

## Basics

- 1.1 Single Nucleotide Polymorphisms & Haplotype Maps
- 1.2 Genomic Structural Variations
- 1.3 Genome-wide genetic marker discovery and genotyping using next-generation sequencing
- 1.4 Single-cell sequencing-based technologies

## Comparative genomics & genome evolution

- 2.1 Ultraconserved elements
- 2.2 Reconstruction of ancestral genomes
- 2.3 Horizontal gene transfer in eukaryotic evolution
- 2.4 Comparative genetics of longevity and cancer
- 2.5 Evolution of the human lineage

## Genome-wide epigenetics

- 3.1 DNA methylation landscapes
- 3.2 Chromatin modification landscapes
- 3.3 Linking DNA methylation and histone modifications

## Functional genome annotation

- 4.1 RNA-seq transcriptomics
- 4.2 MicroRNA profiling
- 4.3 Protein–RNA interactomes
- 4.4 Ribosome profiling for studying translation

## Human diseases

- 5.1 Genetic mapping of human diseases
- 5.2 Genetics of Crohn disease
- 5.3 Genetic architectures of psychiatric disorders
- 5.4 Cancer genomics
- 5.5 Cancer epigenomics
- 5.6 Mapping complex disease traits with global gene expression
- 5.7 Gene mapping of medical traits in model organisms

## Personalized genomics

- 6.1 Exome sequencing as a tool for Mendelian disease gene discovery
- 6.2 Uncovering rare variants through whole-genome sequencing
- 6.3 1000 (human) Genomes Project
- 6.4 Personal genomics & health care