Molecules for bioinformatics, fall 2010

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Lecturer

Sirkka-Liisa Varvio

Scope

4 cu

Description

- This course is suitable for (statistics) students with planned orientation to biometry and also for other students interested in all-round-education on biological applications of statistical inference.
- In Bioinformatics Master program (MBI) this is one of the optionally compulsory courses and in Aalto-TKK-MBI a compulsory course.
- In Aalto-TKK-MBI the accessory course ´Genetic analysis´ is Bfms Module I.
  The accesory course (reading group) Genetic analysis, 2 cu
- is based on the book Griffiths et al. Introduction to genetic analysis, 9th ed. (9780716799023)
- The course covers Chapters 1, The genetic approach to biology, Ch 7, DNA structure and replication, Ch 8, RNA transcription and processing, Ch 9, Proteins and their synthesis, Ch 13, Genomics.
- This is the basic knowledge of molecular genetics assumed in other bioinformatics courses.

The course ´Molecules for bioinformatics' introduces characteristics of molecules as statistical and computational challenges. Part of the lectures will be in computer class.
During the course home-work (exercises) will be given. These are to submitted as informed later.

Submitting exercises gives 20 points, exam gives 40 points. Passing the course with grade 1 requires 30 points, and the limit for maximum grade 5 is 50 points of the total 60.

The lectures do not follow any specific book. Lecture notes will be available here at the beginning of each lecture.

- Sequence databases - how to retrieve sequence information and use it for comparative purposes - online facilities for multiple sequence alignment Introduction to the living world by http://tolweb.org/tree/* (http://tolweb.org/tree/*)and first steps into molecular sequence databases http://www.ncbi.nlm.nih.gov. Assignment_1.pdf, Assignment_2.pdf, Assignment_4.pdf

- The neutral theory of molecular evolution, sequence evolution models and phylogeny inference by distance matrix methods and parsimony, in practice with MEGA-software, http://www.megasoftware.net/, Assignment_3.pdf, Example dataset.txt.
  LECTURE SLIDES: ^The neutral theory of molecular evolution..pdf\, ^Modelling sequence evolution and Phylogeny inference..pdf\

- Molecules in genomes, genomic complexity.
  LECTURE SLIDES: ^Comparative genomics..pdf\

- Basics of genetic inheritance and population genetics, molecular markers, haplotypes, coalescence.
  LECTURE SLIDES: ^Mapping genomes - pedigrees - populations..pdf\

- Structure of life - three domains of life - origins of life - RNA-world - entry into the DNA world – endosymbiosis -> eukaryotic cell - stepwise evolution of the genetic code - eukaryotic big bang – genome repatterning and eukaryotic radiation - "the current status of the central dogma"
  SUGGESTED READINGS:
  What is life.pdf, RNA world.pdf, When DNA replication and protein synthesis come together.pdf, Origins of mitochondria.pdf, Origins of eukaryotes.pdf, The biological Big Bang.pdf, Latest news on codon usage.pdf, Genetic code origins.pdf, Maybe interesting....pdf, Revisiting the central dogma in 21st century.pdf,

SUBMITTING ASSIGNMENTS, GO HERE: Genetic analysis

Lecture times,

Molecules for bioinformatics: 8.9 - 23.9, Tuesdays 14-17, Wednesdays 16-18, Thursdays 14-17, D122, some lectures in computer class C128.

Associated course Genetic analysis: 8.9 - 20.10, (no course sessions in 6. Oct and 13. Oct) Wednesdays 12-16, B120.

Exams, EXAM 141010..doc

Molecules for bioinformatics exam 14.10, 9-12, C128 (computer class), all kinds of information sources can be used in the exam - all except other students or other kind of communication (for example, e-mail) with somebody.

Genetic analysis exam is 27.10, ~~12-16~~, 13-17, B120.

Registration for Molecules for bioinformatics

Registration for Genetic analysis

Did you forget to register? What to do.