LEARNING OBJECTIVES

Course Learning Objectives

1. Provide students with a foundation in principles of DNA sequence based bioinformatics.
2. Students will be able to navigate a unix/linux file system and execute basic commands.
3. Students will be able to describe the principles of DNA sequencing and standard sequence file types in its analysis.
4. Students will become familiar with a set of standard sequence based bioinformatic tools.
5. Students will be able to perform bioinformatic analyses utilizing command line software packages and public web and file-based resources.

Learning Objectives:

1. Define the primary nucleotide sequence databases

1. Describe the NCBI Entrez database retrieval system

2. Understand the difference between hardlinks and neighbors in Entrez

Learning Objectives

- Students will be able to define the functional units of a computer
- Students will be able to define the functioning units of the UNIX operating system
- Students will be able to login and navigate a UNIX filesystem using the command-line interface

Learning Objectives:

1. Define 1st ,2nd and 3rd 'generation' DNA sequencing;

2. Describe the basic molecular biology driving Sanger (1st generation) and Illumina (2nd generation) sequencing;

3. Describe the basic principles of base calling on an Illumina sequencing platform and the FASTQ file.

4. Perform basic operations using the FastQC package and interpret the results.

Learning Objectives

1. Describe the basic principles of high-throughput sequencing read alignment

2. Define sequence mapping quality and a SAM file

3. You will be able to:

   - Perform a BWA alignment starting from a reference sequence and fastq file using default parameters;

   - Understand the scope and purpose of **selected** non-default run time parameters available.

Learning Objectives

You will be able to:

- Interpret the SAM file format
- Use Samtools to convert, sort and index a sam file;
- Perform basic operations on a bam file using the Integrated Genomics Browser.

Learning Objectives

- Understanding the approaches and utility of epigenetic measurements in genomic-based research
- Understanding the underlying principles and challenges of ChIP-seq analysis
- Be familiar with the ChIP-seq analysis workflow and selected quality measures
- Be able to perform a basic ChIP-seq analysis from fastq file to enriched regions

Learning Objectives

- Introduction to the theory and practice of RNA sequencing (RNA-seq) analysis:
  - How do you design your RNA-Seq experiment?
  - What are batch effects and how do you minimize them?

- Describe applications of RNA-seq and its limitations

Learning Objectives

- Describe the RNA-Seq alignment problem and how to solve it
- Compare and contrast RNA-Seq alignment to DNA alignment
- Select the appropriate parameters to generate counts with HTSeq based on your library prep.
- You will be able to:
  - Perform STAR alignments starting from a reference sequence and fastq files
  - Visualize your RNA-Seq alignments using IGV and QC your alignments and counts
  - Generate counts using HTSeq

Learning Objectives

- Understand how and why different normalization is needed to compare between and within samples
- Perform differential gene expression analyses using DESeq2
- Understand why we need to perform multi-test correction
- How to perform functional enrichment to gain biological insights

Learning Objectives

- Describe challenges associated with assembling genomic sequence information *de novo*
- Compare two *de novo* assembly algorithms for whole-genome shotgun sequence information
- Explain the meaning and usage of common genome assembly metrics

Learning Objectives

- Reflect on how sequencing technologies are changing our understanding of microbial diversity and function
- Discuss distributed pathways and microbial community metabolism as ecological design principles
- Recognize basic design elements in metagenomic workflows
- Describe the taxonomic and functional potential of forest soil microbial communities