

Dear colleagues,

For the data analysis part for the workshop we ask you to bring a laptop with you. This laptop should have a working internet connection (there will be WIFI options) and you need to have permission to install software. Please prepare the following two things:

- (1) Please visit <https://uzh.cytobank.org/> and create an account there. Once you do so, Vinko will activate these accounts so that you will have access during the workshop.
- (2) Please download and install the R software (<https://stat.ethz.ch/CRAN/>) and the R studio (<https://www.rstudio.com/>) interface.

In order for the course to go smoothly, please additionally install the following packages which will be needed during the course. To do this, after installing R and R studio, open the R studio application and execute the following lines of code in the R console of the R studio interface:

```
source("http://bioconductor.org/biocLite.R")
biocLite("flowCore")
biocLite("ggplot2")
biocLite("gplots")
biocLite("Rtsne")
biocLite("RColorBrewer")
biocLite("reshape2")
biocLite("FlowSOM")
biocLite("plyr")
```

When asked if you want to update existing packages, choose all (type a and hit enter).

We will of course give a short general introduction to R and R studio in the course but I hope that everyone manages to install these packages as this saves us a lot of time during the course. I am looking forward to seeing all of you next week.

Best wishes, Felix