Dissertation Defense - Kalpana Dommaraju, PhD Bioinformatics and Computational Biology
April 23, 2021 2:00 - 4:00 PM
VIEW EVENT
All are invited to attend the defense. For more information please contact Graduate Coordinator at kharrism@gmu.edu

**Candidate:** Kalpana Dommaraju

**Program:** PhD, Bioinformatics and Computational Biology

**Date:** Friday, April 23, 2021

**Time:** 2:00 PM

**Place:** Zoom Meeting Link: [https://zoom.us/j/92134273132?pwd=bEhBSEswbUhLVEZnblFHBk1oeDQYdz09](https://zoom.us/j/92134273132?pwd=bEhBSEswbUhLVEZnblFHBk1oeDQYdz09)

**Title:** Computational Identification of Viral/Bacterial Epitopes for Type and Strain Characterization, Leading to the Development of Vaccines Against Human Adenovirus, HIV, and Staphylococcus aureus

**Committee Chair:** Dr. Donald Seto

**Committee Members:** Dr. Patrick Gillevet, Dr. Iosif Vaisman

**ABSTRACT:**
Identifying, characterizing, and typing human viral pathogens are the first steps for managing a potential outbreak. Human adenoviruses are one of the first viral pathogens to be isolated and studied, causing respiratory, ocular, and gastrointestinal infections. As a pathway to novel and emergent pathogens, novel forms result from genome recombination, identified through using the major capsid proteins (penton base, hexon and fiber) as markers. A bioinformatics tool is developed to accurately identify and characterize the genotypes based on BLAST results, phylogenetic trees, and sequence identity with the pre-existing epitopes. This tool enables quick and accurate detection of novel strains. Extending the paradigm to a bacterial human pathogen, a similar tool was developed. Staphylococcus aureus is the leading cause of skin and soft tissue infections with high mortality rate worldwide. Strain identification is critical for understanding the epidemiology of the pathogen. The highly variable unique repeat pattern of spa gene provides a sensitive method for distinguishing S. aureus isolates. Spatyper, A bioinformatics pipeline is developed to characterize the strains and identify novel types.