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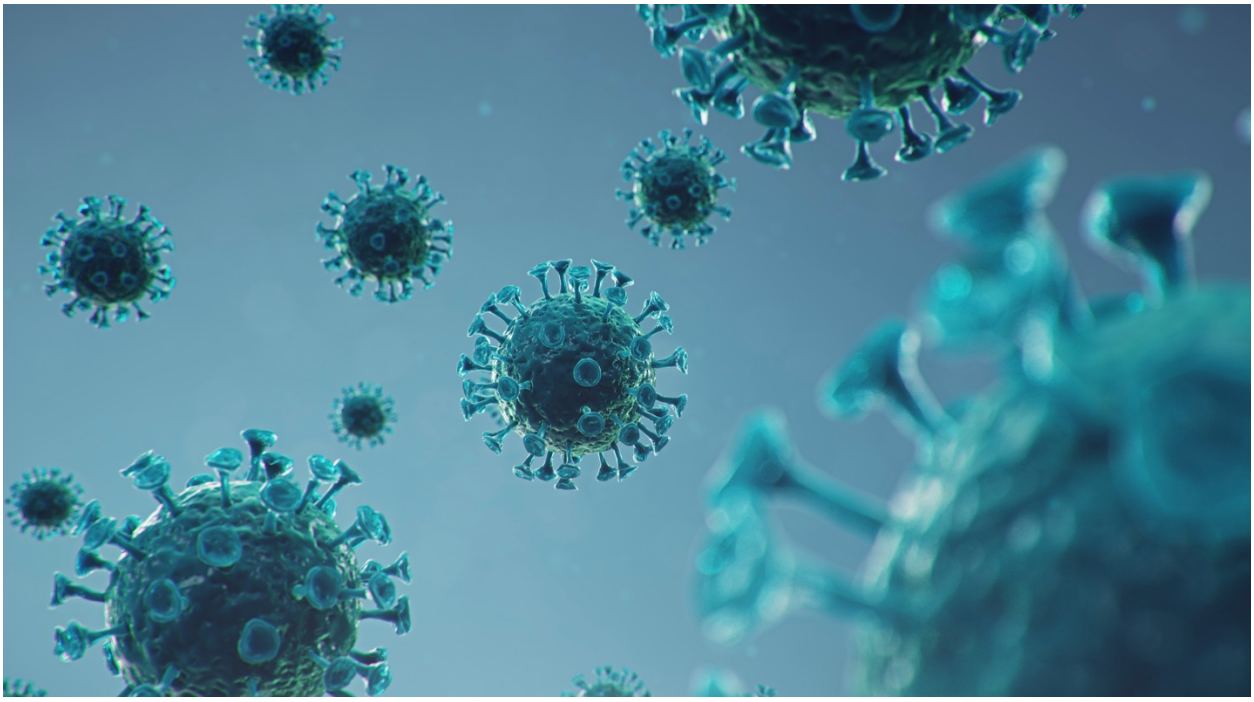
WEBINAR:

Genomic Analysis of SARS-COV-2: New Variants and the Vaccine Rollout

https://edu.tbioinfo.com/genomic-analysis-of-sars-cov-2-webinar

This webinar will cover bioinformatics approaches to sequence analysis in the light of the ongoing pandemic and introduce the upcoming graduate **Bioinformatics for Infectious Diseases Course** at LSU that covers topics, tools and resources developed for infectious disease research



As the vaccine rollout starts around the world, new variants in the spike protein of SARS-COV-2 as well as rapid evolution of this RNA virus are raising concerns about the long-term efficacy of the vaccine. In this webinar, we will discuss the ways significant mutations in viral genomes can be identified and studied in the context of evolution, protein structural changes and how to evaluate the significance of such variants for intervention measures

Topic: BIOIFORMATICS FOR INFECTIOUS DISEASES-WEBINAR
Time: Jan 22, 2021 03:00 PM Central Time (US and Canada)
Registration for attendance: https://edu.tbioinfo.com/genomic-analysis-of-sars-cov-2-webinar

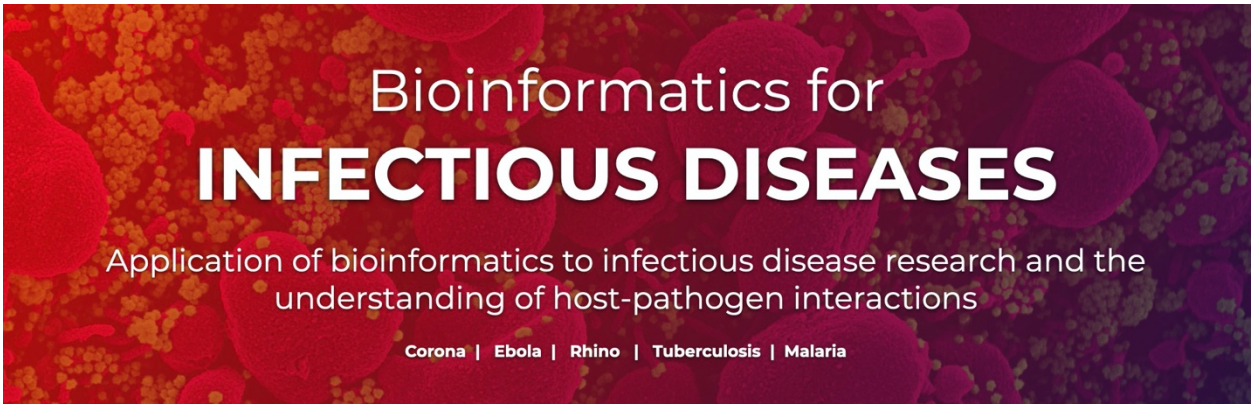
Background: A SARS-CoV-2 variant, referred to as SARS-CoV-2 VUI 202012/01 (Variant Under Investigation, year 2020, month 12, variant 01), has been identified through viral genomic sequencing in the United Kingdom (UK). It is defined by multiple spike protein mutations (deletion 69-70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H) present. Since then, similar mutations have been confirmed in the US and other parts of the world. The emergence of such mutations indicates greater transmissibility and might have other potential impacts, including

- *Ability to spread more quickly in humans*. There is already evidence that one mutation, D614G, has this property to spread more quickly. In the lab, G614 variants propagate more quickly in human respiratory epithelial cells, out-competing D614 viruses. There also is evidence that the G614 variant spreads more quickly than viruses without the mutation.
- *Ability to cause either milder or more severe disease in humans*. There is no evidence that VOC 202012/01 produces more severe illness than other SARS-CoV-2 variants.
- *Ability to evade detection by specific diagnostic tests*. Most commercial polymerase chain reaction (PCR) tests have multiple targets to detect the virus, such that even if a mutation impacts one of the targets, the other PCR targets will still work.
- *Decreased susceptibility to therapeutic agents such as monoclonal antibodies*.
- *Ability to evade vaccine-induced immunity*. FDA-authorized vaccines are "polyclonal," producing antibodies that target several parts of the spike protein. The virus would likely need to accumulate multiple mutations in the spike protein to evade immunity induced by vaccines or by natural infection.

Source: CDC/ECDC

Upcoming graduate Course at LSU that covers topics, tools and resources developed for infectious disease research:

Bioinformatics for Infectious Diseases – Course Overview



Spring Session Graduate Course on Bioinformatics for Infectious Diseases. Fall session graduate course: LSU PBS 7004 course - 3 credits (Online Coursework and scheduled review sessions via ZOOM).

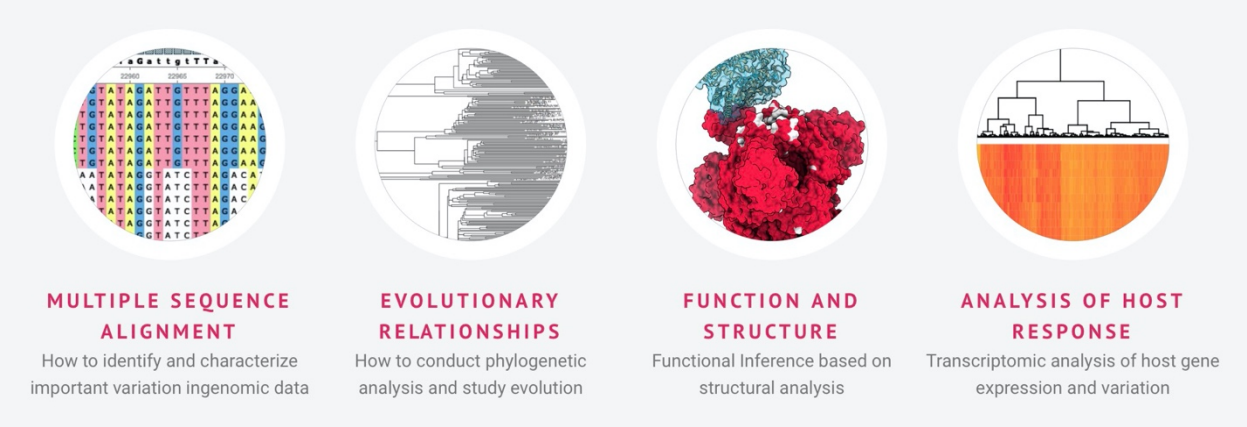
Online Materials: This course was prepared as a collaboration between LBRN, BioMMED and Pine Biotech. **Faculty:** Dr. Gus Kousoulas, Dr. Ramesh Subramanian and Dr. Farhana Mussarat.

Sessions	Topics	Date
Program overview and Hands-On Workshop	1) Syllabus and Program outcomes: review sessions, practical assignments, and asynchronous resources 2) Bioinformatics analysis of public domain data	Feb 11, 2021
Genomics	First- and Second- Generation Sequencing Data types, approaches and resulting data types	Feb 25, 2021
Analytical Challenges	Pathogen Genome Analysis using examples of viral, bacterial and parasite pathogens	Mar 4, 2021
Sequence Alignment	Pairwise and Multiple Sequence Alignment	Mar 18, 2021
Evolutionary Analysis	Phylogenetic Tree Reconstruction, rate of mutation and association with time	April 1, 2021
Association Studies	Genomic Variants and Phenotype: PCA, GWAS, Biological significance of NT and AA variants	April 15, 2021
Variant Significance	Working with Protein Structures to map variants, examine properties and match structures	April 29, 2021
Host Response	RNA-Seq Data Analysis to study immune response to infection and compare treatment effects	May 6, 2021
Final Exam / Review	Review and Exam	May 13, 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 communicable diseases 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 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



Throughout the course, students will gain access to user-friendly analysis pipelines on the T-BioInfo platform, learn how to apply statistical analysis to genomic data and visualize it using Excel and R. In addition, we will show how to utilize tools like UCSF Chimera to explore 3D protein structures to find important features affected by identified genomic variants at the physico-chemical level. Curated datasets will be provided for practice with associated tutorials.

Course REGISTRATION: https://edu.tbioinfo.com/bioinformatics-for-infectious-diseases-lsu