Limma Package Introduction

Gordon Smyth

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Limma is an R package for the analysis of gene expression microarray data, especially the use of linear models for analysing designed experiments and the assessment of differential expression. Limma provides the ability to analyse comparisons between many RNA targets simultaneously in arbitrary complicated designed experiments. Empirical Bayesian methods are used to provide stable results even when the number of arrays is small. The normalization and data analysis functions are for two-color spotted microarrays. The linear model and differential expression functions apply to all microarray technologies including Affymetrix and other single-channel oligonucleotide platforms.

The full Limma User's Guide is available as part of the online documentation. To reach the User's Guide you need to install the limma package. If you've installed the package and you're using Windows, type `library(limma)` at the R prompt then click on "limma" from the drop-down menu called "Vignettes". If you're not using Windows, you can type

```
> library(limma)
> limmaUsersGuide()
```

or alternatively

```
> help.start()
```

and follow the links to the limma package help.