

Course Title (in English) Comparative Genomics of Prokaryotes
Course Title (in Russian) Сравнительная геномика прокариот
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1. Annotation

Course Description

The course covers basic and advanced topics of comparative genomics necessary for deep analysis of bacterial genomes such as databases, functional annotation and orthologs prediction, pangenomics, phylogenetic analysis, prediction of regulatory elements, annotation of genomic rearrangements, and ancestral reconstruction. The lectures include (1) an overview of the biological processes and models, (2) summary of popular approaches and software and (3) scientific context and recent papers in the field. Practice part comprises a set of home assignments which would require basic programming skills. We will discuss the necessary packages and libraries, but the participants are assumed to be comfortable with learning basic tools on their own, with reasonable amount of support. The participants will get an overview of evolutionary processes at genome level and be able to analyze the genomic data in the context of both theoretical and practical genomics problems.

Course Prerequisites

Molecular Biology, Introduction to Bioinformatics, Introduction to Programming (Python)

2. Structure and Content

Course Academic Level Master-level course suitable for PhD students

Lecture	Topic	Summary of Topic
1	Introduction,	History of sequencing technologies, types

	genomic databases	of genomic data, databases, basic genomic characteristics.
2	Functional annotation	Features prediction, functional annotation, sequence alignments, domains, COG-KOG, KEGG database, GO-terms, GO-enrichment,
3	Gene evolution	Orthologs-paralogs, gene content evolution, phyletic patterns, gene trees, gene synteny index
4	Pangenome concept, microevolution	'Genome-Pangenome-Metagenome', criteria of bacterial species, pangenome composition and types, Venn diagrams, evolutionary basics of pangenome
5	Phylogenetic trees	Definition, algorithms, models. Tree of life.
6	Recombination	Homologous recombination, comparison of tree topology, HGT detection
5	Chromosome architecture	Replication of circular chromosome, GC-skew, gene distribution across the chromosome, synteny blocks
6	Genomic rearrangements	Genomic repeats, types of rearrangements, selection on rearrangements, role of insertion sequences, genome reduction
7	Ancestral reconstruction	Reconstruction of ancestral protein sequence, reconstruction of gene content, reconstruction of gene order. Evolutionary experiments.
8	Non-coding regions, regulation	Selection in non-coding regions, binding sites of transcription factors, prediction of operons, phase/antigenic variation
9	Visualization of data	Circular diagrams, phylogenetic trees, gene composition etc.
10	Projects presentation	

3. Assignments - Course Project

Description

The aim of the project is to apply different bioinformatics methods to real genomic data. Given 20-30 fully-assembled bacterial genomes belong to the same species. The analysis includes (1) construction of orthologs and

pangenome description (2) construction of species tree and description of phyletic patterns (3) construction of LCB and estimation of recombination rates (4) comparison of gene trees from different LCB

4. Grading

Type of Assessment Graded

Grade Structure

Activity Type	Activity weight, %
Tests	20%
Course Project	70%
Report	10%

Grading Scale

A: 90
B: 80
C: 70
D: 60
E: 50

5. Textbooks and Internet Resources

Recommended Textbooks

1. Eugene Koonin. The Logic of Chance: The Nature and Origin of Biological Evolution.
2. Pavel A. Pevzner Computational Molecular Biology: An Algorithmic Approach
2. The Pangenome: Diversity, Dynamics and Evolution of Genomes. Editors: Tettelin, Hervé, Medini, Duccio (Eds.)
3. Michael M. Madigan, Kelly S. Bender, Daniel Buckley, W Matthew Sattley, David A. Stahl. Brock Biology of Microorganisms

6. Learning Outcomes

Knowledge

Understanding of basic concepts of molecular evolution and methods of comparative genomics.

Skill

Functional annotation of genes. Construction and comparison of phylogenetic trees. Detection of regions of recombination. Reconstruction of genome rearrangements. Prediction of regulatory elements. Ability to interpret modern genomes in the evolutionary perspective.

Experience

Application of theoretical concepts to real-life problems. Understanding recent developments in molecular evolution and comparative genomics.