# Bioinformatics MSc

Vrije Universiteit Amsterdam - Faculteit der Exacte Wetenschappen - M Bioinformatics - 2015-2016

Research in Bioinformatics in its broadest definition concerns the analysis of informational processes within living systems with the help of computers. To do this succesfully, 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 and the Faculty of Earth and Life 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.

# Inhoudsopgave

## Compulsory optional Courses Systems Biology Major

Vakken:

| Naam | Periode | Credits | Code |
|------|---------|---------|------|
| Advanced Modeling in Systems Biology | Periode 6 | 6.0 | X_418155 |
| Statistics with R | Periode 5 | 6.0 | X_418156 |
| Synthetic Biology and Biomedicine | Periode 4 | 6.0 | X_418125 |

## 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.

Vakken:

| Naam | Periode | Credits | Code |
|------|---------|---------|------|
| Data Mining Techniques | Periode 5 | 6.0 | X_400108 |
| Fundamentals of Bioinformatics and Systems Biology | Periode 1 | 6.0 | X_405114 |
| Machine Learning | Periode 4 | 6.0 | X_400154 |
| Signal Transduction in Health and Disease | Periode 2 | 6.0 | X_432535 |

## 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.

Vakken:

| Naam | Periode | Credits | Code |
|------|---------|---------|------|
| Biosystems Data Analysis | Periode 3 | 6.0 | X_437001 |
| First internship (Major) | Ac. Jaar (september) | 42.0 | X_405027 |
| Fundamentals of Bioinformatics | Periode 1 | 6.0 | X_405052 |
| Introduction to Systems Biology | Periode 1 | 6.0 | X_428565 |
| Second Internship (Minor) | Ac. Jaar (september) | 18.0 | X_405032 |

| Seminar Series and Writing a Research Proposal | Ac. Jaar (september) | 6.0 | X_400594 |
|---|---|---|---|

## Compulsory Courses Bioinformatics Major

Vakken:

| Naam | Periode | Credits | Code |
|---|---|---|---|
| Algorithms in Sequence Analysis | Periode 2 | 6.0 | X_405050 |
| Bioinformatics for Translational Medicine | Periode 5 | 6.0 | X_405092 |
| Structural Bioinformatics | Periode 4 | 6.0 | X_405019 |

## Compulsory Courses Systems Biology Major

Vakken:

| Naam | Periode | Credits | Code |
|---|---|---|---|
| Basic Models of Biological Networks | Periode 4 | 6.0 | X_418154 |
| Systems Biology in Practice | Periode 2 | 6.0 | X_418157 |

## Advanced Modeling in Systems Biology

| Vakcode | X_418155 () |
|---|---|
| Periode | Periode 6 |
| Credits | 6.0 |
| Voertaal | Engels |
| Faculteit | Faculteit der Exacte Wetenschappen |
| Coördinator | prof. dr. F.J. Bruggeman |
| Examinator | prof. dr. F.J. Bruggeman |
| Docent(en) | prof. dr. F.J. Bruggeman |
| Lesmethode(n) | Hoorcollege, Computerpracticum, Werkcollege |
| Niveau | 500 |

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

**Inhoud vak**
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.

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

**Toetsvorm**
Results of computer assignments, written exams

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

## Algorithms in Sequence Analysis

| Vakcode | X_405050 (405050) |
|---|---|
| Periode | Periode 2 |
| Credits | 6.0 |
| Voertaal | Engels |
| Faculteit | Faculteit der Exacte Wetenschappen |
| Coördinator | prof. dr. J. Heringa |
| Examinator | prof. dr. J. Heringa |
| Docent(en) | prof. dr. J. Heringa |
| Lesmethode(n) | Hoorcollege, Werkcollege |
| Niveau | 400 |

**Doel vak**
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.

**Inhoud vak**
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 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 own implementation of Hidden Markov Models and using it to
predict protein domain structure

**Onderwijsvorm**
13 Lectures: 2 two-hour lectures per week
11 Computer practicals and associated assignments: 2 two-hour hands-on
sessions per week

**Toetsvorm**
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).

**Literatuur**
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

**Vereiste voorkennis**
Bachelor in any science discipline (including medicine).
Basic programming skills and an interest in biological problems.

**Doelgroep**
mAI, mBio, mCS

**Overige informatie**
Signing up via bb.vu.nl is mandatory.
The course is taught in English.

## Basic Models of Biological Networks

| Vakcode | X_418154 () |
|---|---|
| **Periode** | Periode 4 |
| **Credits** | 6.0 |
| **Voertaal** | Engels |
| **Faculteit** | Faculteit der Exacte Wetenschappen |
| **Coördinator** | prof. dr. F.J. Bruggeman |
| **Examinator** | prof. dr. F.J. Bruggeman |
| **Docent(en)** | dr. J.P. Bruggeman, prof. dr. F.J. Bruggeman |
| **Lesmethode(n)** | Hoorcollege, Werkcollege, Computerpracticum |
| **Niveau** | 400 |

**Doel vak**

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 indispensible 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.

**Inhoud vak**

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.

**Onderwijsvorm**

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

**Toetsvorm**

Results of computer assignments, written exams.

**Literatuur**

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

# Bioinformatics for Translational Medicine

| Vakcode | X_405092 () |
|---|---|
| Periode | Periode 5 |
| Credits | 6.0 |
| Voertaal | Engels |
| Faculteit | Faculteit der Exacte Wetenschappen |
| Coördinator | dr. S. Abeln |
| Examinator | dr. S. Abeln |
| Docent(en) | prof. dr. J. Heringa |
| Lesmethode(n) | Hoorcollege, Practicum |
| Niveau | 400 |

**Doel vak**

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 algorithms 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.

**Inhoud vak**
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.

Three small data analysis practicals are also given on:
• Exome sequencing
• RNA sequencing
• Proteomics

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

**Toetsvorm**
The final grade for this course will consist of 65% practical work (see above) and 35% theoretical assessment.

Practical assessment (65&):
• CATS assignment (35%)
• 3 data analysis assignments (30%)

Theoretical assessment: (35%)
• Oral or written exam (depending on number of course students).

• As part of the exam a research paper on a Bioinformatics method
needs to be analysed in detail and you need to write a small research
proposal based on the paper.

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

**Aanbevolen voorkennis**
An interest in Biological problems.

**Doelgroep**
mAI, mBio, mCS

**Overige informatie**
Signing up via bb.vu.nl is mandatory.
The course is taught in English.

• Compulsory course for students in MSc of Bioinformatics.
• Optional course for students with Bachelor Physics, Chemistry,
Mathematics, Computer Science, Biology, or Biomedical Sciences.

## Biosystems Data Analysis

| Vakcode | X_437001 (437001) |
|---------|-------------------|
| Periode | Periode 3 |
| Credits | 6.0 |
| Voertaal | Engels |
| Faculteit | Faculteit der Exacte Wetenschappen |
| Niveau | 400 |

**Inhoud vak**
http://studiegids.uva.nl/xmlpages/page/2015-2016/zoek-vak/vak/19661

**Overige informatie**
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

| Vakcode | X_400108 (400108) |
|---------|-------------------|
| Periode | Periode 5 |
| Credits | 6.0 |
| Voertaal | Engels |
| Faculteit | Faculteit der Exacte Wetenschappen |
| Coördinator | dr. M. Hoogendoorn |
| Examinator | dr. M. Hoogendoorn |
| Docent(en) | dr. M. Hoogendoorn |
| Lesmethode(n) | Hoorcollege |
| Niveau | 500 |

**Doel vak**

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.

**Inhoud vak**

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).

**Onderwijsvorm**

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

**Toetsvorm**

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 to 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.

**Literatuur**

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

**Aanbevolen voorkennis**

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

**Doelgroep**

mBA, mCS, mAI, mBio

# First internship (Major)

| Vakcode | X_405027 (405027) |
|---|---|
| Periode | Ac. Jaar (september) |

| Credits | 42.0 |
|---|---|
| **Voertaal** | Engels |
| **Faculteit** | Faculteit der Exacte Wetenschappen |
| **Coördinator** | prof. dr. J. Heringa |
| **Niveau** | 400 |

**Doel vak**

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.

**Inhoud vak**

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.

**Onderwijsvorm**

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.

**Toetsvorm**

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).

**Literatuur**

Course reading will be advised by the host institution.

**Aanbevolen voorkennis**

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.

**Doelgroep**

MSc Bioinformatics and Systems Biology

**Overige informatie**

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

| Vakcode | X_405052 (405052) |
|---|---|
| **Periode** | Periode 1 |
| **Credits** | 6.0 |
| **Voertaal** | Engels |
| **Faculteit** | Faculteit der Exacte Wetenschappen |
| **Coördinator** | dr. ir. K.A. Feenstra |
| **Examinator** | dr. ir. K.A. Feenstra |
| **Docent(en)** | dr. ir. K.A. Feenstra |
| **Lesmethode(n)** | Hoorcollege, Deeltoets extra zaalcapaciteit, Computerpracticum |
| **Niveau** | 400 |

**Doel vak**

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 him/her self. 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.

**Inhoud vak**

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!

**Onderwijsvorm**
• 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

**Toetsvorm**
• [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

**Literatuur**
• 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

**Aanbevolen voorkennis**
Bachelor in any science discipline (including medicine), or strong
programming background.
An interest in programming and biological problems.

**Doelgroep**
mAI, mBio, mCS, mMNS

# Fundamentals of Bioinformatics and Systems Biology

| **Vakcode** | X_405114 () |
|---|---|
| **Periode** | Periode 1 |
| **Credits** | 6.0 |
| **Voertaal** | Engels |
| **Faculteit** | Faculteit der Exacte Wetenschappen |
| **Coördinator** | dr. ir. K.A. Feenstra |
| **Examinator** | dr. ir. K.A. Feenstra |
| **Niveau** | 400 |

**Doel vak**
This master course covers the practical parts and project work of
Fundamentals of Bioinformatics (X_405052) and of Introduction to Systems
Biology, which does not overlap with the bachelor courses Principles of
Bioinformatics (X_401094) and Principles of Systems Biology. The course
is not intended as a stand-alone course and cannot not be chosen by
students, but may only be taken on assignment by the mentors of the
Master Bioinformatics and Systems Biology.

**Inhoud vak**
practical/project work from Fundamentals of Bioinformatics (405052) and
of Introduction to Systems Biology.

**Onderwijsvorm**

see practical/project work in Fundamentals of Bioinformatics (405052)
and of Introduction to Systems Biology.

**Toetsvorm**

see project, group work and presentation in Fundamentals of
Bioinformatics (405052) and of Introduction to Systems Biology.

**Literatuur**

• 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

**Aanbevolen voorkennis**

A bachelor including the courses Principles of Bioinformatics (X_401094)
and Principles of Systems Biology (AM_1037FEW), or equivalent, as
assessed by the mentor.

**Doelgroep**

Students in the Master Bioinformatics and Systems Biology, only on
assignment by mentor.

**Intekenprocedure**

Students should not register directly for this course.

## Introduction to Systems Biology

| Vakcode | X_428565 () |
|---|---|
| **Periode** | Periode 1 |
| **Credits** | 6.0 |
| **Voertaal** | Engels |
| **Faculteit** | Faculteit der Exacte Wetenschappen |
| **Coördinator** | dr. D. Molenaar |
| **Examinator** | dr. D. Molenaar |
| **Docent(en)** | prof. dr. B. Teusink, dr. D. Molenaar, prof. dr. F.J. Bruggeman |
| **Lesmethode(n)** | Hoorcollege, Werkgroep, Werkcollege |
| **Niveau** | 400 |

**Doel vak**

Introduction to Systems Biology is the starting course of the
Bioinformatics and Systems Biology master (together with Fundamentals of
Bioinformatics). It aims to give a broad overview of important topics
relevant to the field of Systems Biology, 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. Based on their background, students will be assigned to
deficiency classes where they will be working to fill gaps in their
background knowledge in mathematics, programming and/or biology.
Goals:
- To make the students aware of gaps in their own background knowledge.
- To make the student acquainted with the major issues, concepts and
methodology in systems biology (to be studied in more detail in the
master)

- To develop a basic understanding of major biological concepts in genomics and cell biology that are relevant to current topics in systems biology
- To work together in a group of diverse backgrounds
- To gain hands-on experience in basic modeling as a means of solving systems biology problems

**Inhoud vak**
Theory:
- Design principles of biological networks, basic modeling approaches, evolution
Practical:
- Exercises during/in between lectures in which methods of systems biology will be applied to several topics.

**Onderwijsvorm**
- Lectures (two hour lecture in the morning, two days per week)
- Computer practicals
- Modeling practicals
- Deficiency classes in biology, mathematics and/or programming

**Toetsvorm**
30% Mathematics, Programming or Biology deficiency classes
60% Final exam of the Systems Biology subjects

**Literatuur**
A course syllabus will be provided

**Aanbevolen voorkennis**
Highschool mathematics

**Doelgroep**
Students with background in Biology, Bioinformatics, Mathematics, Physics

# Machine Learning

| | |
|---|---|
| **Vakcode** | X_400154 (400154) |
| **Periode** | Periode 4 |
| **Credits** | 6.0 |
| **Voertaal** | Engels |
| **Faculteit** | Faculteit der Exacte Wetenschappen |
| **Coördinator** | dr. E.W. Haasdijk |
| **Examinator** | dr. E.W. Haasdijk |
| **Docent(en)** | dr. E.W. Haasdijk |
| **Lesmethode(n)** | Hoorcollege, Werkcollege |
| **Niveau** | 300 |

**Doel vak**
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.

**Inhoud vak**

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.

**Onderwijsvorm**

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 and/or presentation.
The course will be taught in English.

**Literatuur**

NNB

**Doelgroep**

3BA, 3BA-D, 3CS, 3LI, 3IMM, mBio

## Second Internship (Minor)

| Vakcode | X_405032 (405032) |
|---|---|
| Periode | Ac. Jaar (september) |
| Credits | 18.0 |
| Voertaal | Engels |
| Faculteit | Faculteit der Exacte Wetenschappen |
| Coördinator | prof. dr. J. Heringa |
| Examinator | prof. dr. J. Heringa |
| Niveau | 400 |

**Doel vak**

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 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.

**Inhoud vak**
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.

**Onderwijsvorm**
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.

**Toetsvorm**
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).

**Literatuur**
Course reading will be advised by the host institution.

**Aanbevolen voorkennis**
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.

**Doelgroep**
MSc Bioinformatics and Systems Biology

**Overige informatie**
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

| Vakcode | X_400594 (400594) |
|---|---|
| **Periode** | Ac. Jaar (september) |
| **Credits** | 6.0 |
| **Voertaal** | Engels |
| **Faculteit** | Faculteit der Exacte Wetenschappen |
| **Coördinator** | dr. ir. K.A. Feenstra |
| **Examinator** | dr. ir. K.A. Feenstra |
| **Lesmethode(n)** | Hoorcollege |
| **Niveau** | 500 |

**Doel vak**

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 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 topic area.
* The student will have hands-on experience in writing a Bioinformatics research proposal.
* The student will have some exposure to a semi-realistic proposal procedure.

**Inhoud vak**

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

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

**Onderwijsvorm**

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

**Toetsvorm**

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

**Literatuur**

* manual and further material on
http://wiki.cs.vu.nl/mp/index.php/Bioinformatics_and_Systems_Biology_Res
earch_Proposal
* relevant background literature

**Aanbevolen voorkennis**

All compulsory courses in the MSc Bioinformatics and Systems Biology programme, including those of the chosen profile.
A good grasp of major bioinformatics research themes, open questions and methods is recommended; in practice this means this course is best taken after the major internship.

**Doelgroep**
Students in the MSc Bioinformatics and Systems Biology only (mBio).

**Overige informatie**
To start the course please make an appointment with the coordinator.

# Signal Transduction in Health and Disease

| | |
|---|---|
| **Vakcode** | X_432535 (432535) |
| **Periode** | Periode 2 |
| **Credits** | 6.0 |
| **Voertaal** | Engels |
| **Faculteit** | Faculteit der Exacte Wetenschappen |
| **Coördinator** | prof. dr. M.J. Smit |
| **Examinator** | prof. dr. M.J. Smit |
| **Docent(en)** | dr. M.J. Smit |
| **Lesmethode(n)** | Hoorcollege |
| **Niveau** | 600 |

**Doel vak**
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.

**Inhoud vak**
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.

**Onderwijsvorm**
Lectures, self-study.
Students will do a case study in groups on a receptor/protein family
linked to disease. Molecular mechanisms underlying pathology will be
addressed and presented.

**Toetsvorm**
Assignment and presentation, written exam.

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

Papers available on Blackboard

**Aanbevolen voorkennis**

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

**Doelgroep**
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

| | |
|---|---|
| **Vakcode** | X_418156 () |
| **Periode** | Periode 5 |
| **Credits** | 6.0 |
| **Voertaal** | Engels |
| **Faculteit** | Faculteit der Exacte Wetenschappen |
| **Coördinator** | dr. D. Molenaar |
| **Examinator** | dr. D. Molenaar |
| **Docent(en)** | dr. D. Molenaar |
| **Lesmethode(n)** | Hoorcollege |
| **Niveau** | 400 |

**Doel vak**
The goal of the course is to obtain practical skills in the programming
environment R for statistical analyses. The course will provide hands-on
experience in the treatment and investigation of (biological) datasets.
Familiarize the students with the intricacies of the modern techniques
for data generation and analysis. As a bonus, students will become
acquainted with some concepts of higher order programming.

**Inhoud vak**
Systems 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
(http://www.r-project.org/). R is intensively used and developed in the
community of experimental biologists, and most newly published data
analysis techniques are first available as R-packages. 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 uni- and
multivariate analysis (e.g. ANOVA, correlation, regression, clustering,
and ordination). 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.

**Onderwijsvorm**
Lectures, tutorials, computer practical work, self-study

**Toetsvorm**
Computer assignments

**Literatuur**

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

**Aanbevolen voorkennis**
Some knowledge of basic statistics

**Doelgroep**
Master students with a background in Biology, Biomedical Sciences, Bioinformatics, Physics or Mathematics with an interest in the analysis of large datasets.

# Structural Bioinformatics

| | |
|---|---|
| **Vakcode** | X_405019 (405019) |
| **Periode** | Periode 4 |
| **Credits** | 6.0 |
| **Voertaal** | Engels |
| **Faculteit** | Faculteit der Exacte Wetenschappen |
| **Coördinator** | dr. ir. K.A. Feenstra |
| **Examinator** | dr. ir. K.A. Feenstra |
| **Docent(en)** | dr. ir. K.A. Feenstra, dr. S. Abeln |
| **Lesmethode(n)** | Hoorcollege, Practicum |
| **Niveau** | 400 |

**Doel vak**
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.

**Inhoud vak**
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 simulation, &Monte Carlo simulation
• Function from structure

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

**Onderwijsvorm**
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.

**Toetsvorm**
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 you exam through exercises and paper
discussion during the lectures

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

**Aanbevolen voorkennis**
Bachelor in any science discipline (including medicine).
Basic scripting skills (e.g. Python or Pearl) and an interest in
biological problems. 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.

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

**Overige informatie**
- 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

| **Vakcode** | X_418125 () |
| --- | --- |
| **Periode** | Periode 4 |

| Credits | 6.0 |
|---|---|
| Voertaal | Engels |
| Faculteit | Faculteit der Exacte Wetenschappen |

**Inhoud vak**

http://studiegids.uva.nl/xmlpages/page/2015-2016/zoek-vak/vak/14399

**Overige informatie**

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

| Vakcode | X_418157 () |
|---|---|
| Periode | Periode 2 |
| Credits | 6.0 |
| Voertaal | Engels |
| Faculteit | Faculteit der Exacte Wetenschappen |
| Niveau | 400 |

**Inhoud vak**

http://studiegids.uva.nl/xmlpages/page/2015-2016/zoek-vak/vak/20673

**Overige informatie**

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.