DEPARTMENT OF MOLECULAR MEDICINE AND SURGERY

K1F2981, Rare Disease Genomics, 1.5 credits (hec)

Genomik för sällsynta sjukdomar, 1,5 högskolepoäng

Third-cycle level / Forskarnivå

Approval

This syllabus was approved by the The Committee for Doctoral Education on 2023-11-13, and is valid from spring semester 2024.

Responsible department

Department of Molecular Medicine and Surgery, Faculty of Medicine

Prerequisite courses, or equivalent

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

Purpose & Intended learning outcomes

Purpose

This is a course aimed at students actively involved or planning genetic analysis of rare diseases. The course is also appropriate for those working with complex diseases and cancer whose projects involve high throughput DNA sequencing. The purpose of this course is to provide the participants with knowledge and practical experience about current research strategies and tools for analysis of DNA-sequencing data in the field of rare disease genomics. The participants will also be made aware of ethical issues in relation to rare disease genomics.

Intended learning outcomes

After the course, the participants should be able:
1. To select adequate genomic technologies and data analysis strategies to answer research questions in the field of rare disease genetics or in their field of research;
2. To evaluate candidate variants and genes using publicly available databases and tools;
3. To discuss suitable approaches for functional validation of candidate variants and genes;
4. To identify and discuss on ethical issues arising from large-scale sequencing studies.

Course content

The focus of the course is the use of current DNA-sequencing methods and bioinformatics tools to understand the genetic basis of rare genetic diseases. Within the overall theme of clinical and experimental approaches to diagnostics of rare genetic diseases, particular attention will be paid to annotation and classification of different types of genetic variants (single nucleotide variants and structural variants). The course will cover the use of different in-silico pathogenicity scores, phenotype ontology terms, and population and family data for variant and gene interpretation. The course will cover selected experimental strategies to validate genetic findings. The course will also cover current clinical best practice guidelines concerning ethical issues such as report of incidental findings and acquisition of informed consent.

Forms of teaching and learning

The course consists of lectures, seminars, hands-on computer-based exercises, and self-studies. Students are required to bring their laptops with working internet connection.

Language of instruction

The course is given in English

Grading scale

Pass (G) /Fail (U)

Compulsory components & forms of assessment

Compulsory components

All teaching and learning activities are compulsory. Absence from compulsory parts is compensated according to the instructions from the course leader.

Forms of assessment

The examination consists of a take-home examination and a group reflection exercise. To pass the whole course the grade "Pass" must have been obtained for both assessments. Anti-plagiarism tools will be used according to KI guidelines.

Course literature

Reference literature:
- Wright CF et al. Paediatric genomics: diagnosing rare disease in children. Nat Rev Genet. 2018 May;19(5):253-268.
- Eilbeck K, Quinlan A, Yandell M. Settling the score: variant prioritization and Mendelian disease. Nat Rev Genet. 2017 Oct;18(10):599-612.
- Green RC et al. American College of Medical Genetics and Genomics. ACMG recommendations for reporting of incidental findings in clinical exome and genome sequencing. Genet Med. 2013 Jul;15(7):565-74.

- MacArthur DG et al. Guidelines for investigating causality of sequence variants in human disease. Nature. 2014 Apr 24;508(7497):469-76.
- Strande NT et al. Evaluating the Clinical Validity of Gene-Disease Associations: An Evidence-Based Framework Developed by the Clinical Genome Resource. Am J Hum Genet. 2017 Jun 1;100(6):895-906