



LUNDS UNIVERSITET

Medicinska fakulteten

Biomedical, medical and public health training board
(NBMFU)

BIMM15 Tumour Genomics

15 higher education credits

Second cycle

Level 1N

General Information

Main field

Biomedicine

Subject

Genomics

Type of course and its location in the educational system

The course is an elective in-depth course within the Master of Medical Science programme in Biomedicine.

Language of instruction

English

Learning Outcomes

Knowledge and understanding

On completion of the course the student shall be able to

- account for fundamental concepts and principles for mapping the human genome
- account for the most common mechanisms behind genomic change in humans
- explain the principles of the methods for analysing genomic change
- explain the principles for analysing global gene and protein expressions
- explain the principles for statistical and bioinformatical analysis of global gene expressions
- explain the principles for interpreting protein expression data.

Skills and abilities

On completion of the course students shall be able to

- identify and manage information from the most common genome databases
- manage raw data of genomic change and global gene and protein expressions from public databases
- analyse global gene and protein expressions by means of statistical/bioinformatical methods
- present compilations of findings from statistical/bioinformatical investigations, orally and in writing
- plan a genomic investigation of relevance for the onset of sporadic cancer
- choose between alternative approaches to the analysis of genomic data.

Adopted by the NBMFU 28 April 2010

Valid from autumn semester 2010

Judgement and approach

On completion of the course students shall be able to

- handle patient information that is not linked to specific issues and investigations in an ethically acceptable manner.

Course Content

The course consists of four stages. The first stage is a brief introduction to tumour biology, justified by the fact that most of the issues dealt with in the course are related to cancer. The second stage is concerned with genomics, focusing on the Human Genome Project and on how genomic change can be analysed and evaluated bioinformatically with the help of genome databases. A special focus is placed on various types of genetic markers and how they have been used to create genetic and physical maps for cloning and sequencing the human genome. A solid introduction is given to the evolutionary change of the genome, how changes can take place on the chromosome and sequence level in tumour cells, and how these deviations can be analysed and experimentally mapped in order to finally identify cancer-related genes.

The theme of the third stage is gene expression. Methods for the analysis of gene expression (mRNA) as well as different principles for global expression analysis by means of microarray technology are presented. A central part of the stage deals with the use of statistical methods for managing and analysing expression data and with different principles for a biological interpretation of the findings. This also goes for the fourth stage of the course, which deals with the analysis of protein data and global protein expression (proteomics).

Subjects examined

Oral and written presentations, 10 credits

Written exam, 5 credits

Instruction and Examination

Instruction takes the form of general lectures and practical computer exercises.

The introductory stage comprises approximately one week of lectures on the fundamental concepts of tumour biology and the cellular/biological processes that are involved in the development of cancer.

The remaining stages of the course mainly consist of computer exercises. In the genomics stage students are introduced to the Human Genome Project and various types of genomics issues are analysed by means of sequencing programs and genome and gene databases. Statistical and bioinformatical methods are applied both in the stage on gene expression for analysing expressions of various diseases, and in the proteomics stage for analysing protein data of various tumour types.

The assessment is based partly on oral and written presentations of all computer exercises and partly on a written examination. The written examination consists of two sections: a section testing the fundamental knowledge outcomes by questions requiring short answers and a section with essay questions and calculations, testing the ability to apply the knowledge acquired to more complex issues.

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Grades

One of the grades Pass or Fail is awarded.

Admission Requirements

To be admitted to the course students must have passed the course BIMA51 (Molecular Medicine) or 120 credits in science subjects, of which 15 credits must be in basic chemistry (one of the courses KEMA00, KEMA01, KEMA02, KEMA03), 15 credits Chemistry of the Cell (MOBA02).

Literature

Recommended literature is listed separately. An updated list is made available on the course homepage a month before the start of the course.

Further Information

The course replaces BIMM53, Functional Genomics. It is primarily addressed to students who have a background in biomedicine and molecular biology and want to increase their knowledge and skills in managing and interpreting basic biological data and to students with a background in bioinformatics who want to increase their knowledge of biology. The course focuses on issues related to cancer, but the methods and approaches dealt with are general and can be applied to other areas where biological data are handled.