Packages installation Tutorial 3

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## Bioconductor

Bioconductor is a software ecosystem tailored to genome biology field. It contains:  
- Software for analysis and visualization of data.  
- Annotation of diverse aspects of genome biology for various organisms.  
- Packaged and documented data sets from published experiments.

### Install Bioconductor

Start RStudio and enter the commands:

if (!requireNamespace("BiocManager", quietly = TRUE))   
 install.packages("BiocManager")   
 BiocManager::install(version = "3.12")

#### If your R version is < 3.5.0

It is always recommended to update to the most current version of R and Bioconductor. If this is not possible and R < 3.5.0 , please use the following for installing Bioconductor packages:

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

Install specific packages, e.g., “GenomicFeatures” and “AnnotationDbi”, with:

library(BiocInstaller)  
BiocInstaller::biocLite(c("GenomicFeatures", "AnnotationDbi"))

## Packages for Tutorial 3

### Bioconductor packages

Install the IRanges and GenomicRanges packages:

library(BiocManager)  
BiocManager::install(c("IRanges","GenomicRanges"))

Install the BSgenome.Hsapiens.UCSC.hg19 package that will provide us with full genome sequences for Homo sapiens (hg19):

*Please pay attention that this package installation takes time.*

if (!requireNamespace("BiocManager", quietly = TRUE))  
 install.packages("BiocManager")  
  
BiocManager::install("BSgenome.Hsapiens.UCSC.hg19")

Install the msa package:

if (!requireNamespace("BiocManager", quietly = TRUE))  
 install.packages("BiocManager")  
  
BiocManager::install("msa")

### CRAN packages

Install the rmarkdown package:

install.packages("rmarkdown")

Install the seqinr package:

install.packages("seqinr")

Install the ape package:

install.packages("ape")