During the course, we will translate the protocol of the below paper to a Snakemake pipeline. If you are not familiar with RNA-seq analysis or if you want to have a previous understanding of the protocol, the paper is worth the reading.

Nature protocols paper: <https://www.nature.com/articles/nprot.2016.095>

To execute this analysis, there are some computational requirements. If you have an account on HiperGator, all software will be available there. Having a good text editor will help during the development of the code. I use the Atom editor (<https://atom.io/>). It is a great text editor with many packages that you can use to personalize or supplement function to it.

Also, to use Git and Bitbucket to control or code, you will need to create a free account on Bitbucket (<https://bitbucket.org/>) webpage. Don't worry about creating a repository yet, we will do it during the course.

However, if you intend to run the pipeline on your computer, there are some requirements. Initially, you will need a computer with the following configuration:

* Hardware (64-bit computer running either Linux or Mac OS X (10.7 Lion or later); 4 GB of RAM (8 GB preferred);

The following software needs to be installed:

 • HISAT2 software ([http://ccb.jhu.edu/software/hisat2 or http://github.com/ infphilo/hisat2](http://ccb.jhu.edu/software/hisat2%20or%20http:/github.com/%20infphilo/hisat2), version 2.0.1 or later)

 • StringTie software ([http://ccb.jhu.edu/software/stringtie or https://github. com/gpertea/stringtie](http://ccb.jhu.edu/software/stringtie%20or%20https:/github.%20com/gpertea/stringtie), version 1.2.2 or later)

* SAMtools (<http://samtools.sourceforge.net>, version 0.1.19 or later)
* R (<https://www.r-project.org>, version 3.2.2 or later; I am going to use version 3.6)
* Python3 (<https://www.python.org/downloads/>; I am going to use version 3.6.5)
* Snakemake (<https://snakemake.readthedocs.io/en/stable/>; I am going to use version 5.1.3)

You will receive a tutorial file to reproduce all analyses of the course. So, even if you don't have a HiperGator account or a compatible computer, it is possible to attend the course, learn the concepts, and replicate it by yourself in the future.