



Scalable methods for genomic analyses and comparative epigenomics



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Date : Tuesday, February 4th, 2020

Time : 16:00 – 17:00

Venue: E002 room, Graduate School of Science

High-throughput technologies, and in particular next-generation sequencing (NGS), have been revolutionizing biomedical research by enabling the characterization of the genetic and epigenetic components of the molecular processes of the cell with unprecedented resolution. Although these developments promise to have a significant impact on life sciences and health care, an immediate challenge is that the current computing infrastructure and techniques to store, process, analyze and share the vast volumes of data generated by these platforms frequently represents a major bottleneck. In this presentation, we will describe some of the software solutions that we have developed to facilitate large-scale data analysis, which includes open-source data analysis pipelines for whole-genome sequencing, exome sequencing, transcriptome sequencing, metagenomics. We will also present the IHEC Data Portal, which collects data for the International Human Epigenome Consortium (IHEC) and can be used to explore more than 10,000 reference epigenomics maps. Finally, we propose that inter-species epigenomic datasets will be key to better understand the evolution and the role of non-coding DNA. We will present data from different from non-human primate species and show how they can be used to better prioritize non-coding variants.