

Installation of required R packages

The following R packages are required for the successful completion of the following workshop modules: 1. Gene Expression 2. QTL Mapping

Gene Expression

In the gene expression module we will be undertaking a differential gene expression analysis. For this, we will make use of the DESeq2 R package. To install this package, copy and paste the commands below in your R console:

```
source("https://bioconductor.org/biocLite.R")
biocLite("DESeq2")
```

In addition to DESeq2 we will need the following R packages as well:

```
source("https://bioconductor.org/biocLite.R")
#libraries for gene expression analysis
biocLite("DESeq2")
biocLite("vsn")

#libraries for table manipulations
install.packages("DT")
install.packages("plyr")

#libraries for visualization
install.packages("ggplot2")
install.packages("pheatmap")
install.packages("RColorBrewer")

#libraries for gene annotation and enrichment analysis
biocLite("org.Mm.eg.db")
biocLite("topGO")
```

QTL Mapping

QTL mapping workshop will require the installation of the following R libraries. Copy and paste the commands below in you R console:

```
install.packages("qtl2", repos="http://rqtl.org/qtl2cran")
install.packages("GGally")
```

External datasets that need to be downloaded

The QTL mapping workshop, particularly the one on Diversity Outbred mice, has a section on **SNP Association Mapping** that requires the following two files:

- cc_variants.sqlite Download here : These are the variants in the Collaborative Cross founders (3 GB)
- mouse_genes.sqlite Download here : full set of mouse gene annotations (677 MB)