

## Course information Bioinformatics (TFTB45)

“Bioinformatics is an interdisciplinary field that develops methods and *software tools* for understanding biological data. As an interdisciplinary field of science, bioinformatics combines *computer science, statistics, mathematics, and engineering* to analyze and interpret biological data.” <https://en.wikipedia.org/wiki/Bioinformatics>, 20170828.

### Teachers

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### Course Aims

The course aims to provide basic knowledge in bioinformatics, namely the theories and practical applications of computer-based methods for the analysis of DNA and protein sequences as well as for studies of protein structures. This involves both theoretical understanding and practical skills in handling methods.

After the course, you should be able to:

Use the most important open databases for literature, sequence data and structural information.

- Perform comparisons of sequences and give good interpretations of the results.
- Extract important structural information about genes, proteins, and genomes.
- Discuss the possibilities and limitations of bioinformatics tools.
- Plan for new bioinformatics problems and to solve them by combining the tools you learn in this course.

### Course book

Selected Wikipedia articles, see Reading list in Lisam.

## Teaching activities

### Lectures

|    |                                                                                                                                          |
|----|------------------------------------------------------------------------------------------------------------------------------------------|
| F1 | Introduction, Sequence Alignments                                                                                                        |
| F2 | BLAST                                                                                                                                    |
| F3 | Multiple Sequence Alignments (MSA), PSI-BLAST, PSSM                                                                                      |
| F4 | More applications on MSA, uses in machine learning SS, RSA prediction<br>Phylogeny, Clustering, tree building algorithms, build a model. |
| F5 | Application Genome browser                                                                                                               |
| F6 | Summay, Recap.                                                                                                                           |

### Practical exercises.

|    |                                                                                                                                                                                                                                                                                                  |
|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| L1 | Alignment-by-hand                                                                                                                                                                                                                                                                                |
| L2 | BLAST                                                                                                                                                                                                                                                                                            |
| L3 | Patterns, Logos, and Multiple Sequence Alignments                                                                                                                                                                                                                                                |
| L4 | Find out more information about your sequence. Secondary Structure<br>Prediction, Exposed/buried surface area Prediction, Visualize the relationship<br>to other proteins using a tree. Build a 3D structure and compare the predicted<br>secondary structure and surface areas with your model. |
| L5 | Genome Browser Exercise                                                                                                                                                                                                                                                                          |

- Each practical exercise connects to the previous lecture and are performed at a computer, except L1, which is in a class room.
- In L2 you will be given a unique protein sequence that you will use as test case to find out as much information as possible in L2-L4..
- The instructions can be downloaded from LISAM under *submissions/inlämning*.
- The lab report (answer to the question) is submitted in LISAM under *submissions/inlämning*
- Deadline three days after the exercise. This will enable feedback on the practical during the following lecture.
- **BONUS POINTS:** Reports submitted on time, that receive PASS, will gain one extra point on the exam. 5p total (Exam max: 60p)
- Ok to work in pairs for the computer practicals (L2-L5), submit using **spontaneous group submission** in Lisam. Important to add all members to the group otherwise you risk losing bonus points.

## Computer rooms

We will use Asgård and Olympen computer room at ISY in the B-house (entrance B 25, plane 3, corridor B-D), and Boren/Glan/Roxen in Sjösystemet (one time)

