Seminar: Vergleichende & Funktionelle Genomanalyse *WS2011

Basics & Methods

1.1 ✓ Single Nucleotide Polymorphisms & Haplotype Maps
1.2 Genomic Structural Variations
1.3 Genome-wide approaches to studying chromatin modifications
1.4 ✓ RNA-Seq: a revolutionary tool for transcriptomics
1.5 Gene mapping in dogs and other model organisms

Complex diseases

2.1 Genome-wide association studies (GWAS)
2.2 ✓ GWAS: Pathogenesis of Crohn disease
2.3 ✓ GWAS: Genetic susceptibility to SLE (systemic lupus erythematosus)
2.4 ✓ Mapping complex disease traits with global gene expression
2.5 ✓ Psychiatric genetics: progress amid controversy

Functional annotation

3.1 ENCODE project – functional annotation of the human genome
3.2 ✓ Approaches to comparative sequence analysis
3.3 Functional repertoires of metazoan genome
3.4 ✓ Small silencing RNAs: an expanding universe
3.5 Nonsense Mediated Decay: balancing roles in gene and genome regulation

Sequence conservation & Evolution

4.1 Ultraconserved elements in the human genome
4.2 ✓ Reconstruction of ancestral genomes
4.3 ✓ RNA-based gene duplication: mechanistic and evolutionary insights
4.4 ✓ Horizontal gene transfer in eukaryotic evolution

Epigenetics

5.1 ✓ DNA methylation landscapes
5.2 ✓ Linking DNA methylation and histone modification: patterns and paradigms
5.3 ✓ Cancer epigenomics: DNA methylomes and histone-modification maps

Personalized genomics

6.1 Human whole-genome sequencing – challenges and research ethics
6.2 Uncovering rare variants through whole-genome sequencing
6.3 1000-(human)Genomes Project

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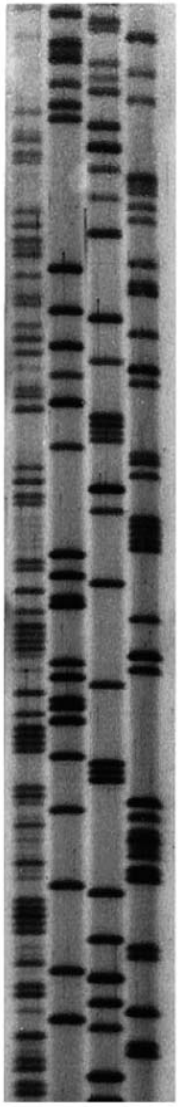
✓ Thema vergeben



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Teaching

Seminars

http://genome.fli-leibniz.de/lectures/download/themenvorschlag.pdf