R for cytometry - introduction

Nello Blaser

Department of Mathematics, University of Bergen

January 12th 2018

R for cytometry

- Getting started
- Working with fcs files
- Plotting
- Interface with cytobank
- Algorithms
    - SPADE
    - tSNE
    - PhenoGraph
    - Citrus
- Any wishes?

Lecture style

- Introduction
- Hands-on
- Questions-based
- Problem solving strategies

R package universe

- R
- RStudio
- CRAN
- Bioconductor
- Github

Installing packages

CRAN:

```
install.packages("ggplot2")
```

Bioconductor

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

Github

```
install.packages("devtools")
devtools::install_github("nolanlab/citrus")
```

Packages for this course

```r
cran_pkgs <- c("Rtsne", "ggplot2", "dplyr",
               "data.table")
bio_pkgs <- c("flowCore", "FlowRepositoryR",
              "flowUtils", "FlowSOM", "spade",
              "flowClust", "flowMerge", "flowMeans",
              "SamSPECTRAL", "flowPeaks",
              "immunoClust")

install.packages(cran_pkgs)
biocLite(bio_pkgs)
devtools::install_github('nolanlab/citrus')
```

Basic data structures

Go through this tutorial.

Reading in data

Use readr:

```
install.packages("readr")
require(readr)
```

Go through this tutorial