

Early Registration Fee
Starting at \$475 + tax

Late Registration Fee
is an additional \$200

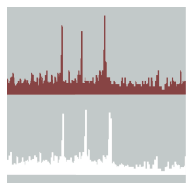
Limited to 30 participants
per workshop

 bioinformatics.ca

Canadian Bioinformatics Workshop Series

Registration and Travel Awards Available

Epigenomic Data Analysis



Date

June 18-19, 2018 - Vancouver, British Columbia

Faculty

Guillaume Bourque, David Bujold, Misha Bilenky, and Martin Hirst

Course Objectives

High-throughput sequencing of Chromatin-Immunoprecipitated libraries (ChIP-seq) and of bisulfite converted DNA (WGBS) have become increasingly common and have largely supplanted microarrays for chromatin and DNA methylation profiling. When processed appropriately, ChIP-seq data has the potential to provide a base-pair resolution view of transcription factor DNA-binding events and the mapping of histone modifications genome-wide. Similarly, WGBS can provide a quantitative genome wide profile of cytosine methylation.

The CBW has developed a **2-day workshop** providing an introduction to ChIP-seq and WGBS data analysis followed by integrated tutorials demonstrating the use of popular ChIP-Seq and WGBS analysis packages. The tutorials are designed as self-contained units that include example data and detailed instructions for installation of all required bioinformatics tools (FASTQC, BWA, MACS2, FindER, samtools, Picard, BisSNP). The course also includes an overview of integrative epigenomic tools that have been developed to explore ChIP-Seq and WGBS data together with other epigenomic datasets such as RNA-seq, DHS-seq and ATAC-seq.

Sponsored by:



CEEHRC NETWORK
Canadian Epigenetics, Environment and Health Research Consortium Network

For information send an email to:
course_info@bioinformatics.ca

For course requirements and to apply
visit: bioinformatics.ca