SPEECH INFORMATION (For Conference Program Book)	
Topic	Identifying antimicrobial resistance gene biomarkers from microbial genomes using explainable machine learning approaches
Abstract	Antimicrobial resistance is becoming a significant issue in contemporary medical settings. Although antibiotic drugs remain the mainstream treatment for most infectious diseases, bacteria have also evolved resistance to these drugs during the treatment process. The MEGA-plate experiment demonstrated that bacteria can evolve strong resistance to antibiotic drugs very quickly and easily, suggesting that we need to pay closer attention to the underlying process of antimicrobial resistance in order to combat infectious diseases. In this talk, I will introduce how we deal with the antimicrobial resistance analysis and prediction problems using bacterial pan-genome-based machine learning feature selection approaches. Since genes are central to the antimicrobial resistance mechanisms, I will introduce how we utilize the gene-based pan-genome to catalogue the bacterial gene content. I will then talk about how we apply a machine learning feature selection algorithm on the gene catalogue to 1) identify genes highly relevant to the resistance patterns, and 2) enhance the prediction of antimicrobial resistance pathogens. I will also introduce our novel feature selection approach, the Cross-Validated Feature Selection algorithm, for extracting the minimum set of genes that may serve as biomarkers for antimicrobial resistance in the prediction process. I hope that through this talk, one can learn how genes can be catalogued using pan-genomes and how machine learning feature selection algorithms can be applied to the resistance prediction problems.