**R FOR BIOLOGISTS**

**Workshop 1 – Introductory concepts in R**

**Monday/Tuesday February 24/25, 2 – 5 pm**

This workshop is designed for new- to novice- level R users. We will cover material that will ensure you are able to get data into R, visualize it, and run preliminary (i.e. simple) analyses.

Topics:

* R projects & R markdown
* Data import, rearrangement, “tidy” data
* Data types in R
* Data visualization for publication-quality graphs
* Basic statistics (e.g. linear modeling, multiple regression, t-tests, ANOVAs)
* Common mistakes
* Error interpretation
* Finding help
* Principles of clean coding

\*NOTE: repeated measures, time-series, and spatial analyses will not be covered in this workshop

**Workshop 2 – Intermediate concepts in R**

**Wednesday/Thursday February 26/27, 2 – 5 pm**

This workshop is designed for users who want to write their own functions, reduce code complexity through conditionals (e.g. if-else statements) and iterations (e.g. for loops), how to troubleshoot user functions, and version control through git and GitHub. We will cover material that will give you the basic tools to begin building more complex analyses.

Topics:

* Iterating your code with for loops
* When to use lists versus dataframes for iterating computations
* Conditionals
* Writing functions
* Troubleshooting functions
* Using git and GitHub for version control

**Workshop 3 – Advanced concepts in R**

This workshop is designed for users who are comfortable with all the above topics and wish to expand upon R by building packages. We will cover material that will give you the tools and resources for writing R packages.

Topics:

* How do packages work?
* Building an R package
* Meta-programming
* Unit tests
* Nested loops and when to avoid them