MODULE DESCRIPTION CARD – SYLLABUS

This module is a part of the Intensive International Education Programs in the field of the … organised at Poznan University of Technology as part of the „IMPACT – Innowacyjne Międzynarodowe Programy w AI, Cyberbezpieczeństwie i Teleinformatyce" project implemented SPINAKER Program of the National Agency for Academic Exchange, financed by the European Social Development Fund 2021–2027 (ESDF).

Module name:	**Number of hours:**	**Lecturer:**
Artificial intelligence in bioinformatics	10	Maciej Piernik, PhD

Module Descriptions:

The module introduces practical applications of artificial intelligence in bioinformatics. Students learn how to formulate biological and medical questions as machine learning tasks, prepare and analyze genomics and transcriptomics data, build and evaluate predictive models (diagnostics, drug-response prediction, virtual cells) and critically assess their limitations.

Purpose of the support under Module:

The overall objective of the Innovative International Education Program in Artificial Intelligence is to develop advanced, practice-oriented competences in designing, implementing and critically assessing AI solutions for complex real-world problems, with particular emphasis on interdisciplinary applications.

The specific objective of the module is to provide competencies and promote activities carried out at the Poznań University of Technology in the area of modern machine learning and deep learning methods in bioinformatics, including diagnostics and drug-response prediction, genomics and transcriptomics analysis, multi-omics integration and virtual cell-based simulations.

Method of support under Module:

Support within the module is provided with the participation of the instructor and divided into the following elements:

- 6-week self-study program using teaching materials provided by the instructor on the e-learning platform;
- 6 weeks of support from the instructor in the form of online consultations using tools that enable meetings to be held;
- a test to verify the acquisition of competences.

Module-related learning outcomes:

Descriptions of the new competences:

After completing the module, the student can formulate basic bioinformatics problems as machine learning tasks, select appropriate models and evaluation metrics, implement simple end-to-end pipelines in Python, interpret model outputs in a biologically meaningful way and critically assess the risks and limitations of AI in biomedical applications.

Knowledge:

1. Knows typical applications of AI in bioinformatics, such as patient diagnostics and prognosis, drug-response prediction, variant effect prediction, functional genomics, transcriptomics analysis, virtual cells and AI-assisted drug discovery.
2. Understands the key challenges of bio/med-tech data (large p, small n, batch effects, label noise, confounders, class imbalance, missing data) and their impact on model design, validation and generalization.
3. Knows the principles, strengths and limitations of core machine learning methods used in bioinformatics, including linear models, tree-based ensembles, gradient boosting and basic deep learning architectures (feedforward nets, CNNs, RNNs, transformers, autoencoders).
4. Understands how different types of biological data (sequences, gene expression, clinical variables, images, graphs, multi-omics) can be represented numerically and used as inputs to ML models.
5. Knows common analysis tasks in genomics and transcriptomics (e.g., differential expression, pathway enrichment, cell-type annotation, trajectory/velocity, regulatory network inference) and how AI methods support these tasks.
6. Understands the role of model evaluation, validation schemes and metrics (ROC-AUC, PR-AUC, calibration, learning curves, regression errors) and the importance of reproducibility, documentation and avoiding data leakage.

Skills:

1. Can translate a concrete biological or clinical question (e.g., diagnostic, prognostic, response prediction, variant effect, perturbation effect) into an ML task with defined inputs, outputs, metrics and baselines.
2. Can prepare real bioinformatics data for modeling: perform basic cleaning, handle high-dimensional data, address batch effects, split data correctly and select an appropriate validation scheme.
3. Can implement, train and evaluate simple ML models in Python (e.g., using scikit-learn/PyTorch) for selected bioinformatics problems, and compare baselines with more advanced models in a reproducible way.
4. Can interpret model performance metrics and diagnostic plots (ROC/PR curves, calibration curves, learning curves, feature importance, simple explainability tools) and use them to refine the modeling pipeline.
5. Can design and implement a minimal end-to-end AI/bio pipeline: from data inspection, through model training and validation, to a simple, usable output (e.g., script or lightweight app) that could realistically support a biological or clinical decision.
6. Can critically analyze AI/bio solutions with respect to confounders, batch effects, overfitting and domain shift, and propose concrete steps to improve them.

Social competences:

1. Is aware of the responsibility associated with using AI in biomedical contexts and is cautious in interpreting, communicating and applying model outputs, especially when they may influence patient-related decisions.
2. Is prepared to work in interdisciplinary teams (computer scientists, biologists, clinicians, pharmacists), communicate assumptions, methods and limitations in accessible language and adjust solutions to the needs of different stakeholders.
3. Is ready to engage in continuous self-learning in AI and bioinformatics, actively seek expert opinions, critically evaluate sources and share knowledge and good practices with others.
4. Demonstrates honesty about model capabilities and limitations (e.g., uncertainty, data gaps, failure modes) and resists overstating results, especially in high-stakes biomedical applications.

Criteria for verifying learning outcomes

Learning outcomes are verified through an online single-choice test that assesses the student’s knowledge of artificial intelligence methods in bioinformatics, types and properties of biomedical data, and typical application scenarios (diagnostics, drug-response prediction, genomics, transcriptomics, multi-omics). The test checks both theoretical understanding and the ability to correctly interpret model outputs, evaluation metrics, and common pitfalls. A minimum of 51% of the answers must be correct to pass.

Method of verification/validation of learning outcomes

Verification is conducted via an online single-choice test delivered on the dedicated e-learning platform. The test is taken individually, without access to supporting materials, and evaluates the extent to which the student has achieved the intended knowledge, skills, and social competencies related to the safe and correct use of AI methods in bioinformatics. The results are automatically recorded and validated according to predefined assessment criteria.

Workload

25 h (including work with teaching materials provided by the lecturer, consultation, and the student's own work) – 1 ECTS point

Level of the European Qualifications Framework