Single Cell RNA-seq

Pre-workshop installation instructions

Research Informatics Core

PREPARATION: Installing R packages

We need several R packages for our analysis today. Some are installed through bioconductor, some from CRAN through install.packages.

- While installing packages, you may get messages about updating other packages. This is generally optional: you can select not to (enter 'n' in the prompt), but at some point it's a good idea to update.

Bioconductor

- If you have not already done so, install BiocManager for Bioconductor tools:

```r
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
```

Seurat

- Seurat requires the multtest package from Bioconductor, but it is installed from CRAN:

```r
BiocManager::install('multtest', update=F)
install.packages('Seurat')
```

Other CRAN packages

- Install Matrix, dplyr, and fossil from CRAN:

```r
install.packages('Matrix')
install.packages('dplyr')
install.packages('fossil')
```

Bioconductor packages

- Install ComplexHeatmap and monocle from Bioconductor:

```r
BiocManager::install("ComplexHeatmap", update=F)
BiocManager::install("monocle", update=F)
```

Check installations

- Try to load each package to confirm that the installation was successful:

```r
library(Seurat)
library(Matrix)
library(dplyr)
library(fossil)
library(ComplexHeatmap)
library(monocle)
```