Installing Seurat 1.4 and working with CellFindR Data (4/2/2019)

1. Make sure to install R 3.4.4: You can find it here: https://cran.cnr.berkeley.edu/
2. Attached is Seurat 1.4.0.16.tg.z file, this is the right installation version necessary to get CellFindR running.
3. To get Seurat loaded onto R, you must install devtools package. One way is to go to RStudio, go to the Packages tab on the right side and press install. If you search for devtools that should work. Once installed, you have to use library(devtools) to initate that package then use the function install.packages() and then put the path name of the Seurat 1.4.0.16.tg.z
4. Alternatively the easy way is to go the packages tab, press install choose Package archive file instead of Repository (CRAN) and locate your Seurat zip.
5. Now that Seurat is installed you have to initialize it everytime you start new R: by library(Seurat).
6. For CellFindR functions, I have attached the CellFindR.R files, you can just select all the function and press Run.

Now Seurat should be loaded and so are the cellFindR functions

1. You can load in the 10x data .Robj now with load(‘path.name.Robj’) IT will come up set as a variable (often tenx or cochobj).
2. Remember the [tenx@data.info](mailto:tenx@data.info) is your best friend.
3. Looks like you have access to this box folder: https://ucsf.box.com/s/dmap9kkd09z6k47xf84mrunfgjv0x4il
4. They should have all of the processed CellFindR outputs for our data sets.
5. Inside each file there should be matrix files that show the differential gene expression of all the groups along with TSNEs and other plots. More importantly, if you go into the mm10 or hg19 (depending on human/mouse alignment) folder or the Robj folder (organization is mixed here), there should be a file\_name.Robj.
6. If you can download the whole folder, and then import the Robj into R, with load(‘path.Robj’) you can continue the analysis! via some cellfindR functions or using the last part of the Seurat tutorial below.
7. I think datasets that would be good to start with:

Cochlea\_adult\_all 2.15.18 (mouse adult dataset)

Vest 1.8.18 (Vestibular 17wk mouse data set)

Helpful tutorials about Seurat with the right format.

<https://satijalab.org/seurat/pbmc3k_tutorial_1_4.html>

CellFindR vignette building on this is attached as the .pdf file. It basically shows the process of loading the 10x data and running through Seurat. All of this is already done if you find the .Robj in the respective dataset folder.