R Class Descriptions (Advanced) with Learning Objectives

# Introduction to Bioconductor

## Description

This class will provide an overview of Bioconductor. We will learn how to identify Bioconductor packages that are appropriate for our project, explore package documentation, and demonstrate how to download and install R packages from Bioconductor.

## Learning Objectives

Upon completion of this class participants should be able to:

* Describe what the Bioconductor project comprises
* Navigate the Bioconductor website to find packages for a particular task
* Install and update Bioconductor package
* Open a package vignette and practice running through the examples that they contain
* Ensure that they are using the correct version of R to reproduce exactly the contents of this lesson
* Describe how to join and communicate with the Bioconductor community

## Assumptions for This Class

This class makes a few assumptions about your understanding of R and RStudio. First, it assumed that you have already installed [R](https://cran.r-project.org/) and [RStudio](https://www.rstudio.com/products/RStudio/#Desktop). Second, is that you have experience with R. If not, here are some resources for getting started:

* NIH Library [Introduction to R and RStudio](https://www.nihlibrary.nih.gov/training/introduction-r-and-rstudio-9) class
* [A (very) short introduction to R](https://cran.r-project.org/doc/contrib/Torfs+Brauer-Short-R-Intro.pdf)
* [Quick-R](http://www.statmethods.net/)
* [Getting up to speed with R](https://rkabacoff.github.io/datavis/Rintro.pdf)

Third, is experience working in RStudio and creating scripts and/or markdown files.

# Working with Data in Bioconductor

## Description

This class will provide an overview of common Bioconductor datatypes and explore options for working with biological sequence data.  Specifically, this class will focus on the object types for storing and manipulating genomic features and sequences.

## Learning Objectives

Upon completion of this class participants should be able to:

* Locate resources on S4Vector classes
* Review standard R datatypes
* List the 6 basic Bioconductor classes
* Discuss methods for working with biological sequences
* Locate information on Bioconductor, Bioconductor packages, and Bioconductor Courses

## Assumptions for This Class

This class makes a few assumptions about your understanding of R and RStudio. First, it assumed that you have already installed [R](https://cran.r-project.org/) and [RStudio](https://www.rstudio.com/products/RStudio/#Desktop). Second, is that you have experience with R. If not, here are some resources for getting started:

* NIH Library [Introduction to R and RStudio](https://www.nihlibrary.nih.gov/training/introduction-r-and-rstudio-9) class
* [A (very) short introduction to R](https://cran.r-project.org/doc/contrib/Torfs+Brauer-Short-R-Intro.pdf)
* [Quick-R](http://www.statmethods.net/)
* [Getting up to speed with R](https://rkabacoff.github.io/datavis/Rintro.pdf)

Third, is experience working in RStudio and creating scripts and/or markdown files.