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local: Molecular Biology/Inovation & CENTD - Butantan Institute

Lecture 02 - install packages

In [1]:

```
library(igraph)
```

Error in library(igraph): there is no package called 'igraph'
Traceback:

1. library(igraph)
2. stop(txt, domain = NA)

Install packages from CRAN

In [2]:

```
#------ Install packages from CRAN ----------------
?install.packages
```

In [3]:

```
.libPaths()
```

'/home/flalix/anaconda3/envs/study/lib/R/library'

In [5]:

```
install.packages("igraph")
```

Updating HTML index of packages in '.Library'
Making 'packages.html' ... done

In [6]:

```
library(igraph)
```

Attaching package: 'igraph'

The following objects are masked from 'package:stats':

    decompose, spectrum

The following object is masked from 'package:base':

    union

In [ ]:

```
install.packages(c("rafalib", "VennDiagram", "Rmisc","plot3D"))
```

In [ ]:

```
install.packages("devtools", dependencies = TRUE)
```

Install packages from github with devtools

In [ ]:

```
library(devtools)
install_github("dosorio/Peptides", force = TRUE)
```

In [ ]:

```
library(Peptides)
?Peptides
```

In [ ]:

```
Peptides::mw
```

In [ ]:

```
Peptides::charge()
```

Install packages from Bioconductor

In [7]:

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

```
Updating HTML index of packages in '.Library'
Making 'packages.html' ... done
Bioconductor version 3.7 (BiocInstaller 1.30.0), ?biocLite for help
A newer version of Bioconductor is available for this version of R,
  ?BiocUpgrade for help
```

In [ ]:

```
biocLite("org.Hs.eg.db")
```

In [ ]:

```
biocLite(c("affy", "limma", "geneplotter"))
```

Install packages from CRAN/Bioconductor in anaconda (shell script)

This is a shell command: conda install -c r r-igraph

In [14]:

```
system("conda install -c r r-igraph")
```