Scaling up reproducible research for single cell transcriptomics using MetaNeighbor (Equipment setup)

Equipment setup

This section walks through the installation process of MetaNeighbor and the packages used in the protocol. The installation process takes 1-20 minutes, depending on the number of dependencies already available. All code blocks can be run in R command line, Rstudio, RMarkdown notebooks or a jupyter notebook with an R kernel. Important: the installation process may create conflicts in the notebook environment. We recommend running the installation process in a separate R shell or to restart the Rstudio R environment after the installation has completed and before starting one of the procedures.

Start by installing the latest MetaNeighbor package from the Gillis lab GitHub page.

```
if (!require("devtools")) {
  install.packages("devtools", quiet=TRUE)
}
devtools::install_github("gillislab/MetaNeighbor")
```

Note that the latest stable version of MetaNeighbor is also available through Bioconductor by running `BiocManager::install("MetaNeighbor")`. We recommend using the latest development version from Github, as some of the functionalities illustrated in this protocol require Bioconductor version 3.12 or higher to work (only available with R version 4.1 or higher).

Next, install the following packages, which are not necessary to run MetaNeighbor itself, but are needed to run the protocol.

```
to_install = c("scRNAseq", "tidyverse", "org.Hs.eg.db", "UpSetR")
installed = sapply(to_install, requireNamespace)
if (sum(!installed) > 0) {
    if (!requireNamespace("BiocManager", quietly = TRUE)) {
        install.packages("BiocManager")
        BiocManager::install()
    }
    BiocManager::install(to_install[!installed])
}
```

Reminder: don't forget to restart the R session at this stage.