

DEPARTMENT OF CELL AND MOLECULAR BIOLOGY

C5F6061, Single-Cell Lineage Tracing, 1.5 credits (hec)

Spårning av släktskapslinjer i singelceller, 1,5 högskolepoäng

Third-cycle level / Forskarnivå

Approval

This syllabus was approved by the The Committee for Doctoral Education on 2025-02-20, and is valid from autumn semester 2025.

Responsible department

Department of Cell and Molecular Biology, Faculty of Medicine

Prerequisite courses, or equivalent

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

Purpose & Intended learning outcomes

Purpose

The course aims to offer participants an understanding about lineage tracing approaches to map the developmental history of cells within a tissue. This knowledge provides fundamental insights into normal tissue development and diseases such as cancer. We cover most recent methods that allow combined lineage tracing and single-cell transcriptomics for detailed comparisons between molecular and developmental histories.

This course introduces the foundational concepts of various single-cell lineage tracing approaches, covering their experimental implementation, computational analysis, and data interpretation. Featuring renowned international speakers who have made pioneering contributions to method development and biological discovery, the course also provides ample opportunities for students to engage with experts and discuss topics relevant to their own research.

Intended learning outcomes

After completing this course, the participant is expected to be able to: summarize the principles, caveats and strengths of single-cell lineage tracing methods and critically compare these; describe applications in which single-cell lineage tracing can provide deeper biological insights; explain the experimental pipeline underlying these types of experiments; and account for the

basics of the bioinformatic principles underlying analysis of these types of data.

Course content

The course covers main lineage tracing methods including prospective lineage tracing based on synthetic barcodes (e.g. integration barcodes, recombined barcodes, CRISPR-generated barcodes) and retrospective lineage tracing based on natural barcodes (e.g. copy number variations, single-nucleotide variants, mitochondrial DNA mutations). We will discuss different methods to deliver synthetic barcodes into complex tissues (e.g. transgenes, plasmids, viruses). We will cover a variety of model systems (e.g. mouse, zebrafish, fly, cell line, tumour, organoid) and barcode readout methodologies (e.g. single-cell and spatial transcriptomics, single-cell chromatin profiling). Course participants will get a hands-on introduction into computational methods to reconstruct, evaluate and interpret single-cell lineage relationships.

Forms of teaching and learning

Lectures by invited international experts, group work and seminar presentations.

Language of instruction

The course is given in English

Grading scale

Pass (G) /Fail (U)

Compulsory components & forms of assessment

Compulsory components

All lectures, group work and the seminar presentation (examination) are compulsory. Any absence must be compensated for in accordance with the instructions of the course director.

Forms of assessment

The assessment comprises a critical evaluation and comparison of methods for single cell lineage tracing. Each student selects two papers from a selection of papers provided by the course supervisors. The student describes two different approaches and explains the experimental as well as computational pipelines. Each student identifies strengths and weaknesses of the two methods and assesses which of the two approaches is preferable for addressing a hypothetical scientific question. This is followed by group discussions about the different methods and possible biological insights.

Course literature

Relevant original research papers and review papers will be provided by the course organizers as recommended reference literature.

Other information

The course corresponds to one full week of studies.