KEYNOTE 1

Statistical and Bioinformatic Tools for the i-BALSAC Multisectoral Infrastructure

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13:00-14:20
CreatorSpace – PRZ 302
(in French)

The i-BALSAC infrastructure for high resolution mapping of the French-Canadian population aims to create a multisectoral platform for cutting-edge research in biological, biomedical and social sciences. The platform will integrate and interrelate genealogical, genetic and geographical data, and develop statistical and cartographical analytical tools to optimize utilization of these data. For health research, the infrastructure will provide Canadians with data and tools to study genetic determinants of health. These data and tools will contribute to the design of projects aiming to identify genetic variations associated with complex diseases and to establish treatment, screening and preventive strategies. This presentation will describe the context that led to the i-BALSAC infrastructure project followed by the plans for the development of the infrastructure and of some statistical and bioinformatics tools for the integration of genealogical and genetic data.

Dr. Marie-Hélène Roy-Gagnon completed her PhD in Genetic Epidemiology at the Johns Hopkins University Bloomberg School of Public Health in 2004, with postdoctoral fellowships at NIH and the University of Michigan. She also holds an MSc in statistics from Université Laval. Before joining the School of Epidemiology and Public Health at the University of Ottawa in 2013, she was an Assistant Research Professor at the University of Montreal and Scientist at Sainte-Justine University Hospital Research Center. Her main research interests lie in the development and optimal use of statistical methods for genetic epidemiological data, in order to address the many challenges faced in uncovering the genetic causes of complex diseases. Dr. Roy-Gagnon's methodological work is done in the context of multidisciplinary collaborations, with current projects including studies on cardiovascular disease and obesity, orofacial clefts and asthma. Her research program includes three themes: 1) the optimal utilization of genealogical resources in genetic epidemiology; 2) the development and utilization of statistical models to capture complex relationships of genetic effects; and 3) the use of quantitative traits as intermediate phenotypes or biomarkers for complex diseases.