

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

Most of the packages will be installed using BiocManager. Our first step therefore, is to install BiocManager (<https://bioconductor.org/install>),

Install BiocManager

```
if (!require("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install()
```

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:

```
BiocManager::install("DESeq2")
```

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

libraries for gene expression analysis

```
BiocManager::install("vsn", force = TRUE)
```

libraries for table manipulations

```
BiocManager::install("DT", force = TRUE)
BiocManager::install("plyr", force = TRUE)
```

libraries for visualization

```
BiocManager::install("ggplot2", force = TRUE)
BiocManager::install("pheatmap", force = TRUE)
BiocManager::install("RColorBrewer", force = TRUE)
```

###libraries for gene annotation and enrichment analysis

```
BiocManager::install("org.Mm.eg.db", force = TRUE)
BiocManager::install("topGO", force = TRUE)
```

QTL Mapping

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

```
BiocManager::install("qtl2", force = TRUE)
BiocManager::install("GGally", force = TRUE)
```

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)