

Epidemiology and Population Health Summer Institute at Columbia University



DIGITAL COURSE

OFFERED THROUGHOUT JUNE 2020

Introduction to Bioconductor

DESCRIPTION

The Bioconductor project provides open-source software based on the R programming language for statistical analysis and visualization of high-throughput genomic data. This course provides a broad introduction to the project, from navigating its large collection of packages to its core functionality for representation, manipulation, and visualization of genomic data. We will learn how to efficiently analyze genomic intervals and SNPs, how to manage experiments of one or more genomic data type with clinical and pathological data, and how to visualize genomic data. This workshop equips participants with essential background for a wide range of applications in statistical genomics and genetic epidemiology, such as GWAS, RNA-seq, DNA methylation, ChIP-seq, metagenomics, and multi'omic experiments.

INSTRUCTORS

- Levi Waldron, PhD
- Ludwig Geistlinger, PhD

OBJECTIVES

The primary objective of this course is to equip students with a basic understanding of how genomic data are represented and analyzed in Bioconductor. By the end of the course, participants will be able to:

- Navigate and install available Bioconductor packages
- Identify and inspect Bioconductor data structures for commonly used 'omic data types
- Perform common visualization methods to genomic data in their own data analysis

EARLY DISCOUNTS
AVAILABLE UNTIL
APRIL 1, 2020

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THROUGH MAY 1, 2020

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