

Intro to Bioinformatics

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Location: TBD

COURSE DESCRIPTION: This course is designed to introduce students to the fundamental concepts and tools in bioinformatics, focusing on biological databases, data analysis in R, and genomic data exploration. By the end of this course, students will be able to effectively use R for various bioinformatics applications, including RNA-Seq data analysis and exploratory data analysis.

Day 1: Introduction to Bioinformatics

- Introduction to Bioinformatics
 - Definition and importance in biomedical sciences
 - Key areas of application
- Basic Biological Concepts
 - DNA, RNA, and proteins
 - Central dogma of molecular biology
 - Genomics, transcriptomics, and proteomics
- Key Bioinformatics Databases
 - Introduction to sequence databases (GenBank, RefSeq, Swiss-Port, PDB, and more)
 - NCBI, Ensembl, UCSC Genome Browser
 - Writing pseudocode in UCSC genome Browser

Day 2: Data Manipulation and Visualization in R

- Data Manipulation using `dplyr` and `tidyr`
 - Data types and structures in R
 - Importing and managing data in R
- Data Visualization with `ggplot2`
 - Grammar of graphics
 - Creating various types of plots (scatter, line, bar, histogram, boxplot)
 - Customizing plots (themes, labels, colors)
- Hands-on Practice
 - Manipulating and visualizing a sample dataset

Day 3: Statistical Analysis and Data Exploration

- Introduction to Statistical Analysis in R
 - Descriptive statistics (mean, median, mode, standard deviation)

- Inferential statistics (t-tests, chi-square tests)
- Exploratory Data Analysis (EDA)
 - Techniques for EDA (summary statistics, visualizations, detecting outliers)
- Introduction to Hypothesis Testing
 - Formulating hypotheses
 - Performing hypothesis tests in R
- Hands-on Practice
 - Conducting statistical analyses on a sample dataset
 - Exploring data using EDA techniques

Day 4: Analysis of scRNA-seq data

- Introduction to RNA-Seq Data Analysis
 - Overview of RNA-Seq
 - Steps in RNA-Seq data analysis
- Using R for RNA-Seq Analysis
 - Differential expression analysis (DESeq2, edgeR)
 - Generating heatmaps
- Gene Ontology analysis
 - Introduction to KEGG, Reactome, GO
- Hands-on Practice
 - Analyzing a small RNA-Seq dataset
 - Generating a report with findings