TULANE UNIVERSITY
SCHOOL *of* MEDICINE

Tulane University Center for Biomedical Informatics & Genomics

TIIDHS Research Seminar

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Statistical and Machine Learning Approaches for the Identification of Viruses and Virus-host Interactions

May 1, 2023 | 3:00PM – 4:00PM

Zoom Link

Abstract

Viruses play important roles in controlling bacterial population size, altering host metabolism, and have broader impacts on the functions of microbial communities, such as human gut, soil, and ocean microbiomes. However, the investigations of viruses and their functions were vastly underdeveloped. Metagenomic studies provide enormous resources for the identifications of novel viruses and their hosts. We developed several statistical and machine learning methods for the identification of viruses like VirFinder and DeepVirFinder and for the identification of virus-host interactions such as VirHostMatcher, VirHostMatcherNet, and ContigNet. We also developed computational methods for the analysis of metagnomic Hi-C data for metagenome assembly and for linking mobile genetic elements to their hosts. Applications of these tools to metagenomic data will help explore mobile genetic elements and their interactions with their hosts.

Biography

Dr. Fengzhu Sun is a professor of Quantitative and Computational Biology at the University of Southern California (USC). He is an elected fellow of the American Association for the Advancement of Sciences (AAAS) and American Statistical Association (ASA). He received the USC Provost's Mellon Mentoring award in 2012 and USC Dornsife College Senior Raubenheimer award for excellence in research, teaching and service in 2017. He has published over 200 papers and developed several widely used algorithms in metagenomics including LSA, GRAMMy, VirFinder, DeepVirFinder, VirHostMatcher, VirHostMatcher-Net, etc.. He has been cited over 13000 times according to google scholar.