

August 7, 2009

## Contents

### 1 Session information 1

```
> library(ExpressionView)
> library(eisa)
> library(genefilter)

> library(ALL)
> data(ALL)
> ALL.T <- ALL[, grepl("^T", ALL$BT)]
> filter <- filterfun(function(x) IQR(x) > 1)
> probes.keep <- genefilter(ALL.T, filter)
> ALL.T.filt <- ALL.T[probes.keep, ]
> modules <- ISA(ALL.T.filt)

Called from: isa.filter.robust.default(data, ...)
Called from: isa.filter.robust.default(data, ...)

> module.order <- orderModules(modules)

ordering 576 genes
ordering genes in module 1
ordering genes in module 2
ordering genes in module 3
ordering 33 samples
ordering samples in module 1
ordering samples in module 2
ordering samples in module 3
ordering done.
```

### 1 Session information

The version number of R and packages loaded for generating this vignette were:

- R version 2.9.1 (2009-06-26), i486-pc-linux-gnu

- Locale: LC\_CTYPE=en\_US.UTF-8;LC\_NUMERIC=C;LC\_TIME=en\_US.UTF-8;LC\_COLLATE=en\_US.UTF-8;LC\_MONETARY=C;LC\_MESSAGES=en\_US.UTF-8;LC\_PAPER=en\_US.UTF-8;LC\_NAME=C;LC\_ADDRESS=C;LC\_IDENTIFICATION=C
- Base packages: base, datasets, graphics, grDevices, methods, stats, utils
- Other packages: ALL 1.4.4, AnnotationDbi 1.6.1, Biobase 2.4.1, Category 2.10.0, DBI 0.2-4, eisa 0.1, ExpressionView 0.1, genefilter 1.24.2, hgu95av2.db 2.2.12, isa2 0.1, RSQLite 0.7-1
- Loaded via a namespace (and not attached): annotate 1.22.0, graph 1.22.2, GSEABase 1.6.0, RBGL 1.20.0, splines 2.9.1, survival 2.35-4, tools 2.9.1, XML 2.3-0, xtable 1.5-5