## Course Specifications

Valid as from the academic year 2018-2019

### Course

**Bioinformatics (O000105)**

### Lecturers in academic year 2018-2019

- **De Neve, Wesley**
  - KR01 lecturer-in-charge
- **Van Messem, Arnout**
  - KR01 co-lecturer

### Offered in the following programmes in 2018-2019

| Bachelor of Science in Molecular Biotechnology | 5 | A |

### Course size

<table>
<thead>
<tr>
<th>Credits</th>
<th>Study time</th>
<th>Contact hrs</th>
</tr>
</thead>
<tbody>
<tr>
<td>5.0</td>
<td>150 h</td>
<td>45.0 h</td>
</tr>
</tbody>
</table>

### Course offerings in academic year 2018-2019

A (semester 1)  
**English**

### Teaching languages

- **English**

### Keywords

- Algorithmic design
- Algorithms
- Bioinformatics
- Creative problem solving
- Complexity analysis
- Datastructures
- Machine Learning
- Programming
- Python

### Position of the course

*The field of bioinformatics was born after biologists discovered how to sequence (digitize) DNA, raising the need for mathematical and computational techniques to decipher the language of DNA, RNA, and proteins. As a result, bioinformatics has become an important part of modern biology, often facilitating new insights and new (data-driven) approaches, driving further biological developments.*

*Primarily taking a computational point-of-view, this course aims at introducing students to the design, implementation, and analysis of standard algorithms in the field of bioinformatics, including exhaustive search algorithms, recursive algorithms, divide-and-conquer algorithms, greedy algorithms, graph algorithms, randomized algorithms, machine learning algorithms, and dynamic programming algorithms. These algorithms and related datastructures (e.g., lists, tuples, sets, dictionaries, graphs, hash tables, and trees) are studied in the context of problems like pattern matching, genome rearrangements, DNA sequencing, DNA sequence alignment, regulatory motif finding, structural genome annotation (splice site and translation initiation site detection), functional genome annotation, and/or medical image analysis.*

### Contents

*Based on capita selecta from the course handbook used, this course deals with the following computational topics, making use of pseudocode and the Python programming language:*

- algorithms and complexity, including asymptotic notation;
- exhaustive search algorithms;
- recursive algorithms;
- divide-and-conquer algorithms;
- greedy algorithms;
- graph algorithms;
- (deep) machine learning algorithms;
- randomized algorithms; and
- dynamic programming algorithms.

### Initial competences

*An understanding of basic probability theory and the behaviour of common functions studied in calculus (e.g., linear functions, logarithmic functions, exponential functions).*

---

(Approved)
Prior experience in at least one high-level programming language (e.g., Python).

Final competences

1. Understand the biological motivation of common bioinformatics problems, as well as their mathematical and computational abstraction.
2. Be familiar with the standard algorithms and data structures used in bioinformatics.
3. Design and implement algorithms for new bioinformatics problems using standard algorithmic techniques.
4. Compare the effectiveness and time/memory efficiency of different algorithmic techniques in solving different bioinformatics problems.

Conditions for credit contract

Access to this course unit via a credit contract is determined after successful competences assessment

Conditions for exam contract

This course unit cannot be taken via an exam contract

Teaching methods

Guided self-study, demonstration, lecture, seminar: practical PC room classes

Learning materials and price


Slides shown during the lectures will be made available on Minerva (in English), together with additional learning materials (e.g., background information and links to relevant websites).

Free digital tools like Eclipse and PyCharm for writing and debugging Python source code.

Students are required to have a personal laptop for use in this course.

References


Course content-related study coaching

The theory lectures touch upon the biological motivation of common bioinformatics problems, as well as their mathematical and computational abstraction.

During the supervised hands-on sessions, students themselves learn how to tackle computational challenges in the field of bioinformatics by solving a series of mandatory computer exercises, mostly on an individual basis.

After each deadline, the solutions of all exercises are made available on Minerva.

Announcements on Minerva are used for counselling, giving feedback, and providing background information.

The lecturer and the teaching assistants have weekly office hours for answering questions about the course in general, the theory, and the exercises. Individual appointments can also be scheduled via email.

Evaluation methods

end-of-term evaluation and continuous assessment

Examination methods in case of periodic evaluation during the first examination period

Written examination with open questions, written examination with multiple choice questions, skills test

Examination methods in case of periodic evaluation during the second examination period

Written examination with open questions, written examination with multiple choice questions, skills test

Examination methods in case of permanent evaluation

Possibilities of retake in case of permanent evaluation

examination during the second examination period is not possible

Calculation of the examination mark

Periodic evaluation (50%) + non-periodic evaluation (50% hands-on sessions). To qualify for passing this course, both the score of the periodic and the non-periodic evaluation should be at least equal to 8/20. If that is not the case, the examination mark will be subject to an upper limit of 7/20.

The non-periodic evaluation cannot be retaken during the second examination period. Therefore, the examination mark for the second examination period is calculated twice. For the first calculation, the score of the non-periodic evaluation, as obtained during the first examination period, accounts for 50% of the examination mark and the score of the periodic evaluation, as obtained during the second examination period, accounts for the remaining 50% of the examination mark. For the second calculation, the examination mark is equal to the score of the periodic evaluation, as obtained during the second examination period. The final examination mark for the second examination period is then equal to the maximum of the above two calculations.

Students who eschew period aligned and/or non-period aligned evaluations for this course unit may be failed by the examiner.