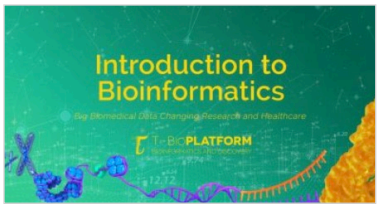
The Louisiana Biomedical Research Network has partnered with Pine Biotech to offer an innovative curriculum that was designed to quickly introduce complex bioinformatics topics in a project-based approach. The modules will be available starting November 5th and culminating with the Annual 2019 Louisiana Bioinformatics Conference.



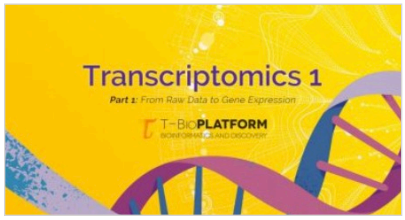
1. Introduction to Bioinformatics

This module is designed to introduce undergraduate and graduate-level students in biology or related fields to the field of bioinformatics, or the intersection of informatics and biology, and the opportunities that come with the available big data for research and industry. Participants will receive an introduction to some of the many exciting ways this discipline is applied in health care, agriculture, environmental sciences, public health, and more.

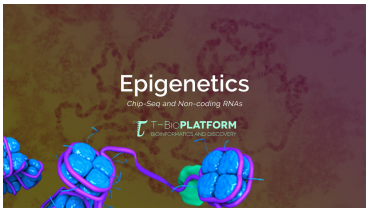
- Data-driven discovery in Life Sciences
- Examples in healthcare and industry
- Available resources for bioinformatics

2. Transcriptomics (RNA-Seq)

This module talks about real-world applications of RNA-seq. We will review methods of quantitative and qualitative analysis of RNA in a sample, how data is generated using Next Generation Sequencing and use several projects to practice generating a table of expression from raw FASTq files and the subsequent analysis of this table of gene and isoform expression.



- Processing RNA-seq data & Differential Gene Expression
- Exploring RNA-seq with advanced methods (PCA, Clustering, Classification)
- Gene and pathway Annotation, Gene Set Enrichment Analysis
- Single cell transcriptomics

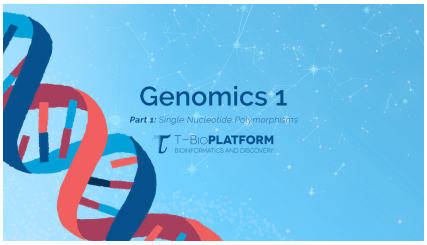


3. Epigenetics

This module talks about regulation of gene expression with regulatory RNAs. These include long non coding RNAs, microRNAs and other non-coding elements. We will also discuss Chromatin Immune Precipitation or CHiP-Seq to study histone modification. Histone modification can make some regions of the genome more open or closed for transcription.

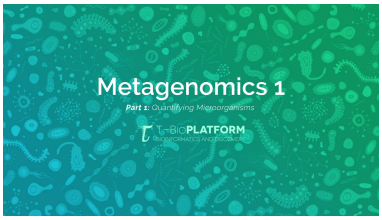
- CHiP-Seq
- microRNA, repeats and RNA editing
- Non-coding RNAs

4. Genomics



This module serves as an introduction to the bioinformatics sub-discipline of genomics. Participants will be familiarized with the biology of genetics and genetic variation, while considering practical applications of genomics to research and medicine. An example analysis of real-world NGS data is then provided in a tutorial, offering a choice of several genomics algorithms using the T-BioInfo platform.

- Somatic and Germline Mutations
- Genome Wide Association Studies
- Copy Number Variation



5. Metagenomics

This is a course on Metagenomics Data analysis and the significance of the microbiome for human health. You will learn about multiple types of sequencing methods, 16S rRNA and DNA, and then practice analysis of 16s sequencing data, including several public-domain methods for processing, analysis and visualization of microbiome data.

- Understanding the role of microbiome in human health
- 16s metagenomics - processing data and analysis of OTU abundance
- Visualization and annotation of metagenomics data

6. Machine Learning for Biomedical Data

Throughout the course, we will rely on advanced statistical methods that have to be conceptually clear. The module on Machine Learning will allow participants to explore various methods and their applications to various types of datasets. As a hot topic, the terminology and uses of machine learning across various domains have been widely discussed. Throughout this module, we will learn how machine learning is utilized for analysis of big biomedical datasets.

- Data exploration, normalization and standardization
- Unsupervised methods - dimensionality reduction and clustering
- classification and feature selection
- Combining methods and visualizing results

To facilitate the learning experience for participants of all levels, we will rely on the interactive and user-friendly T-BioInfo platform. This is a solution developed at the Tauber Bioinformatics Research Center at the University of Haifa, Israel. The sections relevant to the planned modules are highlighted in red.