**CQS 2018 - Discovery Oriented Data Science - scRNA-seq data analysis demo** Ken Lau, Ph.D

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There are just a few things that you will need to do before our class on **Tuesday.** The first section are things that are required for the analysis we will do in class, while the next section includes things that are optional, but will enrich your experience or get you up-to-speed in R.

**Required**

1. Make sure you have **R and RStudio** running on your computer. We will use RStudio, so please make sure it is fully installed. If you have not used it in a while, you may want to update to the newest version.
2. **Install the Seurat package** by following the instructions below (taken from Seurat website).

# Enter commands in R (or R studio, if installed)

install.packages('Seurat')

library(Seurat)

If you see the warning message below, enter y:

package which is only available in source form, and may need compilation of C/C++/Fortran: 'Seurat'

Do you want to attempt to install these from sources?

y/n:

1. **Download the datasets** “immune\_control\_expression\_matrix.txt.gz” and “immune\_stimulated\_expression\_matrix.txt.gz” from the Github site or [here](https://www.dropbox.com/s/79q6dttg8yl20zg/immune_alignment_expression_matrices.zip?dl=1).
2. Create a folder on your computer (desktop, documents, or other) and put the datasets into that folder. Find the directory name of this folder you just created. An example from my computer (OSX format) is below. Copy and paste yours below as well.

“/Users/paigevega/Desktop/CQS\_2018\_DiscoveryOrientedDataScience”

Your pathname:

**Optional**

1. If you want, get familiar with coding in R. There are many ways to do this, and everyone learns differently. Personally, I benefited from the Swirly tutorial – instructions to install and use the package are available [here](https://swirlstats.com/instructors.html). Don’t worry – you don’t need to have any coding experience for our class.
2. We will use Seurat to go over some common methods in scRNA-seq analysis. Check out their paper [here](https://www.nature.com/articles/nbt.4096).
3. If you need help installing R, getting R packages installed, or anything else – come see me before class. See you then!