



SCALABLE TOOLS FOR VIRAL MOLECULAR EPIDEMIOLOGY

Niema Moshiri, Ph.D.

Niema Moshiri is an Assistant Teaching Professor in the Computer Science & Engineering Department at the University of California, San Diego (UCSD). His work is in primarily in computational biology, with a research focus on viral phylogenetics and epidemiology. He also places a heavy emphasis on teaching, namely on the development of online educational content, primarily Massive Adaptive Interactive Texts (MAITs). In this talk, he will provide a brief overview of the key components of viral phylogenetics and molecular epidemiology, and he will also discuss specific steps of standard viral bioinformatics pipelines that are key computational bottlenecks preventing ultra-large scalability.



REVISITING THE ORIGIN AND EMERGENCE OF SARS-COV-2

Joel Wertheim, Ph.D.

Joel Wertheim is a molecular epidemiologist who uses phylogenetic and bioinformatics approach to understand the emergence and spread of infectious diseases. He will present his work on the timing of SARS-CoV-2 emergence in China and the seeding of the COVID-19 pandemic in North America and Europe.