



Bioinformatics Education

Supplement to – Training for translation between disciplines: a philosophy for life and data sciences curricula

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Abstract



Bioinformatics MSc

VU University Amsterdam - Faculteit der Exacte Wetenschappen - M Bioinformatics - 2017-2018

Research in Bioinformatics in its broadest definition concerns the analysis of informational processes within living systems with the help of computers. To do this successfully, Bioinformatics actively uses and integrates contributions from areas such as Mathematics, Computer Science, Chemistry, Medicine and Biology. Bioinformatics has recently become one of the keywords in the life sciences as well as in Biotechnological and Pharmaceutical industries. Although in essence the field exists for over two decades and bioinformatics techniques developed over the years have come of age, the field has gained major prominence relatively recently, owing mostly to the world-wide human genome projects and subsequent structural and functional genomics initiatives. While the complete human genome sequence has been obtained at relatively little cost of around two billion Euros, the current investments in for example proteomics industries amount to orders of magnitude more. Also other genomic technologies, aimed at gaining insight in human physiological functioning such as microarray (gene chip) technology, have attracted multi-billion Euro investments both in industry and academia. Currently, many new small/medium enterprises (SMEs) and large international biotechnological and pharmaceutical companies are actively recruiting bioinformaticians, but experience hardship in doing so due to the lack of individuals with proper training. Similar problems are encountered at national academic centres in The Netherlands, particularly in microarray centres. As the interpretation of the data coming from all the above large-scale projects is crucially depending on the application and creation of new bioinformatics techniques, it is clear that a broad based and integrative master's curriculum in bioinformatics at the Vrije Universiteit is timely.

The international Bioinformatics Master study takes 2 years and is organised by the Integrative Bioinformatics Institute VU (IBIVU) at the Vrije Universiteit since 2003. The IBIVU is a multidisciplinary centre within the Vrije Universiteit in which three faculties (Faculty of Sciences; Faculty of Earth and Life Sciences; and the Faculty of Psychology) and the VU Medical Centre take part. To prepare for the Bioinformatics master course, various Bachelor programmes at the Vrije Universiteit offer integral courses in Bioinformatics, such as Medical Natural Sciences and Biomolecular Sciences. These Bachelor programmes (taking 3 years) are dedicated to providing the student with a broad and thorough basis in each of their areas of study, which is indispensable for starting the Bioinformatics Master programme. The Bioinformatics Master's provides the student with an opportunity to deepen his/her knowledge of the various aspects of Bioinformatics, while the student has ample possibility to specialise in one or a few areas of choice. It is expected that the breadth and flexibility of the masters programme resulting from the multi-disciplinary setup of the Integrative Bioinformatics Institute as well as the emphasis on creating bioinformatics tools from the strong embedding in the Informatics department (e.g. AI, Computer Systems) will be attractive for students.

The Bioinformatics Master studies are currently organised by the Faculty of Sciences. The latest information can always be found at: <http://www.ibi.vu.nl/>.

Depending on the individual furnishing of his/her Master programme, the student can attend lectures in other faculties and centres, for example Biology or the Centre for Neurogenomics and Cognitive Research (CNCR). Graduation projects can vary from practical to rather fundamental, depending on the preferences and capacities of the students. Students can also go to companies, research institutes or universities either in The Netherlands or abroad.

Study advice is open to all. Advisor prof. dr. Jaap Heringa can be contacted at all times. Furthermore, the website <http://www.ibi.vu.nl/> contains information regarding the international Bioinformatics Master programme.

Formal procedures during your master

The full Master's programme in Bioinformatics takes two years and is worth 120 credit points (within the European Community Course Credit Transfer System). The global lay-out of the programme is approximately ten months (60 credits) of practical training and ten months (60 credits) of courses and other theory supported subjects.

Note: Every programme, including the choice of optional courses, has to be discussed and agreed upon with the master coordinator or a personal mentor and approved by the Examination Board.

More information

- All compulsory courses and electives you find in the [year schedule](#);
- A complete description of the programme you find in the [Teaching and Examination Regulations](#);
- For more information about the programme you can contact the [academic advisor](#) (VU students only);
- As a VU student you need to register for all courses via [VUnet](#). Only after you completed your enrollment for the study programme you can register for courses;
- More information on all the courses you find through the links below.

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Compulsory optional Courses Systems Biology Major

Courses:

Name	Period	Credits	Code
Advanced modelling in Systems Biology	Period 6	6.0	X_418155
Statistics with R	Period 5	6.0	X_418156
Synthetic Biology and Biomedicine		6.0	XMU_418125

Compulsory Optional (Alternative) Course

Courses:

Name	Period	Credits	Code
Literature Review	Ac. Year (September)	6.0	XMU_0007
Literature Review	Ac. Year (September)	6.0	XM_0007
Seminar Series and Writing a Research Proposal	Ac. Year (September)	6.0	X_400594

Optional Courses

Three courses (18 credits) in the programme are free choice. Courses from the list below are always approved. Many other optional courses are acceptable, but will have to be discussed and agreed upon with the master coordinator or a personal mentor and approved by the Examination Board.

Courses:

Name	Period	Credits	Code
Data Mining Techniques	Period 5	6.0	X_400108
Machine Learning	Period 4	6.0	X_400154
Signal Transduction in Health and Disease	Period 2	6.0	X_432535

Conversion courses

Courses:

Name	Period	Credits	Code
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Introduction to Programming (PYTHON)	Period 2	6.0	X_401096
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Compulsory Courses

The master includes four compulsory courses (total of 24 credits) that are compulsory for all students. In addition, three courses (18 credits) should be chosen from one of the two profiles: Bioinformatics or Systems Biology. Please refer to 'Compulsory optional courses' for more detail.

Courses:

Name	Period	Credits	Code
Biosystems Data Analysis	Period 3	6.0	XMU_437001
First internship (Major)	Ac. Year (September)	42.0	XM_405027
Fundamentals of Bioinformatics	Period 1	6.0	X_405052
Introduction to Systems Biology	Period 1	6.0	X_428565
Second Internship (Minor)	Ac. Year (September)	18.0	XM_405032

Compulsory Courses Bioinformatics Major

Courses:

Name	Period	Credits	Code
Algorithms in Sequence Analysis	Period 2	6.0	X_405050
Bioinformatics for Translational Medicine	Period 5	6.0	X_405092
Structural Bioinformatics	Period 4	6.0	X_405019

Compulsory Courses Systems Biology Major

Courses:

Name	Period	Credits	Code
Basic Models of Biological Networks	Period 2	6.0	X_418154
Systems Biology in Practice	Period 4	6.0	XMU_418157

Advanced modelling in Systems Biology

Course code	X_418155 ()
Period	Period 6
Credits	6.0

Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen
Coordinator	prof. dr. F.J. Bruggeman
Examinator	prof. dr. F.J. Bruggeman
Teaching staff	prof. dr. F.J. Bruggeman
Teaching method(s)	Lecture, Computer lab, Seminar
Level	500

Course objective

To extend modelling techniques learnt in Basic models of biological networks and to get acquainted with more advanced aspects of modelling biological systems

Course content

In this course we will assume knowledge of Basic models of biological networks. We will go deeper into important issues in modelling biological systems. Issues that will be discussed are model validation (parameter estimation, experimental design), dynamic behaviour (instability, multistability), robustness and sensitivity analysis, more advanced Metabolic Control Analysis and stochastic modelling. After this course, students should be able to make a model, evaluate its dynamic behaviour and explore the structure and parameters of the model. This should provide enough background for students to apply modelling in their own research.

Form of tuition

Lectures, self-study, computer practical work, computer modelling tutorials

Type of assessment

Results of computer assignments, written exams

Course reading

A course syllabus with recent reviews and papers presented by the lecturers and guest researchers (max. 15 euros)

Algorithms in Sequence Analysis

Course code	X_405050 (405050)
Period	Period 2
Credits	6.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen
Coordinator	prof. dr. J. Heringa
Examinator	prof. dr. J. Heringa
Teaching staff	prof. dr. J. Heringa
Teaching method(s)	Lecture, Seminar
Level	400

Course objective

Have you ever wondered how we can track a gene across 3 billion years of evolution? Sequence alignment can be used to compare genes from humans

and bacteria, using a dynamic programming algorithm. In this course we focus on algorithms for biological sequences that can be applied to real scientific problems in biology.

Students will obtain in-depth knowledge about the theory of sequence analysis methods. They will also develop understanding and skills to apply the algorithms to protein and DNA sequences. We would like to stress that no biological knowledge is required to enter this course.

Goals

- At the end of the course, the student will be aware of the major issues, methodology and available algorithms in sequence analysis.
- At the end of the course, the student will have hands-on experience in tackling biological problems using sequence analysis algorithms and applying the general statistical framework of Hidden Markov Models.
- At the end of the course, the student will be able to implement several of the most important algorithms in sequence analysis.

Course content

Theory:

- Dynamic programming, database searching, pairwise and multiple alignment, probabilistic methods including hidden markov models, pattern matching, entropy measures, evolutionary models, and phylogeny.

Practical:

- Programming (in Python) own alignment algorithm based on dynamic programming
- Reverse translation and dynamic programming
- Homology searching and pattern recognition using biological and disease examples
- Multiple alignment of biological sequences
- Entropy-based functional residues prediction
- Programming (in Python) own implementation of Hidden Markov Models and using it to predict protein domain structure

Form of tuition

13 Lectures: 2 two-hour lectures per week

13 Computer practicals and associated assignments: 2 two-hour hands-on sessions per week

Type of assessment

The final grade for this course will consist of 50% practical work (see above) and 50% theoretical assessment.

The theoretical assessment will be an oral and/or written exam (depending on number of students).

Course reading

Course material on bb.vu.nl

Books: Durbin, R., Eddy, S.R., Krogh, A., Mitchison, G.. Biological Sequence Analysis. Cambridge University Press, 1998, 350 pp., ISBN 0521629713.

Recommended reading: Marketa Zvelebil and Jeremy O. Baum Understanding Bioinformatics Garland Science 2008 ISBN-10: 0-8153-4024-9

Entry requirements

Bachelor in any science discipline (including medicine).

Basic programming skills (Python) and an interest in biological problems.

Target group
mAI, mBio, mCS

Remarks
Signing up via bb.vu.nl is mandatory.
The course is taught in English.

Basic Models of Biological Networks

Course code	X_418154 ()
Period	Period 2
Credits	6.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen
Coordinator	prof. dr. F.J. Bruggeman
Examinator	prof. dr. F.J. Bruggeman
Teaching staff	dr. J.P. Bruggeman, prof. dr. F.J. Bruggeman
Teaching method(s)	Lecture, Seminar, Computer lab
Level	400

Course objective

The aim of the course is to learn the basis of modelling of biological systems. Computer models of metabolic networks, signal transduction pathways and transcriptional regulation are becoming indispensable in modern (medical) biology. After this course, students have an understanding of the principles of modelling, have learned to work with modelling tools and have applied these tools to biological examples. This should provide enough background for students to communicate with modellers or read modelling papers.

Course content

In this course we will teach how to set up computer models of biological systems, and how such models can be programmed in common software tools. We will provide some basic theoretical concepts required for understanding how to make models and how to interpret the results. Topics will include: properties of cell components (such as enzyme kinetics), mass and energy balances, stoichiometry and constraint-based modelling, kinetic modelling, Metabolic Control Analysis, modelling software. Topics will be illustrated by computer practicals of biological examples.

Form of tuition

Lectures, self-study, computer practical work, computer modelling tutorials

Type of assessment

Results of computer assignments, written exams.

Course reading

A course syllabus with recent reviews and papers presented by the lecturers and guest researchers (max. 15 euros).

Bioinformatics for Translational Medicine

Course code	X_405092 ()
Period	Period 5
Credits	6.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen
Coordinator	dr. S. Abeln
Examinator	dr. S. Abeln
Teaching staff	prof. dr. J. Heringa
Teaching method(s)	Lecture, Practical
Level	400

Course objective

Observations from biological high-throughput experiments will allow us to improve diagnosis and give a personalised treatment plan for patients. However, integrating data from several sources and using this data for predictions is non-trivial.

This is a theoretical and practical Bioinformatics course on computational methods for Translational Medicine; we will focus on Bioinformatics methods that are used to predict the clinical outcome for patients and analysis methods to obtain deeper understanding of complex diseases, by combining data from various high-throughput experiments such as proteomics, microarrays and next-generation sequencing as well as existing biological databases.

goals

- At the end of the course, students will be aware of Bioinformatics methods that are applicable to the area of Translational Medicine.
- Students should be able to combine these methods to come to a creative solution to get new insights from large scale biological experiments.
- At the end of the course, students will have hands-on experience in handling large biological datasets, and will understand the complexity of the biological data both from high-throughput experiments and existing biological databases.
- The student will become familiar with a few in depth research topics that lie within the expertise area of several (Bioinformatics) researchers at the VU, UvA, AMC, NKI and VUMC.

Course content

Theory

- Computational analysis of molecular profiling techniques, such as: proteomics, RNA sequencing, exome sequencing, arrayCGH.
- Computational methods include: normalisation, feature selection, classification, read mapping, clustering.
- All data analysis is relevant in a clinical setting, for diagnosis, treatment decisions or biomarker discovery.

Practical:

- Classification Assessment of Tumor Subtypes (CATS): This is a large assignment for which you have to build a classifier that can discriminate different tumor subtypes based on arrayCGH profiles. You

need to hand in predictions (class contest), write a paper and give a presentation. Note that this is a group project.

Small data analysis practicals are also given on:

- DNA/ RNA sequence analysis
- Proteomics

Form of tuition

- 13 Lectures (2 two-hour lectures per week)
- 12 computer practicals (2 two-hour sessions per week)

Type of assessment

The final grade for this course will consist of 50% practical work (see above) and 50% theoretical assessment.

Practical assessment (50%):

- CATS assignment (50%)
- 2/3 data analysis assignments (pass/fail)

Theoretical assessment: (50%)

- Oral or written exam (depending on number of course students).
- The exam is based on a selection of 8-10 scientific papers in the field of Bioinformatics & Translational Medicine.

Course reading

- course material on bb.vu.nl
- 8-10 scientific papers are provided, and make up the course syllabus.

Entry requirements

Some basic programming skills, in either R or python are required, as well as some basic knowledge on molecular biology.

If you are not following the MSc Bioinformatics, it is advisable to first follow the MSc course "Fundamentals of Bioinformatics".

Recommended background knowledge

If you are not following the MSc Bioinformatics, it is advisable to first follow the MSc course "Fundamentals of Bioinformatics".

Target group

mAI, mBio, mCS

Remarks

The course is taught in English.

- Compulsory course for students in MSc of Bioinformatics.
- Optional course for students with a Bachelor in Physics, Chemistry, Mathematics, Computer Science, Biology, or Biomedical Sciences (see requirements below).

Biosystems Data Analysis

Course code	XMU_437001 (437001)
Period	Period 3
Credits	6.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen

Level	400
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Course content

<http://studiegids.uva.nl/xmlpages/page/2017-2018/zoek-vak/vak/33367>

Remarks

This course is offered at the UvA. For more information contact: FNWI Education Service Centre, Science Park 904, servicedesk-esc-science@uva.nl, +31 (0)20 525 7100. Enrolment via <https://m.sis.uva.nl/vakaanmelden> is required.

Data Mining Techniques

Course code	X_400108 (400108)
Period	Period 5
Credits	6.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen
Coordinator	dr. M. Hoogendoorn
Examinator	dr. M. Hoogendoorn
Teaching staff	dr. M. Hoogendoorn
Teaching method(s)	Lecture
Level	500

Course objective

The aim of the course is that students acquire data mining knowledge and skills that they can apply in a business environment. How the aims are to be achieved: Students will acquire knowledge and skills mainly through the following: an overview of the most common data mining algorithms and techniques (in lectures), a survey of typical and interesting data mining applications, and practical assignments to gain "hands on" experience. The application of skills in a business environment will be simulated through various assignments of the course.

Course content

The course will provide a survey of basic data mining techniques and their applications for solving real life problems. After a general introduction to Data Mining we will discuss some "classical" algorithms like Naive Bayes, Decision Trees, Association Rules, etc., and some recently discovered methods such as boosting, Support Vector Machines, and co-learning. A number of successful applications of data mining will also be discussed: marketing, fraud detection, text and Web mining, possibly bioinformatics. In addition to lectures, there will be an extensive practical part, where students will experiment with various data mining algorithms and data sets. The grade for the course will be based on these practical assignments (i.e., there will be no final examination).

Form of tuition

Lectures (h) and compulsory practical work (pra). Lectures are planned to be interactive: there will be small questions, one-minute discussions, etc.

Type of assessment

Practical assignments (i.e. there is no exam). There will be two assignments done in groups of three. There is a possibility to get a grade without doing these assignments: to do a real research project instead (which will most likely involve more work, but it can also be more rewarding). For the regular assignments the first assignment counts for 40% and the second for 60%. The grade of both assignments needs to be sufficient to pass the course.

Course reading

Ian H. Witten, Eibe Frank, Mark A. Hall, Data Mining: Practical Machine Learning Tools and Techniques (Third Edition). Morgan Kaufmann, January 2011
ISBN 978-0-12-374856-0

Recommended background knowledge

Kansrekening and Statistiek or Algemene Statistiek (knowledge of statistics and probabilities) or equivalent. Recommended: Machine Learning.

Target group

mBA, mCS, mAI, mBio

First internship (Major)

Course code	XM_405027 (405027)
Period	Ac. Year (September)
Credits	42.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen
Coordinator	prof. dr. J. Heringa
Level	400

Course objective

The first internship (Major) can consist of 30 till 42 credits in steps of 3 credits. The Major and Minor internships together will account for a total of 60 credits.

During the major internship, students will carry out a large in-depth project, thereby learning to work in a consistent and goal-oriented way, whilst enhancing their communication and scientific reporting skills in English, both written and orally.

The Integrative Bioinformatics Centre's (IBIVU) broad, multidisciplinary structure allows you to work on a wide variety of subjects at the VU. External internships, nationally or internationally, in academic institutions, academic hospitals, or R&D departments in industry are also possible. There is no mandatory order of the internships, students can either start with a Major or a Minor internship.

Course content

Depending on the student's profile, i.e. bioinformatics or systems biology, projects can be chosen in fundamental bioinformatics or systems biology research. Projects may also be more applied, but are required to have a dominant bioinformatics or systems biology component.

Form of tuition

The student will have a daily supervisor, with whom interaction takes place according to a master-apprentice model, and a formally responsible supervisor and second supervisor from the VU.

Type of assessment

The internship will be assessed on three components: (i) project progress, (ii) written report, and (iii) final presentation, which will count for 1/2, 1/3 and 1/6, respectively. After one to three months, depending on the duration of the internship, the student will present an initial seminar, explaining the structure of the project and the major research question(s).

Course reading

Course reading will be advised by the host institution.

Recommended background knowledge

It is mandatory that students in the bioinformatics and systems biology master's programme have completed their conversion classes in programming (bioinformatics profile) or mathematics (systems biology profile) before embarking on their major or minor internship.

Target group

MSc Bioinformatics and Systems Biology

Remarks

The internship should be approved by the study mentor prior to commencement, and an internship contract, stipulating the expected number of hours of supervision per week, should be signed by the host institution and the VU.

Note: Every programme, including the choice of optional courses, has to be discussed and agreed upon with the master coordinator or personal mentor and approved by the Examination Board.

Fundamentals of Bioinformatics

Course code	X_405052 (405052)
Period	Period 1
Credits	6.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen
Coordinator	dr. ir. K.A. Feenstra
Examinator	dr. ir. K.A. Feenstra
Teaching staff	dr. ir. K.A. Feenstra, prof. dr. J. Heringa, dr. D. Molenaar, dr. S. Abeln
Teaching method(s)	Lecture, , Computer lab
Level	400

Course objective

Interested in Bioinformatics?

Or you want to find out how biology can make an exciting application domain?

Or you want to learn how what more you could do with your data, and with

less effort? Enter here to start!

Fundamentals of Bioinformatics (FoB) is the starting course of the Bioinformatics master. It aims to give a broad overview of important topics relevant to the field, with a focus on current open problems. Students will be made aware of these open problems during practical sessions that aim to let the student 'stumble upon' these problems by themselves. Based on their background, students will be assigned to separate classes where they will be working to fill gaps in their background knowledge in programming and/or biology.

Goals:

- To make the students aware of gaps in their own background knowledge.
- The student will be aware of the major issues, methodology and available algorithms in bioinformatics.
- To work together in a group of diverse backgrounds.
- To gain hands-on experience in scripting and handling basic mathematical equations as a means of solving bioinformatics problems.
- To develop a basic understanding of major concepts in genomics and molecular cell biology that are relevant to current topics in bioinformatics.

Course content

Theory:

- Evolution, Genomes, Sequences, Blast/PSI-Blast, Semantic Web, Multi-omics, Next-generation Sequencing

Practical:

- Exercises during/in between lectures
- Project in groups to solve a major bioinformatics problem. The groups will be composed to include each of the three major background areas: bioinformatics, biology and computer science. Success of the group project will depend on the level of cooperation!

Form of tuition

- 12 Lectures (two hour lecture in the morning, two days per week)
- 12 Computer practicals (two hour sessions following the morning lectures, two days per week), partially supervised.
- Project work

Feedback (theoretical and practical) will be given during the project and computer practical sessions.

Type of assessment

- [30%] Programming or Biology classes
- [30%] Project and group work
- [40%] Oral or written exam (depending on number of course students) to assess:
 - Exercises
 - Project results (individual)
 - Lecture topics

Course reading

- course material (slides, scientific papers) on bb.vu.nl
- Marketa Zvelebil and Jeremy O. Baum Understanding Bioinformatics Garland Science 2008 ISBN-10: 0-8153-4024-9

Entry requirements

Bachelor in any science discipline (including medicine), or strong programming background.

Recommended background knowledge

An interest in algorithmic approaches to biological problems.

Target group

mAI, mBio, mCS, mMNS

Introduction to Programming (PYTHON)

Course code	X_401096 ()
Period	Period 2
Credits	6.0
Language of tuition	Dutch
Faculty	Faculteit der Exacte Wetenschappen
Coordinator	ir. M.P.H. Huntjens
Examinator	ir. M.P.H. Huntjens
Teaching staff	ir. M.P.H. Huntjens
Teaching method(s)	Lecture, Practical,
Level	100

Introduction to Systems Biology

Course code	X_428565 ()
Period	Period 1
Credits	6.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen
Coordinator	dr. D. Molenaar
Examinator	dr. D. Molenaar
Teaching staff	prof. dr. B. Teusink, dr. D. Molenaar, prof. dr. F.J. Bruggeman
Teaching method(s)	Lecture, Study Group, , Seminar
Level	400

Course objective

Introduction to Systems Biology is the starting course of the Bioinformatics and Systems Biology master (together with Fundamentals of Bioinformatics).

Goals:

- To make the student acquainted with the major approaches and methodology in systems biology (to be studied in more detail in the master).
- To develop a basic understanding of biological concepts that are relevant to current topics in systems biology.
- To gain hands-on experience in basic modelling as a means of solving systems biology problems.
- To repair gaps in background knowledge.

Course content

Theoretical topics:

- The two branches of systems biology
- Data structure, geometrical mapping, PCA, distance metrics, clustering
- Cellular composition, diffusion, time scales, rates
- Mass-action, mass balances, reactions, equilibria, stable/unstable steady states equilibrium binding, affinity, conformational change, ultrasensitivity, transduction cascades, autoregulation, mutual inhibition/activation, bistability, feed-forward loops, steady state metabolism, regulation of metabolism and regulation by demand

Practical:

- Exercises during/in between lectures in which methods of systems biology will be applied to several topics.

- Conversion classes

Depending on their background, students will also be assigned to two out of three deficiency classes where they will be working to fill gaps in their knowledge in mathematics, programming and/or biology.

Form of tuition

- Lectures (two hour lecture in the morning, two days per week)
- Computer- and modelling practicals
- Conversion classes in biology, mathematics and/or programming

Type of assessment

30% Mathematics, Programming or Biology conversion classes
60% Final exam of the Systems Biology subjects

Course reading

A course syllabus will be provided

Recommended background knowledge

Mathematics at highschool level

Target group

Students with a bachelor degree in Biology, Bioinformatics, Mathematics, Physics or similar background

Literature Review

Course code	XMU_0007 ()
Period	Ac. Year (September)
Credits	6.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen

Course content

<http://studiegids.uva.nl/xmlpages/page/2017-2018/zoek-vak/vak/37380>

Remarks

This course is offered at the UvA. For more information contact: FNWI Education Service Centre, Science Park 904, servicedesk-esc-science@uva.nl, +31 (0)20 525 7100.
Enrolment via <https://m.sis.uva.nl/vakaanmelden> is required.

Literature Review

Course code	XM_0007 ()
Period	Ac. Year (September)
Credits	6.0
Faculty	Faculteit der Exacte Wetenschappen

Machine Learning

Course code	X_400154 (400154)
Period	Period 4
Credits	6.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen
Coordinator	P. Bloem MSc
Examinator	P. Bloem MSc
Teaching staff	P. Bloem MSc
Teaching method(s)	Lecture, Seminar
Level	300

Course objective

The goal of this course is to present the dominant concepts of machine learning methods including some theoretical background. We'll cover established machine learning techniques such as Decision Trees, Neural Networks, Bayesian Learning, Instance-based Learning and Evolutionary Algorithms as well as some statistical techniques to assess and validate machine learning results.

Course content

Machine Learning is the study of how to build computer systems that learn from experience. It is a very active subfield of Artificial Intelligence that intersects with statistics, cognitive science, information theory, and probability theory, among others. Recently, Machine Learning has gained great importance for the design of search engines, robots, and sensor systems, and for the processing of large scientific data sets. Further applications include handwriting or speech recognition, image classification, medical diagnosis, stock market analysis, bioinformatics, etc.

Form of tuition

The course will be taught in two parts; the first part consists of lectures with written examination. The second part of the course will have a more do-it-yourself character (e.g., practical assignment and/or literature research) and result in a report. The course will be taught in English.

Type of assessment

Exam and assignment with a written report in teams of 5 students

Course reading

TBA

Target group

Second Internship (Minor)

Course code	XM_405032 (405032)
Period	Ac. Year (September)
Credits	18.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen
Coordinator	prof. dr. J. Heringa
Examinator	prof. dr. J. Heringa
Level	400

Course objective

The second internship (Minor) can consist of 18 till 30 credits in steps of 3 credits. The Major and Minor internships together will account for a total of 60 credits.

During the major internship, students will carry out a large in-depth project, thereby learning to work in a consistent and goal-oriented way, whilst enhancing their communication and scientific reporting skills in English, both written and orally. The minor internship should be different from the major internship, and should be hosted by a different department, section or group, if taking place at the same institution hosting the major internship.

The broad multidisciplinary structure of the Integrative Bioinformatics Centre VU (IBIVU), Swammerdam Institute for Life Sciences (SILS, UvA) and partners allows you to work on a wide variety of subjects. External internships, nationally or internationally, in academic institutions, academic hospitals, or R&D departments in industry are also possible.

Course content

Depending on the student's profile, i.e. bioinformatics or systems biology, projects can be chosen in fundamental bioinformatics or systems biology research. Projects may also be more applied, but are required to have a prominent bioinformatics or systems biology component.

Form of tuition

The student will have a daily supervisor, with whom interaction takes place according to a master-apprentice model, and a formally responsible supervisor from the VU.

Type of assessment

The internship will be assessed on three components: (i) project progress, (ii) written report, and (iii) final presentation, which will count for 1/2, 1/3 and 1/6, respectively. After one to three months in the project, depending on the duration of the internship, the student will present an initial seminar, explaining the structure of the project and the major research question(s).

Course reading

Course reading will be advised by the host institution.

Recommended background knowledge

It is mandatory that students in the bioinformatics and systems biology master's programme have completed their conversion classes in programming (bioinformatics profile) or mathematics (systems biology profile) before embarking on their major or minor internship.

Target group

MSc Bioinformatics and Systems Biology

Remarks

The internship should be approved by the study mentor prior to commencement, and an internship contract, stipulating the expected number of hours of supervision per week, should be signed by the host institution and the VU.

Note: Every programme, including the choice of optional courses, has to be discussed and agreed upon with the master coordinator or personal mentor and approved by the Examination Board.

Seminar Series and Writing a Research Proposal

Course code	X_400594 (400594)
Period	Ac. Year (September)
Credits	6.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen
Coordinator	dr. ir. K.A. Feenstra
Examinator	dr. ir. K.A. Feenstra
Teaching method(s)	Lecture
Level	500

Course objective

You have a brilliant research idea, and would need about a million euro's to try it out – how do you communicate the idea in your mind to others, and make them enthusiastic enough that they will trust you with their money? You will write a real proposal on a current open bioinformatics and/or systems biology problem of your own choosing, and defend it in front of an expert and experienced review committee.

Seminar Series and Writing a Research Proposal is intended to make students acquainted with the academic practice of writing and defending research proposals.

Goals:

- * The student will be aware of the major issues and methodology in a selected bioinformatics and/or systems biology topic area.
- * The student will have hands-on experience in writing a Bioinformatics and/or Systems Biology research proposal.
- * The student will have some exposure to a semi-realistic proposal procedure.

Course content**Theory:**

- * A short induction into research proposals (calls, budgets, Gantt)

Practical:

- * Attendance of a minimum of three scientific seminars on bioinformatics and/or systems biology topics, and short report
- * Design of a one million euro research proposal on a selected bioinformatics and/or systems biology topic
- * Defense of the proposal in front of an ad-hoc committee of bioinformatics and/or systems biology experts
- * Revision of the proposal based on the feedback received after the defense

Form of tuition

on individual basis, possibly with an introductory lecture depending on the number of students

Type of assessment

[50%] Proposal (report)

[50%] Oral proposal defence (10 minutes presentation, 20 minutes questions) in front of a mock committee.

Course reading

* manual and further material on

https://wiki.cs.vu.nl/mp/index.php?title=Bioinf_Sys_Bio_Research_Proposa

* relevant background literature

Entry requirements

All compulsory courses in the MSc Bioinformatics and Systems Biology programme, including those of the chosen profile.

Recommended background knowledge

A good grasp of major bioinformatics and/or systems biology research themes, open questions and methods is recommended; in practice this means this course is best taken after the major internship.

Target group

only Students in the MSc Bioinformatics and Systems Biology (mBio) are allowed to take this course.

Remarks

To start the course please make an appointment with the coordinator.

We will schedule several moments in the academic year where presentations will be held. We may also schedule several starting sessions, depending on the number and spread of participants.

Signal Transduction in Health and Disease

Course code	X_432535 (432535)
Period	Period 2
Credits	6.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen
Coordinator	prof. dr. M.J. Smit
Examinator	prof. dr. M.J. Smit
Teaching staff	dr. ir. A.H. de Boer, dr. M.H. Siderius, prof. dr. M.J. Smit, prof. dr. ir. A.H. de Boer
Teaching method(s)	Lecture

Level	500
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Course objective

At the end of this theoretical course, the students are aware of the latest insights of cellular signal transduction in both healthy and pathological conditions.

Course content

This course will link human genetic variation (somatic and inherited mutations) to the development of disease and will focus on pathological signaling, mutant signaling proteins in disease and possible treatment of resulting disease (small compounds, biologicals, gene therapy). Modern pharmacological concepts, including constitutive receptor activity, receptor regulation, allosteric modulation and dimerization will be addressed in light of signal transduction in health and disease. A special focus will be on signal transduction resulting in pathologies such as Alzheimer, Parkinson's disease, inflammatory diseases and cancer.

Form of tuition

Lectures, self-study.

Students will do a case study in groups on a signaling pathway linked to disease. Molecular mechanisms underlying pathology will be addressed and presented. Therapeutic targets within this signaling pathway will be proposed and discussed.

Type of assessment

Assignment and presentation, written exam.

Course reading

'Cell signaling', Authors: Wendell Lim, Bruce Mayer, Tony Pawson
ISBN: 9780815342441
Format: Paperback
Publication Date: June 15, 2014

Papers available on Canvas

Recommended background knowledge

Bachelor Biology, Medical Biology, Pharmaceutical Sciences, Medical Natural Sciences, Biomolecular Science portal course or equivalent

Target group

mBMS-BC, mDDS-BCCA, mDDS-CMCT, mDDS-DD&S, mDDS-DDSA, mDDS-DDTF, mDDS-C-var, mDDS-E-var, mDDS-M-var, mMNS-MCD, mMNS-MPy

Statistics with R

Course code	X_418156 ()
Period	Period 5
Credits	6.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen
Coordinator	dr. D. Molenaar
Examinator	dr. D. Molenaar
Teaching staff	dr. D. Molenaar

Teaching method(s)	Lecture
Level	400

Course objective

Biologists often have to handle, analyze, and present analysis results of large sets of biological data, originating from genomics, transcriptomics, proteomics, and metabolomics experiments. In many cases, these tasks cannot be performed using standard “press the button” commercial statistical packages. A popular solution to this problem is the use of the open source statistical programming environment R. R is used intensively in the community of experimental biologists, and most newly published data analysis techniques are first available as R-packages.

Goals:

- To obtain knowledge of the structure of the R-language as well as practical skills in the programming, producing graphs and documents with R
- To obtain hands on experience in handling and investigation of data sets
- To obtain an overview of some modern statistical learning techniques

Course content

This course focuses on obtaining the practical skills to perform data handling and analysis tasks from small to large data sets, and to graphically display and interpret the results. Statistical analyses will center on multivariate analysis. Examples of the generation and interpretation of (large) data sets will be presented from the various fields of biology, ranging from cell biology to ecology. The items treated during the lectures will be studied in computer practical sessions using R.

Form of tuition

Lectures, tutorials, computer practical work, self-study

Type of assessment

Assessment will take place by three or four individual assignments. The exact number of assignments and their dates will be announced two months before the start of the course.

Course reading

A course syllabus with theory and computer exercises will be made available

Recommended background knowledge

Knowledge of basic statistics

Target group

Master students having a background in basic statistics

Structural Bioinformatics

Course code	X_405019 (405019)
Period	Period 4
Credits	6.0
Language of tuition	English

Faculty	Faculteit der Exacte Wetenschappen
Coordinator	dr. ir. K.A. Feenstra
Examinator	dr. ir. K.A. Feenstra
Teaching staff	dr. ir. K.A. Feenstra, dr. S. Abeln
Teaching method(s)	Lecture, Practical
Level	400

Course objective

Why Structural Bioinformatics?

Generally speaking, the function of a protein is determined by its three dimensional structure, and therefore structural information is crucial for understanding the working of proteins. However, experiments, prediction and simulation of protein structures remain difficult. This course will provide you an overview of existing computational techniques, to validate, simulate, predict and analyse protein structures. More importantly, it will provide practical knowledge about how and when to use such techniques.

Goals:

- Being able to evaluate protein structures with knowledge of their experimental source and validation techniques
- Being able to compare different protein structures, and evaluate similarity
- Learning how and when to use structure prediction methods
- Being able to create scripts that connect different Structural Bioinformatics methods.
- Being able to compare different simulation techniques for biological macro-molecules, and be able to analyse the simulated data computationally.
- Reading and understanding scientific papers in the field of Structural Bioinformatics.

Course content

Theory:

- Protein and DNA structure sources
- Experimental methods
- Structure validation
- Protein fold prediction (from homology modelling to ab initio prediction)
- Structural classification and structural alignment
- Protein folding and energetics
- Molecular Dynamics & Monte Carlo simulation
- Function from structure

Practical:

- Obtaining geometric features from PDB files
- Homology modelling with Modeller
- Protein interaction as a 'computational experiment' (simulation).

Form of tuition

13 Lectures (2 two-hour lectures per week)

12 computer practicals (2 two-hour sessions per week)

Feedback (theoretical and practical) will be given during the computer practical sessions.

Type of assessment

The final grade for this course will consist of 50% practical work and 50% theoretical assessment.

Practical Assignments: (50%)

- (1) Obtaining geometric features from PDB files
- (2) Homology modelling with Modeller (including structural alignment)
- (3) Protein interaction as a 'computational experiment' (simulation).

Theoretical: (50%)

- Oral or written exam (depending on number of course students).
- As part of the exam a research paper on a Structural Bioinformatics topic needs to be analysed in detail.
- You will be prepared for your exam through exercises and paper discussions during the lectures

Course reading

- course material on bb.vu.nl
- Marketa Zvelebil and Jeremy O. Baum. Understanding Bioinformatics. Garland Science 2008 ISBN-10: 0-8153-4024-9

Entry requirements

Bachelor in any science discipline (including medicine), with an interest in applying algorithmic approaches to molecular structures in biology.

Some experience with programming (preferably python). Note that at the start of the course a small scripting practical will be given, this means that in practice students without scripting experience can follow the course if they are motivated to learn during the course, and willing to put in the extra effort - when in doubt please contact the coordinator.

Target group

mAI, mBio, mCS, mPDCS, mMNS, mBMOL, mNS, mBIO

Remarks

- Compulsory course for students in Bioinformatics Profile of MSc Bioinformatics & Systems Biology (mBIO).
- Optional course for mAI, mCS, mPDCS, mMNS, mBMOL, mNS, mBIO.

Synthetic Biology and Biomedicine

Course code	XMU_418125 ()
Credits	6.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen
Level	500

Course content

<http://studiegids.uva.nl/xmlpages/page/2016-2017/zoek-vak/vak/27846>

Remarks

This course is offered at the UvA. For more information contact: FNWI Education Service Centre, Science Park 904, servicedesk-esc-science@uva.nl, +31 (0)20 525 7100.
Enrolment via <https://m.sis.uva.nl/vakaanmelden> is required.

Systems Biology in Practice

Course code	XMU_418157 ()
Period	Period 4
Credits	6.0
Language of tuition	English
Faculty	Faculteit der Exacte Wetenschappen
Level	400

Course content

<http://studiegids.uva.nl/xmlpages/page/2017-2018/zoek-vak/vak/37407>

Remarks

This course is offered at the UvA. For more information contact: FNWI Education Service Centre, Science Park 904, servicedesk-esc-science@uva.nl, +31 (0)20 525 7100. Enrolment via <https://m.sis.uva.nl/vakaanmelden> is required.

Course Catalogue 2017 - 2018

Course Programme Minor Lecturer

Search course

systems biology

☐ Search text

[> All cours](#)

Biosystems Data Analysis

Course catalogue number 5304BIDA6Y

Credits 6 EC

Language of instruction English

Time period(s)

Sem. 1 **Sem. 2**

[> See also](#)



College/graduate

Graduate School of Life and Earth Sciences

Lecturer(s)

dr. J.A. Westerhuis (co-ordinator)

Contact

dr. J.A. Westerhuis
Science Park 904+31 20 5256546
J.A.Westerhuis@uva.nl

Is part of

Master's Life Sciences
Master's Computational Science (Joint Degree)
Master's Forensic Science

[Register](#)

Objectives

Various data analysis methods are discussed in this course. For each of these methods the students will be provided knowledge on how and when to use the multivariate method for analyzing complex sets of multivariate data in biological systems, and especially how to interpret the data analysis results. After the course:

- Students know the origin of the data and the specific properties of the data.
- Students understand how the data analysis methods work theoretically.
- Students are able to apply the methods, and they are able to interpret the results.
- Students comprehend the pitfalls of multivariate data and validation strategies to prevent overfit.
- Students are able to critically review data analysis applications in which the above mentioned methods have been used.
- Students are able to select the most appropriate method for a given biological question.

Contents

In the analysis of biochemical systems, many measurements are performed, leading to complex multivariate data sets. The tendency is to measure more and more of just a few samples. Multivariate data analysis methods are often used to explore such sets.

This course covers a broad range of multivariate data analysis methods, for e.g. exploration, clustering, classification. The latter is especially important in biomarker discovery. Design of experiments and ANOVA for multivariate data is also discussed. Furthermore, the interpretation of selected features in terms of function and networks is discussed. The course starts with an introduction on the properties of the different types of functional genomics data.

The main goal of this course is to teach students how to interpret the results of the multivariate methods and how this relates to the biological problem that is studied.

Registration

Information about procedures can be found at <http://www.student.uva.nl/ls/az/item/course-registration.html>.

Teaching method

- Lecture
- Self-study
- Laptop seminar

Time

The schedule for this course is published on DataNose.

Study materials

- Literature: Literature will be provided using Blackboard
- Software: Matlab

Min/max participants

The maximum number of participants is 60.

Assessment and testing

There will be two tests. The first test is a practical one. Here students are given a specific data set which they have to analyse using Matlab and interpret given the instructions provided. This test will last 3 hours, at the end of which students hand in their data analysis report.

The second (final) test is a theoretical one in which questions are asked on the data analysis methods, especially on how to interpret their results.

For the final grade, the weights are 1/3 and 2/3 for the practical and the theoretical test respectively.

Remarks

Matlab, Linear Algebra, introduction level Statistics. Admission to the course will depend on capacity, total number of applications, date of registration and background of the individual student. If the number of applications exceeds the capacity of the course, students may have to be selected and priority will be given in the following order:

- First-year students of the master Life Sciences (UvA and VU)
- Second-year students of the master Life Sciences (UvA and VU)
- Students of the master Computational Sciences
- Students of the master Chemistry
- Students of the master Forensic Sciences
- Students of other master programmes

Course Catalogue 2017 - 2018

Course Programme Minor Lecturer

Search course

systems biology

☐ Search text

[> All cours](#)

Literature Review Life Sciences

Course catalogue number	5304TSBB6Y				
Credits	6 EC				
Language of instruction	English				
Time period(s)	<table><tr><td>Sem. 1</td><td>Sem. 2</td></tr><tr><td></td><td></td></tr></table> > See also	Sem. 1	Sem. 2		
Sem. 1	Sem. 2				
					
College/graduate	Graduate School of Life and Earth Sciences				
Lecturer(s)	dr.ir. H.C.J. Hoefsloot (co-ordinator)				
Contact	dr.ir. H.C.J. Hoefsloot Science Park 904+31 20 5255867 H.C.J.Hoefsloot@uva.nl				
Is part of	Master's Life Sciences				

[Register](#)

Registration

Information about procedures can be found at <http://www.student.uva.nl/lis/az/item/course-registration.html>.

Time

The schedule for this course is published on DataNose.

Course Catalogue 2017 - 2018

Course Programme Minor Lecturer

Search course

☐ Search text

[> All cours](#)

Systems Biology in Practice

Course catalogue number	5304SBIP6Y				
Credits	6 EC				
Language of instruction	English				
Time period(s)	<table> <tr> <th>Sem. 1</th><th>Sem. 2</th></tr> <tr> <td></td><td></td></tr> </table> > See also	Sem. 1	Sem. 2		
Sem. 1	Sem. 2				
College/graduate	Graduate School of Life and Earth Sciences				
Organised by	Swammerdam Institute for Life Sciences (SILS)				
Lecturer(s)	dr. F. Branco dos Santos (co-ordinator)				
Contact	dr. F. Branco dos Santos SILS - Science Park 904 kamer C3.264 - F.BrancodosSantos@uva.nl				
Is part of	Master's Life Sciences				

[Register](#)

Objectives

The aim of the course is to get acquainted with the interdisciplinary approach of experimental microbial physiology, transcriptome analysis and proteome analysis. Students will learn how information obtained by experiments at the level of cellular behaviour, genetic profile and enzymatic make-up can be combined in order to get insight in the mechanisms underlying regulation and adaptation of microbial organisms. Students will be introduced to the basic techniques and principles of microbial physiology, transcriptome analysis, massspectrometry and data analysis.

Contents

Throughout the course, the same experimental material will be used. Microorganisms will be cultured under a set of different conditions in the group Molec Microbial Phys and their physiology will be quantified in terms of metabolic fluxes. Transcriptome analysis of the cells will show how and to what extent the environment affects the metabolic network at the genetic level. Finally the same cells will be analyzed at the level of their protein composition by a proteomic analysis and by enzyme activity assays *in vitro*. Lectures on more general subjects of Microbiol Systems Biology will be organized to give the students a flavor of practice and application.

The content of the course can be summarized:

- Theory and practice growth of bacterial growth, flux analysis, biochemical assays;
- Theory and practice of genetic tools, gene expression, transcriptomics;
- Theory and practice of mass spec and proteomics;
- Data analysis, protein identification, systems biology of micro organisms

Registration

Information about procedures can be found at <http://www.student.uva.nl/ls/az/item/course-registration.html>.

Teaching method

Lectures and practicals.

Time

The schedule for this course is published on DataNose.

Study materials

- Literature: Lecture contents.

Assessment and testing

Written thesis, written lecture abstracts and oral presentation.

Remarks

Location: Science Park

Course Catalogue 2015 - 2016







Course Programme Minor Lecturer

Search course

☐ Search text

[> All cours](#)

Synthetic Biology and Biomedicine

Catalogue number	5304SYBB6Y				
Credits	6 (EC)				
Language of the course	English				
Year	Year 1 Master Life Sciences				
Time period(s)	<table border="1"> <thead> <tr> <th>Sem. 1</th><th>Sem. 2</th></tr> </thead> <tbody> <tr> <td></td><td></td></tr> </tbody> </table> 1 February 2016 - 25 March 2016 > See also	Sem. 1	Sem. 2		
Sem. 1	Sem. 2				
					
Educational institute	Graduate School of Life and Earth Sciences				
Lecturer(s)	dr. P.J. Verschure (co-ordinator) prof. dr. H.V. Westerhoff (and guest lecturers)				
Information	dr. P.J. Verschure Science Park 904 kamer C2.270 +31 20 5255151				
Is part of	Master's Life Sciences				

[Register](#)

Objectives

- To obtain knowledge of (1) the use of synthetic biology to understand complex biological behavior, (2) synthetic circuit design both experimental and theoretical, (3) how to apply synthetic biology in (bio)medical research, (4) human practice and the socio-public discussion around synthetic biology. The students will be trained in having a curiosity oriented research-based attitude. Skills obtained:
- To critically read and analyze and draw conclusions of scientific literature in the synthetic biology field.
 - To be able to design and modulate synthetic cell systems both experimentally and computationally
 - To present on paper and through presentations obtained knowledge from lectures, literature and experimental work.
 - To be able to critically assess science and scientific results

Contents

Synthetic biology aims to understand biological behavior by rebuilding or wiring biological behavior to refine biological systems design principles. Synthetic biology tools are expected to be very powerful to understand and eventually rewire the behavior of complex diseases. In this course the students will obtain knowledge of the field of synthetic biology, synthetic biology tools and synthetic circuit design to extract systems behavior (e.g. bistability, oscillation, cascade behavior). This knowledge will be put in the biomedical context touching on e.g. personalized medicine. Moreover, the students will learn facets of getting involved in a constructive dialogue on topics of public debate in the field of synthetic biology. In the practical training of the course the students will experience hands-on experimental building and analysis of a synthetic cell system that exhibits bistable behavior. The students will obtain an experimental update in molecular biology tools and use advanced cloning tools in the field of synthetic biology such as the Gibson assembly. This course will provide perfect background for the students to enter the iGEM competition (international genetically engineered machine competition, <http://igem.org>).

Overview of the course activities:

- Lectures to obtain scientific knowledge and background of the field of synthetic biology.
- Assignment project to use obtained knowledge and gain knowledge from literature to put synthetic biology approaches in the context of biomedicine
- Practical to obtain hands-on experience in building and analyzing synthetic cell systems with defined behavior.

Recommended prior knowledge

Background in Cell Biology

Registration at

Information about the registration procedures and the registration deadlines can be found at <https://student.uva.nl> ; choose Master's programme; A-Z list; Course and Exam Registration.

Format

The course will include theoretical knowledge and practical training. The students are expected to use knowledge from both theory and practice for the assignment project assignment on synthetic biology and biomedicine.

Time

The course schedule can be found at <https://datanose.nl/>

Study materials

Study material will be provided in the form of scientific literature (provided through Blackboard).

Assessment

The assessment will be based on (1) performance during the practical as well as the practical report of the practical, (2) the assignment project (written report and presentation) and (3) the exam.

Examination date

The exam schedule can be found at <https://datanose.nl/>