

edgeR: differential expression analysis  
of digital gene expression data

User's Guide

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# Chapter 1

## Introduction

### 1.1 Scope

This guide provides an overview of the Bioconductor package **edgeR** for differential expression analyses of read counts arising from RNA-Seq, SAGE or similar technologies [Robinson et al., 2010]. The package can be applied to any technology that produces read counts for genomic features. Of particular interest are summaries of short reads from massively parallel sequencing technologies such as Illumina<sup>TM</sup>, 454 or ABI SOLiD applied to RNA-Seq, SAGE-Seq or ChIP-Seq experiments. **edgeR** provides statistical routines for assessing differential expression in RNA-Seq experiments or differential marking in ChIP-Seq experiments.

The package implements exact statistical methods for multigroup experiments developed by Robinson and Smyth [2007, 2008]. It also implements statistical methods based on generalized linear models (glms), suitable for multifactor experiments of any complexity, developed by McCarthy et al. [2012]. Sometimes we refer to the former exact methods as *classic edgeR*, and the latter as *glm edgeR*. However the two sets of methods are complementary and can often be combined in the course of a data analysis. Most of the glm functions can be identified by the letters “**glm**” as part of the function name.

A particular feature of **edgeR** functionality, both classic and glm, are empirical Bayes methods that permit the estimation of gene-specific biological variation, even for experiments with minimal levels of biological replication.

**edgeR** can be applied to differential expression at the gene, exon, transcript or tag level. In fact, read counts can be summarized by any genomic feature. **edgeR** analyses at the exon level are easily extended to detect differential splicing or isoform-specific differential expression.

This guide begins with brief overview of some of the key capabilities of package, and then gives a number of fully worked case studies, from counts to lists of genes.

## 1.2 Citation

The **edgeR** package implements statistical methods from the following publications. Please try to cite the appropriate articles when you publish results obtained using the software, as such citation is the main means by which the authors receive credit for their work.

Robinson, MD, and Smyth, GK (2008). Small sample estimation of negative binomial dispersion, with applications to SAGE data. *Biostatistics* 9, 321–332.

Proposed the idea of sharing information between genes by estimating the negative binomial variance parameter globally across all genes. This made the use of negative binomial models practical for RNA-Seq and SAGE experiments with small to moderate numbers of replicates. Introduced the terminology *dispersion* for the variance parameter. Proposed conditional maximum likelihood for estimating the dispersion, assuming common dispersion across all genes. Developed an exact test for differential expression appropriate for the negative binomially distributed counts. Despite the official publication date, this was the first of the papers to be submitted and accepted for publication.

Robinson, MD, and Smyth, GK (2007). Moderated statistical tests for assessing differences in tag abundance. *Bioinformatics* 23, 2881–2887.

Introduced empirical Bayes moderated dispersion parameter estimation. This is a crucial improvement on the previous idea of estimating the dispersions from a global model, because it permits gene-specific dispersion estimation to be reliable even for small samples. Gene-specific dispersion estimation is necessary so that genes that behave consistently across replicates should rank more highly than genes that do not.

Robinson, MD, McCarthy, DJ, Smyth, GK (2010). edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. *Bioinformatics* 26, 139–140.

Announcement of the **edgeR** software package. Introduced the terminology *coefficient of biological variation*.

Robinson MD, Oshlack A (2010). A scaling normalization method for differential expression analysis of RNA-seq data. *Genome Biology* 11, R25.

Introduced the idea of model-based scale normalization of RNA-Seq data. Proposed TMM normalization.

McCarthy, DJ, Chen, Y, Smyth, GK (2012). Differential expression analysis of multifactor RNA-Seq experiments with respect to biological variation. *Nucleic Acids Research*. Published online 28 January 2012.

Extended negative binomial differential expression methods to glms, making the methods applicable to general experiments. Introduced the use of Cox-Reid approximate

conditional maximum likelihood for estimating the dispersion parameters, and used this for empirical Bayes moderation. Developed fast algorithms for fitting glms to thousands of genes in parallel. Gives a full explanation of the concept of *biological coefficient of variation*.

## 1.3 How to get help

Most questions about **edgeR** will hopefully be answered by the documentation or references. Every function mentioned in this guide has its own help page. For example, a detailed description of the arguments and output of the **exactTest** function can be read by typing **?exactTest** or **help(exactTest)** at the R prompt.

The authors of the package always appreciate receiving reports of bugs in the package functions or in the documentation. The same goes for well-considered suggestions for improvements. Other questions about how to use **edgeR** are best sent to the Bioconductor mailing list **bioconductor@stat.math.ethz.ch**. Often other users are likely to have experienced similar problems, and posting to the list allows everyone to gain from the answers. To subscribe to the mailing list, see <https://stat.ethz.ch/mailman/listinfo/bioconductor>. Please send requests for general assistance and advice to the mailing list rather than to the individual authors. Users posting to the mailing list for the first time may find it helpful to read the posting guide at <http://www.bioconductor.org/doc/postingGuide.html>.

## 1.4 Quick start

A classic **edgeR** analysis might look like the following. Here we assume there are four RNA-Seq libraries in two groups, and the counts are stored in a tab-delimited text file, with gene symbols in a column called **Symbol**.

```
> x <- read.delim("fileofcounts.txt",row.names="Symbol")
> group <- factor(c(1,1,2,2))
> y <- DGEList(counts=x,group=group)
> y <- estimateCommonDisp(y)
> y <- estimateTagwiseDisp(y)
> et <- exactTest(y)
> topTags(et)
```

A glm **edgeR** analysis of the same data would look similar, except that a design matrix would be formed:

```
> design <- model.matrix(~group)
> y <- estimateGLMTrendedDisp(y,design)
> y <- estimateGLMTagwiseDisp(y,design)
> fit <- glmFit(y,design)
> lrt <- glmLRT(y,fit,coef=2)
> topTags(lrt)
```

Many variants are available on this analysis.



# Chapter 2

## Overview of capabilities

### 2.1 Terminology

edgeR performs differential abundance analysis for pre-defined genomic features. For simplicity, we will henceforth refer to the genomic features as “genes”, although they could in principle be transcripts, exons, general genomic intervals or some other type of feature. For ChIP-seq experiments, abundance might relate to transcription factor binding or to histone mark occupancy, but we will henceforth refer to abundance as in terms of gene expression. In other words, the remainder of this guide will use terminology as for a gene-level analysis of an RNA-seq experiment, although the methodology is more widely applicable than that.

### 2.2 Reading the counts

edgeR works on a table of integer read counts, with rows corresponding to genes and columns to independent libraries. The first step in any analysis will usually be to read these counts into an R session. This is straightforward for anyone experienced with R, but can be a hurdle for first-timers.

If the count data is contained in a single tab-delimited or comma-separated text file with multiple columns, one for each sample, then the simplest method is usually to read the file into R using one of the standard R read functions such as `read.delim`. See the quick start above, or the case study on LNCaP Cells, or the case study on oral carcinomas later in this guide for examples.

If the counts for different samples are stored in separate files, then the files have to be read separately and collated together. The edgeR function `readDGE` is provided to do this. Files need to contain two columns, one for the counts and one for a gene identifier. See the SAGE and deepSAGE case studies for examples of this.

## 2.3 The DGEList data class

`edgeR` stores data in a simple list-based data object called a `DGEList`. This type of object is easy to use because it can be manipulated like any list in R. The function `readDGE` makes a `DGEList` object directly. If the table of counts is already available as a matrix or a `data.frame`, `y` say, then a `DGEList` object can be made by

```
> dge <- DGEList(counts=y)
```

A grouping factor can be added at the same time:

```
> group <- c(1,1,2,2)
> dge <- DGEList(counts=y, group=group)
```

The main components of an `DGEList` object are a matrix `counts` containing the integer counts, a `data.frame` `samples` containing information about the samples or libraries, and an optional `data.frame` `genes` containing annotation for the genes or genomic features. The `data.frame` `samples` contains a column `lib.size` for the library size or sequencing depth for each sample. If not specified by the user, the library sizes will be computed from the column sums of the counts. For classic `edgeR` the `data.frame` `samples` must also contain a column `group`, identifying the group membership of each sample.

## 2.4 Normalization

### 2.4.1 Normalization is only necessary for sample-specific effects

`edgeR` is concerned with differential expression analysis, not with the quantification of expression levels. It is concerned with relative changes in expression levels between conditions, and not with estimating absolute expression levels. This greatly simplifies the technical influences that need to be taken into account, because any technical factor that is unrelated to the experimental conditions will cancel out of any differential expression analysis. For example, read counts can generally be expected to be proportional to gene length as well as to gene expression, but `edgeR` does not generally need to adjust for gene length because gene length has the same relative influence on the read counts for each RNA sample. For this reason, normalization issues arise only to the extent that technical factors have sample-specific effects.

### 2.4.2 Sequencing depth

The most obvious technical factor that affects the read counts, other than gene expression levels, is the sequencing depth of each RNA sample. `edgeR` adjusts any differential expression analysis for varying sequencing depths as represented by differing library sizes. This is part of the basic modeling procedure and flows automatically into fold-change or p-value calculations. It is always present, and doesn't require any user intervention.

### 2.4.3 RNA composition

The second most important technical influence on differential expression is one that is less obvious. RNA-seq provides a measure of the relative abundance of each gene in each RNA sample, but does not provide any measure of the total RNA output on a per-cell basis. This commonly becomes important when a small number of genes are very highly expressed in one sample, but not in another. The highly expressed genes can consume a substantial proportion of the total library size, causing the remaining genes to be under-sampled in that sample. Unless this *RNA composition* effect is adjusted for, the remaining genes may falsely appear to be down-regulated in that sample [Robinson and Oshlack, 2010].

The `calcNormFactors` function normalizes for RNA composition by finding a set of scaling factors for the library sizes that minimize the log-fold changes between the samples for most genes. The default method for computing these scale factors uses a trimmed mean of M-values (TMM) between each pair of samples [Robinson and Oshlack, 2010]. We call the product of the original library size and the scaling factor the *effective library size*. The effective library size replaces the original library size in all downstream analyses.

### 2.4.4 GC content

The GC-content of each gene does not change from sample to sample, so it can be expected to have little effect on differential expression analyses to a first approximation. Recent publications, however, have demonstrated that sample-specific effects for GC-content can be detected [Risso et al., 2011, Hansen et al., 2012]. The EDASeq [Risso et al., 2011] and cqn [Hansen et al., 2012] packages estimate correction factors that adjust for sample-specific GC-content effects in a way that is compatible with `edgeR`. In each case, the observation-specific correction factors can be input into the glm functions of `edgeR` as an *offset* matrix.

### 2.4.5 Gene length

Like GC-content, gene length does not change from sample to sample, so it can be expected to have little effect on differential expression analyses. Nevertheless, sample-specific effects for gene length have been detected [Hansen et al., 2012], although the evidence is not as strong as for GC-content.

### 2.4.6 Model-based normalization, not transformation

In `edgeR`, normalization takes the form of correction factors that enter into the statistical model. Such correction factors are usually computed internally by `edgeR` functions, but it is also possible for a user to supply them. The correction factors may take the form of scaling factors for the library sizes, such as computed by `calcNormFactors`, which are then used to compute the effective library sizes. Alternatively, gene-specific correction factors can be entered into the glm functions of `edgeR` as offsets. In the latter case, the offset matrix will

be assumed to account for all normalization issues, including sequencing depth and RNA composition.

Note that normalization in **edgeR** is model-based, and the original read counts are not themselves transformed. This means that users should not transform the read counts in any way before inputting them to **edgeR**. For example, users should not enter RPKM values to **edgeR** in place of read counts. Such quantities will prevent **edgeR** from correctly estimating the mean-variance relationship in the data, which is a crucial to the statistical strategies underlying **edgeR**. Similarly, **edgeR** is not designed to work with estimated expression levels, for example as might be output by Cufflinks.

## 2.5 Negative binomial models

### 2.5.1 Introduction

The starting point for an RNA-Seq experiment is a set of  $n$  RNA samples, typically associated with a variety of treatment conditions. Each sample is sequenced, short reads are mapped to the appropriate genome, and the number of reads mapped to each genomic feature of interest is recorded. The number of reads from sample  $i$  mapped to gene  $g$  will be denoted  $y_{gi}$ . The set of genewise counts for sample  $i$  makes up the expression profile or *library* for that sample. The expected size of each count is the product of the library size and the relative abundance of that gene in that sample.

### 2.5.2 Biological coefficient of variation (BCV)

RNA-Seq profiles are formed from  $n$  RNA samples. Let  $\pi_{gi}$  be the fraction of all cDNA fragments in the  $i$ th sample that originate from gene  $g$ . Let  $G$  denote the total number of genes, so  $\sum_{g=1}^G \pi_{gi} = 1$  for each sample. Let  $\sqrt{\phi_g}$  denote the coefficient of variation (CV) (standard deviation divided by mean) of  $\pi_{gi}$  between the replicates  $i$ . We denote the total number of mapped reads in library  $i$  by  $N_i$  and the number that map to the  $g$ th gene by  $y_{gi}$ . Then

$$E(y_{gi}) = \mu_{gi} = N_i \pi_{gi}.$$

Assuming that the count  $y_{gi}$  follows a Poisson distribution for repeated sequencing runs of the same RNA sample, a well known formula for the variance of a mixture distribution implies:

$$\text{var}(y_{gi}) = E_{\pi} [\text{var}(y|\pi)] + \text{var}_{\pi} [E(y|\pi)] = \mu_{gi} + \phi_g \mu_{gi}^2.$$

Dividing both sides by  $\mu_{gi}^2$  gives

$$\text{CV}^2(y_{gi}) = 1/\mu_{gi} + \phi_g.$$

The first term  $1/\mu_{gi}$  is the squared CV for the Poisson distribution and the second is the squared CV of the unobserved expression values. The total  $\text{CV}^2$  therefore is the technical

$CV^2$  with which  $\pi_{gi}$  is measured plus the biological  $CV^2$  of the true  $\pi_{gi}$ . In this article, we call  $\phi_g$  the dispersion and  $\sqrt{\phi_g}$  the biological CV although, strictly speaking, it captures all sources of the inter-library variation between replicates, including perhaps contributions from technical causes such as library preparation as well as true biological variation between samples.

Two levels of variation can be distinguished in any RNA-Seq experiment. First, the relative abundance of each gene will vary between RNA samples, due mainly to biological causes. Second, there is measurement error, the uncertainty with which the abundance of each gene in each sample is estimated by the sequencing technology. If aliquots of the same RNA sample are sequenced, then the read counts for a particular gene should vary according to a Poisson law [Marioni et al., 2008]. If sequencing variation is Poisson, then it can be shown that the squared coefficient of variation (CV) of each count between biological replicate libraries is the sum of the squared CVs for technical and biological variation respectively,

$$\text{Total } CV^2 = \text{Technical } CV^2 + \text{Biological } CV^2.$$

Biological CV (BCV) is the coefficient of variation with which the (unknown) true abundance of the gene varies between replicate RNA samples. It represents the CV that would remain between biological replicates if sequencing depth could be increased indefinitely. The technical CV decreases as the size of the counts increases. BCV on the other hand does not. BCV is therefore likely to be the dominant source of uncertainty for high-count genes, so reliable estimation of BCV is crucial for realistic assessment of differential expression in RNA-Seq experiments. If the abundance of each gene varies between replicate RNA samples in such a way that the genewise standard deviations are proportional to the genewise means, a commonly occurring property of measurements on physical quantities, then it is reasonable to suppose that BCV is approximately constant across genes. We allow however for the possibility that BCV might vary between genes and might also show a systematic trend with respect to gene expression or expected count.

The magnitude of BCV is more important than the exact probabilistic law followed by the true gene abundances. For mathematical convenience, we assume that the true gene abundances follow a gamma distributional law between replicate RNA samples. This implies that the read counts follow a negative binomial probability law.

### 2.5.3 Estimating BCVs

When a negative binomial model is fitted, we need to estimate the BCV(s) before we carry out the analysis. The BCV, as shown in the previous section, is the square root of the dispersion parameter under the negative binomial model. Hence, it is equivalent to estimating the dispersion(s) of the negative binomial model.

The parallel nature of sequencing data allows some possibilities for borrowing information from the ensemble of genes which can assist in inference about each gene individually. The easiest way to share information between genes is to assume that all genes have the same

mean-variance relationship, in other words, the dispersion is the same for all the genes [Robinson and Smyth, 2008]. An extension to this “common dispersion” approach is to put a mean-dependent trend on a parameter in the variance function, so that all genes with the same expected count have the same variance [Anders and Huber, 2010].

However, the truth is that the gene expression levels have non-identical and dependent distribution between genes, which makes the above assumptions too naive. A more general approach that allows genewise variance functions with empirical Bayes shrinkage was introduced several years ago [Robinson and Smyth, 2007] and has recently been extended to generalized linear models and thus more complex experimental designs [McCarthy et al., 2012]. Only when using tagwise dispersion will genes that are consistent between replicates be ranked more highly than genes that are not. It has been seen in many RNA-Seq datasets that allowing gene-specific dispersion is necessary in order that differential expression is not driven by outliers. Therefore, the tagwise dispersions are strongly recommended in model fitting and testing for differential expression.

In **edgeR**, we first estimate a common dispersion for all the tags and then apply an empirical Bayes strategy for squeezing the tagwise dispersions towards the common dispersion. The amount of shrinkage is determined by the prior weight given to the common dispersion and the precision of the tagwise estimates. The prior can be thought of arising from a number of prior observations, equivalent to `prior.n` tags with common dispersion and the same number of libraries per tag as in the current experiment. The prior number of tags `prior.n` can be set by the user. The precision of the tagwise estimators is roughly proportional to the per-tag degrees of freedom, equal to the number of libraries minus the number of groups or the number of GLM coefficients. We generally recommend choosing `prior.n` so that the total degrees of freedom (`prior.n*df`) associated with the prior is about 20–30. For example, if there are four libraries and two groups, the tagwise degrees of freedom are 2, so we would recommend `prior.n=10`. This is an empirical rule of thumb borne out of experience with a number of datasets. The default behavior of the **edgeR** is to set the prior degrees of freedom to 20.

## 2.6 Pairwise comparisons between two or more groups (classic)

### 2.6.1 Estimating dispersions

**edgeR** uses the quantile-adjusted conditional maximum likelihood (qCML) method for experiments with single factor.

Compared against several other estimators (e.g. maximum likelihood estimator, Quasi-likelihood estimator etc.) using an extensive simulation study, qCML is the most reliable in terms of bias on a wide range of conditions and specifically performs best in the situation of many small samples with a common dispersion, the model which is applicable to Next-

Gen sequencing data. We have deliberately focused on very small samples due to the fact that DNA sequencing costs prevent large numbers of replicates for SAGE and RNA-seq experiments.

The qCML method calculates the likelihood by conditioning on the total counts for each tag, and uses pseudo counts after adjusting for library sizes. Given a table of counts or a `DGEList` object, the qCML common dispersion can be calculated using the `estimateCommonDisp()` function, and the qCML tagwise dispersions can be calculated using the `estimateTagwiseDisp()` function.

However, the qCML method is only applicable on datasets with a single factor design since it fails to take into account the effects from multiple factors in a more complicated experiment. Therefore, the qCML method (i.e. the `estimateCommonDisp()` and `estimateTagwiseDisp()` function) is recommended for a study with a single factor. When an experiment has more than one factor involved, we need to seek a new way of estimating dispersions.

Here is a simple example of estimating dispersions using the qCML method. Given a `DGEList` object `D`, we estimate the dispersions using the following commands.

To estimate common dispersion:

```
D <- estimateCommonDisp(D)
```

To estimate tagwise dispersions:

```
D <- estimateTagwiseDisp(D)
```

Note that common dispersion needs to be estimated before estimating tagwise dispersions.

For more detailed examples, see the case studies in section 3.1 (Zhang's data), section 3.2 ('t Hoen's data) and section 3.3 (Li's data).

## 2.6.2 Testing for DE genes

For all the Next-Gen sequencing data analyses we consider here, people are most interested in finding differentially expressed genes/tags between two (or more) groups. Once negative binomial models are fitted and dispersion estimates are obtained, we can proceed with testing procedures for determining differential expression using the exact test.

The exact test is based on the qCML methods. Knowing the conditional distribution for the sum of counts in a group, we can compute exact  $p$ -values by summing over all sums of counts that have a probability less than the probability under the null hypothesis of the observed sum of counts. The exact test for the negative binomial distribution has strong parallels with Fisher's exact test.

As we discussed in the previous section, the exact test is only applicable to experiments with a single factor. The testing can be done by using the function `exactTest()`, and the function allows both common dispersion and tagwise dispersion approaches. For example:

```
> et <- exactTest(D)
> topTags(et)
```

For more detailed examples, see the case studies in section 3.1 (Zhang’s data), section 3.2 (’t Hoen’s data) and section 3.3 (Li’s data).

## 2.7 More complex experiments (glm functionality)

### 2.7.1 Generalized linear models

Generalized linear models (GLMs) are an extension of classical linear models to nonnormally distributed response data [Nelder and Wedderburn, 1972, McCullagh and Nelder, 1989]. GLMs specify probability distributions according to their mean-variance relationship, for example the quadratic mean-variance relationship specified above for read counts. Assuming that an estimate is available for  $\phi_g$ , so the variance can be evaluated for any value of  $\mu_{gi}$ , GLM theory can be used to fit a log-linear model

$$\log \mu_{gi} = \mathbf{x}_i^T \boldsymbol{\beta}_g + \log N_i$$

for each gene [Lu et al., 2005, Bullard et al., 2010]. Here  $\mathbf{x}_i$  is a vector of covariates that specifies the treatment conditions applied to RNA sample  $i$ , and  $\boldsymbol{\beta}_g$  is a vector of regression coefficients by which the covariate effects are mediated for gene  $g$ . The quadratic variance function specifies the negative binomial GLM distributional family. The use of the negative binomial distribution is equivalent to treating the  $\pi_{gi}$  as gamma distributed.

### 2.7.2 Estimating dispersions

For general experiments (with multiple factors), **edgeR** uses the Cox-Reid profile-adjusted likelihood (CR) method in estimating dispersions. The CR method is derived to overcome the limitations of the qCML method as mentioned above. It takes care of multiple factors by fitting generalized linear models (GLM) with a design matrix.

The CR method is based on the idea of approximate conditional likelihood which reduces to residual maximum likelihood. Given a table counts or a **DGEList** object and the design matrix of the experiment, generalized linear models are fitted. This allows valid estimation of the dispersion, since all systematic sources of variation are accounted for.

The CR method can be used to calculate a common dispersion for all the tags, trended dispersion depending on the tag abundance, or separate dispersions for individual tags. These can be done by calling the functions **estimateGLMCommonDisp()**, **estimateGLMTrendedDisp()** and **estimateGLMTagwiseDisp()**, and the tagwise dispersion approach is strongly recommended in multi-factor experiment cases.

Here is a simple example of estimating dispersions using the GLM method. Given a **DGEList** object **D** and a design matrix, we estimate the dispersions using the following commands.



To estimate common dispersion:

```
D <- estimateGLMCommonDisp(D, design)
```

To estimate trended dispersions:

```
D <- estimateGLMTrendedDisp(D, design)
```

To estimate tagwise dispersions:

```
D <- estimateGLMTagwiseDisp(D, design)
```

Note that we need to estimate either common dispersion or trended dispersions prior to the estimation of tagwise dispersions. When estimating tagwise dispersions, the empirical Bayes method is applied to squeeze tagwise dispersions towards common dispersion or trended dispersions, whichever exists. If both exist, the default is to use the trended dispersions.

For more detailed examples, see the case study in section 3.4 (Tuch's data).

### 2.7.3 Testing for DE genes

For general experiments, once negative binomial models are fitted and dispersion estimates are obtained, we can proceed with testing procedures for determining differential expression using the generalized linear model (GLM) likelihood ratio test.

The GLM likelihood ratio test is based on the idea of fitting negative binomial GLMs with the Cox-Reid dispersion estimates. By doing this, it automatically takes all known sources of variations into account. Therefore, the GLM likelihood ratio test is recommended for experiments with multiple factors.

The testing can be done by using the functions `glmFit()` and `glmLRT()`. Given raw counts, a fixed value for the dispersion parameter and a design matrix, the function `glmFit()` fits the negative binomial GLM for each tag and produces an object of class `DGEGLM` with some new components.

This `DGEGLM` object can then be passed to the function `glmLRT()` to carry out the likelihood ratio test. User can select one or more coefficients to drop from the full design matrix. This gives the null model against which the full model is compared using the likelihood ratio test. Tags can then be ranked in order of evidence for differential expression, based on the  $p$ -value computed for each tag.

As a brief example, consider a situation in which are three treatment groups, each with two replicates, and the researcher wants to make pairwise comparisons between them. A linear model representing the study design can be fitted to the data with commands such as:

```
> group <- factor(c(1,1,2,2,3,3))
> design <- model.matrix(~group)
> fit <- glmFit(y,design,etc)
```

The fit has three parameters. The first is the baseline level of group 1. The second and third are the 2 vs 1 and 3 vs 1 differences.

To compare 2 vs 1:

```
> lrt.2vs1 <- glmLRT(y,fit,coef=2)
> topTags(lrt.2vs1)
```

To compare 3 vs 1:

```
> lrt.3vs1 <- glmLRT(y,fit,coef=3)
```

To compare 3 vs 2:

```
> lrt.3vs2 <- glmLRT(y,fit,contrast=c(0,-1,1))
```

The contrast argument in this case requests a statistical test of the null hypothesis that coefficient3−coefficient2 is equal to zero.

To find genes different between any of the three groups:

```
> lrt <- glmLRT(y,fit,coef=2:3)
> topTags(lrt)
```

For more detailed examples, see the case study in section 3.4 (Tuch’s data) and 3.5 (arabidopsis RNA-Seq data).

## 2.8 What to do if you have no replicates

edgeR is primarily intended for use with data including biological replication. Nevertheless, RNA-Seq and ChIP-Seq are still expensive technologies, so it sometimes happens that only one library can be created for each treatment condition. In these cases there are no replicate libraries from which to estimate biological variability. In this situation, the data analyst is faced with the following choices, none of which are ideal. We do not recommend any of these choices as a satisfactory alternative for biological replication. Rather, they are the best that can be done at the analysis stage, and options 2–4 may be better than assuming that biological variability is absent.

1. Be satisfied with a descriptive analysis, that might include an MDS plot and an analysis of fold changes. Do not attempt a significance analysis. This may be the best advice.
2. Simply pick a reasonable dispersion value, based on your experience with similar data, and use that. Typical values for datasets arising from well-controlled experiments are `dispersion=0.4` for human data, `dispersion=0.1` for data on genetically identical model organisms or `dispersion=0.01` for technical replicates. Note that the p-values obtained and the number of significant genes will be very sensitive to the dispersion value chosen, and be aware that less well controlled datasets, with unaccounted-for batch effects and so on, could have in reality much larger dispersions than are suggested here. Nevertheless, choosing a nominal dispersion value may be more realistic than ignoring biological variation entirely.

3. Remove one or more explanatory factors from the linear model in order to create some residual degrees of freedom. Ideally, this means removing the factors that are least important but, if there is only one factor and only two groups, this may mean removing the entire design matrix or reducing it to a single column for the intercept. If your experiment has several explanatory factors, you could remove the factor with smallest fold changes. If your experiment has several treatment conditions, you could try treating the two most similar conditions as replicates. Estimate the dispersion from this reduced model, then insert these dispersions into the data object containing the full design matrix, then proceed to model fitting and testing with `glmFit` and `glmLRT`. This approach will only be successful if the number of DE genes is relatively small.

In conjunction with this reduced design matrix, you could try `estimateGLMCommonDisp` with `method="deviance"`, `robust=TRUE` and `subset=NULL`. This is our current best attempt at an automatic method to estimate dispersion without replicates, although it will only give good results when the counts are not too small and the DE genes are a small proportion of the whole. Please understand that this is only our best attempt to return something useable. Reliable estimation of dispersion generally requires replicates.

4. If there exist a sizeable number of control transcripts that should not be DE, then the dispersion could be estimated from them. For example, suppose that `housekeeping` is an index variable identifying housekeeping genes that do not respond to the treatment used in the experiment. First create a copy of the data object with only one treatment group:

```
> d1 <- d
> d1$samples$group <- 1
```

Then estimate the dispersion from the housekeeping genes and all the libraries as one group:

```
> d0 <- estimateCommonDisp(d1[housekeeping,])
```

Then insert this into the full data object and proceed:

```
> d$common.dispersion <- d0$common.dispersion
> et <- exactTest(d)
```

and so on. A reasonably large number of control transcripts is required, at least a few dozen and ideally hundreds.

# Chapter 3

## Case studies

### 3.1 SAGE profiles of normal and tumour tissue

#### 3.1.1 Introduction

This section provides a detailed analysis of data from a SAGE experiment to illustrate the data analysis pipeline for `edgeR`. The data come from a very early study using SAGE technology to analyse gene expression profiles in human cancer cells [Zhang et al., 1997].

Zhang et al. [1997] examined human colorectal and pancreatic cancer tumor tissue. In this case study, we analyse the data comparing primary colon tumor tissue with normal colon epithelial cells. Two tumor and two normal RNA samples were available from different individuals.

#### 3.1.2 Reading the data

The tag counts for the four individual libraries are stored in four separate plain text files obtained from the GEO repository:

```
> dir()
[1] "GSM728.txt" "GSM729.txt" "GSM755.txt" "GSM756.txt" "targets.txt"
```

In each file, the tag IDs and counts for each tag are provided in a table.

The file `targets.txt` gives the filename, the group and a brief description for each sample:

```
> targets <- readTargets()
> targets
      files group      description
1 GSM728.txt  NC      Normal colon
2 GSM729.txt  NC      Normal colon
3 GSM755.txt  Tu Primary colonrectal tumour
4 GSM756.txt  Tu Primary colonrectal tumour
```

This makes a convenient argument to the function `readDGE`, which reads the tables of counts, calculates the sizes of the count libraries and produces a `DGEList` object for use by subsequent functions. The `skip` and `comment.char` arguments are used to ignore comment lines:

```
> d <- readDGE(targets, skip=5, comment.char = "!")
> d$samples
```

	files	group	description	lib.size	norm.factors
1	GSM728.txt	NC	Normal colon	50179	1
2	GSM729.txt	NC	Normal colon	49593	1
3	GSM755.txt	Tu Primary	colonrectal tumour	57686	1
4	GSM756.txt	Tu Primary	colonrectal tumour	49064	1

```
> head(d$counts)
```

	1	2	3	4
CCCATCGTCC	1288	1380	1236	0
CCTCCAGCTA	719	458	148	142
CTAAGACTTC	559	558	248	199
GCCCAGGTCA	520	448	22	62
CACCTAATTG	469	472	763	421
CCTGTAATCC	448	229	459	374

```
> summary(d$counts)
```

	1	2	3	4
Min. :	0	Min. : 0	Min. : 0	Min. : 0
1st Qu.:	0	1st Qu.: 0	1st Qu.: 0	1st Qu.: 0
Median :	0	Median : 0	Median : 0	Median : 0
Mean :	1	Mean : 1	Mean : 1	Mean : 1
3rd Qu.:	1	3rd Qu.: 1	3rd Qu.: 1	3rd Qu.: 1
Max. :	1288	Max. : 1380	Max. : 1236	Max. : 1011

There are 57448 unique tags:

```
> dim(d)
[1] 57448 4
```

### 3.1.3 Filter low expression tags

The number of unique tags is greater than the total number of reads in each library, so the average number of reads per tag per sample is less than one. We will filter out tags with very low counts. We want to keep tags that are expressed in at least one normal or tumor samples. Since there are two replicate samples in each group, we keep tags that are expressed at a reasonable level in at least two samples. Our expression cutoff is 100 counts per million (cpm). For the library sizes here, 100 cpm corresponds to a read count of about 5:

```
> keep <- rowSums(cpm(d)>100) >= 2
> d <- d[keep,]
> dim(d)
```

```
[1] 1233    4
```

This reduces the dataset to around 1200 tags. For the filtered tags, there is very little power to detect differential expression, so little information is lost by filtering.

After filtering, it is a good idea to reset the library sizes:

```
> d$samples$lib.size <- colSums(d$counts)
> d$samples
```

	files	group	description	lib.size	norm.factors
1	GSM728.txt	NC	Normal colon	27012	1
2	GSM729.txt	NC	Normal colon	27735	1
3	GSM755.txt	Tu Primary	colonrectal tumour	28696	1
4	GSM756.txt	Tu Primary	colonrectal tumour	22461	1

### 3.1.4 Normalization

Apply TMM normalization:

```
> d <- calcNormFactors(d)
> d$samples
```

	files	group	description	lib.size	norm.factors
1	GSM728.txt	NC	Normal colon	27012	0.989
2	GSM729.txt	NC	Normal colon	27735	1.005
3	GSM755.txt	Tu Primary	colonrectal tumour	28696	0.906
4	GSM756.txt	Tu Primary	colonrectal tumour	22461	1.110

The normalization factors here are all very close to one, indicating that the four libraries are very similar in composition. Although we do see some differences between the tumour samples, which are noticeably different from one another when compared against the normals, which are very similar to each other.

This `DGEList` is now ready to be passed to the functions that do the calculations to determine differential expression levels for the genes.

### 3.1.5 Estimating the dispersions

The first major step in the analysis of DGE data using the NB model is to estimate the dispersion parameter for each tag, a measure of the degree of inter-library variation for that tag. Estimating the common dispersion gives an idea of overall variability across the genome for this dataset:

```
> d <- estimateCommonDisp(d, verbose=TRUE)
Disp = 0.173 , BCV = 0.416
```

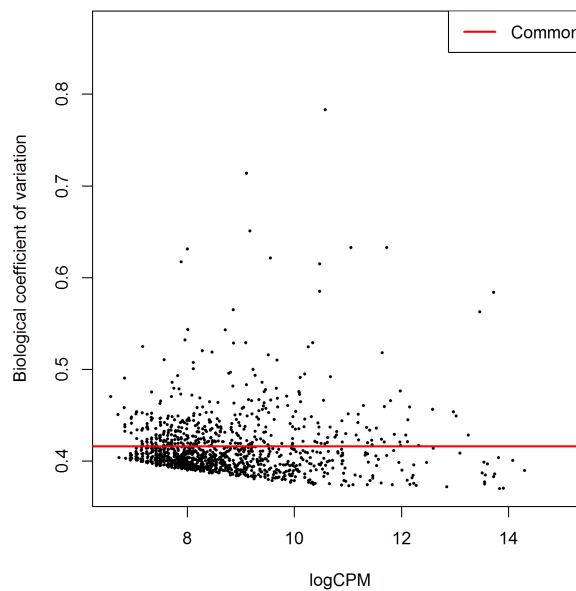
The square root of the common dispersion gives the coefficient of variation of biological variation (BCV). Here the BCV is 41%. This is a relatively large value, but not atypical for observational studies on human tumor tissue where the replicates are independent tumors or individuals.

For routine differential expression analysis, we use empirical Bayes tagwise dispersions. For SAGE data, no abundance-dispersion trend is usually necessary:

```
> d <- estimateTagwiseDisp(d, trend="none")
```

`plotBCV()` plots the tagwise dispersions against log2-CPM:

```
> plotBCV(d, cex=0.4)
```



### 3.1.6 Differential expression

Once the dispersions are estimated, we can proceed with testing procedures for determining differential expression. The function `exactTest` conducts tagwise tests using the exact negative binomial test proposed by Robinson and Smyth [2008]. The test results for the `n` most significant tags are conveniently displayed by the `topTags` function:

```
> et <- exactTest(d)
> topTags(et, n=20)
```

Comparison of groups: Tu-NC

	logFC	logCPM	PValue	FDR
AGCTGTTCCC	12.19	13.46	6.55e-14	8.08e-11
CTTGGGTTTT	8.94	10.19	3.57e-09	2.20e-06

TCACCGGTCA	-4.00	10.88	5.06e-08	2.08e-05
TACAAAATCG	8.19	9.43	8.18e-08	2.15e-05
GTCATCACCA	-7.74	9.00	8.72e-08	2.15e-05
TAATTTTTGC	5.63	9.16	2.71e-07	5.58e-05
TAAATTGCAA	-4.03	10.63	3.40e-07	5.99e-05
GTGCGCTGAG	7.42	8.64	5.25e-07	7.98e-05
GGCTTTAGGG	3.44	12.59	5.82e-07	7.98e-05
ATTTCAAGAT	-5.40	9.05	7.37e-07	9.08e-05
GCCCAGGTCA	-3.42	13.25	1.15e-06	1.19e-04
GTGTGTTTGT	7.31	8.53	1.18e-06	1.19e-04
CGCGTCACTA	4.78	10.09	1.25e-06	1.19e-04
CTTGACATAC	-7.21	8.46	1.44e-06	1.27e-04
GACCAGTGGC	-4.78	9.29	1.57e-06	1.29e-04
CCAGTCCGCC	7.84	9.09	2.22e-06	1.71e-04
GGAAGTGTGA	-3.62	10.76	3.36e-06	2.44e-04
CCTTCAAATC	-5.12	8.77	3.57e-06	2.45e-04
GCAACAACAC	3.81	9.94	3.78e-06	2.45e-04
GATGACCCCC	-3.37	9.84	7.70e-06	4.75e-04

By default, Benjamini and Hochberg's algorithm is used to control the false discovery rate (FDR) [Benjamini and Hochberg, 1995].

The table below shows the counts per million for the tags that **edgeR** has identified as the most differentially expressed. There are pronounced differences between the groups:

```
> detags <- rownames(topTags(et, n=20))
> cpm(d)[detags,]
```

	1	2	3	4
AGCTGTTCCC	0	0.0	4146.9	45011.4
CTTGGGTTTT	0	0.0	731.8	4318.6
TCACCGGTCA	4368	2704.2	209.1	222.6
TACAAAATCG	0	0.0	487.9	2493.2
GTCATCACCA	1296	721.1	0.0	0.0
TAATTTTTGC	0	36.1	1289.4	935.0
TAAATTGCAA	3813	2127.3	104.5	267.1
GTGCGCTGAG	0	0.0	627.3	1024.0
GGCTTTAGGG	777	1298.0	13660.4	8370.1
ATTTCAAGAT	1296	757.2	0.0	44.5
GCCCAGGTCA	19251	16152.9	766.7	2760.3
GTGTGTTTGT	0	0.0	522.7	1024.0
CGCGTCACTA	37	108.2	3066.6	935.0
CTTGACATAC	666	721.1	0.0	0.0
GACCAGTGGC	777	1622.5	0.0	89.0
CCAGTCCGCC	0	0.0	209.1	2181.6
GGAAGTGTGA	3332	3028.7	69.7	489.7
CCTTCAAATC	1074	612.9	0.0	44.5
GCAACAACAC	111	144.2	2265.1	1335.6
GATGACCCCC	1555	1766.7	104.5	222.6

The total number of differentially expressed genes at  $FDR < 0.05$  is:

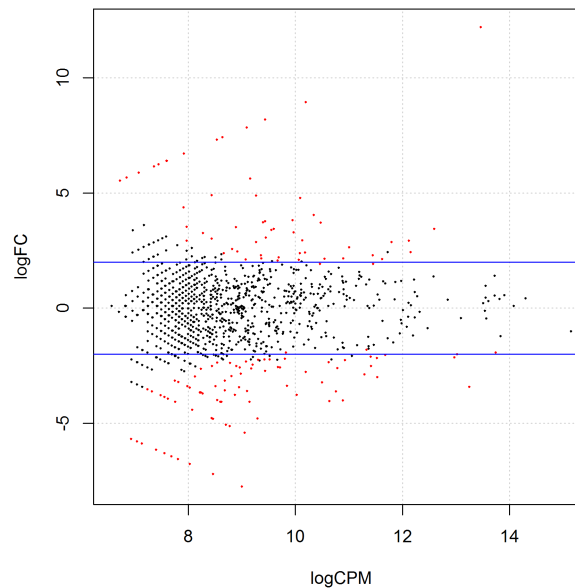


```
> summary(de <- decideTestsDGE(et, p=0.05, adjust="BH"))
      [,1]
-1      87
0    1088
1       58
```

Here the entries for -1, 0 and 1 are for down-regulated, non-differentially expressed and up-regulated tags respectively.

The function `plotSmear` generates a plot of the tagwise log-fold-changes against log-cpm (analogous to an MA-plot for microarray data). DE tags are highlighted on the plot:

```
> detags <- rownames(d)[as.logical(de)]
> plotSmear(et, de.tags=detags)
> abline(h = c(-2, 2), col = "blue")
```



The horizontal blue lines show 4-fold changes.

### 3.1.7 Setup

This analysis was conducted on:

```
> sessionInfo()
R version 2.15.0 (2012-03-30)
Platform: i386-pc-mingw32/i386 (32-bit)

locale:
```

```
[1] LC_COLLATE=English_Australia.1252 LC_CTYPE=English_Australia.1252
[3] LC_MONETARY=English_Australia.1252 LC_NUMERIC=C
[5] LC_TIME=English_Australia.1252
```

attached base packages:

```
[1] stats      graphics  grDevices  utils      datasets  methods   base
```

other attached packages:

```
[1] edgeR_2.7.20 limma_3.13.6
```

loaded via a namespace (and not attached):

```
[1] tools_2.15.0
```

## 3.2 deepSAGE of wild-type vs *Dclk1* transgenic mice

### 3.2.1 Introduction

This section provides a detailed analysis of data from an experiment using deep-sequenced tag-based expression profiling [’t Hoen et al., 2008].

The biological question addressed was the identification of transcripts differentially expressed in the hippocampus between wild-type mice and transgenic mice over-expressing a splice variant of the  $\delta$ C-doublecortin-like kinase-1 (*Dclk1*) gene. The splice variant, DCLK-short, makes the kinase constitutively active and causes subtle behavioural phenotypes.

The tag-based gene expression technology in this experiment could be thought of as a hybrid between SAGE and RNA-seq—like SAGE it uses short sequence tags ( $\sim 17$ bp) to identify transcripts, but it uses the deep sequencing capabilities of the Solexa/Illumina 1G Genome Analyzer greatly to increase the number of tags that can be sequenced.

The RNA samples came from wild-type male C57/BL6j mice and transgenic mice over-expressing DCLK-short with a C57/BL6j background. Tissue samples were collected from four individuals in each of the two groups by dissecting out both hippocampi from each mouse. Total RNA was isolated and extracted from the hippocampus cells and sequence tags were prepared using Illumina’s Digital Gene Expression Tag Profiling Kit according to the manufacturer’s protocol.

Sequencing was done using Solexa/Illumina’s Whole Genome Sequencer. RNA from each biological sample was supplied to an individual lane in one Illumina 1G flowcell. The instrument conducted 18 cycles of base incorporation, then image analysis and basecalling were performed using the Illumina Pipeline. Sorting and counting the unique tags followed, and the raw data (tag sequences and counts) are what we will analyze here. ’t Hoen et al. [2008] went on to annotate the tags by mapping them back to the genome. In general, the mapping of tags is an important and highly non-trivial part of a DGE experiment, but we shall not deal with this task in this case study.

The tag counts for the eight individual libraries are stored in eight separate plain text files:

In each file, the tag IDs and counts for each tag are provided in a table. It is best to create a tab-delimited, plain-text ‘Targets’ file, which, under the headings ‘files’, ‘group’ and ‘description’, gives the filename, the group and a brief description for each sample.

	files	group					
1	GSM272105.txt	DCLK	Dclk1	transgenic	mouse	hippocampus	
2	GSM272106.txt	WT		wild-type	mouse	hippocampus	
3	GSM272318.txt	DCLK	Dclk1	transgenic	mouse	hippocampus	
4	GSM272319.txt	WT		wild-type	mouse	hippocampus	
5	GSM272320.txt	DCLK	Dclk1	transgenic	mouse	hippocampus	
6	GSM272321.txt	WT		wild-type	mouse	hippocampus	
7	GSM272322.txt	DCLK	Dclk1	transgenic	mouse	hippocampus	
8	GSM272323.txt	WT		wild-type	mouse	hippocampus	

```
> d <- readDGE(targets, skip = 5, comment.char = "!")
> colnames(d) <- c("DCLK1", "WT1", "DCLK2", "WT2", "DCLK3", "WT3", "DCLK4", "WT4")
> d$samples
```

	files	group					description	lib.size	norm.factors
DCLK1	GSM272105.txt	DCLK	Dclk1	transgenic	mouse	hippocampus	2685418		1
WT1	GSM272106.txt	WT		wild-type	mouse	hippocampus	3517977		1
DCLK2	GSM272318.txt	DCLK	Dclk1	transgenic	mouse	hippocampus	3202246		1
WT2	GSM272319.txt	WT		wild-type	mouse	hippocampus	3558260		1
DCLK3	GSM272320.txt	DCLK	Dclk1	transgenic	mouse	hippocampus	2460753		1
WT3	GSM272321.txt	WT		wild-type	mouse	hippocampus	294909		1
DCLK4	GSM272322.txt	DCLK	Dclk1	transgenic	mouse	hippocampus	651172		1
WT4	GSM272323.txt	WT		wild-type	mouse	hippocampus	3142280		1

```
> dim(d)
[1] 844316      8
```

### 3.2.3 Filtering

For this dataset there were over 800,000 unique tags sequenced, most of which have a very small number of counts in total across all libraries. We want to keep tags that are expressed in at least one of wild-type or transgenic mice. In either case, the tag should be expressed in at least four libraries. We seek tags that achieve one count per million for at least four libraries:

```
> keep <- rowSums(cpm(d) > 1) >= 4
> d <- d[keep,]
> dim(d)
[1] 44882      8
```

Having filtered, reset the library sizes:

```
> d$samples$lib.size <- colSums(d$counts)
```

### 3.2.4 Normalization

For this SAGE data, composition normalization is not so strongly required as for RNA-Seq data. Nevertheless, we align the upper-quartiles of the counts-per-million between the libraries:

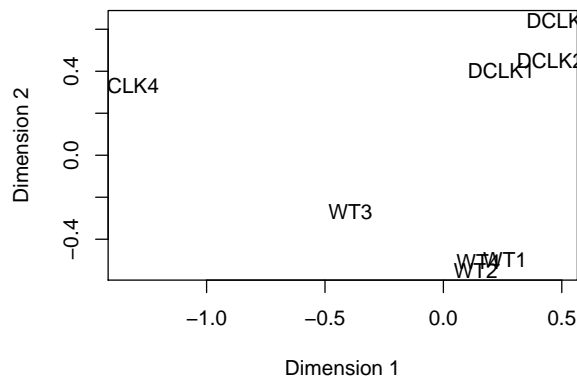
```
> d <- calcNormFactors(d,method="upperquartile")
> d$samples
```

	files	group				description	lib.size	norm.factors
DCLK1	GSM272105.txt	DCLK	Dclk1	transgenic	mouse	hippocampus	2441387	1.033
WT1	GSM272106.txt	WT		wild-type	mouse	hippocampus	3198460	0.979
DCLK2	GSM272318.txt	DCLK	Dclk1	transgenic	mouse	hippocampus	2895690	1.051
WT2	GSM272319.txt	WT		wild-type	mouse	hippocampus	3210704	0.975
DCLK3	GSM272320.txt	DCLK	Dclk1	transgenic	mouse	hippocampus	2225219	1.016
WT3	GSM272321.txt	WT		wild-type	mouse	hippocampus	271817	0.960
DCLK4	GSM272322.txt	DCLK	Dclk1	transgenic	mouse	hippocampus	601062	1.013
WT4	GSM272323.txt	WT		wild-type	mouse	hippocampus	2855960	0.975

### 3.2.5 Data exploration

Before proceeding with the computations for differential expression, it is possible to produce a plot showing the sample relations based on multidimensional scaling:

```
> plotMDS(d)
```



The DCLK and WT samples separate quite nicely.

### 3.2.6 Estimating the dispersion

First we estimate the common dispersion to get an idea of the overall degree of inter-library variability in the data:

```
> d <- estimateCommonDisp(d, verbose=TRUE)
Disp = 0.152 , BCV = 0.39
```

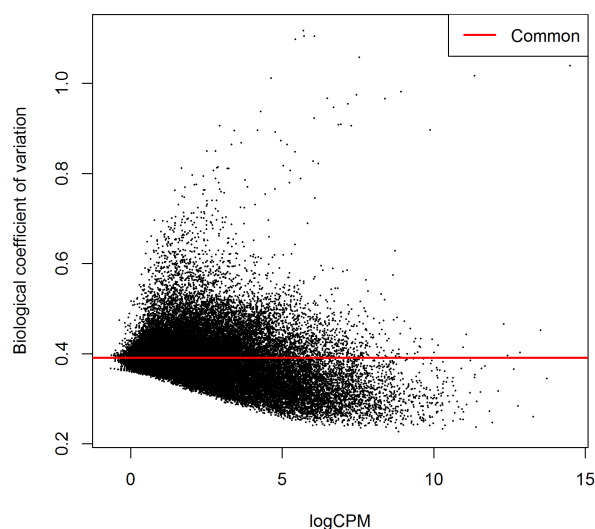
The biological coefficient of variation is the square root of the common dispersion.

Generally it is important to allow tag-specific dispersion estimates, so we go on to compute empirical Bayes moderated tagwise dispersion estimates. The trend is turned off as it is not usually required for SAGE data:

```
> d <- estimateTagwiseDisp(d, trend="none")
```

The following plot displays the estimates:

```
> plotBCV(d)
```



### 3.2.7 Differential expression

Conduct exact conditional tests for differential expression between the mutant and the wild-type:

```
> et <- exactTest(d, pair=c("WT", "DCLK"))
```

Top ten differentially expressed tags:

```
> topTags(et)
```

Comparison of groups: DCLK-WT

	logFC	logCPM	PValue	FDR
TCTGTACGCAGTCAGGC	9.33	5.46	5.52e-19	2.48e-14
CATAAGTCACAGATCG	9.78	3.58	4.50e-18	1.01e-13
CCAAGAATCTGGTCGTA	3.83	3.65	1.85e-14	2.76e-10
ATACTGACATTTCGTAT	-4.40	4.49	1.29e-13	1.21e-09
GCTAATAAATGGCAGAT	3.11	5.92	1.35e-13	1.21e-09
CTGCTAAGCAGAAGCAA	3.34	3.91	1.65e-13	1.24e-09
AAAAGAAATCACAGTTG	9.45	3.17	2.16e-13	1.39e-09
TTCCTGAAAATGTGAAG	3.57	3.92	6.26e-13	3.51e-09
TATTTTGTTTGTGTCGTA	-4.04	4.08	3.00e-12	1.49e-08
CTACTGCAGCATTATCG	2.95	4.06	7.93e-12	3.56e-08

The following table shows the individual counts per million for the top ten tags. `edgeR` chooses tags that both have large fold changes and are consistent between replicates:

```
> detags <- rownames(topTags(et)$table)
> cpm(d)[detags, order(d$samples$group)]
```

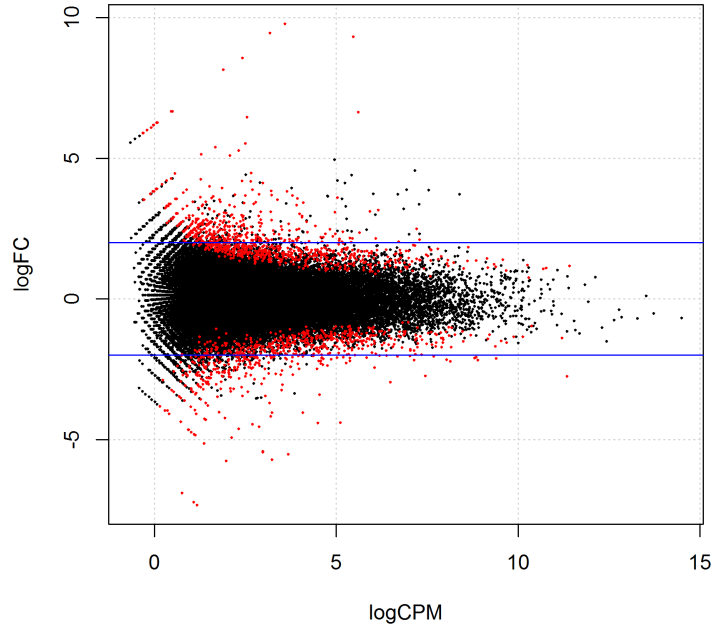
	DCLK1	DCLK2	DCLK3	DCLK4	WT1	WT2	WT3	WT4
TCTGTACGCAGTCAGGC	65.54	34.88	197.73	54.90	0.000	0.311	0.00	0.00
CATAAGTCACAGAGTCG	27.44	26.59	26.06	11.65	0.000	0.000	0.00	0.00
CCAAGAATCTGGTCGTA	28.67	22.79	21.12	21.63	0.938	1.557	0.00	2.45
ATACTGACATTTCGTAT	2.05	1.73	3.60	1.66	35.330	71.012	14.72	36.42
GCTAATAAAATGGCAGAT	158.52	110.85	59.32	118.12	14.069	9.967	3.68	13.31
CTGCTAAGCAGAAGCAA	31.13	30.39	23.37	24.96	2.189	2.180	0.00	3.85
AAAAGAAATCACAGTTG	12.70	31.08	18.87	4.99	0.000	0.000	0.00	0.00
TTCCTGAAAATGTGAAG	30.31	24.17	38.65	16.64	1.876	2.803	0.00	2.45
TATTTTGTGTTTGTGCGTA	4.10	1.73	1.35	0.00	27.513	53.259	14.72	23.46
CTACTGCAGCATTATCG	30.31	33.50	31.46	21.63	3.752	3.426	0.00	4.55

The total number of differentially expressed genes at  $FDR < 0.05$ :

```
> summary(de <- decideTestsDGE(et, p=0.05))
[,1]
-1  679
0 43332
1   871
```

A smearplot displays the log-fold changes with the DE genes highlighted:

```
> detags <- rownames(d)[as.logical(de)]
> plotSmear(et, de.tags=detags)
> abline(h = c(-2, 2), col = "blue")
```



Blue lines indicate 4-fold changes.

### 3.2.8 Setup

This analysis was conducted on:

```
> sessionInfo()
R version 2.15.0 (2012-03-30)
Platform: i386-pc-mingw32/i386 (32-bit)

locale:
[1] LC_COLLATE=English_Australia.1252 LC_CTYPE=English_Australia.1252
[3] LC_MONETARY=English_Australia.1252 LC_NUMERIC=C
[5] LC_TIME=English_Australia.1252

attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods   base

other attached packages:
[1] edgeR_2.7.10 limma_3.13.1

loaded via a namespace (and not attached):
[1] tools_2.15.0
```

## 3.3 Androgen-treated prostate cancer cells (RNA-Seq, two groups)

### 3.3.1 Introduction

This case study considers RNA-Seq data from a treatment vs control experiment with relatively low biological variability.

### 3.3.2 RNA Samples

Genes stimulated by androgens (male hormones) are implicated in the survival of prostate cancer cells and are potential target of anti-cancer treatments. Three replicate RNA samples were collected from prostate cancer cells (LNCaP cell line) after treatment with an androgen hormone (100uM of DHT). Four replicate control samples were also collected from cells treated with an inactive compound [Li et al., 2008].

### 3.3.3 Sequencing

35bp reads were sequenced on an Illumina 1G Genome Analyzer using seven lanes of one flow-cell. FASTA format files are available from <http://yeolab.ucsd.edu/yeolab/Papers.html>.



### 3.3.4 Read mapping

Reads were mapped and summarized at the gene level as previously described by Young et al. [2010]. Reads were mapped to the NCBI36 build of the human genome using Bowtie, allowing up to two mismatches. Reads not mapping uniquely were discarded. The number of reads overlapping the genomic span of each Ensembl gene (version 53) was counted. Reads mapping to introns and non-coding regions were included. The tab-delimited file of read counts can be downloaded as `pnas_expression.txt` from <http://sites.google.com/site/davismcc/useful-documents>.

### 3.3.5 Reading the data

Read the targets file associating treatments with samples:

```
> targets <- readTargets()
> targets
```

	Lane	Treatment	Label
Con1	1	Control	Con1
Con2	2	Control	Con2
Con3	2	Control	Con3
Con4	4	Control	Con4
DHT1	5	DHT	DHT1
DHT2	6	DHT	DHT2
DHT3	8	DHT	DHT3

Read the file of counts:

```
> x <- read.delim("pnas_expression.txt", row.names=1, stringsAsFactors=FALSE)
> head(x)
```

	lane1	lane2	lane3	lane4	lane5	lane6	lane8	len
ENSG00000215696	0	0	0	0	0	0	0	330
ENSG00000215700	0	0	0	0	0	0	0	2370
ENSG00000215699	0	0	0	0	0	0	0	1842
ENSG00000215784	0	0	0	0	0	0	0	2393
ENSG00000212914	0	0	0	0	0	0	0	384
ENSG00000212042	0	0	0	0	0	0	0	92

Put the counts and other information into a `DGEList` object:

```
> y <- DGEList(counts=x[,1:7], group=targets$Treatment, genes=data.frame(length=x[,8]))
> colnames(y) <- targets$Label
> dim(y)
```

[1] 37435 7

### 3.3.6 Filtering

We filter out very lowly expressed tags, keeping genes that are expressed at a reasonable level in at least one treatment condition. Since the smallest group size is three, we keep genes that achieve at least one count per million (cpm) in at least three samples:

```
> keep <- rowSums(cpm(y)) >= 3
> y <- y[keep,]
> dim(y)
[1] 17829      7
```

Re-compute the library sizes:

```
> y$samples$lib.size <- colSums(y$counts)
```

### 3.3.7 Normalizing

Compute effective library sizes using TMM normalization:

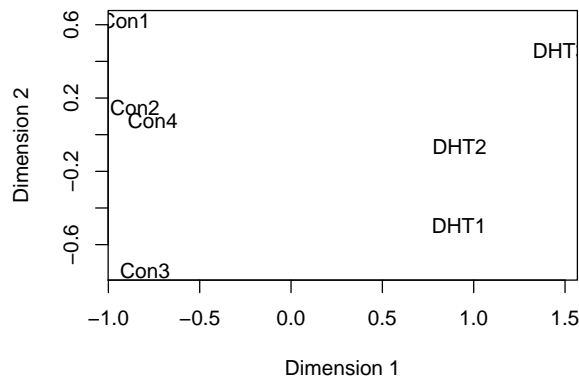
```
> y <- calcNormFactors(y)
> y$samples
```

	group	lib.size	norm.factors
Con1	Control	977853	1.029
Con2	Control	1155906	1.037
Con3	Control	1440803	1.028
Con4	Control	1484150	1.029
DHT1	DHT	1821968	0.942
DHT2	DHT	1832876	0.938
DHT3	DHT	681389	1.003

### 3.3.8 Data exploration

An MDS plots shows distances, in terms of biological coefficient of variation (BCV), between samples:

```
> plotMDS(y)
```



Dimension 1 clearly separates the control from the DHT-treated samples. This shows that the replicates are consistent, and we can expect to find lots of DE genes.

### 3.3.9 Estimating the dispersion

The common dispersion estimates the overall BCV of the dataset, averaged over all genes:

```
> y <- estimateCommonDisp(y, verbose=TRUE)
Disp = 0.0212 , BCV = 0.146
```

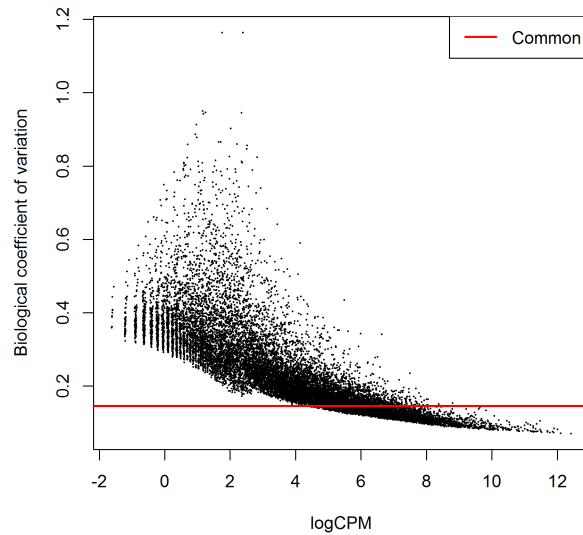
The BCV (square root of the common dispersion) here is 14%, a typical size for a laboratory experiment with a cell line or a model organism.

Now estimate gene-specific dispersions:

```
> y <- estimateTagwiseDisp(y)
```

Plot the estimated dispersions:

```
> plotBCV(y)
```



### 3.3.10 Differential expression

Compute exact genewise tests for differential expression between androgen and control treatments:

```
> et <- exactTest(y)
> top <- topTags(et)
> top
```

Comparison of groups: DHT-Control

	Length	logFC	logCPM	PValue	FDR
ENSG000000151503	5605	5.82	9.70	0.00e+00	0.00e+00
ENSG000000096060	4093	5.00	9.94	0.00e+00	0.00e+00
ENSG000000166451	1556	4.66	8.83	1.21e-244	7.18e-241
ENSG000000162772	1377	3.32	9.73	1.50e-194	6.67e-191
ENSG000000127954	3919	8.17	7.20	4.76e-183	1.70e-179
ENSG000000115648	2920	2.63	11.47	7.73e-167	2.30e-163
ENSG000000130066	868	2.58	9.97	8.06e-154	2.05e-150
ENSG000000113594	10078	4.08	8.03	3.74e-152	8.34e-149
ENSG000000123983	4305	3.59	8.57	1.45e-149	2.87e-146
ENSG000000116133	4286	3.26	8.78	1.76e-141	3.14e-138

Check the individual cpm values for the top genes:

```
> cpm(y)[rownames(top), ]
```

	Con1	Con2	Con3	Con4	DHT1	DHT2	DHT3
ENSG000000151503	35.8	30.3	34.01	39.75	1815	1876	1796
ENSG000000096060	66.5	68.3	72.88	76.14	2182	2033	2129
ENSG000000166451	41.9	45.0	39.56	38.41	960	902	1068
ENSG000000162772	175.9	176.5	173.51	204.83	1631	1784	1632

ENSG00000127954	0.0	0.0	2.08	2.02	333	328	323
ENSG00000115648	961.3	937.8	914.07	906.24	5340	5424	4802
ENSG00000130066	316.0	333.9	344.95	321.40	1755	1804	2016
ENSG00000113594	37.8	31.1	39.56	28.97	514	523	613
ENSG00000123983	63.4	65.7	65.24	72.77	743	686	922
ENSG00000116133	99.2	92.6	106.88	96.35	896	879	815

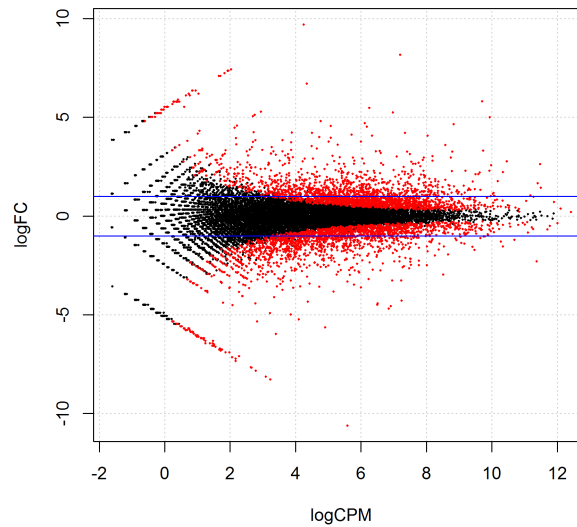
The total number of DE genes at 5% FDR is given by

```
> summary(de <- decideTestsDGE(et))
      [,1]
-1   1983
 0  13722
 1   2124
```

Of the 4373 tags identified as DE, 2085 are up-regulated in DHT-treated cells and 2288 are down-regulated.

Plot the log-fold-changes, highlighting the DE genes:

```
> detags <- rownames(y)[as.logical(de)]
> plotSmear(et, de.tags=detags)
> abline(h=c(-1, 1), col="blue")
```



The blue lines indicate 2-fold changes.

### 3.3.11 Setup

The analysis of this section was conducted with:

```
> sessionInfo()
R version 2.15.0 (2012-03-30)
Platform: i386-pc-mingw32/i386 (32-bit)

locale:
[1] LC_COLLATE=English_Australia.1252 LC_CTYPE=English_Australia.1252
[3] LC_MONETARY=English_Australia.1252 LC_NUMERIC=C
[5] LC_TIME=English_Australia.1252

attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods   base

other attached packages:
[1] edgeR_2.7.10 limma_3.13.4

loaded via a namespace (and not attached):
[1] tools_2.15.0
```

### 3.3.12 Acknowledgements

Thanks to Matthew Young for the file of read counts.

## 3.4 RNA-Seq of oral carcinomas vs matched normal tissue

### 3.4.1 Introduction

This section provides a detailed analysis of data from a paired design RNA-seq experiment, featuring oral squamous cell carcinomas and matched normal tissue from three patients [Tuch et al., 2010]. The aim of the analysis is to detect genes differentially expressed between tumor and normal tissue, adjusting for any differences between the patients. This provides an example of the GLM capabilities of `edgeR`.

RNA was sequenced on an Applied Biosystems SOLiD System 3.0 and reads mapped to the UCSC hg18 reference genome [Tuch et al., 2010]. Read counts, summarised at the level of refSeq transcripts, are available in Table S1 of Tuch et al. [2010].

### 3.4.2 Reading in the data

The read counts for the six individual libraries are stored in one tab-delimited file. To make this file, we downloaded Table S1 from Tuch et al. [2010], deleted some unnecessary columns

and edited the column headings slightly:

```
> rawdata <- read.delim("TableS1.txt", check.names=FALSE, stringsAsFactors=FALSE)
> head(rawdata)
      RefSeqID      Symbol NbrOfExons   8N 8T   33N 33T   51N 51T
1   NM_182502  TMPRSS11B      10 2592   3  7805 321  3372   9
2   NM_003280    TNNC1       6 1684   0  1787   7  4894  559
3   NM_152381    XIRP2      10 9915  15 10396  48 23309 7181
4   NM_022438     MAL       3 2496   2  3585 239  1596   7
5 NM_001100112    MYH2      40 4389   7  7944  16  9262 1818
6   NM_017534    MYH2      40 4402   7  7943  16  9244 1815
```

For easy manipulation, we put the data into a `DGEList` object:

```
> library(edgeR)
> y <- DGEList(counts=rawdata[,4:9], genes=rawdata[,1:3])
```

### 3.4.3 Annotation

The study by Tuch et al. [2010] was undertaken a few years ago, so not all of the RefSeq IDs provided by match RefSeq IDs currently in use. We retain only those transcripts with IDs in the current NCBI annotation, which is provided by the `org.Hs.eg.db` package:

```
> library(org.Hs.eg.db)
> idfound <- y$genes$RefSeqID %in% mappedRkeys(org.Hs.egREFSEQ)
> y <- y[idfound,]
> dim(y)
[1] 15610      6
```

We add Entrez Gene IDs to the annotation:

```
> egREFSEQ <- toTable(org.Hs.egREFSEQ)
> head(egREFSEQ)
  gene_id accession
1      1  NM_130786
2      1  NP_570602
3      2  NM_000014
4      2  NP_000005
5      3  NR_040112
6      9  NM_000662
> m <- match(y$genes$RefSeqID, egREFSEQ$accession)
> y$genes$EntrezGene <- egREFSEQ$gene_id[m]
```

Now use the Entrez Gene IDs to update the gene symbols:

```
> egSYMBOL <- toTable(org.Hs.egSYMBOL)
> head(egSYMBOL)
```

```

      gene_id symbol
1         1   A1BG
2         2   A2M
3         3  A2MP1
4         9   NAT1
5        10   NAT2
6        11  AACP
> m <- match(y$genes$EntrezGene, egSYMBOL$gene_id)
> y$genes$Symbol <- egSYMBOL$symbol[m]
> head(y$genes)
      RefSeqID      Symbol NbrOfExons EntrezGene
1  NM_182502  TMPRSS11B         10    132724
2  NM_003280    TNNC1          6       7134
3  NM_152381    XIRP2         10    129446
4  NM_022438      MAL          3       4118
5 NM_001100112    MYH2         40       4620
6  NM_017534    MYH2         40       4620

```

### 3.4.4 Filtering

Different RefSeq transcripts for the same gene symbol count predominantly the same reads. So we keep one transcript for each gene symbol. We choose the transcript with highest overall count:

```

> o <- order(rowSums(y$counts))
> y <- y[o,]
> d <- duplicated(y$genes$Symbol)
> y <- y[!d,]
> nrow(y)
[1] 10529

```

Normally we would also filter lowly expressed genes. For this data, all transcripts already have at least 50 reads for all samples of at least one of the tissues types.

Recompute the library sizes:

```

> y$samples$lib.size <- colSums(y$counts)

```

Use Entrez Gene IDs as row names:

```

> rownames(y$counts) <- rownames(y$genes) <- y$genes$EntrezGene
> y$genes$EntrezGene <- NULL

```



### 3.4.5 Normalization

TMM normalization is applied to this dataset to account for compositional difference between the libraries.

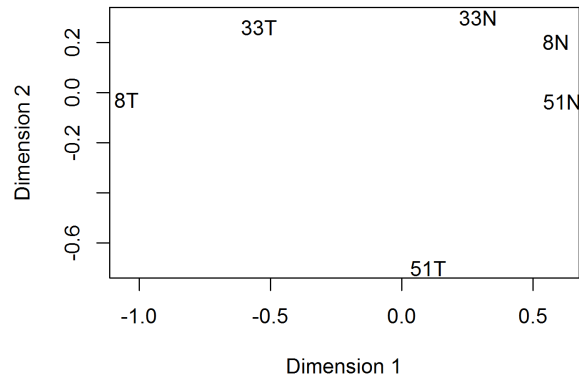
```
> y <- calcNormFactors(y)
> y$samples
```

	group	lib.size	norm.factors
8N	1	7413954	1.155
8T	1	7140100	1.062
33N	1	15308019	0.656
33T	1	13704190	0.948
51N	1	19374726	1.089
51T	1	14430515	1.203

### 3.4.6 Data exploration

The first step of an analysis should be to examine the samples for outliers and for other relationships. The function `plotMDS` produces a plot in which distances between samples correspond to leading biological coefficient of variation (BCV) between those samples:

```
> plotMDS(y)
```



In the plot, dimension 1 separates the tumor from the normal samples, while dimension 2 roughly corresponds to patient number. This confirms the paired nature of the samples. The tumor samples appear more heterogeneous than the normal samples.

### 3.4.7 The design matrix

Before we fit negative binomial GLMs, we need to define our design matrix based on the experimental design. Here we want to test for differential expression between tumour and normal tissues within patients, i.e. adjusting for differences between patients. In statistical terms, this is an additive linear model with patient as the blocking factor:

```
> Patient <- factor(c(8,8,33,33,51,51))
> Tissue <- factor(c("N","T","N","T","N","T"))
> data.frame(Sample=colnames(y),Patient,Tissue)
  Sample Patient Tissue
1     8N        8      N
2     8T        8      T
3    33N       33      N
4    33T       33      T
5    51N       51      N
6    51T       51      T
> design <- model.matrix(~Patient+Tissue)
> rownames(design) <- colnames(y)
```

This sort of additive model is appropriate for paired designs, or experiments with batch effects.

### 3.4.8 Estimating the dispersion

First we estimate the overall dispersion for the dataset, to get an idea of the overall level of biological variability:

```
> y <- estimateGLMCommonDisp(y, design, verbose=TRUE)
Disp = 0.162 , BCV = 0.402
```

The square root of the common dispersion gives the coefficient of variation of biological variation. Here the common dispersion is found to be 0.162, so the coefficient of biological variation is around 0.402.

Then we estimate gene-wise dispersion estimates, allowing a possible trend with average count size:

```
> y <- estimateGLMTrendedDisp(y, design)
> y <- estimateGLMTagwiseDisp(y, design)
```

### 3.4.9 Differential expression

Now proceed to determine differentially expressed genes. Fit genewise glms:

```
> fit <- glmFit(y, design)
```

Conduct likelihood ratio tests for tumour vs normal tissue differences and show the top genes:

```
> lrt <- glmLRT(fit)
> topTags(lrt)
Coefficient: TissueT
```

	RefSeqID	Symbol	NbrOfExons	logFC	logCPM	LR	PValue	FDR
4118	NM_022440	MAL	2	-7.16	6.66	108.9	1.73e-25	1.82e-21
27179	NM_014440	IL36A	4	-6.14	5.48	99.9	1.58e-23	8.32e-20
5737	NM_000959	PTGFR	3	-5.21	4.81	95.9	1.21e-22	4.25e-19
5837	NM_005609	PYGM	20	-5.48	6.07	93.0	5.17e-22	1.36e-18
132724	NM_182502	TPR51B	10	-7.41	7.72	88.7	4.66e-21	9.80e-18
3850	NM_057088	KRT3	9	-5.83	6.57	81.6	1.71e-19	3.00e-16
487	NM_173201	ATP2A1	22	-4.62	6.03	79.4	5.01e-19	7.54e-16
4606	NM_004533	MYBPC2	28	-5.47	6.57	79.1	5.92e-19	7.80e-16
2027	NM_053013	ENO3	12	-5.18	6.39	76.6	2.13e-18	2.49e-15
1160	NM_001099735	CKMT2	10	-5.50	4.77	73.2	1.17e-17	1.23e-14

Note that `glmLRT` has conducted a test for the last coefficient in the linear model, which we can see is the tumor vs normal tissue effect:

```
> colnames(design)
[1] "(Intercept)" "Patient33" "Patient51" "TissueT"
```

The genewise tests are for tumor vs normal differential expression, adjusting for baseline differences between the three patients. (The tests can be viewed as analogous to paired *t*-tests.) The top DE tags have tiny *p*-values and FDR values, as well as large fold changes.

Here's a closer look at the counts-per-million in individual samples for the top genes:

```
> o <- order(lrt$table$PValue)
> cpm(y)[o[1:10],]
```

	8N	8T	33N	33T	51N	51T
4118	279.6	0.14	191.9	7.005	69.7	0.4851
27179	49.5	1.40	119.2	3.284	41.4	0.0693
5737	61.4	0.98	18.5	0.876	89.5	3.1184
5837	188.7	3.08	82.8	1.168	112.1	7.1377
132724	349.6	0.42	509.9	23.423	174.0	0.6237
3850	144.2	0.98	246.5	26.123	45.7	0.3465
487	131.9	3.50	101.4	3.794	116.9	11.1569
4606	130.3	1.54	31.7	0.438	415.2	31.6690
2027	146.3	0.56	84.1	5.400	249.4	15.4534
1160	48.2	0.14	23.9	0.511	85.9	6.7219

We see that all the top genes have consistent tumour vs normal changes for the three patients.

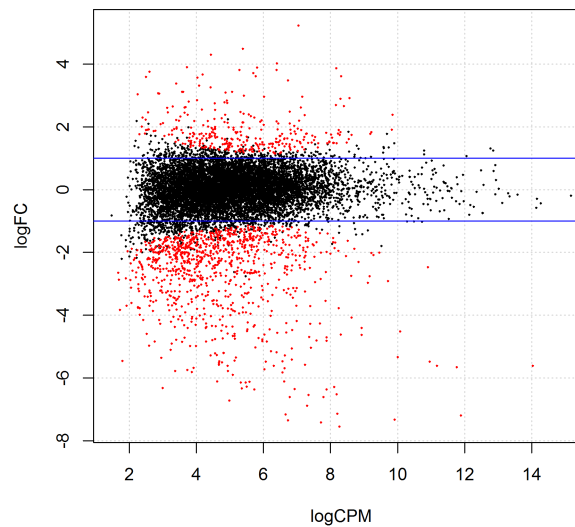
The total number of differentially expressed genes at 5% FDR is given by:

```
> summary(de <- decideTestsDGE(lrt))
```

```
[,1]
-1  978
0   9242
1    309
```

Plot log-fold change against log-counts per million, with DE genes highlighted:

```
> detags <- rownames(y)[as.logical(de)]
> plotSmear(lrt, de.tags=detags)
> abline(h=c(-1, 1), col="blue")
```



The blue lines indicate 2-fold changes.

### 3.4.10 Setup

This analysis was conducted on:

```
> sessionInfo()
R version 2.15.0 (2012-03-30)
Platform: i386-pc-mingw32/i386 (32-bit)

locale:
[1] LC_COLLATE=English_Australia.1252 LC_CTYPE=English_Australia.1252
[3] LC_MONETARY=English_Australia.1252 LC_NUMERIC=C
[5] LC_TIME=English_Australia.1252

attached base packages:
[1] splines      stats      graphics  grDevices  utils      datasets  methods
[8] base
```

```
other attached packages:
[1] org.Hs.eg.db_2.7.1   RSQLite_0.11.1      DBI_0.2-5
[4] AnnotationDbi_1.18.0 Biobase_2.16.0      BiocGenerics_0.2.0
[7] edgeR_2.7.27         limma_3.13.6
```

```
loaded via a namespace (and not attached):
[1] IRanges_1.14.3 stats4_2.15.0 tools_2.15.0
```

## 3.5 RNA-Seq of pathogen inoculated Arabidopsis with batch effects

### 3.5.1 Introduction

This case study re-analyses *Arabidopsis thaliana* RNA-Seq data described by Cumbie et al. [2011]. Summarized count data is available as a data object in the CRAN package `NBPSeq` comparing  $\Delta$ hrcC challenged and mock-inoculated samples [Cumbie et al., 2011]. Samples were collected in three batches, and adjustment for batch effects proves to be important. The aim of the analysis therefore is to detect genes differentially expressed in response to  $\Delta$ hrcC challenge, while correcting for any differences between the batches.

### 3.5.2 RNA samples

*Pseudomonas syringae* is a bacterium often used to study plant reactions to pathogens. In this experiment, six-week old *Arabidopsis* plants were inoculated with the  $\Delta$ hrcC mutant of *P. syringae*, after which total RNA was extracted from leaves. Control plants were inoculated with a mock pathogen.

Three biological replicates of the experiment were conducted at separate times and using independently grown plants and bacteria.

### 3.5.3 Sequencing

The six RNA samples were sequenced one per lane on an Illumina Genome Analyzer. Reads were aligned and summarized per gene using GENE-counter. The reference genome was derived from the TAIR9 genome release ([www.arabidopsis.org](http://www.arabidopsis.org)).

### 3.5.4 Filtering and normalization

Load the data from the `NBPSeq` package:

```

> library(NBPSeg)
> library(edgeR)
> data(arab)
> head(arab)
      mock1 mock2 mock3 hrcc1 hrcc2 hrcc3
AT1G01010   35   77   40   46   64   60
AT1G01020   43   45   32   43   39   49
AT1G01030   16   24   26   27   35   20
AT1G01040   72   43   64   66   25   90
AT1G01050   49   78   90   67   45   60
AT1G01060    0   15    2    0   21    8

```

There are two experimental factors, treatment (hrcc vs mock) and the time that each replicate was conducted:

```

> Treat <- factor(substring(colnames(arab),1,4))
> Treat <- relevel(Treat, ref="mock")
> Time <- factor(substring(colnames(arab),5,5))

```

There is no purpose in analysing genes that are not expressed in either experimental condition. We consider a gene to be expressed at a reasonable level in a sample if it has at least two counts for each million mapped reads in that sample. This cutoff is ad hoc, but serves to require at least 4–6 reads in this case. Since this experiment has three replicates for each condition, a gene should be expressed in at least three samples if it responds to at least one condition. Hence we keep genes with at least two counts per million (CPM) in at least three samples:

```

> keep <- rowSums(cpm(arab)>2) >= 3
> arab <- arab[keep, ]
> table(keep)
keep
FALSE  TRUE
 9696 16526

```

Note that the filtering does not use knowledge of what treatment corresponds to each sample, so the filtering does not bias the subsequent differential expression analysis.

Create a DGEList and apply TMM normalization:

```

> y <- DGEList(counts=arab,group=Treat)
> y <- calcNormFactors(y)
> y$samples
      group lib.size norm.factors
mock1  mock 1896802      0.979
mock2  mock 1898690      1.054
mock3  mock 3249396      0.903
hrcc1  hrcc 2119367      1.051
hrcc2  hrcc 1264927      1.096
hrcc3  hrcc 3516253      0.932

```

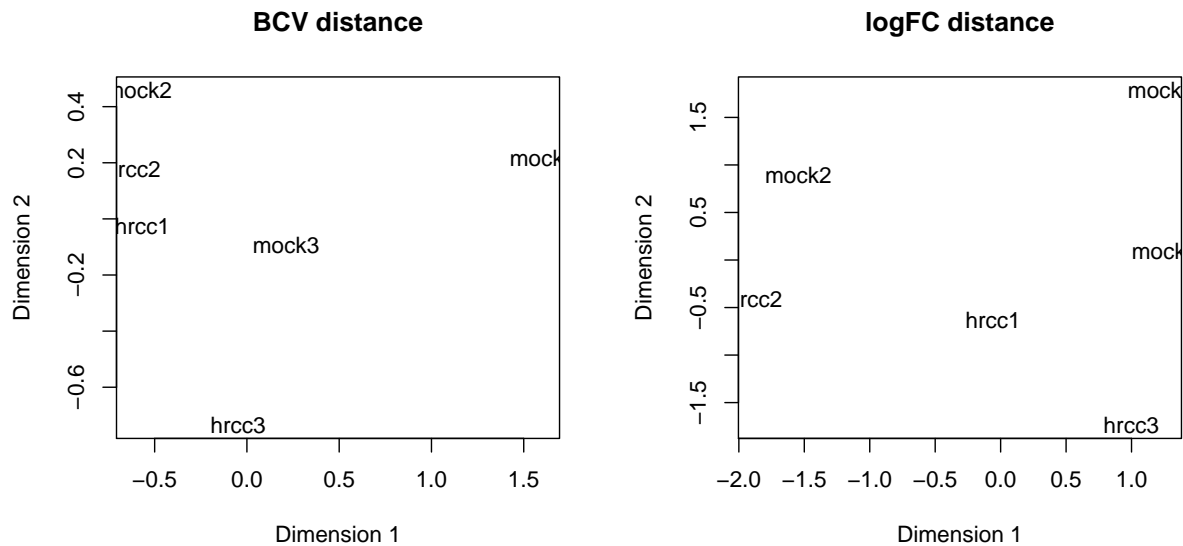
### 3.5.5 Data exploration

An MDS plot shows the relative similarities of the six samples. Distances on an MDS plot of a DGEList object correspond to *leading BCV*, the biological coefficient of variation between each pair of samples using the 500 genes with most heterogeneous expression.

```
> plotMDS(y, main="BCV distance")
```

For comparison, we also make an MDS plot with distances defined in terms of shrunk fold changes.

```
> els <- y$samples$lib.size * y$samples$norm.factors
> aug.count <- 2*ncol(arab)*els/sum(els)
> logCPM <- log2( t(t(arab)+aug.count) )
> plotMDS(logCPM, main="logFC distance")
```



The two plots give similar conclusions. Each pair of samples extracted at each time tend to cluster together, suggesting a batch effect. The hrcc treated samples tend to be above the mock samples for each time, suggesting a treatment effect within each time. The two samples at time 1 are less consistent than at times 2 and 3.

To examine further consistency of the three replicates, we compute predictive log2-fold-changes (logFC) for the treatment separately for the three times.

```
> design <- model.matrix(~Time+Time:Treat)
> logFC <- predFC(y,design,prior.count=1)/log(2)
```

The logFC at the three times are positively correlated with one another, as we would hope:

```
> cor(logFC[,4:6])
```

	Time1:Treathrcc	Time2:Treathrcc	Time3:Treathrcc
Time1:Treathrcc	1.000	0.241	0.309
Time2:Treathrcc	0.241	1.000	0.369
Time3:Treathrcc	0.309	0.369	1.000

The correlation is highest between times 2 and 3.

### 3.5.6 The design matrix

Before we fit GLMs, we need to define our design matrix based on the experimental design. We want to test for differential expressions between  $\Delta$ hrcC challenged and mock-inoculated samples within batches, i.e. adjusting for differences between batches. In statistical terms, this is an additive linear model. So the design matrix is created as:

```
> design <- model.matrix(~Time+Treat)
> rownames(design) <- colnames(y)
> design
```

	(Intercept)	Time2	Time3	Treathrcc
mock1	1	0	0	0
mock2	1	1	0	0
mock3	1	0	1	0
hrcc1	1	0	0	1
hrcc2	1	1	0	1
hrcc3	1	0	1	1

```
attr("assign")
[1] 0 1 1 2
attr("contrasts")
attr("contrasts")$Time
[1] "contr.treatment"

attr("contrasts")$Treat
[1] "contr.treatment"
```

### 3.5.7 Estimating the dispersion

Estimate the average dispersion over all genes:

```
> y <- estimateGLMCommonDisp(y, design, verbose=TRUE)
Disp = 0.0706 , BCV = 0.266
```

The square root of dispersion is the coefficient of biological variation (BCV). Here the common dispersion is 0.0706, so the BCV is 0.266. The common BCV is on the high side, considering that this is a designed experiment using genetically identical plants.

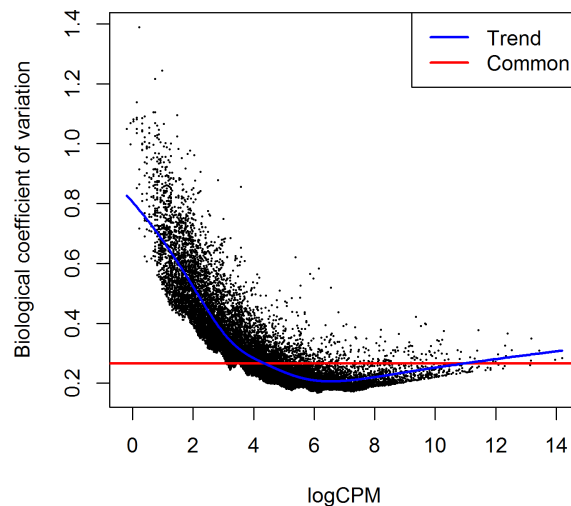
Now estimate genewise dispersion estimates, allowing for a possible abundance trend:



```
> y <- estimateGLMTrendedDisp(y, design)
> y <- estimateGLMTagwiseDisp(y, design, prior.df=6)
```

Here we have chosen `prior.df` slightly smaller than the default, which is 20, after inspecting the following BCV plot. The genewise dispersions show a decreasing trend with expression level. At low logCPM, the dispersions are very large indeed:

```
> plotBCV(y)
```



### 3.5.8 Differential expression

Now proceed to determine differentially expressed genes. Fit genewise glms:

```
> fit <- glmFit(y, design)
```

First we check whether there was a genuine need to adjust for the experimental times. We do this by testing for differential expression between the three times. There is considerable differential expression, justifying our decision to adjust for the batch effect:

```
> lrt <- glmLRT(fit, coef=2:3)
> topTags(lrt)
```

```
Coefficient: Time2 Time3
logFC.Time2 logFC.Time3 logCPM LR PValue FDR
AT5G66800      5.59      -1.075   5.43 271 1.61e-59 2.66e-55
AT5G31702      5.84      -2.605   5.90 223 3.01e-49 2.49e-45
AT5G23000      5.62      -0.289   5.68 199 6.28e-44 3.46e-40
AT3G33004      4.82      -1.764   5.60 195 4.38e-43 1.81e-39
```

```

AT2G45830      5.43      -0.596    4.65 181 4.01e-40 1.33e-36
AT2G11230      3.50      -1.532    5.56 166 8.64e-37 2.38e-33
AT2G07782      3.49      -1.618    5.23 151 1.59e-33 3.75e-30
AT2G23910      3.60      -0.386    5.07 141 1.95e-31 4.03e-28
AT5G35736      5.44      -0.994    4.57 134 7.95e-30 1.42e-26
AT2G27770      2.47      -1.571    5.37 134 8.60e-30 1.42e-26
> FDR <- p.adjust(lrt$table$PValue, method="BH")
> sum(FDR < 0.05)
[1] 3276

```

Now conduct likelihood ratio tests for the pathogen effect and show the top genes. By default, the test is for the last coefficient in the design matrix, which in this case is the treatment effect:

```

> lrt <- glmLRT(fit)
> topTags(lrt)
Coefficient: Treathrcc
      logFC logCPM  LR   PValue    FDR
AT2G19190  4.50   7.37 255 2.38e-57 3.93e-53
AT5G48430  6.34   6.71 231 2.86e-52 2.36e-48
AT2G39530  4.34   6.70 220 9.01e-50 4.96e-46
AT2G39380  4.95   5.75 201 1.01e-45 4.19e-42
AT3G46280  4.78   8.09 194 4.76e-44 1.57e-40
AT1G51800  3.97   7.70 192 9.60e-44 2.64e-40
AT2G44370  5.43   5.17 174 1.20e-39 2.83e-36
AT1G51850  5.33   5.39 167 2.80e-38 5.79e-35
AT1G51820  4.34   6.36 162 5.07e-37 9.31e-34
AT3G55150  5.80   4.86 158 2.74e-36 4.53e-33

```

Here's a closer look at the individual counts-per-million for the top genes. The top genes are very consistent across the three replicates:

```

> top <- rownames(topTags(lrt)$table)
> cpm(y)[top,order(y$samples$group)]
      hrcc1 hrcc2 hrcc3  mock1 mock2 mock3
AT2G19190 358.6 279.1 327.3 16.343 12.64 12.00
AT5G48430 198.6 344.7 116.6  4.218  4.74  0.00
AT2G39530 166.1 210.3 226.7  6.854  9.48 12.00
AT2G39380  96.3  92.5 126.0  2.109  3.16  4.31
AT3G46280 404.4 410.3 765.3 18.452 17.91 16.62
AT1G51800 380.8 381.0 432.6 28.469 17.38 27.70
AT2G44370  59.9  73.5  80.2  2.109  1.05  1.54
AT1G51850  82.1  61.7 101.5  1.054  1.05  3.39
AT1G51820 127.4 171.6 178.3  9.490  7.90  5.54
AT3G55150  45.3  71.2  60.0  0.527  1.05  1.23

```

The total number of genes significantly up-regulated or down-regulated at 5% FDR is summarized as follows:

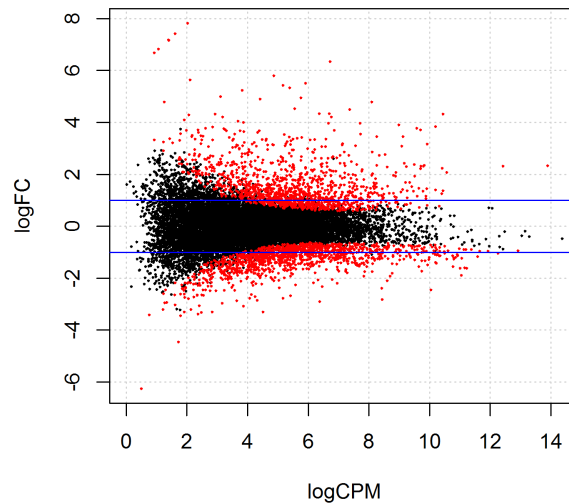
```
> summary(dt <- decideTestsDGE(lrt))
      [,1]
-1  1291
0  13959
1   1276
```

We can pick out which genes are DE:

```
> isDE <- as.logical(dt)
> DEnames <- rownames(y)[isDE]
```

Then we can plot all the logFCs against average count size, highlighting the DE genes:

```
> plotSmear(lrt, de.tags=DEnames)
> abline(h=c(-1,1), col="blue")
```



The blue lines indicate 2-fold up or down.

### 3.5.9 Setup

This analysis was conducted on:

```
> sessionInfo()
R version 2.15.0 (2012-03-30)
Platform: i386-pc-mingw32/i386 (32-bit)

locale:
```

```
[1] LC_COLLATE=English_Australia.1252 LC_CTYPE=English_Australia.1252
[3] LC_MONETARY=English_Australia.1252 LC_NUMERIC=C
[5] LC_TIME=English_Australia.1252
```

attached base packages:

```
[1] splines    stats      graphics  grDevices  utils      datasets  methods
[8] base
```

other attached packages:

```
[1] edgeR_2.7.24 limma_3.13.6 NBPSeg_0.1.4 qvalue_1.30.0
```

loaded via a namespace (and not attached):

```
[1] tcltk_2.15.0 tools_2.15.0
```

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