

## Workshop: Computational Genomics

# **Molecular Diversity Analysis of Genome-Wide Human Population Data**

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Recent available genome-wide high density variation data and the advent of next generation of whole-genome sequencing data for human populations marked transition from single-locus based studies to genomics analysis of human population diversity. In this workshop I will give an overview of the methods and software for human population genetic analysis. I will focus on the genome-wide microarray data and demonstrate the work flow we established to handle large genomic dataset. People attend this workshop will learn how to do computational genomics analysis of population data, particularly, they will learn how to analyze genetic diversity, how to reconstruct phylogenetic trees, how to infer population structure, how to estimate linkage disequilibrium, how to do population-based genome-wide association studies etc.