Workshop on Computational Advances in Molecular Epidemiology

Yury Khudyakov
Division of Viral Hepatitis
Centers of Disease Control
and Prevention
Atlanta, GA 30329
yek0@cdc.gov

Ion Mandoiu
Computer Science &
Engineering Department
University of Connecticut
Storrs, CT 06269
ion@engr.uconn.edu

Pavel Skums
Department of Computer
Science
Georgia State University
Atlanta, GA 30303
pskums@gsu.edu

Alexander Zelikovsky
Department of Computer
Science
Georgia State University
Atlanta, GA 30303
alexz@cs.gsu.edu

Welcome to the 8th *Workshop on Computational Advances in Molecular Epidemiology*, held on September 7, 2019 in Niagara Falls, NY in conjunction with the 10th *ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)*.[1]

Molecular epidemiology is essentially an integrative scientific discipline that considers molecular biological processes in specific epidemiological settings. It relates molecular biological events to etiology, distribution and prevention of disease in human populations. Over years, molecular epidemiology has become extensively fused with mathematical and computational science and immensely benefitted from this tight association. The CAME workshop aims to provide a forum for presentation and discussion of the latest computational research in molecular epidemiology. This multidisciplinary workshop brings together field practitioners of molecular epidemiology, molecular evolutionists, population geneticists, medical researchers, bioinformaticians, statisticians and computer scientists interested in the latest developments in algorithms, mining, visualization, modeling, simulation and other methods of computational, statistical and mathematical analysis of genetic and molecular data in the epidemiological context.

This year's workshop builds upon 7 prior editions successfully held in Atlanta (Nov. 12-15, 2011, in conjunction with the *2011 IEEE International Conference on Bioinformatics and Biomedicine*), New Orleans (June 12-14, 2013, in conjunction with the *3rd IEEE International Conference on Computational Advances in Bio and Medical Sciences*), Miami Beach (June 2-4, 2014, in conjunction with the *4th IEEE International Conference on Computational Advances in Bio and Medical Sciences*), Norfolk, Virginia (June 7-10, 2015, in conjunction with the *11th International Symposium on Bioinformatics Research and Applications*), Atlanta (October 13-15, 2016, in conjunction with the *6th IEEE International Conference on Computational Advances in Bio and Medical Sciences*), Boston (August 20, 2017 in conjunction with the *8th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics*), and Washington, D.C. (August 29, 2018 in conjunction with the *9th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics*).

This year the workshop program includes 15 invited talks that cover the following topics:

- computational methods for viral transmissions inference and molecular surveillance, including phylogenetic and phylodynamics methods for inference of transmission histories and outbreak response, development of computational tools and platforms for epidemiological networks construction and analysis, applications of analysis of genomic data for outbreak investigation.
- Study of intra-host viral evolution, including algorithms for reconstruction of intra-host viral populations from Next-generation sequencing data, inference of fitness landscapes of heterogeneous populations, differentiation between recent and chronic infections, study of viral resistance and immune adaptation.
- computational methods for immunogenomics and cancer genomics, including an inference and prediction of cancer evolutionary and progression history, identification of epitopes and immunodiagnostics.

Speakers will be invited to submit full length articles to special issue of *BMC Bionformatics*.