RNA-seq data analysis for Biologists

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Install R studio

Check R version Make sure you have installed R version $>= 3.4.0$. by typing in your terminal `R` and once you check `q()` to quit R. If your version is not updated run `sudo apt install r-base`.

Install R studio Check Linux version by typing in terminal `uname -mrs`. Follow the instructions.

Checking installed packages

```r
source("https://bioconductor.org/biocLite.R")
biocLite()
library(BiocInstaller)

check.packages.bioc <- function(pkg) {
    new.pkg <- pkg[!(pkg %in% installed.packages()[, "Package"])]
    if (length(new.pkg))
        source("https://bioconductor.org/biocLite.R")
    biocLite(new.pkg)
    sapply(pkg, require, character.only = TRUE)
}




check.packages.cran <- function(pkg) {
    new.pkg <- pkg[!(pkg %in% installed.packages()[, "Package"])]
    if (length(new.pkg))
        install.packages(new.pkg, dependencies = TRUE)
    sapply(pkg, require, character.only = TRUE)
}

packages_bioc <- c("BiocInstaller", "BiocParallel", "SummarizedExperiment",
    "GenomicAlignments", "BiocGenerics", "DESeq2", "Rsamtools",
    "GO.db", "biomaRt", "GenomicFeatures", "DO.db", "GenomicRanges",
    "clusterProfiler")
packages_cran <- c("reshape2", "plyr", "tidyr", "tibble", "dplyr",
    "data.table", "RColorBrewer", "ggplot2")

check.packages.bioc(packages_bioc)
```

```
##        BiocInstaller          BiocParallel SummarizedExperiment
##                 TRUE                  TRUE                 TRUE
##    GenomicAlignments          BiocGenerics               DESeq2
##                 TRUE                  TRUE                 TRUE
##            Rsamtools                 GO.db              biomaRt
##                 TRUE                  TRUE                 TRUE
##      GenomicFeatures                 DO.db        GenomicRanges
##                 TRUE                  TRUE                 TRUE
```

```
##     clusterProfiler
##               TRUE
```

```
check.packages.cran(packages_cran)
```

```
##     reshape2          plyr         tidyr        tibble         dplyr
##         TRUE          TRUE          TRUE          TRUE          TRUE
##   data.table RColorBrewer       ggplot2
##         TRUE          TRUE          TRUE
```