Bioinformatics for INFECTIOUS DISEASES

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

Corona | Ebola | Rhino | Tuberculosis | Malaria

LSU School of Veterinary Medicine

LSU Pathobiological Sciences

Graduate Course on Bioinformatics for Infectious Diseases
offered by the Department of Pathobiological Sciences (PBS), LSU School of Veterinary Medicine (SVM)
Spring, 2021 session graduate course: LSU PBS 7003 course - 3 credits
(Online Coursework and scheduled review sessions via Zoom).

Online Materials: This course has been prepared and taught as a collaboration between the Louisiana Biomedical Research Network (LBRN), The SVM Division of Biotechnology & Molecular Medicine (BioMMED) and Pine Biotech.

Sessions	Topics	Date
Program overview	Syllabus and Program outcomes: review sessions, practical assignments, and asynchronous resources	Jan 14, 2021
Hands-On Workshop	Bioinformatics analysis of public domain data	Jan 28, 2021
Genomics	First- and Second- Generation Sequencing Data types, approaches and resulting data types	Feb 11, 2021
Analytical Challenges	Pathogen Genome Analysis using examples of viral, bacterial and parasite pathogens	Feb 25, 2021
Sequence Alignment	Pairwise and Multiple Sequence Alignment	Mar 4, 2021
Evolutionary Analysis	Phylogenetic Tree Reconstruction, rate of mutation and association with time	Mar 18, 2021
Association Studies	Genomic Variants and Phenotype: PCA, GWAS, Biological significance of NT and AA variants	April 1, 2021
Variant Significance	Working with Protein Structures to map variants, examine properties and match structures	April 15, 2021
Host Response	RNA-Seq Data Analysis to study immune response to infection and compare treatment effects	April 29, 2021
Final Exam / Review	Review and Exam	May 6, 2021

Bioinformatics for Infectious Diseases is a course designed to introduce graduate students to the role and the applications of bioinformatics to the study of pathogens that cause infectious diseases of animals and humans and examine their interaction with the host.

Using examples from peer-reviewed publications, participants will learn to apply bioinformatics tools to publicly available genomic and transcriptomic data on Ebolavirus, Sars-COV-2, *Mycobacterium tuberculosis*, *Plasmodium falciparum* and other pathogens.

Topics we will cover

- Analysis methods and tools for genomic and transcriptomic data analysis of host-pathogen interactions
- 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
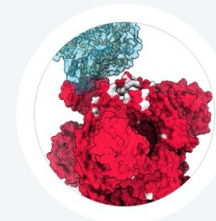- Host-pathogen interaction and treatment response

MULTIPLE SEQUENCE ALIGNMENT
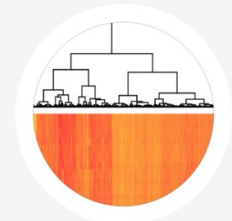How to identify and characterize important variation ingenomic data
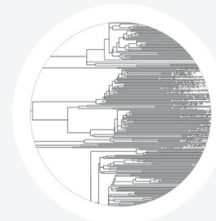
EVOLUTIONARY RELATIONSHIPS
How to conduct phylogenetic analysis and study evolution

FUNCTION AND STRUCTURE
Functional Inference based on structural analysis

ANALYSIS OF HOST RESPONSE
Transcriptomic analysis of host gene expression and variation

Throughout the course, students will gain access to user-friendly analysis pipelines on the T-BioInfo platform available through the GeneLab Core Facility of the LSU School of Veterinary Medicine, which is supported by the LBRN -INBRE (PI: Kousoulas) and the NIH-funded Center for Lung Disease (CLBD: PI, Jeyaseelan). Attendees will learn how to apply statistical analysis to genomic data and visualize it using Excel and R. In addition, attendees will utilize tools like the University of California San Francisco (UCSF) Chimera to explore 3D protein structures to find important features affected by identified genomic variants at the physicochemical level. Curated datasets will be provided for practice with associated tutorials.