edgeR Package Introduction

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edgeR is a package for the differential expression analysis of digital gene expression data, that is, of count data arising from DNA sequencing technologies. It is especially designed for differential expression analyses of RNA-Seq or SAGE data, or differential marking analyses of ChIP-Seq data.

edgeR implements novel statistical methods based on the negative binomial distribution as a model for count variability, including empirical Bayes methods, exact tests, and generalized linear models. The package is especially suitable for analysing designed experiments with multiple experimental factors but possibly small numbers of replicates. It has unique abilities to model transcript specific variation even in small samples, a capability essential for prioritizing genes or transcripts that have consistent effects across replicates.

The full edgeR User's Guide is available as part of the online documentation. To reach the User's Guide, install the edgeR package and load it into an R session by `library(edgeR)`. In R for Windows, the User's Guide will then be available from the drop-down menu called "Vignettes". In other operating systems, type

```
> library(edgeR)
> edgeRUsersGuide()
```

at the R prompt to open the User's Guide in a pdf viewer.