Core courses

# Core Courses

Faculty of Science and Engineering

# Systems Biology

## Full course description

This course introduces the field of Systems Biology, giving a birds-eye-view of key publications, successful applications, novel developments, and ongoing research. You will get acquainted with the large diversity in model types and mathematical frameworks used in systems biology, and their application to a range of biological systems and processes. Furthermore, you will familiarize yourself with the writing of a research proposal with a strong experimental design, and presenting/orally defending your research proposal.

This course is suitable for everyone who wants to become familiar with the breadth and depth of the field of systems biology. In this course you will focus on:

- Applications of Systems Biology
- The multi-scale and multi-disciplinary nature of Systems Biology
- Current research topics within the field
- Ongoing Systems Biology research projects within Maastricht University
- Writing and presenting a competitive research proposal.

## Course objectives

This course introduces the field of Systems Biology, giving a birds-eye- view of key publications, successful applications, novel developments, and ongoing research. You will get acquainted with the large diversity of model types and mathematical frameworks used in systems biology, and their application to a range of biological systems and processes.

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Furthermore, students will familiarize themselves with the writing of a research proposal with a strong experimental design, and presenting/orally defending their research proposal.

## Recommended reading

**Journal club papers:**
Papers to be discussed during the journal club meetings will be provided through Canvas.

Systems Biology and Bioinformatics

**Textbooks as further reading material:**
1. Voit, E.O. A First Course in Systems Biology, Garland Science, 2013.
2. Edda Klipp, Wolfram Liebermeister, Christoph Wierling, Axel Kowald. Systems Biology: A Textbook, 2nd Edition, ISBN: 978-3-527-33636-4, Wiley-Blackwell, 2016.

MSB1001
Period 1
2 Sep 2024
25 Oct 2024
Print course description
ECTS credits:
6.0
Coordinators:

- I.C.W. Arts
- M.E. Adriaens

Teaching methods:
Lecture(s), PBL, Skills, Assignment(s)
Assessment methods:
Assignment, Final paper
Faculty of Science and Engineering

# Biology and Physiology

## Full course description

This course introduces the field of biology and physiology. Understanding the basics of biology and physiology is crucial in systems biology. During this course, human physiology, the cell, cellular processes, genetics and evolution will be discussed. You will get acquainted with the different cellular compartments and functions as well as the molecular processes within cells in relation to genetics/genomics and metabolism. Moreover, you will receive hands on experience with basic molecular biological experiments.

## Course objectives

The overall aim of this course is to introduce the basic concepts of (molecular) biology and physiology to students with a limited biology background. The student gets an overview of the basic biological concepts and laboratory experiments important within the field of systems biology.

The topics within this course include:
- Human physiology
- Basic cell biology and cellular organelles
- Genetics and Genomics
- Evolution and Phylogenetics
- Regulation of gene expression (eg epigenetics)
- Membranes and cellular transport
- Cellular Metabolism and Respiration

Intended learning outcomes:

- ILO1002.1 – Describe basic biological concepts discussed in the tutorials and lectures
- ILO1002.2 – Describe basic molecular techniques to analyze DNA, RNA, protein and metabolites
- ILO1002.3 – Identify experimental approaches to generate data needed to answer specific research questions in the field of systems biology
- ILO1002.4 – Perform basic molecular genetic experiments, including Immuno stainings, DNA isolation and PCR
- ILO1002.5 – Analyze and explain data obtained from experiments described in ILO1002.2
- ILO1002.6 – Critically assess experimental procedures used in scientific papers

## Recommended reading

**Mandatory Literature:**
Campbell, Urry, Cain, Wasserman, Minorsky, Reece. Biology: a Global Approach. 11th edition. Pearson, 2017.
**this is the main book for this course, copies are available at the MaCSBio library. However, these copies should not leave the MaCSBio department**

**Additional Literature:**

- Alberts, B. Molecular Biology of the cell
- Edda Klipp, Wolfram Liebermeister, Christoph Wierling, Axel Kowald. Systems Biology: A Textbook, 2nd Edition, ISBN: 978-3-527-33636-4, Wiley-Blackwell, 2016.

**Journal Clubs:**
Journal club 1: A subcellular map of the human proteome https://science.sciencemag.org/content/356/6340/eaal3321
Journal club 2: Genetic diagnosis of Mendelian disorders via RNA sequencing https://www.nature.com/articles/ncomms15824
Journal club 3: A Genome-wide CRISPR Death Screen Identifies Genes Essential for Oxidative Phosphorylation
https://www.sciencedirect.com/science/article/pii/S1550413116304338?via%3Dihub

**Online resources:**
In this course, Padlet is used as a platform for references to course relevant video and web material. The Padlets provide a convenient way to organize weblinks. To help things started, a few links that contain explanations of the important concepts have been added. We highly recommend you to add materials yourself if you come across something useful on the web to share with other students. The following walls are available (arranged on topics). Just double click on the wall to add URL's to the wall.
https://padlet.com/MSB4102/Physiology
https://padlet.com/MSB4102/cell_biology
https://padlet.com/MSB4102/Genetics
https://padlet.com/MSB4102/Evolution
https://padlet.com/MSB4102/membranes_Transport
https://padlet.com/MSB4102/Metabolism_Respiration

MSB1002
Period 1
2 Sep 2024
25 Oct 2024

Systems Biology and Bioinformatics

Print course description
ECTS credits:
6.0
Coordinator:

- M. Gerards

Teaching methods:
Lecture(s), PBL, Research, Skills
Assessment methods:
Presentation, Written exam, Assignment
Faculty of Science and Engineering

# Mathematics of Biological Systems

## Full course description

This course gives a basic grounding in several key areas of mathematics; calculus, linear algebra, basic skills, statistics and additionally will provide an introduction to Matlab. These topics are grouped into four strands. As students enter this course with differing backgrounds, the aim here is to bring everyone up to a level which will enable them to engage with the later compulsory courses and electives. An initial self- assessment will be completed by all students and the teaching will be adapted based on these results.

Finally, the aim of this course is that students can not only solve mathematical problems when presented with them in a mathematical formulation, but also that students are able to independently generate simple mathematical formulations of biological problems and then solve them.

## Course objectives

1. Calculus Students should be able to:

1. Appreciate the difference between functions using discrete and continuous time and be able to suggest when each is appropriate.
2. Be able to calculate limits
3. Be able to integrate and differentiate a wide range of functions
4. Solve basic differential equations

2. Basic skills and statistics Students should be able to:

1. Distinguish between the forms of linear, polynomial, rational, exponential and logarithmic functions and know their properties.
2. Work with real and complex numbers, understand their properties and graphical representations.
3. Sketch graphs, using function, its first derivative, and the second derivative.
4. Apply different types of curve fitting in the biological context.
5. Understand the basic principles of probability including Bayes theorem.
6. Understand the definitions of discrete and continuous variables, probability and cumulative distribution functions.
7. Calculate expectation, variance, covariance and correlation.
8. Appreciate the basic components of hypothesis testing.

3. Linear algebra Students should be able to:

1. Solve systems of linear equations, understand different types of possible solutions, and use the ideas in applied problems.
2. Perform the common operations of matrix algebra and use them to solve applied problems.
3. Compute determinant of a square matrix and understand its properties.
4. Understand the concepts of linear independence, spanning set, basis, rank of matrix, vector space and subspace, and linear transformation.
5. Understand eigenvectors and eigenvalues, how they characterize the action of some linear transformations and how to used them to solve applied problems.
6. Use the ideas of inner products, orthogonality, and projections to determine least square solutions to a linear systems.

4. Matlab Students should be able to:

1. Use Matlab to import/export data and produce figures based on this data
2. Understand and run code provided to them, and interpret the output
3. Computationally check results from any of the other strands of the course
4. Adapt code provided to them to improve or alter its functionality

5. Applying mathematics to biological problems: Students should be able to:

1. Formulate equations from simple textual descriptions of biological problems
2. Select the appropriate method from those covered in this course for solving a mathematical problem described in biological terms

## Recommended reading

There are many good textbooks for all areas of this course, in particular due to their emphasis on the connection between mathematics and biology and their many biological examples, we recommend;
● Calculus for biology and medicine Claudia Neuhauser (2014) Pearson.
● Elementary linear algebra - Applications version Howard Anton and Chris Rorres (10th edition) John Wiley&Sons, Inc.
● Mathematics for the life sciences Erin N. Bodine, Suzanne Lenhart and Louis J. Gross (2014) Princeton University Press

MSB1003
Period 1
2 Sep 2024
25 Oct 2024
Print course description
ECTS credits:
6.0
Coordinators:

- R. Cavill
- A.M.F. Carlier
- R.B. Jolivet

Teaching methods:
Lecture(s), PBL, Research, Skills
Assessment methods:

Systems Biology and Bioinformatics

Written exam, Assignment
Faculty of Science and Engineering

# Modelling Biosystems

## Full course description

The complexity of biological systems manifests itself in many features. For example, biological systems consist of a very large number of components (e.g. thousands of genes in one cell, billions of neurons in the human brain). Moreover, these components are linked by a multitude of processes, which are often nonlinear. As a consequence, we cannot make reliable predictions about these complex biosystems with intuition alone. Interestingly, mathematics naturally deals with thousands of variables and non-linearities, providing us with an excellent tool to explore complex biosystems.

The aim of this course is to provide an overview over various “mechanistic” or “white box” modeling approaches. The course will introduce the generic modeling process, important modeling concepts and terminology, and focus on equation-based modeling (and in particular ordinary and partial differential equations), agent-based modeling and constraint-based modeling. We will also touch upon the challenges of multiphysics and multiscale modeling and the inspiring avenues of in silico clinical trials and computational modeling for regulatory approval. To illustrate the various modeling approaches we cover different biological scales (intracellular, cellular/tissue and organ/patient) as well as different applications.

The course will not only provide theoretical knowledge, but will apply the various modeling approaches in hands-on practicals, thereby equipping students with Matlab skills needed in the curriculum later on. The course is thus complementary to the parallel MSB1005 Experimental Design and Data Management course which focuses on data management and analysis and introduces R. It is furthermore complementary to the preceding MSB1001 Systems Biology, in that it focuses specifically on mechanistic modeling approaches (in contrast to –omics approaches) and provides both a theoretical comprehension as well as practical training in these mechanistic approaches.

## Course objectives

The general aims of this course are to give the student a thorough overview and understanding of mechanistic modelling approaches. Students will learn the theoretical concepts of equation-based models (Ordinary Differential Equations, ODEs/Partial Differential Equations, PDEs), agent-based models and constraint-based models. Students will also gain practical experience in Matlab and some other specific modelling software tools.

The intended learning outcomes of this course are:
1. Students are able to explain important concepts of mechanistic modeling in biology.
2. Students are able to describe and distinguish the scope and limitations of mechanistic modeling approaches in biology.
3. Students are able to identify and propose appropriate modeling paradigms and approaches for a given biological research problem.
4. Students are able to indicate challenges in and possible approaches to combining different

mechanistic modeling paradigms to address biological problems that could not be handled through a single modeling paradigm.
5. Students are able to abstract a mathematical description in the form of ODEs or PDEs from a biological problem.
6. Students are able to apply Matlab for scientific applications.
7. Students are able to discuss the scope and limitations of important software tools for mechanistic modeling in biomedical contexts.
8. Students are able to explain important applications of mechanistic models in biomedical contexts.
9. Students are able to discuss the specific requirements of the application of mechanistic modeling approaches in clinical contexts.

### Recommended reading

**Mandatory Literature:**
The mandatory literature comprises of the five articles discussed during the journal clubs. These articles will be provided throughout the course, in advance of the respective journal club session.

**Additional Literature:**
Suggested textbooks:
- Voit: 'A first course in systems biology', Taylor & Francis Inc, 2017, ISBN: 9780815345688
- Wilensky & Rand: 'An introduction to agent-based modelling: modelling natural, social and engineered complex systems with Netlogo', MIT press, 2015, ISBN 9780262731898
- Palsson: 'Systems Biology: Constraint-based Reconstruction and Analysis', Cambridge University Press, 2015, ISBN: 9781107038851

In addition, students are encouraged to study the articles cited in the lecture slides.

MSB1004
Period 2
28 Oct 2024
20 Dec 2024
Print course description
ECTS credits:
6.0
Coordinators:

- A.M.F. Carlier
- M. Breuer

Teaching methods:
Lecture(s), PBL, Assignment(s), Skills
Assessment methods:
Assessment
Faculty of Science and Engineering

## Experimental Design and Data Management

### Full course description

When publishing in a scientific journal, you often have the choice to make your findings available

freely, openly accessible for the entire world. Additionally, a standard requirement is that all of the source data underlying your findings are openly shared using the FAIR ('Findable, Accessible, Interoperable, and Reusable') data principles. In Systems Biology research, these datasets are generally huge. Hence, next to proper experimental design, data management has become of utmost importance in Systems Biology research. This course covers all aspects of study design and data management, including statistical data analysis and the FAIR data principles. Additionally, you will learn how to perform basic as well as advanced data analyses in the scientific programming language R.

## Course objectives

1. Learn to explain important aspects of sample collecting and sample storage in biobanks;
2. Learn to distinguish between the relative merits and use cases for the diversity of study designs used in the field of Systems Biology research;
3. Learn to perform analyses on biomedical research data in the statistical programming language R;
4. Learn to explain important aspects of scientific data management, including statistical data analysis, data visualization and data sharing;
5. Learn to explain the principles of FAIR data sharing and open-access publishing.

## Recommended reading

### Mandatory Literature:


- Rundle et al. 2012: Better cancer biomarker discovery through better study design. Eur J Clin Invest; 42(12): 1350–1359.
- Vineis et al. 2005: Environmental tobacco smoke and risk of respiratory cancer and chronic obstructive pulmonary disease in former smokers and never smokers in the EPIC prospective study. BMJ; 330(7486):277
- Rundle et al. 2005: Design Options for Molecular Epidemiology Research within Cohort Studies. Cancer Epidemiol Biomarkers Prev; 14(8):1899-907.
- Gallo et al. 2012: STrengthening the Reporting of OBservational studies in Epidemiology - Molecular Epidemiology (STROBE-ME): an extension of the STROBE statement. Eur J Clin Invest.; 42(1):1-16.
- Lall et al. 2017: Personalized risk prediction for type 2 diabetes: the potential of genetic risk scores. Genetics in Medicine; 19(3):322-329.
- Lemesle et al. 2015: Multimarker proteomic profiling for the prediction of cardiovascular mortality in patients with chronic heart failure. PLoS One; 10(4):e0119265.
- Wang et al. 2011: Assessing the role of circulating, genetic, and imaging biomarkers in cardiovascular risk prediction. Circulation; 123(5):551-65.
- Vaux et al. 2012: Research methods: Know when your numbers are significant. Nature; 492(7428):180-1.
- Button et al. 2013: Power failure: why small sample size undermines the reliability of neuroscience. Nature Reviews Neuroscience; 14:365–376.
- Sham et al. 2014: Statistical power and significance testing in large-scale genetic studies. Nat Rev Genet; 15(5):335-46.
- Uitterlinden et al. 2016: An Introduction to Genome-Wide Association Studies: GWAS for Dummies. Semin Reprod Med; 34:196–204.
- Langfelder et al. 2008: WGCNA: an R package for weighted correlation network analysis. BMC Bioinformatics; 9:559.
- Yuan et al. 2017: Co-expression network analysis identified FCER1G in association with

progression and prognosis in human clear cell renal cell carcinoma. Int J Biol Sci; 13(11):1361-1372.
- Zerbino et al. 2017: Ensembl 2018. Nucleic Acids Res; 46(D1):D754-D761.
- Rodriguez et al. 2016: Publishing FAIR Data: An Exemplar Methodology Utilizing PHI-Base. Front Plant Sci; 7:641.
- Wilkinson et al. 2016: The FAIR Guiding Principles for scientific data management and stewardship. Sci Data; 3:160018.

**Additional Literature:**

- Boothby et al. 2015: Evidence for extensive horizontal gene transfer from the draft genome of a tardigrade. PNAS; 112(52): 15976–15981.
- Koutsovoulos et. Al 2016: No evidence for extensive horizontal gene transfer in the genome of the tardigrade Hypsibius dujardini, PNAS; 113(18): 5053–5058.

Additional literature may be provided by the lecturers at their lecture and tutorial sessions. All literature will be provided via Canvas.

MSB1005
Period 2
28 Oct 2024
20 Dec 2024
Print course description
ECTS credits:
6.0
Coordinators:

- M.E. Adriaens
- A.J. Isaacs

Teaching methods:
Lecture(s), PBL, Skills
Assessment methods:
Assignment, Written exam
Elective courses

# Elective Courses

Faculty of Science and Engineering

# Omics

## Full course description

In this course, you will explore the rich world of omics technologies and their applications. This not only includes the detailed study of the technological possibilities, but also of the data generated by experiments using these. The course will combine biological understanding with computational understanding, and discuss which methods can be applied to bring the two together.

We will discuss how a wide variety of omics technologies work, what they require and what they can deliver and we will detail their features and limitations. Also we will explore the entire trajectory of applying an omics method, checking and pre-processing the data to make them suited for statistical evaluation, perform the statistical tests, and apply further methods to help interpret the results and put them in a biological context. The initial phases of the analytical process will mainly depend on the exact technology used, whereas the later steps rather depend on the specific scientific questions to be answered.

Also we will look into specific examples of domains and specific studies in which omics technologies are applied.

Some follow-up methods to further explore data generated by omics methods and biologically interpret the findings of the experiments will be studied in more detail in modules MSB1011 (Machine Learning, period 5, year 1) and MSB1014 (Network Biology, period 1, year2).

## Course objectives

The aim of this course is to obtain applied understanding of omics technologies and the processing of the data obtained using these technologies in research or other domains.

Specifically, the student should be able:

1. To describe commonly used technologies for genomics applications
   1.1. DNA/cDNA microarrays
   1.2. Next generation sequencing/ Massive parallel sequencing
      - Whole-genome and whole-exome
      - RNA (mRNA, miRNA, ncRNA)
      - Bisulphite-based
      - In combination with immunoprecipitation

2. To discuss commonly used applications of high-throughput biological profiling
   2.1. Genetics / Genetic variation
   2.2. Comparative genomics
   2.3. Transcriptomics
   2.4. Epigenomics
   2.5. Metabolomics
   2.6. Proteomics
   2.7. Microbiomics

3. To retrieve, process, analyse and interpret omics data and experimental results
   3.1 To query repositories for omics data and to use retrieved data and meta-data for integrative or comparative analysis
   3.2 To apply the initial processing steps required to check data quality and prepare high-throughput data for statistical or biological analysis
   3.3 To apply the statistical methods used for analysis of high-throughput data
   3.4 To apply and explain the results of overrepresentation analysis methods, including:
      - Pathway analysis
      - Gene Ontology analysis

Systems Biology and Bioinformatics

3.5 To describe other methods used for further data processing:
- Clustering-based methods
- Correlation-based methods
- Classification-based methods
- Network analysis-based methods

4. To explain the possibilities and limitations and examine the advantages and disadvantages of omics technologies, applications and data analysis methods
4.1 Genomics technologies
4.2 Applications of high-throughput biological profiling
4.3 Pre-processing and statistical methods for processing of high-throughput data
4.4 Analysis methods for further processes and biological interpretation of the results

5. To report how multiple types of omics data can be brought together and jointly analysed to increase biological understanding.

6. To discuss the societal (legal and ethical) implications of application of omics technologies and the big data generated.

7. To formulate and analyse use cases for each of the applications studied and to design an experiment tuned to answer a specific biological question using omics technologies.

## Recommended reading

During this course, we will make use of scientific papers, dedicated study guides, and online study materials related to several tools and techniques. For the PBL tutorials, recommended literature is provided with each case (after the pre-discussion). For the journal clubs, the papers are provided at least a week before the meeting is scheduled. For skills labs and lectures materials are provided before, during and/or after the skills lab or lecture takes place, including example answer for skills lab assignments.

MSB1006
Period 4
27 Jan 2025
28 Mar 2025
Print course description
ECTS credits:
6.0
Coordinator:

- L.M.T. Eijssen

Teaching methods:
Lecture(s), PBL, Skills
Assessment methods:
Assignment, Written exam
Faculty of Science and Engineering

# Cardiovascular Systems Biology

## Full course description

The course consists of lectures and journal clubs on the following topics:

1) Cardiac ion channels and cellular electrophysiology

2) Fundamental arrhythmia mechanisms

3) Computational modeling of cardiac electrophysiology

4) Signal processing and imaging of cardiac electrophysiology

5) Clinical arrhythmia syndromes and antiarrhythmic therapies

6) Cardiac arrhythmia management in the era of complex genetics

In parallel, participants will obtain hands-on research experience working on a project investigating the potential proarrhythmic consequences of ion-channel mutations using computational modeling (in Python and/or Matlab). The mathematical and programming skills needed for this research (e.g., parameter optimization techniques) will be trained during a number of computer labs. Finally, a demonstration of experimental cellular electrophysiology (patch-clamp) techniques will be given during a lab visit.

## Course objectives

In this course, participants will explore te experimental, computational and clinical components of cardiovascular systems biology with particular emphasis on cardiac electrophysiology and arrhythmogenesis. We will highlight the multidisciplinary nature of this topic, addressing fundamental pathophysiological concepts, computational approaches and clinical implications.

**Intended learning outcomes:**

1. Students have knowledge on the fundamental mechanisms of cardiac arrhythmias and can identify the most likely mechanisms for a given pathological condition.
2. Students can summarize the role of systems biology approaches in clinical cardiac arrhythmia management.
3. Students can distinguish the core principles, (clinical) applications and limitations of existing cardiac electrophysiological models.
4. Students can create a Markov model of an ion channel model and analyse its output under various conditions.
5. Students can apply numerical optimization techniques to fit a Markov model to experimental data.
6. Students can critique scientific papers about cardiovascular systems biology.
7. Students can explain the clinical implications of cardiovascular simulations in written and oral form by simulating the effects of an ion-channel mutation.

## Recommended reading

**Mandatory Literature:**
References supporting the information presented during lectures will be noted on the lecture slides. These can be employed to obtain additional information to answer questions and expand your knowledge on topics of interest.
In addition, the following papers provide a relevant general introduction into cardiovascular systems biology:
1. Grace AA, Roden DM. Systems biology and cardiac arrhythmias. Lancet. 2012 Oct 27;380(9852):1498-508.
2. Rudy Y, Silva JR. Computational biology in the study of cardiac ion channels and cell electrophysiology. Q Rev Biophys. 2006 Feb;39 (1):57-116.
3. Heijman J, Erfanian Abdoust P, Voigt N, Nattel S, Dobrev D. Computational models of atrial cellular electrophysiology and calcium handling, and their role in atrial fibrillation. J Physiol. 2016 Feb 1;594(3):537-53.
4. Trayanova NA, Doshi AN, Prakosa A. How personalized heart modeling can help treatment of lethal arrhythmias: A focus on ventricular tachycardia ablation strategies in post-infarction patients. Wiley Interdiscip Rev Syst Biol Med. 2020 May;12(3):e1477.
5. Viceconti M, Hunter P. The Virtual Physiological Human: Ten Years After. Annu Rev Biomed Eng. 2016 Jul 11;18:103-23.
6. Cluitmans M, Brooks DH, MacLeod R, Dössel O, Guillem MS, van Dam PM, Svehlikova J, He B, Sapp J, Wang L, Bear L. Validation and Opportunities of Electrocardiographic Imaging: From Technical Achievements to Clinical Applications. Front Physiol. 2018 Sep 20;9:1305.
7. Wilde AA, Behr ER. Genetic testing for inherited cardiac disease. Nat Rev Cardiol. 2013 Oct;10(10):571-83.
All of these papers can be accessed via the Maastricht University library.

**Additional Literature:**
None

MSB1007
Period 4
27 Jan 2025
28 Mar 2025
Print course description
ECTS credits:
6.0
Coordinators:

- J. Heijman
- M.J.M. Cluitmans

Teaching methods:
Lecture(s), PBL, Assignment(s), Skills
Assessment methods:
Written exam, Presentation and paper
Faculty of Science and Engineering

# Dynamical Systems and Non-Linear Dynamics

## Full course description

The course Dynamical Systems and Nonlinear Dynamics will provide you an introduction into the analysis and visualization of the complex behavior of dynamical systems. We will look at a many features of nonlinear systems, starting from first-order differential equations, covering phase- plane analysis and eventually study the famous Lorenzequations.
Topics will include fixed points and stability, numerical methods, bifurcations, oscillators, attractors, chaos, fractals and recurrence analysis. The theory will be
supported by practical examples and applications, and assignments will be mostly done with the help of the computer, using MATLAB and/or Octave. Journal clubs/case studies
will provide further insight into various applications of dynamical systems theory in the field of Systems Biology.

## Course objectives

Intended learning outcomes (ILO's)
1. Describe the behavior of a low-dimensional nonlinear system by identifying its fixed points and classifying their stability
2. Explain how a change in a property of a system can lead to change in its behavior and categorize the type of change
3. Discover deterministic chaos in continuous- and discrete-time systems and compute the properties of a strange attractor
4. Create visualizations of the dynamical behavior of a system using various computational tools that illustrate fixed points, stability, periodicity and chaotic
behavior.
5. Summarize scientific publications that feature applications of nonlinear dynamical system analysis in systems biology and discuss the added value of the techniques
used.

## Recommended reading

**Mandatory Literature:**
The course will be given following the material discussed in: Steven H. Strogatz,
Nonlinear Dynamics and Chaos, 2nd edition. Students are strongly recommended to obtain a copy of this book, as it provides a gentle but thorough introduction into the analysis of nonlinear systems with many examples from physics, biology, chemistry and engineering.

**Additional Literature:**
Additional literature (journal clubs, background material) will be made available through the student portal.

MSB1008
Period 4
27 Jan 2025
28 Mar 2025
Print course description
ECTS credits:
6.0
Coordinator:

Systems Biology and Bioinformatics

- S. Zeemering

Teaching methods:
Lecture(s), PBL, Skills
Assessment methods:
Assignment, Written exam
Faculty of Science and Engineering

# Fundamental and Systems Neuroscience

## Full course description

The brain and its neural circuitry are among the most complex and perplexing natural systems. Brain networks have a storage capacity and flexibility that far exceed modern supercomputers, or any artificial intelligent system. A main question in neuroscience is how such complex networks process incoming multisensory information and match these percepts to stored mnemonic information to guide behaviour. In this course, you will gain more insights in these processes by examining brain functions at various scales, i.e., at the micro-, meso- and macro-level.

You will get an overview of the full spectrum of neuroscience, from neuron to brain to mind, and from experiment to advanced theory and models. Furthermore, by learning how to unify novel findings in Fundamental Neuroscience and Systems Neuroscience into a neuroscientific concept embedded in a system theoretic framework, you will develop an integrated and multidisciplinary perspective on neuroscience and its relation to Systems Biology.

Finally, the practical will provide you with hands-on experience on various state-of-the-art neuroscientific techniques and methods (e.g., fMRI, real-time fMRI, EEG, fNIRS, Brain-Computer Interfaces).

## Course objectives

The intended learning outcomes of this course are that students can:
1. Describe and compare neural processes at the microlevel (fundamental, cellular), mesolevel (neural circuits), and macrolevel (brain systems, network integration), and how they influence each other.
2. Describe and compare major cognitive brain functions, such as Vison, Audition, SensoriMotor control, Memory, Communication, Attention & Consciousness and how the emerge from multiscale neural (integration) mechanisms.
3. Apply the major neuroscientific techniques and methods and can evaluate their possibilities & limitations in relation to an experimental study objective.
4. Design a state-of-the-art neuroscientific experiment
5. Appraise how to synthesise results of various multiscale, neuroscientific datasets multimodal into a comprehensive brain model (i.e., interpretation and integration of neuroscientific results across brain scales and modalities) and how this can be further used to construct and investigate systems biological questions.

### Recommended reading

During this course, we will make use of study books, scientific papers, and dedicated study guides as mentioned in the course manual.

MSB1009
Period 5
31 Mar 2025
23 May 2025
Print course description
ECTS credits:
6.0
Coordinator:

- J.C. Peters

Teaching methods:
Lecture(s), PBL, Skills
Assessment methods:
Attendance, Assignment, Written exam
Faculty of Science and Engineering

# Modeling Metabolism

### Full course description

The ever-increasing availability of large-scale omics and other types of data for human subjects in health and disease calls for appropriate computational means of extracting insights out of the massive amounts of data. Individualized computational models furthermore hold out the prospect of contributing to the expansion of personalized medicine.

In this course, students will get acquainted with a metabolic modeling framework known as constraint-based modeling. This framework allows for the efficient study of genome-scale metabolic networks, i.e. networks encompassing all known metabolic reactions in a given cell type. By studying possible steady state reaction flux distributions of the network under different conditions, this framework studies metabolic functional states beyond the network's topology only; while at the same time bypassing the need for detailed kinetic information, which is not available for entire human cellular networks. In this way, constraint-based modeling also allows for the incorporation of omics data, thus allowing to analyze big data in the context of established metabolic networks.

The course will familiarize students with constraint-based metabolic modeling and its applications, with a particular focus on biomedical applications. To this end, the course introduces the fundamentals of constraint-based modeling; discusses the content of genome-scale metabolic models; presents different constraint-based modeling methods to analyze these metabolic models; and shows how omics data can be used to obtain metabolic models that describe particular cell types and disease conditions. Further topics include other ways of incorporating omics data, as well as the incorporation of constraint-based models into multi-scale models.

## Course objectives

During this course, students will learn theoretical concepts of and gain practical experience with constraint-based modeling of (genome-scale) metabolic models.
Intended learning outcomes are:
1. Students should be able to apply theoretical concepts of constraint-based metabolic modeling.
2. Students should be able to explain the content and elements of metabolic reconstructions.
3. Students should be able to inspect, manipulate and analyze metabolic models in Matlab through constraint-based modeling methods.
4. Students should be able to integrate omics data into metabolic models to construct context-specific models.
5. Students should be able to assess the strengths and limitations of constraint-based metabolic modeling methods in relation to other metabolic modeling approaches.

## Recommended reading

**Mandatory Literature:**
The mandatory literature comprises of the two articles discussed during the journal clubs. These articles will be provided throughout the course, in advance of the respective journal club session.

**Additional Literature:**
Suggested textbook:
Palsson: 'Systems Biology: Constraint-based Reconstruction and Analysis', Cambridge University Press, 2015, ISBN: 9781107038851
In addition, students are encouraged to study the articles cited in the lecture slides.

MSB1010
Period 5
31 Mar 2025
23 May 2025
Print course description
ECTS credits:
6.0
Coordinator:

- M. Breuer

Teaching methods:
Lecture(s), PBL, Skills
Assessment methods:
Assignment, Written exam
Faculty of Science and Engineering

# Machine Learning and Multivariate Statistics

## Full course description

Machine Learning (ML) is the scientific study of algorithms and (multivariate) statistical methods that computer systems use to perform a task relying on patterns in the available data and inference. In its more general formulation, machine learning algorithms build a mathematical model in order to

make predictions or decisions on new data. ML is related to computational statistics and uses methods and theories drawn from of mathematical optimization. Generally, ML tasks are classified into several broad categories. In supervised learning, a mathematical model is built from a set of data that contains both the inputs and the desired outputs (“training data”).
Classification algorithms and regression algorithms are types of supervised learning. Classification algorithms are used when the outputs are restricted to a limited set of values. Regression algorithms are used when the output may have any value within a range. In unsupervised learning, a mathematical model is built from a set of data which contains only inputs and no desired output labels (also named Data Mining). Unsupervised learning algorithms are used to find structure in the data, like grouping or clustering of data points. Unsupervised learning can discover patterns in the data, and can group the inputs into categories, as in feature learning. Dimensionality reduction is the process of reducing the number of "features", or inputs, in a set of data.

In System Biology, ML algorithms can aid in several ways. In data-rich scenarios (e.g. omics data) ML can help identifying the relevant pieces of information given a question, and how to make sense out of it (a "data mining" issue). Additionally, ML algorithms allow understanding how biological systems behave as the result of the integration and interaction between many individual components that can be monitored simultaneously. At the same time bioinformatics and systems biology have already induced significant new developments of general interest in ML, for example in the context of learning with structured data, graph inference, semi-supervised learning, system identification, and novel combinations of optimization and learning algorithms.

In this course, ML will be applied in the context of neuroscientific investigations that on the basis of brain signals try to make sense of how the human brain processes information (visual auditory tactile) as well as in the analysis of omics data. You will study basic theoretical concepts of multivariate statistics and optimization that are fundamental to all ML algorithms. The problems of supervised (classification and regression) and unsupervised (clustering and dimensionality reduction methods) will be introduced formally together with common algorithmic solutions (e.g. Naïve Bayes, Support Vector Machines, Ridge Regression, [deep] neural networks, K-Means clustering). Practical examples of applications will be discussed highlighting best practices in the use of ML as well as in the communication of the obtained results. Finally, you will be tasked to use ML on available data to answer a specific question and report your results in the form of code and a written report.

## Course objectives

During this course, you will acquire the fundamentals to machine learning approaches and their application to system biology. By relating theoretical knowledge with practical examples, you will be inspired to develop a critical view on ML applications and the way they are reported. You will train, theoretical and analytical skills, and (verbal as well as written) communication skills.

The course specific intended learning outcomes (ILOs) are:

1. The ability to describe fundamental concepts in machine learning.
2. Compare algorithms tasked to specific machine learning problems on theoretical grounds.
3. The ability to apply the acquired theoretical knowledge to solve practical examples.
4. Practice the scientific method by devising a Machine Learning analysis strategy to solve a problem within the System Biology field.
5. The ability to justify choices in the methodological approach, critically assess its outcomes.
6. The ability to effectively communicate results in writing together with the dissemination of the analysis methods and pipeline with particular attention to fostering reproducibility of the results.

7. The ability to critically evaluate the usage of machine learning in the biological literature and identify potential issues.

## Recommended reading

### Mandatory Literature:

Pattern Classification – R.O. Duda, P.E. Hart, D.G. Stork; John Wiley & Sons (2012)

### Additional Literature:

In addition, various articles for the Journal clubs will be selected by the tutors and are available through the university library subscriptions.

MSB1011
Period 5
31 Mar 2025
23 May 2025
Print course description
ECTS credits:
6.0
Coordinators:

- F. de Martino
- R. Cavill

Teaching methods:
Lecture(s), PBL, Skills
Assessment methods:
Participation, Assignment, Final paper
Faculty of Science and Engineering

# Computational Neuroscience

## Full course description

This course introduces to you the philosophy, methods and tools of computational neuroscience. You will gain insights into information processing in the brain at several scales (from the spiking behaviour of single neurons to whole-brain dynamics) and levels of abstraction (from cognitive capacities to their biophysical implementation). In parallel, you will receive hands-on training on how to design, simulate and interpret mathematical models of brain processing.

This course is closely related to Fundamental and Systems Neuroscience (year 1) in that computational neuroscience constitutes the theoretical underpinning of systems neuroscience. It addresses similar scientific questions with a stronger emphasis on mathematical modelling (often from the perspective dynamical systems theory) and computer simulations. The emphasis on dynamical models and their numerical simulations relates the present elective to the MSB courses Dynamical Systems and Nonlinear Dynamics (year 1) and Scientific Computing (years 1 & 2).

The human brain is often regarded as the most complex object in the known universe. It is not

surprising therefore that studying the brain and its function is a challenging task, which requires several perspectives and complementary insights. If we want to understand neural systems, we need to describe them at three levels of abstraction. At the first level, we need to identify their function: what do these systems do and why? At the second level, we need to identify potential mechanisms underlying a certain function: how do neural systems realize functions algorithmically? Finally, we need to identify the hardware (i.e. biological) implementation of these algorithms: what are the physical and biological building blocks underlying neural information processing?

Computational neuroscience integrates knowledge across these three levels as it studies information processing carried out by neural structures in terms of biologically constrained models of brain structure and function. While all three levels are equally important in general, the specific question addressed by any one study may place different weights on each level. Computational neuroscience also addresses questions at several spatio-temporal scales from subthreshold activity exhibited by single neurons to whole-brain dynamics.

You will get an overview of models and techniques employed in computational neuroscience as well as of the philosophy underlying the three levels of abstraction (tri-level hypothesis). Finally, you will receive hands-on experience on how to design and simulate models at distinct levels of abstraction and spatio-temporal scales.

## Course objectives

The intended learning outcomes of this course are that students can:
1. Describe and compare the three levels of abstraction put forth by the tri-level hypothesis and how they influence each other
2. Describe and implement mathematical models at the micro-level (point neurons), meso-level (neural circuits & neural mass models) and macro-level (cortical networks)
3. Describe and implement learning rules applicable at different spatio-temporal scales / levels of abstraction such as spike-timing dependent plasticity
4. Conduct a computational neuroscience study from formulating a research question to interpreting simulation results

## Recommended reading

The provided literature accompanies the Lectures and Computer Exercises. In the spirit of RBL, you will conduct your own literature search for Peer Group meetings.

• Frigg, R., & Hartmann, S. (2012). Models in Science. In E. N. Zalta (Ed.), The Stanford Encyclopedia of Philosophy.
• Kaplan, D. M. (2011). Explanation and description in computational neuroscience. Synthese, 183(3), 339–3s73. https://doi.org/10.1007/s11229-011-9970-0
• GitHub Guides
• Gerstner, W., Kistler, W. M., Naud, R., & Paninski, L. (2014). Neuronal Dynamics. Cambridge: Cambridge University Press.
• Potjans, T. C., & Diesmann, M. (2014). The Cell-Type Specific Cortical Microcircuit: Relating Structure and Activity in a Full-Scale Spiking Network Model. Cerebral Cortex, 24(3), 785–806. https://doi.org/10.1093/cercor/bhs358
• Martí, D., Deco, G., Giudice, P. D., & Mattia, M. (2006). Reward-biased probabilistic decision-

making: Mean-field predictions and spiking simulations. Neurocomputing, 69(10–12), 1175–1178. https://doi.org/10.1016/j.neucom.2005.12.069
 Background: Platt, M. L., & Glimcher, P. W. (1999). Neural correlates of decision variables in parietal cortex. Nature, 400(6741), 233–238. https://doi.org/10.1038/22268
• Gancarz, G., & Grossberg, S. (1998). A neural model of the saccade generator in the reticular formation. Neural Networks, 11(7), 1159–1174. https://doi.org/10.1016/S0893-6080(98)00096-3

• Rolls, E. T. (2016). Pattern separation, completion, and categorisation in the hippocampus and neocortex. Neurobiology of Learning and Memory, 129, 4–28. https://doi.org/10.1016/j.nlm.2015.07.008
• Lange, Senden, Radermacher, and De Weerd (in press). Interfering with a memory without erasing its trace.
• Background: Schoups, A., Vogels, R., Qian, N., & Orban, G. (2001). Practising orientation identification improves orientation coding in V1 neurons, 412, 549–553. https://doi.org/10.1038/35087601
• Background: Teich, A. F., & Qian, N. (2003). Learning and Adaptation in a Recurrent Model of V1 Orientation Selectivity. Journal of Neurophysiology, 89(4), 2086–2100. https://doi.org/10.1152/jn.00970.2002

MSB1013
Period 1
2 Sep 2024
25 Oct 2024
Print course description
ECTS credits:
6.0
Coordinator:

- M. Senden

Teaching methods:
Lecture(s), PBL, Skills
Assessment methods:
Written exam, Final paper
Faculty of Science and Engineering

# Network Biology

## Full course description

We are surrounded by complex systems and their understanding, mathematical description, and interpretation are major challenges of the 21st century. In this course, students will be introduced into the world of networks and their application in the analysis of biomedical data. A human body consists of more than 37 billion cells and our existence depends on the harmonious interaction between thousands of genes, proteins and metabolites within our cells. Networks are the ideal tool to capture, explore and evaluate these interactions.

The course covers both the fundamental graph theory concepts and their application in network biology. After completing this course, the student is able to analyse biomedical research data using network science approaches. Additionally, the student will be aware of best practises in network

visualisation to facilitate interpretation and communication of research results.

In the skills training, the students apply the topics discussed in the lectures and tutorials. The content of the training will be directly linked to tutorials. Importantly, in the final project the students will apply the acquired skills to answer their biological research question.

### Course objectives

In this network biology course, students will learn to:

1. Describe basic concepts of graph theory and network science
2. Interpret and distinguish network biology algorithms and resources
3. Assess and explain network biology algorithms and resources
4. Develop and examine network biology analyses using biomedical data
5. Interpret and report the results of a network biology study
6. Apply and discover software to analyse, visualise and interpret biological networks

### Recommended reading

Books; papers; other resources
Literature will be available on the student portal.

MSB1014
Period 1
2 Sep 2024
25 Oct 2024
Print course description
ECTS credits:
6.0
Coordinators:

- S.L.M. Steinbusch - Coort
- M. Summer - Kutmon

Teaching methods:
Lecture(s), PBL, Skills
Assessment methods:
Written exam, Presentation, Final paper
Faculty of Science and Engineering

## Scientific Programming

### Full course description

Scientific programming can be seen like any other type of the laboratory experiment. During the experiment it is required to create a protocol, where each aspect of the experiment is properly described, so it can be reproduced with small experimental error every time it is done and independently of the user. The same applies to a scientific writing. The main objectives is to produce the results, which can be obtained independently of the user.

In this course, you will be introduced into several aspects relevant for programming and for working in the data science/machine learning filed. The course will introduce the relevance of automated statistical analysis, parallel computing, data visualization, interactive notebooks.

Format

The course follows the problem-based learning (PBL) approach. Characteristic of this approach is that learning is the result of an engaged interaction between academic staff and students, fuelled by their experience and knowledge, with the objective of developing understanding and insights.

The course consists of lectures, journal clubs and project meetings. Lectures and journal clubs are meant to introduce the specific topic and give broad understanding of its application and relevance. The project meetings are meant to give the opportunity to go more into depth of each presented subject. During those project meetings, the students will have an opportunity to apply the knowledge and extend it in the project under guidance of the supervisor. Here, the students will be solving problems to new situations by applying acquired knowledge, facts, techniques and rules in a different way.

## Course objectives

The main aim of the course is to give a clear overview of the important parts of scientific programming. This will include but won't be limited to reproducibility aspects of the created computational tools, interactive notebooks, parallel computing and visualization of the outcomes.

The intendent learning outcomes (ILOs) of the course are:

1. The student compiles information to develop software to answer biological/biomedical question
2. The student is able to create and evaluate someone else an interactive lab-journal (Git)
3. The student is able to design multivariate statistic in reproducible way
4. The student is able to explain, apply and implement software in appropriate way.
5. The student learn about parallel computing and apply it in the software where it is possible.
6. The student is able to evaluate different visualization options for the examined data and decide the most informative option.

## Recommended reading

Each literature indicated in this section aims at giving information relevant to the course. Those are only examples of the literature and additional literature will be provided.

**Mandatory Literature:**

1. List M, Ebert P, Albrecht F. Ten Simple Rules for Developing Usable Software in Computational Biology. Markel S, editor. PLOS Computational Biology. 2017 Jan 5;13(1):e1005265.
2. Perez-Riverol Y, Gatto L, Wang R, Sachsenberg T, Uszkoreit J, Leprevost F da V, et al. Ten Simple Rules for Taking Advantage of Git and GitHub. Markel S, editor. PLOS Computational Biology. 2016 Jul 14;12(7):e1004947.
3. Website: https://towardsdatascience.com/getting-started-with-git-and-github-6fcd0f2d4ac6
4. Website :https://jwiegley.github.io/git-from-the-bottom-up/
5. Website: https://www.youtube.com/watch?v=iv8rSLsi1xo

6. Website: https://towardsdatascience.com/the-ultimate-guide-to-data-cleaning-3969843991d4
7. Website: Reproducibility and Replicability in Science: https://www.ncbi.nlm.nih.gov/books/NBK547546/
8. Website:https://www.kdnuggets.com/2019/11/reproducibility-replicability-data-science.html
9. Website:https://medium.com/science-uncovered/reproducibility-crisis-84ae0a5af2f

**Additional Literature:**

It will be provided during the course.

MSB1015
Period 1
2 Sep 2024
25 Oct 2024
Print course description
ECTS credits:
6.0
Coordinator:

- A.M. Blanchet - Smolinska

Teaching methods:
Lecture(s), PBL, Skills
Assessment methods:
Presentation, Assignment
Faculty of Science and Engineering

# Commercialization and Entrepreneurship

## Full course description

At Commercialization & Entrepreneurship, we combine the best aspects of Lean Startup Methodology, Business Model Canvas, Customer Development with our own insights and experience.

The program curriculum is aimed at crafting a strong sustainable, business model. It is a combination of masterclasses and work sessions. The aim is that you validate your assumptions between masterclass and work session. Rapid iteration will allow your project to stay lean and achieve your goals considerably faster.

## Course objectives

At the end of this course, students will be able to:

1. Create and validate your Business Model.
2. Know your Value Proposition. Determine the real value you offer to your customers.
3. Research the Business Model Environment. Analyze trends and developments that are relevant for your business.
4. Validate your Assumptions through interviews with relevant stakeholders. You will become more specific and concrete.
5. Create a strong story and give a pitch.

Systems Biology and Bioinformatics

### Recommended reading

#### Mandatory Literature:

None

#### Additional Literature:

1. The Start-up Owner’s Manual. Vol. 1, by Steve Blank & Bob Dorf
2. Business Model Generation, by Alexander Osterwalder & Yves Pigneur
3. Value Proposition Design, by Alexander Osterwalder & Yves Pigneur

MSB1017
Period 1
2 Sep 2024
25 Oct 2024
Print course description
ECTS credits:
6.0
Instruction language:
English
Coordinator:

- R.P.M.G. Broersma

Teaching methods:
Lecture(s), PBL, Skills
Assessment methods:
Assignment, Presentation
Projects

# Projects

Faculty of Science and Engineering

# Research project 1

### Full course description

The project period is based on research based learning (RBL). In RBL, you are challenged with a real-life problem and have to come up with a creative solution. You have to embrace the project, make it your own, and take responsibility in order to make it a worthwhile learning experience. In addition, you should experience that research is challenging, sometimes a bit frustrating, but above all fun. This way of working is very challenging, but it also offers opportunity to learn teamwork by sharing responsibilities, which is important for your future career.  Furthermore, in the projects you have to use all knowledge and skills you gathered in the programme up to that point. Only when you work together, you can truly excel. That is, you can propose and execute a project that surpasses the regular master level. Innovation and creativity are important, as well as solid scientific method and proper argumentation and discussion. The success of the project depends on your enthusiasm and

Systems Biology and Bioinformatics

motivation.

PRO4002
Period 3
6 Jan 2025
24 Jan 2025
Print course description
ECTS credits:
6.0
Instruction language:
English
Coordinator:

- A.J. Isaacs

Faculty of Science and Engineering

# Research project 2

## Full course description

The project period is based on research based learning (RBL). In RBL, you are challenged with a real-life problem and have to come up with a creative solution. You have to embrace the project, make it your own, and take responsibility in order to make it a worthwhile learning experience. In addition, you should experience that research is challenging, sometimes a bit frustrating, but above all fun. This way of working is very challenging, but it also offers opportunity to learn teamwork by sharing responsibilities, which is important for your future career.  Furthermore, in the projects you have to use all knowledge and skills you gathered in the programme up to that point. Only when you work together, you can truly excel. That is, you can propose and execute a project that surpasses the regular master level. Innovation and creativity are important, as well as solid scientific method and proper argumentation and discussion. The success of the project depends on your enthusiasm and motivation.

PRO4003
Period 6
26 May 2025
13 Jun 2025
Print course description
ECTS credits:
6.0
Instruction language:
English
Coordinators:

- M.M.L. Moerel
- R.B. Jolivet

Teaching methods:
Lecture(s), PBL
Assessment methods:
Attendance, Assignment
Thesis

# Master Thesis Research

Faculty of Science and Engineering

# Master Thesis Systems Biology

## Full course description

The curriculum of the UM master Systems Biology culminates in the master thesis research project. This part of the curriculum is a final proof-of-capability for the master students. It allows the students to demonstrate that they have gained sufficient knowledge, competences and skills to do independent scientific research.

Thesis projects can be carried out under supervision of staff of the MaCSBio, UM research groups, at other faculties, universities, research institutes or companies in the Netherlands or abroad. Irrespective of the internship location or organization, the topic of the thesis should be scientific and directly related to the field of systems biology. The master thesis is concluded with the written master thesis report and an in depth defense of the conducted research, its results and conclusions.

Description of skills training during the course

Ideally, the thesis project allows students to integrate all knowledge, competences and skills they have gained throughout the master programme and their academic career.

## Course objectives

The master thesis is an individual research project in which the students should be able to:

1. demonstrate the ability to plan and perform an individual high-level scientific research project in the field of systems biology;
2. work in a research team and communicate with the members of this team while performing the master thesis;
3. solve the scientific problems that are encountered during the master thesis research;
4. write and defend the master thesis research describing the results, conclusions and the relevance of the conducted research.

MSB5000
Semester 2
3 Feb 2025
4 Jul 2025
Print course description
ECTS credits:
48.0
Coordinator:

- M.M.L. Moerel

Faculty of Science and Engineering

# Ethics

MSB5003
Year
1 Sep 2024
31 Aug 2025
Print course description
ECTS credits:
0.0
Coordinator:

- G.D.A. Hazell