Hooray!!! You have the code for **Machine Learning, a Microscope for Genomics**

I have provided you with code that will run in **Python** or **R**. The **Python** code and annotations are wrapped up in something called a **Jupyter Notebook** and the **R** code and annotations are wrapped in a webpage (an HTML file).

For Python:

If you don't have Python 3 installed, I highly recommend Anaconda (it has all of the scientific computing modules included): https://www.anaconda.com/products/individual

If you don't have Jupyter, installing it is a snap if you have Anaconda, just run:

conda install -c conda-forge jupyterlab

If you have another Python distribution, you can find installation instructions for Jupyter here: https://jupyterlab.readthedocs.io/en/stable/getting_started/installation.html

Then, using the terminal, navigate to to the directory that contains the Jupyter Notebook: **genomics_and_ml_in_python.ipynb**

Then run:

jupyter lab

...and from there you can double click on the notebook and should be good to go.

For R:

If you don't have R installed, you can get it from here: http://archive.linux.duke.edu/cran/

If you don't have RStudio installed: https://rstudio.com/products/rstudio/download/

Now you can double click on the HTML file: **genomics_and_ml_in_R.html** and it should appear in a web-browser and you can see the code and annotations. To run the code, open up RStudio, and copy the code in the web page and paste into the RStudio console.

NOTE: You may have to change the working directory for RStudio to be the location where you saved all of the files in this tutorial. For example, from the **Session** menu, select **Set Working Directory** and **Choose Directory**. Then navigate to the directory that contains all of the files in this tutorial and you should be good to go.

Thanks again and Quest On!!!
Josh