## The "Happy Scientist" Seminar Series: #3

## **Building R packages**

We are pleased to announce the third in the series of educational seminars sponsored by Cores C and D of the Biostats Program Project award. This series, the "Happy Scientist" seminar series, is aimed at providing educational material for members of Biostats, both students and faculty, about a variety of tools and methods that might prove useful to them. If you have any suggestions for subjects that you would like to learn about in future, please send email to Paul Marjoram at (pmarjora@usc.edu). Our agenda will be driven by your specific interests as far as is possible.



Marie Curie
"Have no fear of perfection; you'll
never reach it."

This meeting will be held on Thursday December 8th, at 1pm, and will describe methods for building R-packages, including how to construct *unit tests* to ensure your software runs well and how to use C code within R scripts. We will aim to cover the following topics:

- 1a. Cloning the RPackageTemplate project with git and Rstudio.
- 1b. Compiling and installing the package using Rstudio.

In the background RStudio uses the <u>devtools</u> package to run these commands. The bulk of the presentation will illustrate how to use this package (in conjunction with Rcpp(Armadillo)), to document, test, and build an R package.

- 2a. Automatically generating R functions that "export" C++ functions using Rcpp's compileAttributes method.
- 2b. Using devtools and roxygen2 to automatically generate documentation for exported R functions.
- 2c. Creating and running unit tests using the testthat and devtools packages.
- 2d. Building, installing, and exporting R source packages using devtools.

The seminar will be given by Patrick Muchmore.

**Please note:** Patrick has added a default README file to the RPackageTemplate repository. (If that link doesn't work, the address is: <a href="https://github.com/patrickmuchmore/RPackageTemplate">https://github.com/patrickmuchmore/RPackageTemplate</a>.) It lists the commands he intends to run during the presentation. The package contains C++ code, so a compiler is required, and there are also a few R package prerequisites. He has provided instructions on installing the required software as part of that README. If you would like to be able to run the commands yourself during the presentation (recommended), it would be helpful if you have everything installed ahead of time (by following the instructions in the README file). If you run into issues, we can try to fix them before the seminar (please show up 10-15 minutes early in that case).

As ever, all are welcome to attend, whether involved in the Biostats Program Project or not. We will hold the seminar in the common area on the second floor of Soto between the Biostats kitchen and the restrooms.

Happy Scientist Seminar #3: Title: Building R packages

Time: 1:00-2:30pm, Thursday Dec. 8th

Where: Second floor Soto common area, next to Biostats kitchen