THE UNIVERSITY OF ARIZONA
Mel & Enid Zuckerman College of Public Health

Mel and Enid Zuckerman College of Public Health
University of Arizona

BIOS 685 Special Topics in Biostatistics - Statistical Methods in Bioinformatics

Catalog Description: This course introduces statistical methods commonly used in bioinformatics. The course reviews basic probability and NGS technologies such as RNA-seq and single-cell RNA-seq. Then, we proceed to topics more specific to bioinformatics research, including negative binomial regression, differentially expressed genes detection, and kernel regression for time-course sequencing data. Students will learn the principles behind the statistical methods and how they can be applied to analyze NGS data. (3 units)

Course Topics:

- RNA-seq Data Analysis
- Quality Control and Preprocessing
- Quantitation of Gene Expression
- Statistical Models
- Differential Expression Analysis

Course Objectives: During this course, students will:

- Gain an understanding of computational and biological fundamentals.
- Be able to use R for
    - creating variables and entering FASTQ data
    - retrieving sequences from NCBI
    - applying statistical methods to perform NGS data analysis
- Learn how to perform sequence alignments and quality control of NGS data.
- Learn to present the data and write technical reports.

Learning Outcomes (Competencies Obtained): Upon completion of this course students will be able to:

1. Understand the basic concepts and statistical methods of NGS data collection and analysis
2. Integrate, synthesize and apply knowledge through cumulative and experiential activities
3. Explain basic concepts of bioinformatics-specific communication, including technical and professional writing and the use of mass media and electronic technology