Seminar: Vergleichende & Funktionelle Genomanalyse WS2017/18

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   Personal genomics & health care

✓ Thema vergeben