**Prep-work:**

***Install software***:

We will need up-to-date versions of **R, Rstudio**, **STRUCTURE, GENECLASS,** and **CLUMPP**,installed for the workshop. You should install all of these on your machine, in roughly that order.

**R:** The actual programming language! R can be installed via the links (or instructions in the case of a Linux machine) on [this page](https://cran.rstudio.com/).

**Rstudio:** An Integrated Development Environment (IDE) designed specifically for R, but that also works for python, bash, and a handful of other languages. IDEs make coding *much* more comfortable. They are incredibly useful--I would never try to do any serious coding without one. You can download Rstudio [here](http://www.rstudio.com/products/rstudio/download/). The free version is totally fine.

**STRUCTURE:** STRUCTURE is a tool for finding and visualizing population structure that works with both microsatellite, RAD or whole-genome SNP data, and quite a few other types of data as well! **We need to install both the command line and graphical user interface (GUI) version of the program.** Both are available [here](https://web.stanford.edu/group/pritchardlab/structure_software/release_versions/v2.3.4/html/structure.html). Download the versions both with and without the graphical front-end for your operating system.

* Run the installer for the graphical version and follow the prompts to install STRUCTURE.
* Unzip the zipped file for the version without the graphical front end—no need to install!

***Linux extra steps***:

If you have a linux machine, you'll probably also need to install a handful of other tools: r-base-dev, libxml2-dev, and libcurl4-openssl-dev. The install method will depend on your distro, so you'll need to google it. I used

sudo apt-get install r-base-dev

sudo apt-get install libxml2-dev

sudo apt-get install libcurl4-openssl-dev

on my up-to-date Ubuntu distro without issue, but your mileage may vary. These are needed to install some of the packages we'll be using in R, and there may be a few others you'll end up needing as well.

**Schedule:**

Monday, July 25th (17:00-19:00): Introduction to R

* Introduction to R and Rstudio
* File structures and reading in data
* Objects, classes, object access, and vectorized operations
* Logical operators and subsetting
* Functions and getting help
* Git, Github, and R
* Overview of genetics tools in R (as time permits)

Tuesday, July 26th (17:00-19:00): Next steps in R and R for population genetics

* Packages
* Plotting in R with ggplot2
* Writing functions
* Collaboration with Github
* Population Genetics in R with snpR
* Basic phylogenetics in R
* Open office hours (as time permits)

Looking forward to seeing all of you on Monday!

Best,

Will Hemstrom