

Bioinformatics for **INFECTIOUS DISEASES**

Application of bioinformatics to infectious disease research and the understanding of host-pathogen interactions

Corona | Ebola | Rhino | Tuberculosis | Malaria

We welcome you to join us for a free webinar on bioinformatics for Infectious Diseases. In this session, we will discuss how genomic data and bioinformatics are being used to study viral and bacterial pathogens and play a major role in the current biomedical research around the COVID-19 pandemic. The webinar is designed for students and faculty interested in methods of analysis, including RNA and DNA sequencing data.

October 30, 2020, 1 PM CST, ZOOM

Registration: <https://edu.tbioinfo.com/bioinformatics-for-infectious-diseases-webinar>

Topics we will cover:

- Analysis methods and tools for genomic and transcriptomic data analysis of host-pathogen interaction
- Methods to study relationships based on local and global multiple sequence alignment (MSA)
- Phylogenetic analysis and evolutionary studies used for genome ancestry and population fitness
- Chemical and structural implications of sequence variation mapped on PDB models
- Host-pathogen interaction and treatment response



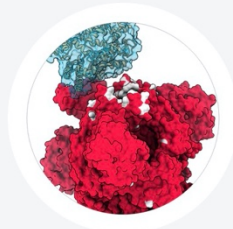
MULTIPLE SEQUENCE ALIGNMENT

How to identify and characterize important variation in genomic data



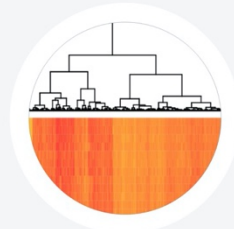
EVOLUTIONARY RELATIONSHIPS

How to conduct phylogenetic analysis and study evolution



FUNCTION AND STRUCTURE

Functional Inference based on structural analysis



ANALYSIS OF HOST RESPONSE

Transcriptomic analysis of host gene expression and variation

We will also showcase some of the latest developments on the T-BioInfo platform designed for virology studies and introduce the upcoming Omics Logic training programs for those interested in effective utilization of bioinformatics for infectious diseases, immunology and microbiology.