

SDC

The university partnership
Denmark – China

Master's Programme in

OMICS



Curriculum

2017

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Legal Frame

Students enrolled in this programme are admitted as full-time students at University of Chinese Academy of Sciences.

This curriculum applies to students enrolled in the programme from 2017.

This master's programme is established within the framework of the following:

- Partnership Agreement between Graduate University of Chinese Academy of Sciences and University of Copenhagen (KU), Aarhus University (AU), University of Southern Denmark (SDU), Aalborg University (AAU), Roskilde University (RUC), Technical University of Denmark (DTU), Copenhagen Business School (CBS), IT University of Copenhagen (ITU), on the establishment of the Sino-Danish *Centre for Education and Research*, Graduate University of Chinese Academy of Sciences, signed on 12 April 2010
- Agreement between Graduate University of Chinese Academy of Sciences (GUCAS) and University of Copenhagen (KU), Aarhus University (AU), University of Southern Denmark (SDU), Aalborg University (AAU), Roskilde University (RUC), Technical University of Denmark (DTU), Copenhagen Business School (CBS), IT University of Copenhagen (ITU) concerning *Master's Programmes at Sino-Danish Centre for Education and Research*, Graduate University of Chinese Academy of Sciences, signed on 29 August 2011
- Agreement between Graduate University of Chinese Academy of Sciences and University of Southern Denmark concerning Provision of the *Master's Programme in Omics* at Sino-Danish Centre for Education and Research (SDC), Graduate University of Chinese Academy of Sciences, signed on 29 August 2011.

Students must observe and act accordingly to the following rules issued by the SDC Directors:

- Courses and Exams
- Exam regulations
- Thesis regulations 10 steps
- Avoid cheating on exams
- Student complaints

Students must also observe and act accordingly to Rules and Regulations for UCAS International Students.

SDC rules are published on Moodle. Title and degree

The degree awarded by University of Southern Denmark is Master of Science in Omics. The degree awarded by University of Chinese Academy of Sciences is Master of Biochemistry and Molecular Biology/ Bioinformatics/ Genomics.

Duration

The master's programme has a duration of two academic years equivalent to 120 ECTS points (European Credit Transfer System). 60 ECTS points correspond to one year of full-time studies.

When choosing thesis period *Danish/International students* must be aware of UCAS' 4 years limit for awarding diploma. UCAS' degree application procedure **STEP 10 CN** (see Thesis regulations 10 steps) has to be completed within four years from the enrolment. This period includes leave of absence.

Admission requirements

- Admission to the Master's programme in Omics is based on a successfully completed bachelor's degree (or equivalent) in:
 - Biochemistry and Molecular Biology from University of Southern Denmark or from a Chinese university.
 - Biochemistry and Molecular Biology with a minor in Chemistry from University of Southern Denmark or from a Chinese university.
 - Biomedicine from University of Southern Denmark or from a Chinese university.
 - Pharmacy from University of Southern Denmark or University of Copenhagen or from a Chinese university.
 - Biotechnology from Technical University of Denmark or from a Chinese university.
 - Technical Biomedicine from Technical University of Denmark or from a Chinese university.
 - Molecular Medicine from Aarhus University or from a Chinese university.
 - Molecular Biology from Aarhus University or from a Chinese university.
 - Biotechnology from Aarhus University or from a Chinese university.
 - Biology from Aarhus University or from a Chinese university.
 - Biochemistry from University of Copenhagen or from a Chinese university.
 - Biology and Biotechnology from University of Copenhagen or from a Chinese university.
 - Molecular Biomedicine from University of Copenhagen or from a Chinese university.
 - Food Science from University of Copenhagen or from a Chinese university.
 - Animal Science from University of Copenhagen or from a Chinese university.
 - Or Veterinary Medicine from University of Copenhagen or from a Chinese university.

The following bachelor degrees may grant admission to the Master's Programme in Omics on an individual assessment:

- Either a BSc in Computer Science from a Chinese university, supplemented with additional knowledge in Molecular Life Sciences
- Or a BSc in Chemistry from a Chinese university, supplemented with additional knowledge in Molecular Life Sciences

Other bachelor programmes that are similar to the above in level, extent or content within the Life Science area may grant admission. The institution receiving the application individually determines this.

High-level English language proficiency.

All applicants may be interviewed prior to admission to assess skills, motivation and knowledge of English.

General programme regulations

The language of instruction in the SDC master's programmes is English. Teaching, supervision and assessment will be carried out in English.

Students will be graded according to both the Chinese and the Danish grading scale. However, for the Master's Thesis, students will be graded according to the Chinese 4-point scale. See Thesis regulations 10 steps.

DK	12	10	7	4	02	00	-3
CN	100-95	94-90	89-76	75-61	60	(59-40)	39-0

Leave of absence can be granted to students on the grounds of becoming a parent, illness, military service or exceptional circumstances

Students who wish to complete degree programme elements at another university or institution of higher education in Denmark, China or abroad as part of their degree programme may apply the Teaching Committee for advance approval of transfer credit for planned subject elements.

Students can maximum be granted 30 ECTS credit transfer.

Either the Teaching Committee or the SDC Directors may grant exemptions to this curriculum or other SDC rules. Applications for exemption are submitted to the SDC Secretariat

Qualifications

Purpose

Omics is a post-genome life science research discipline, in which publicly available DNA sequence data are crucial in both experimental design and data interpretation. It is a holistic-oriented research approach, which contrasts with the traditional reductionistic methodology used in biochemistry, molecular biology etc., in that Omics attempts to give an unbiased survey of the situation within the biological entity of interest. Omics is an extension of central life science disciplines, such as cell biology, molecular biology, biochemistry, physiology, microbiology etc., where the large-scale approach is the novel dimension. Omics utilises knowledge and methods from other scientific disciplines – especially bioinformatics, computer science, statistics and analytical biochemistry; but knowledge in other scientific disciplines – especially within life science – is required for a full understanding of a given project.

The MSc programme in Omics deals with large-scale surveys of defined groups of biomolecules that are present in a biological entity. Omics includes, but is not limited to, the genetic constitution of an organism (Genomics), expression of genes at the RNA level (Transcriptomics), the protein profile of a biological entity (Proteomics), the products of complex metabolic processes (Metabolomics) and variations in the above between different situations (“quantitative Omics”). The programme includes experimental design based on statistics and existing database information, knowledge of the various technological platforms used to perform large-scale studies, computer-based analysis and interpretation of very large data sets, and the extraction of biologically relevant information for the development of testable hypothesis. The integration of different Omics datasets will be addressed theoretically as well as in practice with the students’ own data.

Qualification Profile

Knowledge

The graduate must:

- possess knowledge regarding post-genomic molecular life science, analytical biochemistry or bioinformatics, based on the highest international research within one field defined by the master’s thesis project.
- be able to understand and reflect on knowledge regarding post-genomic molecular life science, analytical biochemistry and bioinformatics, based on a scientific approach.
- be able to identify scientific problems connected to omics-approaches and reflect on application of the different available techniques.

Skills

The graduate must master specific scientific tools and methods within post-genomic molecular life science, analytical biochemistry and bioinformatics:

- Tools and databases used in Omics
- DNA-sequencing
- mRNA expression analyses by sequencing and micro arrays

- Qualitative and quantitative proteomics using mass spectrometry and electrophoretic techniques
- Metabolite analyses by chromatography, NMR and mass spectrometric detection
- Quantification in connection with gene expression
- Interaction analyses
- Chromatography and electrophoresis

The graduate must master the following general skills which are connected to employment in scientific research:

- Acquisition of knowledge within a defined area of topics
- General experimental design
- Detailed planning of experiments
- Interpretation of experimental data
- Keeping of laboratory journals in execution of experiments

The graduate must:

- be able to choose among scientific theories, methods, tools and general properties within analytical biochemistry, bioinformatics and different Omics approaches and apply these on scientific questions.
- on the basis of experiments and newly obtained knowledge be able to establish testable hypotheses or improve on existing ones.
- be able to design experiments to verify or falsify a given hypothesis.
- be able to discuss and arrange new experimental data in context of already existing knowledge.
- be able to disseminate research based knowledge and discuss professional and scientific problems with both peers and non-specialist.

Competences

The graduate must be able to:

- control and develop complex processes within different Omics approaches and suggest novel options if unexpected situations occur.
- The graduate must be able to independently initiate and implement disciplinary and interdisciplinary cooperation and to assume professional responsibility based on professional expertise.
- The graduate must be able to independently take responsibility for his/her own professional development and specialisation.

Structure

Semester	Course / Programme element	Exam	Grading	Examiners	ECTS
1	Omics brush-up	Oral	Pass/Not-pass	Internal	5
	Introduction to Omics	Assignment and oral	Pass/Not-pass	Internal	6
	Analytical biochemistry and sample preparation for Omics	Written	7/100 scale	Internal	8
	Contemporary topic in Omics	Assignment	7/100 scale	Internal	5
	Personalized Track	Assignment and oral	Pass/Not-pass	Internal	7
2	Molecular genetics and epigenetics	Oral	7/100 scale	Internal	5
	Central techniques in Omics	Written	7/100 scale	Internal	9
	Bioinformatics and Systems Biology	Assignments	Pass/Not-pass	Internal	7
	Biostatistics	Assignment and oral	7/100 scale	Internal	3
	Food Omics	Assignment and oral	7/100 scale	Internal	5
3	Thesis	Assignment and oral	7/4 scale	External	60
4					

The programme contains these elements

The first two semesters provide the common core of the programme. In the 3rd and 4th semester, the student will write the thesis.

Course and exam descriptions

Omics brush-up

5 ECTS

CONTENT

The course will provide the student with theoretical knowledge at a level corresponding to a 5 ECTS bachelor study course, which covers the topic that the student should upgrade. The course will give the student the essential minimum knowledge to follow the first courses in (analytical) biochemistry, molecular biology and bioinformatics offered in the master's programme. Experimental work will generally not be a part of the curriculum, but computer-based exercise may be relevant.

Precise details will exclusively depend on the student's qualifying bachelor degree

LEARNING OBJECTIVES

At the end of the course, the students should be able to:

- communicate basic concepts and knowledge within the individualised topics in oral form.
- independently acquire additional knowledge related to the individualised topics.

EXAMINATION

Oral Exam in the form of a presentation on the "Brush up" topic.

RE-EXAMINATION

Same as the ordinary exam.

GRADING

Pass/not pass.

Introduction to Omics

6 ECTS

CONTENT

1. Omics: history and prospects
2. Introduction to genomics
3. Transcriptomics: from microarray to deep-sequencing
4. Introduction to Proteomics
5. Interaction studies using Omics
6. Introduction to metabolomics
7. Genomics and systematic biology
8. Bioinformatics and computational biology

LEARNING OBJECTIVES

At the end of the course, the students should be able to:

- understand information contained - and outline the methods used - in genomics.
- understand and describe the use of microarrays in transcriptomics.
- describe and understand the information obtained by qualitative and quantitative proteomics and outline the methods used.
- describe the role of posttranslational protein modifications and the use of proteomics to determine these.
- discuss the importance of protein interaction and outline the methods used to study these.
- understand and describe the levels of metabolomics and the methods involved.
- outline the use of bioinformatics tools in various Omics studies.
- explain how systems biology is used to describe the function of biological systems.

EXAMINATION

Report describing the use of Omics in a hypothetical research project. 30 minutes oral defence of the report.

RE-EXAMINATION

Same as the ordinary exam.

GRADING

Pass/not pass.

Analytical biochemistry and sample preparation for Omics

8 ECTS

CONTENT

The theory behind methods used for separation and purification of RNA, DNA, proteins, peptides and metabolites will be covered, including methods based on affinity, hydrophobicity, polarity, charge and size:

- Extraction and purification of proteins, RNA, DNA and metabolites from biological samples.
- Chromatographic techniques
- Electrophoretic techniques
- Selective purification/enrichment for post-translational modifications
- Labelling and quantitation for proteomics
- Sample preparation and data analysis in metabolomics
- Sample preparation for lipidomics
- Sample preparation for genomics/transcriptomics
- Digestion of biomolecules
- Interfacing chromatography with mass spectrometry

Practical laboratory work will include:

- Reverse phase liquid chromatography
- Gas chromatography
- Lipid purification
- Protein purification
- Two-dimensional electrophoresis
- MALDI peptide mass finger printing and MALDI MS/MS for identification; data analysis
- Sample preparation for transcriptomics
- Sample preparation for genomics

LEARNING OBJECTIVES

At the end of the course, the students should be able to:

- explain the principles behind the analytical techniques presented in the course.
- evaluate strengths and limitations of different separation/purification techniques.
- select the best separation/purification technique(s) for a specific omics investigation.
- assess the quality of data from separation/purification analyses as presented in original scientific literature.

- evaluate and reflect on the use of separation/purification techniques applied in original research articles.
- operate equipment and perform experiments using the techniques taught in the practical laboratory exercises.

EXAMINATION

Mandatory participation in Laboratory exercises. 4-hours written exam at the end of the semester.

All aids except internet access and communication with others.

RE-EXAMINATION

Same as the ordinary exam.

GRADING

Grades are given according to the Danish 7 step and the Chinese 100 points grading scales.

Contemporary topics in Omics

5 ECTS

CONTENT

The first semester of the Omics programme introduces the students to the main omics disciplines and gives an overview of the sample preparation required for an omics experiment. Various analytical techniques are presented, also in lab demonstrations and exercises. Hence, first semester, and to a large extent also second semester, is "tools" focused with no substantial presentation of a project-oriented application of an omics strategy.

The aim of the course is to present a contemporary "biological" question or problem that is best addressed by the generation of large data sets via the application of one or more omics techniques. Interpretation of data obtained for the elucidation of the "biological" question and the biological significance of the data will be emphasised along with pros and cons of the selected experimental approach. Thus, the students will be given a coherent picture of a specific topic or research field, and how omics have been crucial in the progression of our knowledge. This will put previously obtained technical knowledge into the perspective of real life applications.

The precise topic of the course may vary from year to year, but should fulfil the above described aims. Therefore, a specific course description for topic in question will be forwarded to the SDC Life Science Teaching Committee for approval in due time before teaching is initiated. The specific course description will include - as a minimum - aim, course content, learning objectives, expected learning outcome, teaching form and evaluation forms.

EXAMINATION

To be announced on Moodle.

RE-EXAMINATION

To be announced on Moodle.

GRADING

Grades are given according to the Danish 7 step and the Chinese 100 points grading scales.

Personalized Track

7 ECTS

CONTENT

The main objective of this part of the Omics programme is to provide the individual student with the basic knowledge required to select a theme for the master's thesis, and more over provide a contact that can serve as a "help-desk" throughout the whole study, although with main emphasis on the final master's thesis. Thus, this course will be the glue of the entire study programme.

The objective is to introduce a range of applications of Omics and presentation of various relevant areas of research, which will help the student in selecting his/her personal "biological" question that will follow the student through the study programme and form the basis for the master's thesis. Skills acquired in the courses focused on technical, analytical, biological and bioinformatics as well as "entrepreneurship" will be applied to the personal "biological" question selected.

Moreover, the student will learn about project management, scientific writing and oral presentation of a scientific topic to peers and to non-experts. Standards in publication ethics and scientific conduct will be discussed. Scientific standards that are expected by peer-reviewed journals will be presented.

Suggested topics for biological areas:

- Omics in medical applications (e.g. metabolic-, degenerative-, and cancer diseases)
- Omics and microbiology
- Omics and plant biology
- Omics and agriculture (e.g. animal breeding, food and soil).

LEARNING OBJECTIVES

At the end of the course, the student is expected to be able to:

- critically evaluate scientific results in the original research literature.
- present scientific results in an oral seminar given in English.
- discuss strengths and limitations of modern techniques in Omics.
- identify scientific problems connected to Omics-approaches and reflect on application of the different available techniques to solve relevant biological questions.
- identify the "method of choice" for analysis of a given biological sample.
- select the "method of choice" for answering a specific biological question.
- demonstrate skills in general experimental design, planning of experiments, interpretation of experimental data and note keeping in execution of experiments.
- independently take responsibility for his/her own professional development and specialisation, including application for financial research support.

- disseminate research based knowledge and discuss professional and scientific problems with both peers and non-experts.
- write a scientific paper presenting the results from the Thesis. This paper should ideally be submitted to a peer-reviewed scientific journal.

EXAMINATION

Project assignment.

RE-EXAMINATION

Re-exam will follow the same format.

GRADING

Pass/Not-pass

Molecular genetics and epigenetics

5 ECTS

CONTENT

The course will provide the students with the skills to understand and explain the basic molecular architectures of plant and animal genomes as well as the basic mechanisms that regulate genome functions. Furthermore, the course will provide the students with the ability to understand and discuss principles of molecular genetics including an insight into and the use of methods to identify complex traits and disease genes.

- The organisation of plant and animal genomes
- Identification and characterization of DNA sequences, genes and molecular genetic variation
- Molecular methods used to map Mendelian and complex traits
- Basic mechanisms in genetic regulation of genome function
- Basic mechanisms underlying epigenetic phenomena, including DNA methylation, chromatin modification, RNA methylation and noncoding RNA
- Reading, understanding and oral presentations of scientific papers

Teaching continuously over eight weeks with two to four sessions per week. Teaching comprises lectures, discussion, student presentations and exercises.

LEARNING OBJECTIVES

By the end of the course, the student is expected to have the skills to:

- explain the architecture of plant and animal genomes.
- discuss the mechanisms that regulate the functions of the genome.
- discuss the principles of molecular genetic methods and the techniques used to identify complex traits and disease genes.
- explain principles and mechanisms underlying epigenetic phenomena.
- critically read, understand, and orally present scientific papers.

EXAMINATION

25 minutes oral exam including assessment. Students will be given 5 minutes to prepare answers for a draw from random test questions, and give 20 minutes for oral presentation.

RE-EXAMINATION

Re-exam will follow the same format.

GRADING

Grades are given according to the Danish 7 step and the Chinese 100 points grading scales.

Central techniques in Omics

9 ECTS

CONTENT

Biosciences in the post genome era are a technology driven field. Progress depends on investigating molecular changes with large-scale technologies. This course aims to build basic understanding of the technologies and methods used to characterise and detect variations in genome, transcriptome, proteome, and metabolites of humans, animals, plants and microorganisms, and to provide students with knowledge sufficient for evaluating the specific strengths, weaknesses and possibilities of individual basic methods for characterising biological systems at molecular levels.

The course will provide the students with the skills to understand, explain and select the relevant basic methods for characterising biological systems by large-scale molecular mapping methods. The students will develop the skills to evaluate the strengths and shortcomings of specific technological approaches currently available for describing genome, proteome, transcriptome and metabolome changes in biological systems. The competences achieved are appropriate for preparing the students for designing their own experimental approaches for their final master projects.

Content and perspective:

- Mass spectrometry technology (Instrumentation, Electrospray ionization, Maldi-TOF, ion optics, mass analysers and operation)
- Practical introduction to Protein id and characterization in Proteomics and Metabolomics. Interpretation of data including post-translational modifications.
- Protein and metabolite quantification (LC-MS/MS, SRM and MRM methods)
- Array technology applied in omics
- Advanced Imaging in omics (EM, MALDI Imaging)
- NMR based metabolomics
- Next generation DNA sequencing
- RNAseq based transcriptomics
- microRNA technology

LEARNING OBJECTIVES

The student who has met the objectives of the course will be able to:

- evaluate strengths and limitations of various statistical methods.
- explain the overall theoretical principles behind the statistical methods introduced during the course.
- account for the preconditions, assumptions and limitations in the individual steps of the statistical analysis.
- independently perform a basic analysis of the various omics data using R.

By the end of the course, the student is expected to have the skills to be able to:

- evaluate strengths and limitations of individual central technologies for structural and quantitative analyses of DNA, mRNA, proteins and metabolites from biological samples.
- evaluate the quality of data from proteome, genome, transcriptome and metabolome analyses as presented in original scientific literature.
- evaluate and reflect on the shortcomings of the specific methods and technologies chosen to describe specific biological systems in original research articles.
- suggest alternative approaches to those presented in original scientific literature.
- motivate the choice of experimental methods and approaches for describing and investigating specific biological problems.

Learning outcome from the theoretical part:

Being able to read, understand, explain, and to evaluate critically the methods and information from primary research articles using the following omics methods:

- Protein identification by Maldi-TOF based peptide mass fingerprinting
- Protein id by ESI-MS/MS.
- Metabolite id and quantification analyses by Mass spectrometry.
- Protein quantification by Mass spectrometry
- Discovery based comparative proteome mapping
- Hypothesis based (targeted) comparative proteome mapping.
- Selected reaction monitoring MS. (SRM).
- Proteogenomic data integration.
- Mapping of posttranslational modification of proteins.
- Microarray based transcriptome mapping.
- Next-generation based transcriptome mapping.
- Genome sequencing

Learning outcome from the laboratory part:

Being able to plan experiments, interpret raw data, critically evaluate data quality and to integrate data across the following omics technologies:

- Protein identification by Maldi-TOF based peptide mass fingerprinting
- Protein id by ESI-MS/MS.
- Protein quantification by Mass spectrometry
- Discovery based comparative proteome mapping
- Hypothesis based (Targeted) comparative proteome mapping.
- Selected reaction monitoring MS (SRM).

- Mapping raw instrument data against reference genome data.
- Microarray based transcriptome mapping.
- Next-gen based transcriptome mapping.

EXAMINATION

2-hour closed book written exam followed by 3-hour open book written exam.

RE-EXAMINATION

Same as the ordinary exam.

GRADING

7 Grades are given according to the Danish 7 step and the Chinese 100 points grading scales.

Bioinformatics and Systems Biology

7 ECTS

CONTENT

Bioinformatics is today essential for almost all branches of life sciences, as data generation has become more accessible globally. For instance, the advent of Next Generation Sequencing (NGS) technologies has transformed how biological research is being performed and today almost all biological fields use the technology for innovative discoveries. Whole human genomes can today be sequenced cost effectively and rapidly providing unprecedented possibilities for investigating human traits, evolution and diseases. Similarly, whole bacterial communities and their interplay with the environment can be studied, unravelling novel enzymes and organisms. As these experiments produce massive amounts of data, skills with bioinformatics and large data supercomputing are crucial for analysis. The aim of the course is to give the students a good basic handling of the Unix command line for handling large data sets, knowledge of the NGS technology and steps for sequence data analysis as well as a background to bioinformatics in general and an introduction to systems biology.

This course introduces elementary Unix, basic programming principles and good programming practices. The Unix introduction covers basic commands, file manipulation and input/output redirection. The idea is to equip the student for handling common bioinformatics file formats and forming a good basis for the computer exercises, which are integrated with the lectures.

The student will get an introduction to the most commonly used bioinformatics databases, such as Genbank, PDB, UniProt and SwissProt and work with bioinformatics algorithms such as BLAST, PSI-BLAST and pairwise- and multiple alignment. Weight-matrix based methods will be introduced and how to search using weight-matrices.

An introduction to broader topics such as network biology and metagenomics informatics will also feature on the course to provide a vision for the breadth of omics data and how their utilisation leads to impact.

LEARNING OBJECTIVES

A student who has met the objectives of the course will be able to:

- work from the Unix command line for handling data and operating tools.
- use basic programming skills to extract and analyse data.
- demonstrate insight in structured problem solving.
- break down real-world data problems.
- recognise patterns in data and generalize from them.
- parse (read and extract) (bioinformatics data) files for needed information. Understand and operate with common formats for representing DNA and protein sequence data.

- search for sequence and structure data from the publicly available databases, such as GenBank, UniProt and PDB.
- generate and critically evaluate DNA and peptide alignments.
- query sequence databases using alignment based methods (BLAST) and critically evaluate the results.
- explain the applications of the different NGS technologies, including the weakness and strengths of the approaches, learn to implement the steps involved in a general NGS data analysis.
- give a basic introduction to network biology and metagenomics informatics.
- explain basic concepts of machine learning.
- understand B and T cell epitopes, and MHC presentation with bioinformatics applications.
- cooperate in groups and communicate results.

EXAMINATION

Most sub-courses are designed with exercises involving hands-on work and/or answering questions based on content taught in the classroom. These are evaluated, and comprise a final grade according to sub-course weight (see below). Final grading for the course will be based on the 7-step scale/100 scale.

In case of students failing the course or otherwise requiring a re-examination, they will be offered a written re-examination covering the whole course. This examination will be conducted in a single 4-hour session that comprises evaluation of all the modules. Each module will contribute to a different weight in the final evaluation (weights specified below). The written examination is a combination of a) programming exercises, b) multiple choice questions and c) descriptive questions.

The sub-courses and respective assessment criteria and weighting are listed below:

Module 1 - Introduction to programming, 25% of the final grade.

Covering the basics of the Python programming language along with introducing basic programming principles and good programming practices. Various looping and control structures, built-in data and container types (lists and dictionaries), regular expressions and more advanced data structures are covered. Additionally, a basic introduction to awk for command line manipulation of data. Examples from programming will focus on parsing and manipulating data files including bioinformatics file formats. A large part of the course is spent on computer exercises, which are integrated with the lectures. Intense classroom teaching will be tightly woven in with exercises conducted in class and as homework.

Module assessment: All exercises are done individually and will be assessed. Students will have exercises every day, which will be graded and together give a combined grade for this module.

Module 2 - Introduction to bioinformatics, 20% of the final grade.

The lectures introduce the students to the basics of bioinformatics including the electronic data formats for storing information about biological macromolecules, such as DNA, RNA and proteins, as well introduce them to publicly available sequence and structure databases such as GenBank, UniProt and PDB. The

section will provide students with knowledge of a number of new methods for molecular structure and sequence analysis. Second half of each lecture day includes hands-on sessions of computer exercises, where the methods are learned through practical use.

Module assessment: Based on the completion of the daily exercises, which include searching data, running different tools and based on the results replying to the questions included in the exercises. These exercises are to be completed in the class or at home.

Module 3 – Introduction to NGS and Metagenomics, 10 % of the final grade.

The aim of this module is to give a solid knowledge of NGS and NGS data processing, the microbiome concept and methods for analysing metagenome data. Students should be able to understand and apply this information to practical uses, such as screening large segments of sequenced DNA extracted from wide-ranging environmental samples (in microbiome samples in particular). Furthermore, it is a goal that the students learn to formulate scientific questions in relation to the microbiome that can be addressed by advanced metagenomics analysis and integration with other data types related to the micro biome (association analysis).

Module assessment: Students are asked to work on exercises/assignments. Answers have to be handed in and will be evaluated.

Module 4 – NGS-2, 10 % of the final grade.

This module builds on module 3 – Introduction to NGS. Here the student will be introduced to NGS methods aimed at the analysis of gene regulatory networks, both at the transcriptional and post-transcriptional level.

Students will learn about Transcription Factor-DNA interactions, mRNA expression, micro-RNAs. They will be introduced to the methods currently used for studying such mechanisms and molecules and how these data can be used to understand the genetic events involved in various stages of life.

We will also learn introductory notions of network biology and graph theory, by which gene and/or protein interactions can be studied in a systems-wide manner.

Finally, two practical examples of projects in which these methods are used will be discussed.

Module assessment: Students will be evaluated on a combination of short questions, short exercises and the analysis of a paper (in the form of targeted questions relative to such paper)

Module 5 – Machine Learning and Immunology, 15 % of the final grade.

Basic knowledge of machine learning concepts: training and evaluation, cross validation will be discussed.

Application to simple cases (HMM profiles of proteins). Fundamentals of adaptive immunity: B and T cell epitopes, MHC presentation. Training of neural networks for predicting MHC presentation from experimental data. Usage of the tools in a real-case example (vaccine case study)

Module assessment: Combination of short questions (50%), and a written report on the vaccine case study (50%).

Module 6 - Integrative Systems Biology and Human Genetics, 20 % of the final grade.

This module will focus on Integrative Systems Biology and Applied Human Genetics. Current bioinformatics usage in medical genetics, interspersed with application of methods learned in previous weeks. Students will learn about genome-wide association studies along with some disease-insight, further learn about analysis of RNA-seq biobank data, its combination into functional genetics approaches, eQTL and allelic imbalance. Students will then learn about the application to drug discovery (mendelian randomisation) as well as drug response stratification. Finally, the students will be introduced to one-at-the-time personal genetics and how to analyse their own genome.

Module assessment: The students will be assessed using a combination of assignment evaluation and multiple choice tests.

RE-EXAMINATION

A written re-examination covering the whole course. This examination will be conducted in a single four-hour session that comprises evaluation of all the modules. Each module will contribute to a different weight in the final evaluation (weights specified below). The written examination shall be a combination of a) programming exercises, b) multiple choice questions and c) descriptive questions.

GRADING

Pass/fail

Biostatistics

3 ECTS

CONTENT

Sophisticated statistical methods for analysing omics data are increasingly employed to deal with the complex data sets from the high-throughput experiments. With statistical tools, scientists generate testable hypotheses and draw the scientific conclusions supported by data. This course aims to build a basic understanding of the theoretical and practical aspects of various biostatistical concepts and analytical methods commonly used in the omics field. It focuses on the concepts of experimental design, qualitative and quantitative analysis of data, and statistical inferences. The course also aims to provide the students with knowledge sufficient for evaluating the specific strengths, weaknesses and possibilities of individual statistical methods as well as the capability to read articles on the subject critically. In addition, this course will provide a hands-on tutorial on analysing data with R, the most important statistical tool in the academy.

Content and perspective

- Descriptive statistics
- Introduction to probability
- Introduction to hypothesis testing (for two groups of numbers)
- Introduction to multiple hypothesis testing
- Introduction to analysis of variance (ANOVA)
- 2 by 2 contingency table
- Linear regression
- Correlation
- Principal component analysis (PCA) and cluster analysis
- Statistical power
- Data transformation
- Data visualisation

LEARNING OBJECTIVES

Knowledge

The student who has met the objectives of the course will be able to:

- explain the overall theoretical principles behind the statistical methods introduced in the course.
- evaluate strengths and limitations of various statistical methods.
- account for the preconditions, assumptions and limitations in the individual steps of the statistical analysis.
- apply reasonable statistical methods in analysing empirical data.
- independently perform a basic analysis of the various omics data using R.

Skills

By the end of the course, the student is expected to have the skills to:

- explain the basic principles underlying statistical methods.
- evaluate strengths and limitations of various statistical methods for data analysis.
- use R language to perform statistical tests.

EXAMINATION

Final exam is a report based on the use of statistics in a hypothetical research project. The student describes how they solve a given biostatistics assignment. Details on the individual assignment will be discussed during the exercises. The report should consist of between 5 pages and 10 pages (excluding references). The report must contain the following sections: a) introduction and description of assignment; b) overview of the student's procedure to solve the task; and c) evaluation of results and conclusion.

RE-EXAMINATION

The Re-examination will have the same format as the ordinary exam but a new topic must be chosen.

GRADING

7 Grades are given according to the Danish 7 step and the Chinese 100 points grading scales.

Food Omics

5 ECTS

CONTENT

The omics disciplines are strongly in demand in the sectors of food, agriculture, biotechnology and applied microbiology. In these areas, omics represent a largely underexploited potential of technologies with great promise to advance developments to gain insights at the molecular level into e.g. quality of foods, feed and raw materials, nutritional values, probiotics, crop plant breeding, processes in food production, biotechnology and fermentation and food ingredients. The use of omics techniques is rapidly implemented in these fields of fundamental and applied research with anticipated huge benefits involving also development of dedicated emerging omics tools.

The course aims to provide a broad knowledge of the use of omics in food science concerned with cereals, vegetables, probiotic bacteria, livestock, meat and dairy products. It will provide background to the technical sub-disciplines of proteomics with reported application in the various areas of food and agricultural sciences. It focuses on the experimental design from sample preparation to qualitative and quantitative analysis of data.

Case stories will be selected to cover various thematics including also functional properties of key proteins involved e.g. 1) uptake and metabolism of prebiotic oligosaccharides by probiotic bacteria from the human gut, 2) redox control systems in cereals and microbes in relation to food biotechnology, 3) quality of selected foods. The course also aims to provide the students with knowledge sufficient for proposing research strategies to address objectives to be pursued in the areas of food and agricultural sciences and to evaluate the specific strengths, weaknesses and possibilities of individual experimental plans and projects as well as the competence to critically read articles on the subject.

Content and perspective

- Lectures on relevant techniques in proteomics
- Introduction to the area of food and agricultural sciences
- Description of case stories on "omics" in probiotics bacteria
- Description of case stories "omics" in crop cereals for functional properties and quality
- Description of case stories "omics" in livestock, vegetables, other raw materials
- Description of case stories "omics" redox-active processes in lactic acid bacteria and cereal crops
- The discovery chain from "2D spots to 3D structures" and "omics"-based identification of key proteins
- Production using recombinant techniques and characterization of key proteins in cereals and probiotics
- PULs gene clusters (PULs = polysaccharide utilization loci) in probiotic bacteria, "omics" and phylogenetic analysis
- Future perspectives

LEARNING OBJECTIVES

The student who has met the objectives of the course will be able to:

- evaluate strengths and limitations of selected relevant experimental plans in the area of food and agricultural proteomics.
- explain the possibility of integration of “omics” techniques for individual food and agricultural raw materials and products.
- account for the preconditions to provide experimental design to achieve given objectives.
- independently present a critical account of the application of “omics” in a selected theme within food and agricultural sciences.

Module structure and teaching approach

The course will run over three weeks intensively, with up to eight hours per day. Teaching comprises lectures, discussion, group work on 3-4 selected topics, student presentations with students as opponents.

EXAMINATION

The final exam is held at the end of the course, based on the report (15-30 pages) made of groups of 2-4 students, who work on a chosen subject within the course content. Individual oral presentation (15 min) of the report and a defence (15 min) of the subject chosen for the report where the questions at the exam will take a starting point in the report and be covering also general topics from the lectures as well as the journal club. Total examination of each student is thus 35 min inclusive grading by the examiner and the external examiner.

Assignments, reports and oral defence will be graded with one final grade.

RE-EXAMINATION

3 hour written exam in the form of an essay addressing a theme within the topic.

GRADING

7 Grades are given according to the Danish 7 step and the Chinese 100 points grading scales.

Thesis

60 ECTS

CONTENT

The student will be assigned a Danish and a Chinese supervisor who are to approve the topic.

The student must submit a thesis contract signed by the supervisors and the student to the SDC Office before the start of the thesis period, which is 1 September. An individual thesis period may be arranged with the supervisors, as stated in the general rules for an SDC Master thesis.

The thesis contract contains the thesis topic, a description of the thesis with appropriate selected references, name of the institute and laboratory for execution of the practical work, and submission deadline.

The submission deadline for thesis is 15 June. The thesis is to be delivered digitally at the SDC Office.

An oral thesis defence will be held in the first week of July.

The thesis and the oral defence are assessed by the supervisors and an external examiner.

LEARNING OBJECTIVES

After completing the thesis, the student is expected to master and be able to:

- state the purpose of an experimental omics project in context of the background of the research field.
- independently retrieve scientific literature relevant to the thesis, and outline the current knowledge based on this literature.
- describe materials and methods used in the thesis in such details that an equally qualified person can reproduce the experiments.
- describe, document and explain results obtained in the thesis, so professionals in the field can follow the experiments and the experimental strategy.
- Discuss the thesis results in context of existing knowledge on the topic, relate the outcome of the experimental work to the purpose of the thesis, and devise obvious future work and perspectives.
- present his/her own research in the format of a scientific manuscript.
- orally disseminate his/her own research, and discuss it with peers.
- explain the principles of the main methods used in the thesis.
- describe the biological foundation central to the thesis.

EXAM

The thesis must be written in English throughout. The thesis should be built around the outline of a manuscript for an international scientific journal. The exact journal, from which the format is observed, will depend on the topic of the thesis and should be chosen by the student and the supervisors in agreement. The thesis should be constructed as follows:

- A cover page with all relevant information on thesis title, student, supervisors, study programme and period of thesis work.
- A scientific manuscript prepared according to the guidelines provided by the chosen scientific journal.
- List of abbreviations if this is not requested by the journal's guidelines
- Supplementary material, which presents e.g. elaboration on methods, relevant data not included in the manuscript and discussions on such methods/data with references. Supplementary material is not a compulsory section, but may be useful depending on the thesis project and outcome.
- An electronic media for software developed as part of the thesis, when relevant.

The scientific manuscript must not exceed 40 pages including all figures and tables when following the journals' guidelines for formatting. There is no minimum for supplementary material, since it is not compulsory, but the maximum length is 80 pages all included.

Defence

The defence has the form of an oral exam, which is initiated by an approximately 30 minutes student presentation on the thesis. The subsequent examination should not exceed 90 minutes.

RE-EXAMINATION

The same as the ordinary exam attempt. For more information, see Moodle's 10-step guide.

GRADING

For the Danish/international students, grades are given according to the Danish 7 step and the Chinese thesis grading scales.

For the Chinese students, grades are given according to the Danish 7 step grading scale only.

The details of the thesis procedure are described in SDC Thesis Regulations 10 Steps.

Commencement

Effective as of 01.09.2017

Changes to the curriculum

2018.05.16: Change of exam and re-exam in Biostatistics. The exam has been changed from a report of between 1000 and 2000 words with oral defence to a report of between 5 and 10 pages without oral defence. Furthermore, the re-exam has been changed from being a revision of the previous exam paper to writing a new report.