BioC 2012: Analyzing RNA-seq data for differential exon usage with the DEXSeq package

Alejandro Reyes, Simon Anders, Wolfgang Huber
European Molecular Biology Laboratory (EMBL), Heidelberg, Germany
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Abstract

This vignette describes how to use the Bioconductor package DEXSeq to detect quantitatively different usage of exons from shotgun RNA sequence (RNA-seq) data. The statistical model is based on generalised linear models of the Negative Binomial family (NB-GLMs) and aims to detect changes between experimental conditions of interest that are significantly larger than the technical and biological variability among replicates. The method is described in [2]. It is a specialisation of the NB-GLM approach at the overall gene level provided by the DESeq [1] and edgeR [4] packages. As input, DEXSeq uses the number of reads mapping to each of the exons of a genome. Here, the method is demonstrated on the data from the package pasilla. To cite this software, please refer to citation("DEXSeq").

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The Pasilla data set

Brooks et al. [3] investigated the effect of siRNA knock-down of the gene *pasilla* on the transcriptome of fly S2-DRSC cells. The *pasilla* protein is known to bind to mRNA in the spliceosome and is thought to be involved in the regulation of splicing. The *pasilla* gene is the Drosophila melanogaster ortholog of mammalian NOVA1 and NOVA2. The data set, which is provided by NCBI Gene Expression Omnibus (GEO) under the accession number GSE18508\(^1\), contains 3 biological replicates of the knockdown as well as 4 biological replicates of the untreated control.

Here, we will use these data to demonstrate the DEXSeq package. They are provided in the object pasillaExons in the pasilla package. We start by loading the DEXSeq package and the example data.

```r
> library("DEXSeq")
> library("pasilla")
> data("pasillaExons", package="pasilla")
```

The data command above has loaded the object pasillaExons, which is an object of class ExonCountSet. This is the central data class of DEXSeq: at the beginning of an analysis, the user creates an ExonCountSet object that contains all the required data and metadata. In the course of the analysis workflow, the intermediate and final results of computations are stored in the object, too.

We defer the discussion of how you can create such an object from your own data to Section 9 and instead start with inspecting the example data object.

The ExonCountSet class is derived from eSet, Bioconductor’s standard container class for experimental data. As such, it contains the usual accessor functions for sample, feature and assay data (including pData, fData, experimentData), and some specific ones. The accessor function design shows the available sample annotations.

```r
> design(pasillaExons)
```

<table>
<thead>
<tr>
<th>condition</th>
<th>type</th>
</tr>
</thead>
<tbody>
<tr>
<td>treated1fb</td>
<td>treated</td>
</tr>
<tr>
<td>treated2fb</td>
<td>paired-end</td>
</tr>
<tr>
<td>treated3fb</td>
<td>paired-end</td>
</tr>
<tr>
<td>untreated1fb</td>
<td>single-read</td>
</tr>
<tr>
<td>untreated2fb</td>
<td>single-read</td>
</tr>
<tr>
<td>untreated3fb</td>
<td>paired-end</td>
</tr>
<tr>
<td>untreated4fb</td>
<td>paired-end</td>
</tr>
</tbody>
</table>

The read counts can be accessed with the counts function. We print the first 20 rows of this table:

```r
> head( counts(pasillaExons), 20 )
```

<table>
<thead>
<tr>
<th>treated1fb</th>
<th>treated2fb</th>
<th>treated3fb</th>
<th>untreated1fb</th>
<th>untreated2fb</th>
<th>untreated3fb</th>
<th>untreated4fb</th>
</tr>
</thead>
<tbody>
<tr>
<td>FBgn0000256:E001: 92</td>
<td>28</td>
<td>43</td>
<td>54</td>
<td>131</td>
<td>51</td>
<td>49</td>
</tr>
<tr>
<td>FBgn0000256:E002: 124</td>
<td>80</td>
<td>91</td>
<td>76</td>
<td>224</td>
<td>82</td>
<td>95</td>
</tr>
<tr>
<td>FBgn0000256:E003: 340</td>
<td>241</td>
<td>262</td>
<td>347</td>
<td>670</td>
<td>260</td>
<td>297</td>
</tr>
<tr>
<td>FBgn0000256:E004: 250</td>
<td>189</td>
<td>201</td>
<td>219</td>
<td>507</td>
<td>242</td>
<td>250</td>
</tr>
<tr>
<td>FBgn0000256:E005: 96</td>
<td>38</td>
<td>39</td>
<td>71</td>
<td>76</td>
<td>57</td>
<td>62</td>
</tr>
<tr>
<td>FBgn0000256:E006: 1</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>2</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td>FBgn0000256:E007: 149</td>
<td>70</td>
<td>71</td>
<td>130</td>
<td>281</td>
<td>115</td>
<td>94</td>
</tr>
<tr>
<td>FBgn0000256:E008: 190</td>
<td>124</td>
<td>129</td>
<td>137</td>
<td>345</td>
<td>137</td>
<td>136</td>
</tr>
<tr>
<td>FBgn0000256:E009: 43</td>
<td>17</td>
<td>25</td>
<td>4</td>
<td>9</td>
<td>2</td>
<td>4</td>
</tr>
<tr>
<td>FBgn0000256:E010: 26</td>
<td>13</td>
<td>11</td>
<td>8</td>
<td>20</td>
<td>6</td>
<td>5</td>
</tr>
<tr>
<td>FBgn0000256:E011: 14</td>
<td>3</td>
<td>8</td>
<td>4</td>
<td>20</td>
<td>3</td>
<td>2</td>
</tr>
<tr>
<td>FBgn0000256:E012: 1</td>
<td>2</td>
<td>2</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>FBgn0000256:E013: 2</td>
<td>2</td>
<td>4</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>FBgn0000256:E014: 2</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>FBgn0000256:E015: 58</td>
<td>28</td>
<td>44</td>
<td>46</td>
<td>131</td>
<td>96</td>
<td>69</td>
</tr>
<tr>
<td>FBgn0000256:E016: 93</td>
<td>22</td>
<td>34</td>
<td>73</td>
<td>209</td>
<td>54</td>
<td>36</td>
</tr>
<tr>
<td>FBgn0000256:E017: 1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>FBgn00000578:E001: 2</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>FBgn00000578:E002: 3</td>
<td>4</td>
<td>0</td>
<td>2</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>FBgn00000578:E003: 96</td>
<td>34</td>
<td>27</td>
<td>74</td>
<td>64</td>
<td>18</td>
<td>26</td>
</tr>
</tbody>
</table>

The rows are labelled with gene IDs (here Flybase IDs), followed by a colon and a counting bin number. A counting bin corresponds to an exon or part of an exon. The table content indicates the number of reads that have been mapped to each counting bin in the respective sample.

To see details on the counting bin, we also print the first 6 lines of selected columns of the feature data annotation:

```r
> head(fData(pasillaExons)[,c(1,2,9:12)])
geneID exonID chr start end strand
FBgn0000256:E001 FBgn0000256 E001 chr2L 3872658 3872947 -
FBgn0000256:E002 FBgn0000256 E002 chr2L 3873019 3873322 -
FBgn0000256:E003 FBgn0000256 E003 chr2L 3873385 3874395 -
FBgn0000256:E004 FBgn0000256 E004 chr2L 3874450 3875302 -
FBgn0000256:E005 FBgn0000256 E005 chr2L 3878895 3879067 -
FBgn0000256:E006 FBgn0000256 E006 chr2L 3879652 3880038 -
```

`pasillaExons` contains only a subset of 46 genes that we selected from the genome-wide data set of [3]; we consider this subset so that this vignette can be run quickly. For your own analyses, you would typically consider a genome-wide data set. Of the 46 genes, there is one with 36 exons, and three with 16 exons:

```r
> table(table(geneIDs(pasillaExons)))
0 1 2 3 4 5 6 7 8 9 10 11 12 15 16 17
14424 2 3 3 2 4 2 3 3 3 2 3 2 1 3 2
19 22 23 24 25 36
1 1 3 1 1 1
```

In Section 9, we explain how you can create analogous data objects from your own data.

## 2 Normalisation

Different samples might be sequenced with different depths. In order to adjust for such coverage biases, we estimate size factors, which measure relative sequencing depth. DEXSeq uses the same method as DESeq, which is provided in the function `estimateSizeFactors`.

```r
> pasillaExons <- estimateSizeFactors(pasillaExons)
> sizeFactors(pasillaExons)
treated1fb treated2fb treated3fb untreated1fb untreated2fb untreated3fb untreated4fb
1.336 0.800 0.922 0.991 1.568 0.838 0.830
```

### 2.1 Helper functions

The `.Rnw` file that underlies this document contains the definition of helper functions that this lab uses for the preparation of plots: `plotDispEsts` and `plotMA`. Before proceeding, please run the code chunk where these functions are defined, so you have them available in your workspace. (In future versions of the `DEXSeq` package, these functions will already be defined in the package.)

## 3 Dispersion estimation

To test for differential expression, we need to estimate the variance of the data. This is necessary to be able to distinguish technical and biological variation (noise) from real effects on exon expression due to the different conditions. The information on the size of the noise is inferred from the biological replicates in the data set. However, in RNA-seq experiments the number of replicates is often too small to estimate variance or dispersion parameters individually exon by exon. Instead, variance information is shared across exons and genes, in an intensity dependent manner.

The first step is to get a dispersion estimate for each exon. This task is performed by the function `estimateDispersions`, using Cox-Reid (CR) likelihood estimation (our method follows that of the package `edgeR` [4]). Before starting estimating the CR dispersion estimates, `estimateDispersions` first defines the "testable" exons, which fulfill the following criteria:

1. The exon’s total sum of counts over all samples is higher than the parameter `minCount`,
2. the exon comes from a gene that has at most `maxExon` exons, and
3. the exon comes from a gene that has more than one “testable” exon.

These testable exons are marked in the column testable of the feature data. Then, a CR estimate is computed for each gene, and the obtained values are stored in the feature data column dispBeforeSharing.

> pasillaExons <- estimateDispersions(pasillaExons)

Note that for a full, genome-wide data set, execution of this function may take a while. To indicate progress, one dot is printed on the console whenever 100 genes have been processed. If you have a multicore machine, you may want to use the nCores option to instruct the function to parallelize the task over several CPU cores. See Section 7 and the function’s help page for details.

Afterwards, the function fitDispersionFunction needs to be called, in which a dispersion-mean relation \( \alpha(\mu) = \alpha_0 + \alpha_1/\mu \) is fitted to the individual CR dispersion values (as stored in dispBeforeSharing). The fit coefficients are stored in the slot dispFitCoefs and finally, for each exon, the maximum between the dispersion before sharing and the fitted dispersion value is taken as the exon’s final dispersion value and stored in the dispersion slot. See our paper [2] for the rationale behind this “sharing” scheme.

> pasillaExons <- fitDispersionFunction(pasillaExons)

> head(fData(pasillaExons)$dispBeforeSharing)
[1] 0.00930 0.00826 0.01669 0.01912 0.07736 NA

> pasillaExons@dispFitCoefs

(Intercept) 1(1/means[good])
0.0429 2.0872

> head(fData(pasillaExons)$dispFitted)
[1] 0.0787 0.0631 0.0493 0.0511 0.0773 2.6909

As a fit diagnostic, we plot the per-exon dispersion estimates versus the mean normalised count.

> plotDispEsts( pasillaExons )

The plot (Figure 1) shows the estimates for all exons as dots and the fit as red line. The red line follows the trend of the dots in the upper cluster of dots. The lower cluster stems from exons for which the sample noise happens to fall below shot noise, i.e., their sample estimates of the dispersion is zero or close to zero and hence form another cluster at the bottom. The fact that these two clusters look so well separated is to a large extent an artifact of the logarithmic y-axis scaling. Inspect the fit and make sure that the regression line follows the trend of the points within the upper cluster.

In Section 5, we will see how to incorporate further experimental or technical variables into the dispersion estimation.

---

Figure 1: Per-gene dispersion estimates (shown by points) and the fitted mean-dispersion function (red line).

---

[2] Especially when the dispersion estimates are very large, this fit can be difficult, and has occasionally caused the function to fail. In these rare cases please contact the developers.
4 Testing for differential exon usage

Having the dispersion estimates and the size factors, we can now test for differential exon usage. For each gene, we fit a generalized linear model with the formula

$$\text{sample} + \text{exon} + \text{condition} \times I(\text{exon} == \text{exonID})$$  \hspace{1cm} (1)

and compare it to the smaller model (the null model)

$$\text{sample} + \text{exon} + \text{condition}.$$  \hspace{1cm} (2)

The deviances of both fits are compared using a $\chi^2$-distribution. Based on that, we will be able to decide whether the null model (2) is sufficient to explain the data, or whether it can be rejected in favour of the alternative, model (1).

The function `testForDEU` performs such a test, one after another, for each exon in each gene and fills the `pvalue` and `padjust` columns of the `featureData` slots of the `ExonCountSet` object with the results. Here, `pvalue` contains the p values from the $\chi^2$ test, and `padjust` is the result of performing Benjmini-Hochberg adjustment for multiple testing on Robjctpvalue.

```r
> pasillaExons <- testForDEU( pasillaExons )
> head( fData(pasillaExons)[, c( "pvalue", "padjust" ) ] )
  pvalue  padjust
FBgn0000256:E001 0.851        0.999
FBgn0000256:E002 0.560        0.999
FBgn0000256:E003 0.768        0.999
FBgn0000256:E004 0.680        0.999
FBgn0000256:E005 0.943        0.999
FBgn0000256:E006  NA         NA
```

For some usages, we may also want to estimate fold changes. To this end, we call `estimatelog2FoldChanges`:

```r
> pasillaExons <- estimatelog2FoldChanges( pasillaExons )
```

Now, we can get a table of all results with `DEUresultTable`.

```r
> res1 <- DEUresultTable(pasillaExons)
> head( res1 )
  geneID exonID dispersion pvalue  padjust  meanBase log2fold(untreated/treated)
FBgn0000256:E001 FBgn0000256 E001 0.0787 0.851        0.999        58.343
FBgn0000256:E002 FBgn0000256 E002 0.0631 0.560        0.999       103.333
FBgn0000256:E003 FBgn0000256 E003 0.0493 0.768        0.999       326.476
FBgn0000256:E004 FBgn0000256 E004 0.0511 0.680        0.999       253.654
FBgn0000256:E005 FBgn0000256 E005 0.0774 0.943        0.999       60.638
FBgn0000256:E006 FBgn0000256 E006 2.6909   NA         NA          0.788
```

Controlling false discovery rate (FDR) at 0.1 (10%), we can now ask how many counting bins show evidence of differential exon usage:

```r
> table( res1$padjust < 0.1 )
FALSE  TRUE
 376       7
```

We may also ask how many genes are affected

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Figure 2: Mean expression versus log₂ fold change plot. Significant hits (at \( p_{adj} < 0.1 \)) are colored in red.

```r
> table( tapply( res1$padjust < 0.1, geneIDs(pasillaExons), any ) )

<table>
<thead>
<tr>
<th>FALSE</th>
<th>TRUE</th>
</tr>
</thead>
<tbody>
<tr>
<td>16</td>
<td>6</td>
</tr>
</tbody>
</table>
```

Remember that our example data set contains only a selection of genes. We have chosen these to contain interesting cases; so this large fraction of affected genes is not typical.

To see how the power to detect differential exon usage depends on the number of reads that map to an exon, a so-called MA plot is useful, which plots the logarithm of fold change versus average normalized count per exon and marks by red colour the exons with adjusted \( p \) values of less than 0.1 (Figure 2). There is of course nothing special about the number 0.1, and you can specify other thresholds in the call to `plotMA`. For the definition of the function `plotMA`, see Section 2.1.

```r
> plotMA(with(res1, data.frame(baseMean = meanBase, 
+ log2FoldChange = `log2fold(untreated/treated)' ,
+ padj = padjust)), 
+ ylim=c(-4,4), cex=0.8)
```

## 5 Additional technical or experimental variables

In the previous section we performed the analysis of differential exon usage ignoring the information regarding the library type of the samples. In this section, we show how to introduce this additional variable into the analysis. In this case, `type` is a technical variable, but additional experimental variables can be introduced in the same manner.

```r
> design(pasillaExons)

<table>
<thead>
<tr>
<th>condition</th>
<th>type</th>
</tr>
</thead>
<tbody>
<tr>
<td>treated1fb</td>
<td>treated</td>
</tr>
<tr>
<td>treated2fb</td>
<td>paired-read</td>
</tr>
<tr>
<td>treated3fb</td>
<td>paired-end</td>
</tr>
<tr>
<td>untreated1fb</td>
<td>untreated</td>
</tr>
<tr>
<td>untreated2fb</td>
<td>single-read</td>
</tr>
<tr>
<td>untreated3fb</td>
<td>single-read</td>
</tr>
<tr>
<td>untreated4fb</td>
<td>paired-end</td>
</tr>
</tbody>
</table>
```

First, we need to provide the function `estimateDispersions` with a model formula that makes it aware of the additional factor. Note that if the function `estimateDispersions` is called with no value for its `formula` argument (as we did in Section 3), the factor condition is considered by default.

```r
> formuladispersion <- count ~ sample + ( condition + type ) * exon 
> pasillaExons <- estimateDispersions( pasillaExons, formula = formuladispersion ) 
> pasillaExons <- fitDispersionFunction(pasillaExons)
```

Second, for the testing, we will also change the two formulae to take into account the library type.
Figure 3: Comparison of differential exon usage \( p \) values from analysis with \( (y\text{-axis}, \text{res2}) \) and without \( (x\text{-axis}, \text{res1}) \) consideration of batch (library type) effects.

> `formula0 <- count ~ sample + type * exon + condition`
> `formula1 <- count ~ sample + type * exon + condition + I(exon == exonID)`
> `pasillaExons <- testForDEU( pasillaExons, formula0=formula0, formula1=formula1 )`
> `res2 <- DEUresultTable( pasillaExons )`

We can now compare with the previous result:

> `table( res2$padjust < 0.1 )`

<table>
<thead>
<tr>
<th>FALSE</th>
<th>TRUE</th>
</tr>
</thead>
<tbody>
<tr>
<td>375</td>
<td>8</td>
</tr>
</tbody>
</table>

> `table(res1$padjust < 0.1, res2$padjust < 0.1)`

<table>
<thead>
<tr>
<th>FALSE</th>
<th>TRUE</th>
</tr>
</thead>
<tbody>
<tr>
<td>375</td>
<td>1</td>
</tr>
<tr>
<td>0</td>
<td>7</td>
</tr>
</tbody>
</table>

> `bottom = function(x) pmax(x, 1e-6)`
> `plot(bottom(res1$padjust), bottom(res2$padjust), log="xy", pch=20)`
> `abline(a=0, b=1, col="red3")`
> `abline(y=0.1, h=0.1, col="blue")`

We can see from Figure 3 and the table above that with the type-aware analysis, detection power for differential exon usage due to condition is improved.

### 6 Visualization

\textit{DEXSeq} has a function to visualize the results of testForDEU.

> `plotDEXSeq(pasillaExons, "FBgn0010909", cex.axis=1.2, cex=1.3, lwd=2, legend=TRUE)`

The result is shown in Figure 4. This plot shows the fitted expression values of each of the exons. The function plotDEXSeq takes at least two arguments, the pasillaExons object and the gene ID. The option legend=TRUE causes a legend to be included. The three remaining arguments in the code chunk above are ordinary plotting parameters.
Figure 4: The plot represents the expression estimates from a call to testForDEU. Shown in red is the exon that showed significant differential exon usage, which are simply handed over to R’s standard plotting functions. They are usually not needed and included here only to improve appearance of the plots for this vignette. See the help page for par for details.

Optionally, one can also visualize the transcript models (Figure 5), which might be useful for putting differential exon usage results into the context of isoform regulation.

```r
> plotDEXSeq(pasillaExons, "FBgn0010909", displayTranscripts=TRUE,
+ cex.axis=1.2, cex=1.3, lwd=2, legend=TRUE)
```

Other useful options are to look at the count values from the individual samples, rather than at the model effect estimates. For this display (option norCounts=TRUE), the counts are normalized by dividing them by the size factors (Figure 6).

```r
> plotDEXSeq(pasillaExons, "FBgn0010909", expression=FALSE, norCounts=TRUE,
+ cex.axis=1.2, cex=1.3, lwd=2, legend=TRUE)
```

As explained in detail in the paper, DEXSeq is designed to find difference in exon usage, i.e. differences in expression that only some but not all exons show, while differences in the overall expression of a gene but not in the isoform abundance ratios (and hence affecting all exons in the same way) will not be considered evidence of differential exon usage. Hence, it may be advantageous to remove overall differences in expression also from the plots. Use the option splicing=TRUE for this purpose.

```r
> plotDEXSeq(pasillaExons, "FBgn0010909", expression=FALSE, splicing=TRUE,
+ cex.axis=1.2, cex=1.3, lwd=2, legend=TRUE)
```

To generate an easily browsable, detailed overview over all analysis results, the package provides an HTML report generator, implemented in the function DEXSeqHTML. This function uses the package hwriter to create a result table with links to plots for the significant results, allowing a more detailed exploration of the results. To see an example, visit http://www.embl.de/~reyes/DEXSeqReport/testForDEU.html. The report shown there was generated using the code:

```r
> DEXSeqHTML( pasillaExons, FDR=0.1, color=c("#FF000080", "#0000FF80") )
```
Figure 5: As in Figure 4, but including the annotated transcript models.

Figure 6: As in Figure 4, with normalized count values of each exon in each of the samples.

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Figure 7: The plot represents the splicing estimates, as in Figure 4, but taking away the overall gene expression.

7 Parallelization

DEXSeq analyses can be computationally heavy, especially with data sets that comprise a large number of samples, or with genomes containing genes with large numbers of exons. While some steps of the analysis work on the whole data set, the two parts that are most time consuming (the functions estimateDispersions and testForDEU) can be parallelized by setting the parameter nCores. These functions will then distribute the ExonCountSet object into smaller objects that are processed in parallel on different cores. This functionality uses the multicore package.

> data("pasillaExons", package="pasilla")
> library(multicore)
> pasillaExons <- estimateSizeFactors( pasillaExons )
> pasillaExons <- estimateDispersions( pasillaExons, nCores=3, quiet=TRUE)
> pasillaExons <- fitDispersionFunction( pasillaExons )
> pasillaExons <- testForDEU( pasillaExons, nCores=3)

8 Perform a standard differential exon usage analysis in one command

In the previous sections, we went through the analysis step by step. Once you are sufficiently confident about the workflow for your data, its invocation can be streamlined by the wrapper function makeCompleteDEUAnalysis, which runs the analysis shown above through a single function call.

> data("pasillaExons", package="pasilla")
> pasillaExons <- makeCompleteDEUAnalysis("pasillaExons",
+ formulaDispersion=formuladispersion,
+ formula0=formula0,
+ formula1=formula1,
+ nCores=1)
9 Creating ExonCountSet objects

9.1 From files produced by HTSeq

In this section, we describe how to create an ExonCountSet from an alignment of the RNA-seq reads to the genome, in SAM format, and a file describing gene and transcript models in GTF format.

The first steps of this workflow involve two scripts for the Python library HTSeq [5]. These scripts are provided as part of the R package DEXSeq, and are installed in the sub-directory texttt\python\scripts of the package's installation directory. To find the latter, use system.file.

```r
> pkgDir = system.file(package="DEXSeq")
> pkgDir
[1] "/home/reyes/R/x86_64-unknown-linux-gnu-library/2.16/DEXSeq"
```

```r
> list.files(pkgDir)
[1] "CITATION" "DESCRIPTION" "doc" "help" "html"
[6] "INDEX" "Meta" "NAMESPACE" "NEWS" "python_scripts"
```

```r
> list.files(file.path(pkgDir, "python_scripts"))
[1] "dexseq_count.py" "dexseq_prepare_annotation.py"
```

To use the scripts, you need to first install HTSeq as explained on the web site [5]. Run the scripts from the command line. Both scripts display usage instructions when called without arguments.

The first script, dexseq_prepare_annotation.py, parses an annotation file in GTF format to define non-overlapping exonic parts: for instance, consider a gene whose transcripts contain either of two exons whose genomic regions overlap. In such a case, the script defines three exonic regions: two for the non-overlapping parts of each of the two exons, and a third one for the overlapping part. The script produces as output a new file in GTF format. The second script, dexseq_count.py, reads the GTF file produced by dexseq_prepare_annotation.py and an alignment in SAM format and counts the number of reads falling in each of the defined exonic parts.

The files that were used in this way to create the pasillaGenes object are provided within the pasilla package:

```r
> dir(system.file("extdata",package="pasilla"))
[1] "Dmel.BDGP5.25.62.DEXSeq.chr.gff" "geneIDsinsubset.txt"
[3] "pasilla_gene_counts.tsv" "treated1fb.txt"
[5] "treated2fb.txt" "treated3fb.txt"
[7] "untreated1fb.txt" "untreated2fb.txt"
[9] "untreated3fb.txt" "untreated4fb.txt"
```

The vignette\(^3\) of the package pasilla provides a complete transcript of these steps.

The DEXSeq function read.HTSeqCounts is then able to read the output from these scripts and returns an ExonCountSet object with the relevant information for differential exon usage analysis and visualization.

9.2 From elementary R data structures

Users can also provide their own data, contained in elementary R objects, directly to the function newExonCountSet in order to create an ExonCountSet object. The package GenomicRanges in junction with the annotation packages available in Bioconductor give alternative options that allow users to create the objects necessary to make an ExonCountSet object using only R. The minimum requirements are

1. a per-exon count matrix, with one row for every exon and one column for every sample,
2. a vector, matrix or data frame with information about the samples, and
3. two vectors of gene and exon identifiers that align with the rows of the count matrix.

\(^3\)Data preprocessing and creation of the data objects pasillaGenes and pasillaExons

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> bare <- newExonCountSet(
+   countData = counts(pasillaExons),
+   design=design(pasillaExons),
+   geneIDs=geneIDs(pasillaExons),
+   exonIDs=exonIDs(pasillaExons))

With such a minimal object, it is possible to perform the analysis for differential exon usage, but the visualization functions will not be so useful. The necessary information about exons start and end positions can be given as a data frame to the newExonCountSet function, or can be added to the ExonCountSet object after its creation via the featureData accessor. For more information, please see the manual page of newExonCountSet.

10 Lower-level functions

The following functions are not needed in the standard analysis work-flow, but may be useful for special purposes.

10.1 Single-gene functions

While the function counts returns the whole read count table, the function countTableForGene returns the count table for a single gene:

> head(countTableForGene(pasillaExons,"FBgn0010909"))

```
treated1fb treated2fb treated3fb untreated1fb untreated2fb untreated3fb untreated4fb
E001   1997    494    562     1150     2514     570     547
E002     122    112    180      69      203      156      142
E003     276    293    305      190      398      312      259
E004     420    200    182     230      446     183      185
E005     416    217    279      146      372      237      231
E006     486    357    471      190      337      418      364
```

Both function counts and function countTableForGene can also return normalized counts (i.e., counts divided by the size factors). Use the option normalized=TRUE:

> head(countTableForGene(pasillaExons,"FBgn0010909", normalized=TRUE))

```
treated1fb treated2fb treated3fb untreated1fb untreated2fb untreated3fb untreated4fb
E001   1494.8    618    609     1160.6     1603     680     659
E002     91.3   140    195      69.6      129      186      171
E003    206.6   366    331     191.7      254      372      312
E004    314.4   250    197     232.1      284      218      223
E005    311.4    271    302     147.3      108      283      278
E006    363.8    446    511     191.7      215      499      439
```

The function modelFrameForGene returns a model frame that can be used to fit a GLM for a single gene.

> mf <- modelFrameForGene( pasillaExons, "FBgn0010909" )
> head( mf )

```
sample exon sizeFactor condition type dispersion count
1 treated1fb E001  1.34 treated single-read 0.0166 1997
2 treated1fb E002  1.34 treated single-read 0.0562 122
3 treated1fb E003  1.34 treated single-read 0.0208 276
4 treated1fb E004  1.34 treated single-read 0.0221 420
5 treated1fb E005  1.34 treated single-read 0.0945 416
6 treated1fb E006  1.34 treated single-read 0.0405 486
```

This model frame can then be used, e.g., to estimate dispersions:

> mf <- estimateExonDispersionsForModelFrame( modelFrameForGene( pasillaExons, "FBgn0010909" ) )

Internally, the function estimateDispersions calls these two functions for each gene. It also stores the model frames for later use by testForDEU.

A single-gene version of testForDEU is also provided, by testGeneForDEU:
> testGeneForDEU( pasillaExons, "FBgn0010909" )

<table>
<thead>
<tr>
<th></th>
<th>deviance</th>
<th>df</th>
<th>pvalue</th>
</tr>
</thead>
<tbody>
<tr>
<td>E001</td>
<td>1.24e-01</td>
<td>1</td>
<td>0.72448</td>
</tr>
<tr>
<td>E002</td>
<td>7.09e-01</td>
<td>1</td>
<td>0.39981</td>
</tr>
<tr>
<td>E003</td>
<td>2.79e+00</td>
<td>1</td>
<td>0.09512</td>
</tr>
<tr>
<td>E004</td>
<td>2.90e+00</td>
<td>1</td>
<td>0.08867</td>
</tr>
<tr>
<td>E005</td>
<td>5.13e+00</td>
<td>1</td>
<td>0.02353</td>
</tr>
<tr>
<td>E006</td>
<td>7.61e+00</td>
<td>1</td>
<td>0.00581</td>
</tr>
<tr>
<td>E007</td>
<td>1.14e+00</td>
<td>1</td>
<td>0.28482</td>
</tr>
<tr>
<td>E008</td>
<td>1.57e-01</td>
<td>1</td>
<td>0.69153</td>
</tr>
<tr>
<td>E009</td>
<td>4.97e-01</td>
<td>1</td>
<td>0.48091</td>
</tr>
<tr>
<td>E010</td>
<td>1.47e+02</td>
<td>1</td>
<td>0.00000</td>
</tr>
<tr>
<td>E011</td>
<td>5.50e-02</td>
<td>1</td>
<td>0.81463</td>
</tr>
<tr>
<td>E012</td>
<td>4.77e-01</td>
<td>1</td>
<td>0.48985</td>
</tr>
<tr>
<td>E013</td>
<td>2.38e+00</td>
<td>1</td>
<td>0.12298</td>
</tr>
<tr>
<td>E014</td>
<td>1.44e-07</td>
<td>1</td>
<td>0.99970</td>
</tr>
<tr>
<td>E015</td>
<td>5.36e-01</td>
<td>1</td>
<td>0.46389</td>
</tr>
<tr>
<td>E016</td>
<td>5.33e-01</td>
<td>1</td>
<td>0.46516</td>
</tr>
<tr>
<td>E017</td>
<td>2.36e+00</td>
<td>1</td>
<td>0.12463</td>
</tr>
<tr>
<td>E018</td>
<td>1.99e+00</td>
<td>1</td>
<td>0.15851</td>
</tr>
<tr>
<td>E019</td>
<td>9.57e-04</td>
<td>1</td>
<td>0.97532</td>
</tr>
<tr>
<td>E020</td>
<td>2.03e+00</td>
<td>1</td>
<td>0.15441</td>
</tr>
<tr>
<td>E021</td>
<td>4.39e-03</td>
<td>1</td>
<td>0.94716</td>
</tr>
<tr>
<td>E022</td>
<td>2.17e-01</td>
<td>1</td>
<td>0.64119</td>
</tr>
<tr>
<td>E023</td>
<td>7.30e-01</td>
<td>1</td>
<td>0.39288</td>
</tr>
</tbody>
</table>

See the help pages of these function for further options (e.g., to specify formulae).

### 10.2 Gene count table

The function `geneCountTable` computes a table of gene counts, which are obtained by summing the counts from all exons with the same geneID. This might be useful for the detection of differential expression of genes, where the table can be used as input e.g. for the packages `DESeq` or `edgeR`. This kind of table can also be produced with the package `GenomicRanges`, e.g. function `summarizeOverlaps`.

> head(geneCountTable(pasillaExons))

<table>
<thead>
<tr>
<th>treated1fb</th>
<th>treated2fb</th>
<th>treated3fb</th>
<th>untreated1fb</th>
<th>untreated2fb</th>
<th>untreated3fb</th>
</tr>
</thead>
<tbody>
<tr>
<td>FBgn0000256</td>
<td>1482</td>
<td>857</td>
<td>966</td>
<td>1169</td>
<td>2626</td>
</tr>
<tr>
<td>FBgn0000578</td>
<td>4386</td>
<td>2301</td>
<td>2827</td>
<td>3541</td>
<td>6381</td>
</tr>
<tr>
<td>FBgn0002921</td>
<td>11305</td>
<td>7135</td>
<td>8001</td>
<td>7433</td>
<td>11980</td>
</tr>
<tr>
<td>FBgn0003089</td>
<td>8</td>
<td>4</td>
<td>4</td>
<td>6</td>
<td>9</td>
</tr>
<tr>
<td>FBgn0010226</td>
<td>129</td>
<td>100</td>
<td>113</td>
<td>106</td>
<td>126</td>
</tr>
<tr>
<td>FBgn0010280</td>
<td>2693</td>
<td>1776</td>
<td>2187</td>
<td>2088</td>
<td>3963</td>
</tr>
</tbody>
</table>

Note that a read that mapped to several exons of a gene is counted for each of these exons by the `dексseq_count.py` script. The table returned `geneCountTable` will hence count the read several time for the gene, which may skew downstream analyses in subtle ways. Hence, we recommend to use `geneCountTable` with care and use more sophisticated counting schemes where appropriate.

### 10.3 Further accessors

The function `geneIDs` returns the gene ID column of the feature data as a character vector and the function `exonIDs` return the exon ID column as a factor.

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head(geneIDs(pasillaExons))

FBgn0000256:E001 FBgn0000256:E002 FBgn0000256:E003 FBgn0000256:E004 FBgn0000256:E005
FBgn0000256 FBgn0000256 FBgn0000256 FBgn0000256 FBgn0000256
FBgn0000256:E006
14470 Levels: FBgn0000003 FBgn0000008 FBgn0000014 FBgn0000015 FBgn0000017 ... FBgn0261575

head(exonIDs(pasillaExons))

FBgn0000256:E001 FBgn0000256:E002 FBgn0000256:E003 FBgn0000256:E004 FBgn0000256:E005
"E001" "E002" "E003" "E004" "E005"
FBgn0000256:E006
"E006"

These functions are useful for subsetting an ExonCountSet object.

References


11 Session Information

> sessionInfo()

R Under development (unstable) (2012-07-06 r59735)
Platform: x86_64-unknown-linux-gnu (64-bit)

locale:
[1] LC_CTYPE=en_US.UTF-8 LC_NUMERIC=C LC_TIME=en_US.UTF-8
[7] LC_PAPER=C LC_NAME=C LC_ADDRESS=C
[10] LC_TELEPHONE=C LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C

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

other attached packages:
[1] pasilla_0.2.13 DESeq_1.9.10 lattice_0.20-6 locfit_1.5-8
[5] DEXSeq_1.3.14 Biobase_2.17.6 BiocGenerics_0.3.0

loaded via a namespace (and not attached):
[1] annotate_1.35.3 AnnotationDbi_1.19.28 biomaRt_2.13.1 DBI_0.2-5
[5] geneplotter_1.35.0 grid_2.16.0 hwriter_1.3
[9] IRanges_1.15.2 plyr_1.7.1 RCcolorBrewer_1.0-5 RCurl_1.91-1
[13] RSQLite_0.11.1 splines_2.16.0 stats_2.14.14 stats4_2.16.0
[17] stringr_0.6 survival_2.36-12 tools_2.16.0 XML_3.9-4
[21] xtable_1.7-0

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