microhaplot practical session

For this, we are going to be focusing on familiarizing ourselves with the user interface and all the features. We won’t be discussing, in this session, the bioinformatic preludes to this.

To follow along you will need to have RStudio (https://www.rstudio.com/) and a recent version of R (<https://cran.r-project.org/>) installed.

Then, you can go to <https://github.com/ngthomas/microhaplot> and scroll down the page to the README section. There you will find directions on how to install microhaplot from within R and how to open up the vignette which holds the verbiage that we will use to explore through the program.

In a nutshell this is what it asks you to do:

1. install devtools if you don’t have it
2. install microhaplot
3. provide a directory for microhaplot’s shiny app
4. open the vignette
5. launch the microhaplot shiny app

We will then follow along with that vignette.