.umi,y=value))+
  geom_point()+geom_line()+
  facet_wrap(~variable,ncol=2,scales="free")
```



```
#Fit relationship between gamma parameters and UMI values
gamma.linear.fit.new<-umi.gamma.relation(gamma.fits)
print(gamma.linear.fit.new)
#>   parameter    intercept    meanUMI
#> 1      p1 0.1286864527 -1.039166e-05
#> 2    mean1 -0.0014228140 1.085265e-05
#> 3    mean2 0.0174808132 6.942078e-04
#> 4      sd1 -0.0007532525 2.215104e-05
#> 5      sd2 0.0616897948 2.066408e-03
#> 6      p3 0.0510183280 0.000000e+00
```

Estimation of median dispersion function for each cell type For the dispersion parameter, no relation with the UMI counts was found. Therefore, simply the median value over all subsampling runs is taken for each parameter of the mean-dispersion function.

```
disp.fun.general.new<-dispersion.function. estimation(disp.param)
print(disp.fun.general.new)
#>      asymptDisp extraPois
#> 1 0.06854555 0.1783971
```

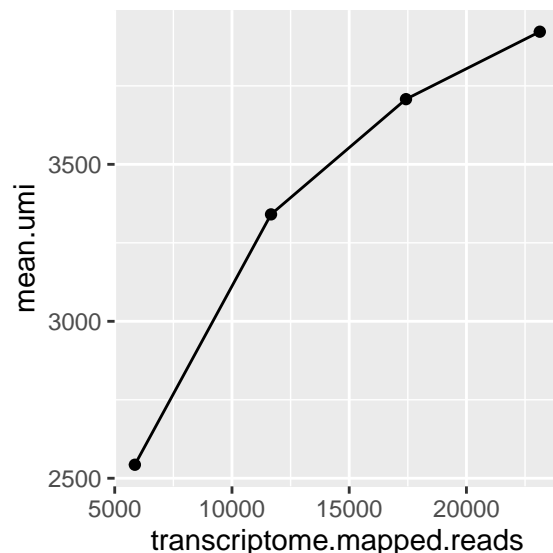
Annotation of cell type for all fitted data frames Multiple fits, e.g. from different cell types or other cell states, can be combined in the gamma fit and dispersion fit data frames. To extract the correct fits for a specific cell type in the power calculation later, an additional column ct is required.

```
gamma.linear.fit.new$ct<-"New_ct"
disp.fun.general.new$ct<-"New_ct"
```

Fitting a functions for UMI counts dependent on read depth As a last point, the relationship between reads and UMIs is fitted logarithmically. Therefore, the number of mapped reads is necessary, which can be gained from summary statistics after the mapping (e.g. in the cellranger summary statistics).

```
#Number of mapped reads taken from cellranger summary statistics
mapped.reads<-data.frame(matrix=c("complete","subsampled75","subsampled50","subsampled25"),
                             transcriptome.mapped.reads=c(23130,17422,11666,5859))

#Plot relationship between mean reads per cell and mean UMI per cell
read.umis<-merge(umi.values,mapped.reads,by="matrix")
print(read.umis)
#>      matrix mean.umi transcriptome.mapped.reads
#> 1 complete 3922.559                23130
#> 2 subsampled25 2543.046                5859
#> 3 subsampled50 3340.644               11666
#> 4 subsampled75 3707.690               17422
ggplot(read.umis,aes(x=transcriptome.mapped.reads,y=mean.umi))+
  geom_point()+geom_line()
```



```
#Fit relationship between mean reads per cell and mean UMI per cell
read.umi.fit.new<-umi.read.relation(read.umis)
```

```
print(read.umi.fit.new)
#>           intercept      reads
#> (Intercept) -6223.204 1014.588
```

Validation of expression probability model In the section “Counting observed expressed genes”, the number of expressed genes in our example count matrices were calculated and saved in the data frame “expressed.genes.df”. To validate our model, we try to predict the same number of expressed genes using our fitted model.

```
#Merge the observed numbers of expressed genes with the read depth
expressed.genes.df<-merge(expressed.genes.df,mapped.reads,
                          by="matrix")

#Choose the same number of donors in the example count matrix
nDonors <- length(unique(annot.df$individual))

#Get the number of cells per cell type and individual
expressed.genes.df$num.cells<-expressed.genes.df$num.cells/nDonors
expressed.genes.df$estimated.genes<-NA
for(i in 1:nrow(expressed.genes.df)){

  #Vector with the expression probability for each gene
  expr.prob<-estimate.exp.param(nSamples=nDonors,
                                readDepth=expressed.genes.df$
                                transcriptome.mapped.reads[i],
                                nCellsCt=expressed.genes.df$num.cells[i],
                                read.umi.fit = read.umi.fit.new,
                                gamma.mixed.fits = gamma.linear.fit.new,
                                ct="New_ct",
                                disp.fun.param=disp.fun.general.new,
                                min.counts = 3,
                                perc.indiv = 0.5)

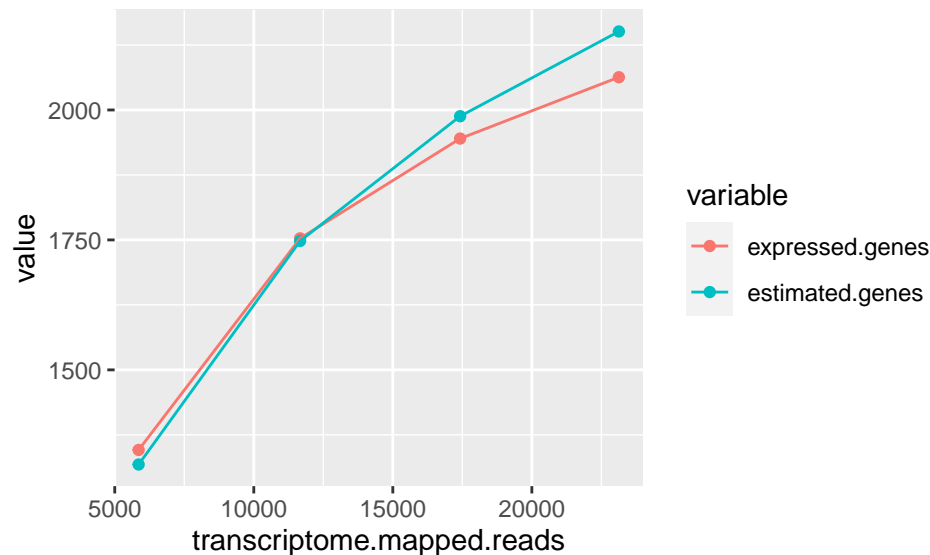
  #Expected number of expressed genes
  expressed.genes.df$estimated.genes[i]<-round(sum(expr.prob))

}

print(expressed.genes.df)
#>           matrix num.cells expressed.genes transcriptome.mapped.reads cells.indiv
#> 1 complete      410      2063      23130      29.28571
#> 2 subsampled25    409      1346      5859      29.21429
#> 3 subsampled50    410      1753     11666      29.28571
#> 4 subsampled75    410      1945     17422      29.28571
#> estimated.genes
#> 1      2151
#> 2      1318
#> 3      1748
#> 4      1988

plot.expressed.genes.df<-reshape2::melt(expressed.genes.df,
                                         id.vars=c("matrix","num.cells","cells.indiv",
                                         "transcriptome.mapped.reads"))
```

```
ggplot(plot.expressed.genes.df, aes(x=transcriptome.mapped.reads, y=value,
                                   color=variable)) +
  geom_point() + geom_line()
```



The estimated numbers of expressed genes match already in the small example data set quite well the observed numbers. A larger data set with more observations improves of course the fit in general. For a proper validation, the fits need to be validated not only on the training data set used for the fits, but also on an independent test data set. This is performed in our publication.

Use of expression probability model for power calculation The fitted values can adapt the power calculation to the specific conditions of the experiment, e.g. a specific cell type of interest. The new data frames are added as parameters instead of the standard example fits of the package. The cell type is set to “New_ct”, as saved in the dispersion and gamma fit data frames above.

```
power<-power.general.restrictedDoublets(nSamples=100,nCells=1500,readDepth=25000,
  ct.freq=0.2,type="eqtl",
  ref.study=scPower::eqtl.ref.study,
  ref.study.name="Blueprint (Monocytes)",
  cellsPerLane=20000,
  read.umi.fit = read.umi.fit.new,
  gamma.mixed.fits = gamma.linear.fit.new,
  ct="New_ct",
  disp.fun.param=disp.fun.general.new,
  mappingEfficiency = 0.8,
  min.UMI.counts = 3,
  perc.indiv.expr = 0.5,
  sign.threshold = 0.05,
  MTmethod="Bonferroni")
```

```
print(power)
```

```
#>           name powerDetect exp.probs      power sampleSize totalCells
#> 1 Blueprint (Monocytes)  0.2627253 0.5105964 0.3353059      100      1500
#>   usableCells multipletFraction ctCells readDepth readDepthSinglet
#> 1          1276          0.149565    255    25000      22272.64
#> mappedReadDepth expressedGenes
```

```
#> 1      17818.11      7455
```

Simplified gamma model without optimizing the read depth

If only the sample size and the number of cells per sample should be evaluated and the same read depth is kept as in the pilot experiment, the power can be calculated directly on the gamma fitted models, without the parameterization for the UMI counts. This has the advantage that no subsampling for different read depths is necessary. The functions `power.sameReadDepth.restrictedDoublets` (for restriction of cells per lane) and `power.sameReadDepth.withDoublets` (for restriction of samples per lane) can be used for this.

```
#Set the cell type specification
gamma.fits$ct<-"New_ct"

power<-power.sameReadDepth.restrictedDoublets(nSamples=100,nCells=1500,
  ct.freq=0.2,type="eqtl",
  ref.study=scPower::eqtl.ref.study,
  ref.study.name="Blueprint (Monocytes)",
  cellsPerLane=20000,
  gamma.parameters = gamma.fits[gamma.fits$matrix=="complete",],
  ct="New_ct",
  disp.fun.param=disp.fun.general.new,
  mappingEfficiency = 0.8,
  min.UMI.counts = 3,
  perc.indiv.expr = 0.5,
  sign.threshold = 0.05,
  MTmethod="Bonferroni")

print(power)
#>               name powerDetect exp.probs      power sampleSize totalCells
#> 1 Blueprint (Monocytes)  0.2702008 0.5246731 0.3418129      100      1500
#>   usableCells multipletFraction ctCells expressedGenes
#> 1      1276      0.149565      255      7645
```

Generating new cell type specific expression priors (plate-based methods)

Power analysis for plate-based methods, such as Smart-seq2, follows a very similar approach, however, a few small adaptations are necessary. As explained already in the section “Case 4: Smart-seq2”, Smart-seq2 data contains read counts instead of UMI counts and reads are obtained from the full length of the transcript, i.e. counts dependent on the gene length. For these reasons, the gamma-mixed distribution is directly parameterized over the read depth, a UMI-read fit is not necessary and the gene length of the eQTL/DE genes is required as an additional parameter for the power calculation.

In the following, the differences are shown based on a small toy data set from Smart-seq2 data (sampled from GSE81547). The dataset comprise a count matrix (read counts instead of UMI counts), an annotation data frame with cell type and donor annotation and additionally a gene length data frame, which shows the gene length for each gene in the count matrix. The length information was obtained from UCSC here (gene annotation GRCh37hg19, exonic regions), but any gene annotation can be used.

```
data(smartseqExample)

#Smart-seq2 read count matrix
dim(counts_smartseq)
#> [1] 22000      83

#Smart-seq2 annotation data frame
```

```

head(annot_smartseq)
#>      cell  cell_type individual
#> 1 GSM2171934 default_ct      S2
#> 2 GSM2171936 default_ct      S1
#> 3 GSM2172062 default_ct      S3
#> 4 GSM2172099 default_ct      S2
#> 5 GSM2172108 default_ct      S2
#> 6 GSM2172131 default_ct      S4

#Cell ordering is identical between count matrix and annotation data frame
all(colnames(counts_smartseq)==annot_smartseq$cell)
#> [1] TRUE

#Gene length data frame
head(gene_length)
#>      gene.symbol geneLength
#> A1BG           A1BG      4027
#> A1BG-AS1      A1BG-AS1    2793
#> A1CF           A1CF      9567
#> A2M            A2M       4653
#> A2ML1          A2ML1     6309
#> A2MP1          A2MP1     1201

#Also the gene ordering is identical between the count matrix and the data frame
all(rownames(counts_smartseq)==gene_length$gene.symbol)
#> [1] TRUE

```

Counting observed expressed genes The number of expressed genes for Smart-seq2 is estimated in a very similar way as for the droplet-based technologies, based on the pseudobulk matrix and two expression thresholds - an expressed gene has a certain number of counts in a certain percentage of individuals. However, as the number of counts per gene depends on the gene length, the first threshold is normalized separately for each gene using its respective length.

```

#Create pseudobulk matrix
pseudo.bulk<-create.pseudobulk(counts_smartseq,annot_smartseq,colName="cell_type")

#Normalize the minimal number of read counts per gene
min_counts<-10
min_counts_norm<-ceiling(min_counts*gene_length$geneLength/1000)

#Calculate the number of expressed genes
expressed.genes<-calculate.gene.counts(pseudo.bulk,
                                       min_counts_norm,perc.indiv=0.5)

nrow(expressed.genes)
#> [1] 8423

```

Fitting the first two steps of the expression prior Similar adaptations are required when fitting the expression priors. The negative binomial fit is done on the raw count matrix, the same way as for the droplet-based methods. However, afterwards the estimated mean values need to be normalized based on the gene length before running the gamma mixed fits. The downstream processing afterwards is again equivalent to the droplet-based methods and not shown in this code (fitting gamma mixed model for different read depth and parameterizing the gamma parameters based on the read depth).

The fitted priors are only suitable for the functions specifically implemented for Smart-seq data, i.e. `power.smartseq`, `optimize.constant.budget.smartseq` and `estimate.exp.prob.count.param` (with the parameter `countMethod="read"`).

```
#Negative binomial curve fitting
fit<-nbinom.estimate(counts_smartseq,sizeFactorMethod="poscounts")
#> Warning: glm.fit: algorithm did not converge
means.deseq<-fit[[1]]
disp.fun<-fit[[3]]

#Normalize the NB means by the gene length
mean.length.norm<-means.deseq$mean/gene_length$geneLength*1000

#Gamma mixed fits
censoredPoint<-1/ncol(counts_smartseq)
gamma.fit<-mixed.gamma.estimate(mean.length.norm,
                                censoredPoint = censoredPoint,
                                return.df=TRUE)
#> Warning in em(mean.vals, ncomp = 3, prop = c(zero.prop, 1 - (zero.prop + :
#> Problem in the EM algorithm: likelihood is decreasing!
gamma.fit
#>
#> shape 0.07892405 0.8649277 0.1993986 0.03624688 0.03374072 0.0004711928
```

Generating new priors for effect sizes and expression ranks

To use other effect size and expression rank priors either data from other DE / eQTL studies or simulated data can be taken.

Priors from DE / eQTL studies Effect sizes from other studies can be taken directly from the summary statistics of the study (FoldChange for DE genes and R^2 value for eQTL genes). A function of `scPower` extracts the gene ranks, if the normalized (!) count matrix is provided and a vector with the names of the significant DE / eQTL genes. To show the function, an example count matrix of `scPower` is processed in the following. For normalization, a simple normalization by counts per cell is done here. Depending on the data, other normalization strategies, e.g. incorporating also the gene length, might be more appropriate.

```
data(countMatrixExample)
#Choose one of the example matrices given by scPower
example.matrix<-count.matrix.example[["complete"]]

#To speed up computation, remove all 0 genes
example.matrix<-example.matrix[rowSums(example.matrix)>0,]

#Normalize by count per cell
example.matrix<-t(t(example.matrix)/colSums(example.matrix))

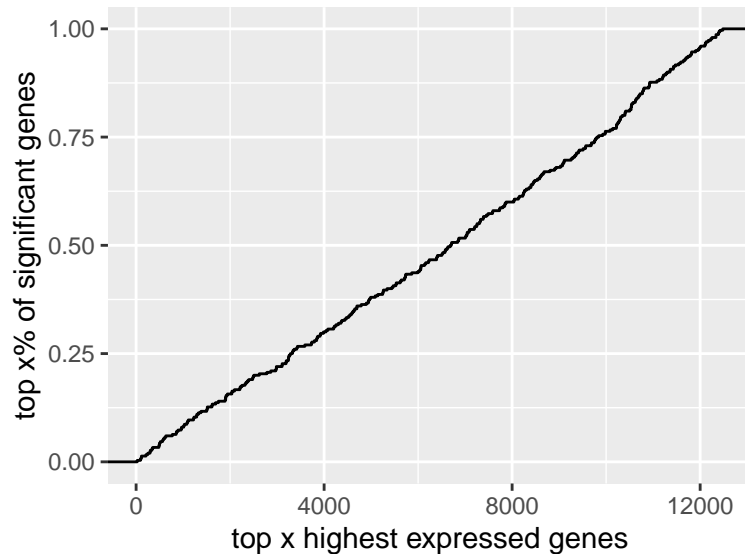
#Randomly select a fraction of the gene to be significant DE genes
sign.genes<-rownames(example.matrix)[1:300]

#Calculate gene ranks
gene.ranks<-gene.rank.calculation(example.matrix,sign.genes)

head(gene.ranks)
#>
gene_symbol cumFraction rank
```

```
#> ENSG00000142676 ENSG00000142676 0.001919232 24
#> ENSG00000116251 ENSG00000116251 0.007357057 92
#> ENSG00000169442 ENSG00000169442 0.008556577 107
#> ENSG00000162511 ENSG00000162511 0.009036385 113
#> ENSG00000142669 ENSG00000142669 0.016873251 211
#> ENSG00000198830 ENSG00000198830 0.019912035 249
```

```
#Plot cumulative density function of significant genes
ggplot(gene.ranks, aes(rank)) + stat_ecdf(geom = "step") +
  xlab("top x highest expressed genes") + ylab("top x% of significant genes")
```



Simulated priors If a data from a suitable study is not available or extreme cases, such as very small or very large effect sizes, shall be tested, the priors can also be simulated using functions of `scPower`. Gene ranks can be either sampled randomly or if an uniform distribution in a certain interval is preferred, generated with the function `uniform.ranks.interval`.

For eQTL genes, the R^2 value are simulated by transformation of Z-Scores using the Fisher Z Transformation. The Z-Scores are sampled from a normal distribution with parameters mean and sd.

```
#Uniform distributed gene ranks for 200 genes in the interval from 5,001-10,000
ranks<-uniform.ranks.interval(start=5001,end=10000,numGenes=200)
#Simulation of fold changes
Rsqr<-effectSize.eQTL.simulation(mean=0.5,sd=0.2,numGenes=200)
#> Loading required package: HardyWeinberg
#> Loading required package: mice
#>
#> Attaching package: 'mice'
#> The following object is masked from 'package:stats':
#>
#> filter
#> The following objects are masked from 'package:base':
#>
#> cbind, rbind
#> Loading required package: Rsolnp
#> Loading required package: nnet
```



```

simulated.eqtl.genes<-data.frame(ranks=ranks,
                                Rsq=Rsq,
                                name="Simulated")

power<-power.general.withDoublets(nSamples=100,nCells=1500,readDepth=25000,
                                ct.freq=0.2,type="eqtl",
                                ref.study=simulated.eqtl.genes,
                                ref.study.name="Simulated",
                                samplesPerLane=4,
                                read.umi.fit = scPower::read.umi.fit[
                                  read.umi.fit$type=="10X_PBMC_1",],
                                gamma.mixed.fits = scPower::gamma.mixed.fits,
                                ct="CD14+ Monocytes",
                                disp.fun.param=scPower::disp.fun.param,
                                mappingEfficiency = 0.8,
                                min.UMI.counts = 3,
                                perc.indiv.expr = 0.5,
                                sign.threshold = 0.05,
                                MTmethod="Bonferroni")

print(power)
#>      name powerDetect exp.probs      power sampleSize totalCells usableCells
#> 1 Simulated  0.5132651  0.62118 0.7580492      100      1500      1431
#>      multipletFraction ctCells readDepth readDepthSinglet mappedReadDepth
#> 1          0.04602      286      25000      24091.28      19273.02
#>      expressedGenes
#> 1          8094

```

For DE genes, the log fold changes are simulated from a normal distribution with parameters mean and sd and transformed to fold changes.

```

#Uniform distributed gene ranks for 200 genes in the interval from 5,001-10,000
ranks<-uniform.ranks.interval(start=5001,end=10000,numGenes=200)
#Simulation of fold changes
foldChange<-effectSize.DE.simulation(mean=2,sd=0.5,numGenes=200)

simulated.de.genes<-data.frame(ranks=ranks,
                                FoldChange=foldChange,
                                name="Simulated")

power<-power.general.withDoublets(nSamples=100,nCells=1500,readDepth=25000,
                                ct.freq=0.2,type="de",
                                ref.study=simulated.de.genes,
                                ref.study.name="Simulated",
                                samplesPerLane=4,
                                read.umi.fit = scPower::read.umi.fit[
                                  read.umi.fit$type=="10X_PBMC_1",],
                                gamma.mixed.fits = scPower::gamma.mixed.fits,
                                ct="CD14+ Monocytes",
                                disp.fun.param=scPower::disp.fun.param,
                                mappingEfficiency = 0.8,
                                min.UMI.counts = 3,
                                perc.indiv.expr = 0.5,
                                sign.threshold = 0.05,

```

```

MTmethod="FDR")

print(power)
#>      name powerDetect exp.probs      power sampleSize totalCells usableCells
#> 1 Simulated  0.6210964  0.62118 0.9957711      100      1500      1431
#>      multipletFraction ctCells readDepth readDepthSinglet mappedReadDepth
#> 1      0.04602      286      25000      24091.28      19273.02
#>      expressedGenes
#> 1      8094

```

Part 3: Power estimation to detect a sufficient number of cells in a specific cell types

To perform the cell type specific DE and eQTL analysis described in part 1 and 2, a sufficient number of cells of the target cell type needs to be detected for each individual. The package provides two functions, either to calculate the power for a specific parameter combination or to calculate the number of cells per sample to reach a certain power. In both cases, important parameters are the cell type frequency of the cell type of interest, which can be gained for example by literature research, here set to 2%. The minimal number of cells which should be detected was set to 10 and the sample size to 100.

In case of the power calculation, we assume to measure 1000 cells per individual. This leads to a detection power of:

```

scPower::power.detect.celltype(nCells=1000,min.num.cells = 10,
                               cell.type.frac=0.02,nSamples=100)
#> [1] 0.6255188

```

In case of estimating the number of cells, we set the detection threshold to 0.95, i.e. the function returns the number of cells to reach a detection power of at least 95%. The required number of cells per person is then:

```

scPower::number.cells.detect.celltype(prob.cut=0.95,min.num.cells = 10,
                                       cell.type.frac=0.02,nSamples=100)
#> [1] 1179

```