Computational Biology (DA7070)

Orga

Department of Mathematics
Stockholm University

About this course

All information / news / exercises etc.pp. can be found online:
`https://kurser.math.su.se/` (Course: DA7065)

Lectures are weekly: TUE and FRI 10-12pm

Lectures in week 7 (Feb 10 and 13) will be replaced by video-lectures
(more details will be announced)

Course examination:

- 3 home assignments (total 6 credis)
- 1 oral or written exam (1.5 credits, P/F)

You pass the course, if you have in total at least 50% of the home assignments correct and if you pass the exam

For those taking this course as PhD-course, additional assignment(s) are required [will be specified at homepage]

Q: How many Phd-students?

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About this course (HOME ASSIGNMENTS)

All solutions must be provided in English

Team work to discuss the exercises is allowed and also recommended, BUT:

- everyone has to hand in an individual and independent solution of the exercies
- you must be able to explain your solutions upon request
- no copies of solutions
- never forget name + student number
- No hand-ins using ChatGPT, AI & Co without explicit declaration are allowed (and will be treated as cheating/plagiarism)!

The deadlines when to hand-in are specified at DA7070 web page.

When handing in programming exercises, always document how to compile and run your program (if needed). Well-commented source code is required.

Do NEVER copy source-code from WWW! NOTE algorithms as for finding genes can easily be applied to find plagiarism ;) **(Exercise!)**

Upload the files (as pdf / zipped source code of prgs) at the DA7070 web page under the respective assignment link.

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And now: “Happy Computational Biology!”

Questions?

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From a general point of view, the aim of this course is to learn about:

- … common problems in molecular biology
- … to formalize biological problems (i.e.: how to turn a fuzzily described problem to a mathematical/computational problem)
- … algorithmic techniques for solving common problems in molecular biology
- … function and implementation of important bioinformatics software

All these need (some) knowledge in computer science and mathematics.

The knowledge about biology you need here, will be provided in this course.

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Tentative outline:

1. Some history (Warm Up + Cracking the genetic code)
2. DNA sequencing
3. String matching (Z-Alg and Suffixtrees)
4. Comparing sequences (Alignments and Co)
5. RNA structures
6. Phylogenomics
7. Homology Relations
8. Phenotypespaces and Graph Products