NAVOI STATE UNIVERSITY

BIF15608 BIOPHYSICS & BIOINFORMATICS — COURSE SYLLABUS

Faculty of Natural Sciences - 60510100 Biology

COURSE PASSPORT & ACADEMIC METADATA

Course Title: Biophysics and Bioinformatics (BIF15608)

Course Type: Mandatory (Compulsory)
Field of Study: 100000

Program: 60510100 Biology

Academic Year: 2026–2027
Semesters: 5 & 6

Form of Education: Full-time

Language of Instruction: English / Uzbek / Russian
Weekly Hours: 4 hrs/week (Sem 5 & 6)

Total Workload: 240 Hours

Credits: 8 ECTS

Assessment: Examination
International Benchmark: Aligned with Lomonosov Moscow State University (MSU) Top-100 QS Curriculum
Aligned UN SDGs: SDG 9 (Industry, Innovation & Infrastructure), SDG 4 (Quality Education), SDG 3 (Good Health)



1. Course Description & International Benchmarking

Biophysics and Bioinformatics is an interdisciplinary course bridging physics, molecular biology, computational algorithms, and genomic data science. Benchmarked against Lomonosov Moscow State University (QS World Rank #94), the curriculum combines biological thermodynamics, bioelectrogenesis, molecular modeling, genomic sequence alignment, and in silico drug design.

The course supports SDG 9 (Innovation & Infrastructure) and SDG 4 (Quality Education) by equipping students with high-tech computational skills, neural network applications, and computational biology techniques.

2. Course Aims & Learning Outcomes

Course Aim: To provide theoretical foundation and practical skills in biophysical thermodynamics, membrane transport, genomic sequence analysis, molecular visualization, and computational drug discovery.

- Knowledge: Understand biological thermodynamics, ion channels, bioelectrogenesis, BLAST algorithms, hidden Markov models, and 3D protein folding.
- Skills: Execute sequence alignment (BLAST, ClustalW), molecular visualization (PyMOL, RasMol), protein structure prediction (I-TASSER), and docking (AutoDock).
- Practical Competency: Measure membrane potentials, isolate mitochondria, analyze genomic databases (GenBank, UniProt, PDB), and construct phylogenetic trees.
- SDG Competencies: Leverage bioinformatics tools for biopharmaceutical innovation, personalized medicine, and genetic resource conservation (SDG 3, SDG 9).

3. Prerequisites

Prerequisites: General Physics, Higher Mathematics, Organic & Biological Chemistry, Molecular Biology, Molecular Genetics.

4. Course Structure & Workload Allocation

Activity Type	Sem 5 Hours	Sem 6 Hours	Total Hours
Lectures	30 Hours	30 Hours	60 Hours
Laboratory Classes	30 Hours	30 Hours	60 Hours
Independent Study	60 Hours	60 Hours	120 Hours
Total Workload	120 Hours	120 Hours	240 Hours (8 ECTS)

5. Detailed Course Curriculum Outline

5.1 Lecture Syllabus Outline

• **L1: Introduction & Biological Thermodynamics:** Thermodynamic laws, Onsager coefficients, Prigogine theorem, open systems, synergetics.

• **L2: Kinetics & Molecular Biophysics:** Michaelis-Menten kinetics, Volterra models, macromolecular forces, spectroscopy, NMR, circular dichroism.

• **L3: Biomembranes & Bioelectrogenesis:** Active/passive membrane transport, Nernst equation, Goldman-Hodgkin-Katz equation, ion channels, action potential.

• **L4: Introduction to Bioinformatics & Databases:** Biological sequence databases: GenBank, EMBL, UniProt, PDB, NCBI structure search tools.

• **L5: Sequence Alignment & Phylogenetics:** BLAST algorithms, pairwise/multiple sequence alignment (ClustalW, T-Coffee), phylogenetic tree building.

• **L6: Protein Structure Prediction & Drug Design:** Ramachandran plots, in silico folding (I-TASSER, Modeller), PyMOL, molecular docking (AutoDock), drug discovery pipelines.

5.2 Practical & Laboratory Outline

- Measurement of diffusion and membrane potentials in biological tissue models.
- Isolation of mitochondria from biological tissues and oxygen consumption rate analysis.
- NCBI GenBank nucleotide and protein sequence extraction and BLAST analysis.
- Multiple sequence alignment and phylogenetic dendrogram construction using ClustalW.
- 3D Protein structure visualization using PyMOL/RasMol and molecular docking in AutoDock.

5.3 Independent Study (Mustaqil Ta'lim) Topics

- Human Genome Project data mining and eukaryotic gene prediction using ORF Finder.
- In silico drug design project for targeted protein-ligand binding.
- Population genetic analysis using WinPepi and PopGene software.

6. Recommended Literature & Information Sources

- Voznesenskiy S.A., Kozlova E.K. Biophysics. Vlados, 2000.
- Ogurtsov A.N. Fundamentals of Bioinformatics. NTU KhPI, 2013.
- Lesk A.M. Introduction to Bioinformatics. Oxford University Press, 2019.
- NCBI, EBI, and ExpASy Proteomics Web Repositories.