

The following are adapted from: <https://rnabio.org/>

Laptop setup instructions

Complete the following before coming to the workshop to ensure that your laptop/computer is setup correctly:

1. Install R which can be downloaded from [CRAN](#).
2. Download and install the most recent version of [R Studio desktop](#). If prompted to install git, select yes.
3. Install the BioConductor core packages. Open R or RStudio and at the '>' prompt, paste the commands:

```
install.packages("BiocManager");  
library(BiocManager);  
BiocManager::install()
```
4. Install the Integrative Genomics Viewer 2.8.12 (IGV). Follow the [IGV Install Instructions](#) for your operating system.
5. Install an SSH client if needed. Mac users already have a command line ssh program that can be run from the terminal. For Windows users, please download [PuTTY](#).

Prerequisites

Do these before coming to the workshop:

1.) R tutorial

You are expected to be familiar with **R** before the workshop. If you are unfamiliar with **R**, here is a suggested tutorial and command reference. Using R installed on your computer please work through the tutorial.

- The [GenViz Intro R tutorial](#)
- The [R command cheat sheet](#)

2.) Command line tutorial

You are expected to be familiar with basic command line usage before the workshop. If you are unfamiliar with **the command line**, below is a suggested tutorial. If you have a Mac computer you can use the "Terminal" application to complete this tutorial. If you have access to a linux server at your institution you could do it there. If neither of those is available you can try a free online termline application that runs in your browser such as [COCALC](#).

- [UNIX Intro Tutorial](#)
- [Unix Cheat sheet](#)

3.) Reading materials

Please read these two articles before coming to the workshop:

- RNA-seq data fundamentals. [RNA Sequencing: The Teenage Years](#).
- RNA-seq analysis and statistics fundamentals. [RNA Sequencing Data: Hitchhiker's Guide to Expression Analysis](#).

Use Minerva – Mount Sinai's supercomputer

Request an Account

If you have not, you shall request to have an account on Minerva:

<https://labs.ica hn.mssm.edu/minervalab/request-an-account/>

Some training materials to get you started:

<https://labs.ica hn.mssm.edu/minervalab/resources/the-minerva-user-group-and-training-classes/>

The Minerva team has agreed to provide a dedicated machine for us to use it interactively during the course. In order for you to gain access, you need to provide your Minerva ID to the course director beforehand.

Minerva provides a unified environment for all participants and has all the packages preinstalled. This way, you can avoid all the hassles of installing packages locally, which may take a significant amount of time/effort.

Li Shen

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