DEPARTMENT OF MICROBIOLOGY, TUMOR AND CELL BIOLOGY

Karolinska Institutet

C1F3230   Genomics for Biomedical Scientists: Handle your Gene Expression Data, 3 credits (hec)

Genomik för biomedicinforskare: att hantera genuttrycksdata, 3 högskolepoäng

Third-cycle level / Forskarnivå

Approval

This syllabus is approved by the The Committee for Doctoral Education on 2023-12-01, and is valid from Spring semester 2024.

Responsible department
Department of Microbiology, Tumor and Cell Biology, Faculty of Medicine

Prerequisite courses, or equivalent

No prerequisite courses, or equivalent, demanded for this course.

Purpose & Intended learning outcomes

Purpose

The biomedical field has experienced a revolution thanks to the development of the massive parallel sequencing technologies. We can now obtain the complete genetic information of a patient in a few days at low costs. However, there is a gap between the application of classical molecular biology tools and the full use of the current genomic and computational approaches. To bridge this gap, the course is designed to give students an introduction to genomic approaches in gene regulation. The emphasis is that the students learn to apply genomic tools in their research without prior knowledge in computational biology. The students will also be made aware of ethical aspects in relation to technical progress.

Intended learning outcomes

At the end of the course the student should be able to:
- Understand the crosstalk across the different levels of gene expression regulation, with special emphasis on chromatin organization, polymerase activity and RNA biology.
- Know the principles of high-throughput technologies applied to the study of gene expression, their advantages and limitations.

- Get a deeper understanding about investigating the dynamics of chromatin and gene regulation, and how deregulation of such states contributes to human diseases.
- Design genome-wide experiments for studying the transcriptome and chromatin state, and to critically evaluate results obtained with those approaches.
- Use common bioinformatics tools to analyse ChIP-Seq and RNA-Seq experiments.
- Make use of publicly available genome-wide databases and publications to complement their own research

Course content

The course covers the use of genome-wide approaches for the study of gene expression regulation and how these approaches have become key for biomedical research. Particular attention will be paid to the understanding of advantages and limitations of those approaches, and applications to the study of human disease. The course will include both lectures and hands-on data analysis session, and provide the students tools to successfully navigate through the jungle of public available genome-wide datasets.

Forms of teaching and learning

Prior knowledge of programming is not required. The learning activities used in the course include lectures, practical training in data analysis, group discussions and problem-based learning activities. The students will be able to use gene expression data analysis software during the course. Students will be grouped in learning groups and present the results of their analysis of a preselected dataset from a recent publication in form of an oral presentation as well as design and develop a research project in which they apply what they have learned into their own ongoing research. Students will also be encouraged to actively participate in the course during the quiz and Q&A (question and answer) sessions. There will be substantial time for practising and discussing after the lectures.

Language of instruction
The course is given in English.

Grading scale

Pass (G) /Fail (U)

Compulsory components & forms of assessment

Compulsory components

Students will be asked to describe a (e.g. their own) research problem prior to the course. The seminars, group discussions and presentations are compulsory. Absence cannot be compensated for.

Forms of assessment

The students will be examined for all learning outcomes. The examination is based on:
- The student's contribution to the discussions during the course.

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- The performance during the bioinformatic hands-on sessions.
- The student's individual contribution to the analysis and presentation at the last day of the course.

Course literature

Literature will consist of recent research articles and online documentation of genomic tools. Those documents will be provided to students as PDF files prior to the course start.