

Setup Installation for Lecture on PCA and PLS

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Abstract

This document presents the way to install R packages required for the lecture on PCA and PLS. The main packages used for the lecture is bigstatsr and mixOmics. So no matter if you have trouble to install the other packages.

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1 Setup Installation :computer

Please make sure that you have recent R and RStudio installed.

- R : <https://cran.r-project.org/>
- RStudio : <https://www.rstudio.com/products/rstudio/download/preview/>

1.1 R packages from CRAN

It is also recommended that you pre-install the packages I will use during my lecture. The package installation instructions are as follows

```
# Install

from_cran <- c("bigstatsr", "sgPLS", "bigmemory")

install.packages(from_cran, repos = "http://cran.rstudio.com")

# Load
library(bigstatsr)
library(sgPLS)
library(bigmemory)
```

The `install.packages` command may install additional packages, which can take some time. Hence it is recommended that you install them ahead of time.

For Mac users, you might have to get an error for packages which require **Xquartz**

Please install it from <https://www.xquartz.org>

1.2 R packages from Bioconductor

Please use the following code to install the new version of *mixOmics* which is on Bioconductor.

```
#install for mixOmics
if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install("mixOmics")
```

```
library(mixOmics)
```

You also have to install first `impute` R package from Bioconductor before `elasticnet` R package from CRAN.

```
source("https://bioconductor.org/biocLite.R")
biocLite("impute")
install.packages("elasticnet")
library(impute)
library(elasticnet)
```

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1.3 R packages from Github

To download some packages from Github you have first to install the R packages *devtools* from cran

```
install.packages("devtools", repos = "http://cran.rstudio.com")
```

then you can install the R package **bigsgPLS** using from R

```
library(devtools)
install_github("matt-sutton/bigsgPLS")
library(bigsgPLS)
```

you can install the R package **sgsPLS** using from R

```
library(devtools)
install_github("matt-sutton/sgspls")
```