Title: Bioinformatics Applications in Public Health Microbiology
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Abstract
Despite advances in medical, sanitary, and public health practices, bacterial communicable diseases remain a serious threat to the health and economies of people worldwide. The role of public health microbiology laboratory is to diagnose and report pathogens that are threats to health of a population. At the frontlines of outbreak detection and response, public health investigators are our key first responders. The work of the public health investigators, however, can be limited by the effectiveness of available diagnostics and tests. Many of these tests, developed pre-genomics era, have low sensitivity and are labour-intensive to perform. While the public is familiar with large-scale outbreaks (i.e. epidemics and pandemics) from the media, outbreaks, defined as an increase in the number of cases of a disease above what is normally expected in a defined population in a given area and time, occur much more frequently than realized. Therefore, it is necessary and important to improve our ability to combat infectious disease outbreaks.

As DNA sequencing cost dropped significantly due to the invention of next generation sequencers, for the first time in human history, it is possible to obtain the whole genome sequence of a disease causing bacteria (pathogen) in real time to aid outbreak investigations. Whole genome sequencing of pathogens provides the highest resolution and most comprehensive data available to identify and track these organisms. The large amount of data also presents unprecedented challenges for public health investigators to process and interpret the data. In this talk, I'll present several Bioinformatics applications useful for public health microbiology with the focus on approaches taken by our Genome Canada funded IRIDA (Integrated Rapid Infectious Disease Analysis Platform) project. These approaches include using ontologies to facilitate the design of software applications, building federated databases, and using semantic web technologies. I will also highlight some outstanding bioinformatics challenges in public health microbiology and invite bright computer science/information systems trainees and researchers to solve these issues.

Dr. William Hsiao joined BCCDC Public Health Microbiology & Reference Laboratory in September 2011 as chief bioinformatician to lead the effort of applying microbial genomics and bioinformatics in public health diagnostic and reference laboratory. He is also cross-appointed in 2012 as a clinical assistant professor in the department of Pathology and Laboratory Medicine, University of British Columbia. He completed his PhD at Simon Fraser University under Dr. Fiona Brinkman's supervision and a post-doctoral fellowship in Dr. Claire Fraser's laboratory at the Institute for Genome Sciences, University of Maryland School of Medicine.

His current research focuses on developing bioinformatics applications and using next generation sequencing technologies to study microbial pathogens and microbial communities (microbiomes). He has participated in several genomics and metagenomics projects and is currently leading the effort to develop a bioinformatics platform to use whole genome sequencing to facilitate public health infectious disease outbreak investigations. This will be achieved by integrating data from genomic sequencing, clinical records, laboratory test results, and epidemiological investigations using semantic web technologies. Overall, his research aims to improve our understanding of the pathogens that make us sick and the microbiota that keep us healthy.