

Please install the below packages using the following commands:

Install Bioconductor Packages

To install core packages, type the following in an R command window:

```
if (!require("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install(version = "3.18")
```

Installation

To install this package, start R (version "4.3") and enter:

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

BiocManager::install("limma")
```

Installation

To install this package, start R (version "4.3") and enter:

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

BiocManager::install("GEOquery")
```

```
# install pheatmap package
install.packages("pheatmap")
```

References:

1. https://biocoreerg.github.io/CRG_RIntroduction_2021/pheatmap-function-from-the-pheatmap-package.html
2. Ritchie ME, Phipson B, Wu D, Hu Y, Law CW, Shi W, Smyth GK (2015). "limma powers differential expression analyses for RNA-sequencing and microarray studies." *Nucleic Acids Research*, **43**(7), e47. doi:10.1093/nar/gkv007.
3. Davis S, Meltzer P (2007). "GEOquery: a bridge between the Gene Expression Omnibus (GEO) and BioConductor." *Bioinformatics*, **14**, 1846–1847.