Seminar: Vergleichende & Funktionelle Genomanalyse WS2016/17

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 linage

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 Challenges in the clinical application of whole-genome sequencing

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