# COURSE DESCRIPTION CARD - SYLLABUS

Course name
Structural Visualization [S1Bioinf1>WIZST]

## Course

| | |
|---|---|
| Field of study<br>Bioinformatics | Year/Semester<br>4/7 |
| Area of study (specialization)<br>– | Profile of study<br>general academic |
| Level of study<br>first-cycle | Course offered in<br>Polish |
| Form of study<br>full-time | Requirements<br>elective |

## Number of hours

| | | |
|---|---|---|
| Lecture<br>15 | Laboratory classes<br>15 | Other<br>0 |
| Tutorials<br>0 | Projects/seminars<br>0 | |

## Number of credit points

2,00

| Coordinators | Lecturers |
|---|---|
| dr hab. inż. Tomasz Żok prof. PP<br>tomasz.zok@put.poznan.pl | |

## Prerequisites

A student entering this course should have a basic knowledge of structural biology, programming and computer graphics. He or she should also have the ability to obtain information from external sources and should have creativity and curiosity.

## Course objective

To provide students with knowledge regarding visualization of structural data. Familiarize with best practices and methods for both reliable and interesting for the viewer presentation of data on the structures of biological molecules.

## Course-related learning outcomes

Knowledge:
1. Is familiar with selected methods for visualizing the structures of biological molecules.
2. Knows best practices for creating charts and graphs.
3. Is familiar with software tools and libraries for preparing data visualizations.

Skills:

1. Is able to prepare charts and diagrams and visualize secondary and tertiary structures of biological molecules.
2. Is able to use visual methods to distinguish important features in the structure of a biological molecule.
3. Is able to design and develop custom software to analyze structural data and visualize results.

Social competences:
1. Understands the importance of visuals in effective communication related to the profession.
2. Understands that creation of an appropriate visualization requires preparation and diligence.
3. Understands the need for constant improvement of his/her own competences, especially in the context of knowledge of the latest data visualization methods.

## Methods for verifying learning outcomes and assessment criteria

Learning outcomes presented above are verified as follows:

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Knowledge acquired in the lecture is verified by a colloquium during the last lecture in the semester. The test consists of 10-15 questions (closed or open), with different numbers of points. Pass mark: 50% of the points. Examination topics will be presented during the lectures.
The skills acquired in laboratory classes will be verified on the basis of the evaluation of projects carried out by the students during the semester. The project will be evaluated depending on the complexity of the problem (students will be able to work on basic or complex problems), the quality of the prepared code and report, as well as the presentation during which the student will present the results obtained.

## Programme content

- General data visualization
- Classical and contemporary algorithms for visualizing RNA structures
- Structural alignment
- Basic and advanced use of the PyMOL tool
- Electron density maps and EM

## Course topics

The course consists of seven lectures. The first lectures will cover basic information about the secondary and tertiary structures of proteins and RNAs with special emphasis on classical approaches to their visualization. Structural motifs and other elements that can be visually distinguished will be discussed. Subsequent lectures will present selected methods for extraction of additional information and its visualization e.g. contact map or Ramachandran plot. Further lectures will present visual ways to compare multiple structures of biological molecules. The lectures will also introduce students to the basics of color selection and best practices for preparing charts, graphs and visualizations.
Laboratory exercises are linked thematically to lectures. In the computer lab, students will complete assignments based on a prepared script and publicly available structural data. The tasks include the use of publicly available tools and the design and implementation of their own software. The results in the form of graphs, charts, drawings and videos will be part of the report, which together with the presentation will be evaluated.

## Teaching methods

1. Lecture: multimedia presentation
2. Laboratory exercises: multimedia presentation, practical exercises, preparing reports

## Bibliography

Basic
1. F. J. Burkowski „Computational and Visualization Techniques for Structural Bioinformatics Using Chimera”
2. T. Skern, „Exploring Protein Structure: Principles and Practice"
Additional
1. E. Picardi, „RNA Bioinformatics”
2. J. Gu, P. E. Bourne, „Structural Bioinformatics”

3. F. Biecek, „Odkrywać! Ujawniać! Objaśniać! Zbiór esejów o sztuce prezentowania danych”

## Breakdown of average student's workload

| | Hours | ECTS |
|---|---|---|
| Total workload | 50 | 2,00 |
| Classes requiring direct contact with the teacher | 30 | 1,00 |
| Student's own work (literature studies, preparation for laboratory classes/ tutorials, preparation for tests/exam, project preparation) | 20 | 1,00 |