**Tutorial R, RStudio and Seurat**

This is a small tutorial helping you to prepare for the single-cell RNA-Seq analysis workshop using R. The full tutorial takes about 20-30 minutes, so please read, download and load the necessary apps and packages before the meeting.

If you already have the latest version of R (**R-3.6.0**) installed and R studio running please jump to point 3 of the tutorial. If not start by:

1. Download R

R is a free and open-source language and environment for statistical computing and graphics.

1.1 go to <https://www.r-project.org/>

1.2 select ‘CRAN’ on the left side of the screen

1.3 select the mirror closest to you (probably within Germany)

1.4 download the R 3.6.0 version of R; either for Linux or for (Mac) OS X or for Windows.

(1.5 read ’install R for the first time’ for any extra details)

1.6 open the R\*.exec file

1.7 save it in an appropriate place on your computer. Select the default settings for a swift installation

1.8 ready to go! Check if you can open R wherever you have saved it in your computer and then close it.

2. Download RStudio

RStudio is a free and open-source integrated development environment for R, a programming language for statistical computing and graphics.

2.1 go to <https://www.rstudio.com/products/rstudio/>download

2.2 select RStudio Desktop (open Source License) and click Download Now

2.3 select the appropriate version of RStudio; either for Linux, (Mac) OS X or Windows.

2.4 open RStudio\*.exec file

2.5 save it in an appropriate place on your computer.

2.6. ready to go! Try to open RStudio where you saved it, the Rversion 3.6.0 should be open in the left side of the RStudio screen.

3. Get or update Packages

These are the packages that will be necessary to run the single-cell RNASeq analysis based on Seurat.

3.1 write and enter the following commands (one by one) in the console of you Rstudio.

install.packages(“ggplot2”, dependencies=T)

install.packages(“reshape2”, dependencies=T)

install.packages(“dplyr”, dependencies=T)

install.packages(“devtools”,dependencies=T)

install.packages(“Seurat”, dependencies=T)

3.2 load all the packages we just installed using library command.

library(“ggplot2”)

library(“reshape2”)

library(“dplyr”)

library(“devtools”)

library(“Seurat”)

If you get an error throughout the tutorial please contact [j.pimentabernardes@ikmb.uni-kiel.de](mailto:j.pimentabernardes@ikmb.uni-kiel.de) by email with SC-Workshop error as title and a copy of the error message in the dialogue box.

If you have some free time please read the workflow we will be using in advance under

<https://satijalab.org/seurat/v3.0/pbmc3k_tutorial.html>