MINISTRY OF SCIENCE AND HIGHER EDUCATION OF THE RUSSIAN FEDERATION
Federal State Autonomous Educational Institution of
Higher Education
"Ural Federal University named after the First President of Russia B.N. Yeltsin"

Institute of Natural Sciences and Mathematics

APPROVED BY
Vice-Rector for Research
_____ A.V. Germanenko
«___» _____ 2023 г.

PROGRAM OF THE DISCIPLINE
BIOINFORMATICS

List of information about the program of the discipline	**Credentials**
Postgraduate Program Biotechnology	**Code PP** 1.5.6.
Group of specialties Biological Sciences	**Код** 1.5.
Federal State requirements (FSR)	Order of the Ministry of Science and Higher Education of the Russian Federation № 951 dated 20.10.2021.
Self-approved requirements (SAR)	Order "On the implementation of the "Requirements for the development and implementation of training programs for scientific and scientific-pedagogical personnel in the graduate school of UrFU" dated 31.03.2022 №315/03

Yekaterinburg
2023

The program of discipline was compiled by the authors:

№	Full name	Academic degree, Academic title	Position	Affiliation
1	Irina S. Kiseleva	PhD, docent	Head of Department	Department of experimental biology and biotechnology Institute of Natural Sciences and mathematics
2	Anastasya S. Tugbaeva	PhD	Associate Professor	Department of experimental biology and biotechnology Institute of Natural Sciences and mathematics

Recommended by:

Educational and methodological board of Institute of Natural Sciences and Mathematics

Head of the Educational and Methodological board of the Institute of Natural Sciences and Mathematics
Record № _1_ от 19.01.2023 г.

E. S. Buyanova

Agreed by:

Head of academic staff training department

E.A. Butrina

1. GENERAL CHARACTERISTIC OF THE DISCIPLINE "BIOINFORMATICS"

1.1. Annotation

The discipline «Bioinformatics» refers to the optional part of the PhD program and is aimed at training of highly qualified competent specialists in the field of biotechnology.

The aim of the discipline: the formation of skills in the use of modern technical means and information technologies for solving analytical and research problems in biology and biotechnology.

The content of the discipline covers a range of issues related to the basic concepts of informational biology, the objects of study of informational biology, methods and algorithms for obtaining, presenting and analyzing data in informational biology.

The study of the discipline involves the following tasks:

- the study of the theoretical foundations of bioinformatics;
- the study of methods of bioinformatics
- information search and work with databases

1.2. The language of study - English

1.3. Expected discipline outcomes

As a result of mastering the discipline, the PhD student should:

Know:

- the subject of bioinformatics and its role in modern biology
- bioinformatics databases and their purpose
- methods for searching and functional annotation of biopolymer sequences methods for conducting phylogenetic analysis, its main stages and limitations
- methods of structural modeling of polypeptides
- algorithms for information search in the field of biology and biotechnology

Be able to:

- apply the mastered methods of bioinformatics in research, choose the right methods of analysis depending on the task

Demonstrate skills and experience in:

- primary processing and analysis of biopolymer sequences
- working with different bioinformatic databases
- phylogenetic analysis
- depositing information in databases
- modeling the structure of polypeptides.

1.4. The scope of the course

N	Types of academic work	Scope of the discipline		The distribution of the hours in the 4 semester
		Total hours	Including contact work (hours)*	
1	Lectures	4	4	4
2	Self-study work, including preparation for attestation	104		104
3	Semester attestation	Test	0.25	Test, 4
4	**Total scope, hours**	**108**	**4.25**	**108**
5	**Total scope, credits**	**3**		**3**

2. THE CONTENT OF THE COURSE

№	Topic	Content
T 1	Bioinformatics databases	Introduction to bioinformatics. Information technologies in bioinformatics. Databases and information systems in bioinformatics, their classification and purpose (NCBI GenBank, EMBL, SWISS-Prot, UniProt, PDB)
T 2	Methods and algorythms	Methods of data and text information analysis in biology. Algorithms for the analysis of genetic sequences and their adaptation to high-performance computing systems. Algorithms for structural and functional annotations of genomic sequences. Primary work with sequences (alignment, correction of erroneous data), search for homologous sequences (BLAST), development of primers for amplification (Primer Blast), search for restriction sites and open reading frames within the sequence. Depositing nucleotide sequences in the international GenBank database (using the Sequin program)
T 3	Phylogenetic analyses	Methods for aligning sequences and constructing dendrograms, their statistical evaluation. Algorithms of molecular evolution. Building a phylogenetic tree. Advantages and limitations of some methods. Interpretation of the received data.
	Amino acid sequences and protein structures	Protein databases (Uniprot, PDB, TrEMBL). Search methods. Modeling of the three-dimensional structure of proteins based on homology, visualization of the obtained structures (RasMol program).

3. ORGANIZATION OF PRACTICE AND SELF-STUDY WORK

3.1. Practice

Not provided.

3.2. Approximate topic of independent work

3.2.1. Approximate list of essay topics

The essay should perform analytical review of literature on the corresponding topic

- GenBank database, processing sequences.
- Sequence analysis (UGENE package). Annotating sequences to send to GenBank using Sequin.
- Phylogenetic analysis, work with trees.
- Protein databases and 3D protein models.

The essay volume is 20-25 typewritten pages in A-4 format.

3.2.2. Approximate topics of individual or group projects

Not provided

4. THE SET OF TOOLS FOR INTERMEDIATE AND FINAL ATTESTATION

4.1. The evaluation criteria for the results of current and intermediate attestation

Approved evaluation criteria of the achievements are based on three levels of mastering the competence components: intermediate, advanced, and high.

Competence components	Characteristics of the level of development the components of competencies		
	threshold	**advanced**	**high**
Knowledge	A PhD student demonstrates knowledge-acquaintance, knowledge-copy: he recognizes objects, phenomena and concepts, finds differences in them, knows of the sources of information, can independently reproduce knowledge.	A PhD student demonstrates analytical knowledge: confidently reproduces and understands the acquired knowledge, classifies them into one or another classification group, independently systematizes	A PhD student can independently get new knowledge from the world around him, creatively use it to make decisions in new and non-standard situations.

		them, establishes relationships between them, productively applies in common situation.	
Skills	A PhD student is able to correctly perform prescribed actions according to an instruction, an algorithm in a known situation, independently solve typical problems that require a choice from known methods in a predictably changing situation	A PhD student is able to independently solve non-standard tasks that require a choice based on a combination of known methods in an unpredictably changing situation	A PhD student is able to independently solve research problems, demonstrates the creative use of skills (technologies)
Personal qualities	A PhD student has a low motivation for studying, shows an indifferent, irresponsible attitude to learning, and assigned work	A PhD student has a pronounced motivation for studying, demonstrates a positive attitude towards learning and future work, and is active. `	A PhD student has a developed motivation for studying and work activities, shows perseverance and dedication, diligence, independence, and creativity.

4.2. The tools for current and intermediate attestation

Assessment of knowledge, skills and (or) experience that characterize step-by-step formation of competencies in the discipline "Bioinformatics" is carried out in the form of current control and intermediate attestation. Current control is carried out during the semester in order to determine the level of assimilation of knowledge by PhD students, the formation of skills and abilities in the field of bioinformatics. To assess knowledge, skills, abilities and (or) experience at the university, a point-rating system is used.

4.2.1. List of sample questions for attestation:

1. Databases and information systems in bioinformatics, their classification and purpose (NCBI GenBank, EMBL, SWISS-Prot, UniProt, PDB)
2. Methods of data and text information analysis in biology.
3. Algorithms for the analysis of genetic sequences and their adaptation to high-performance computing systems.
4. Algorithms for structural and functional annotations of genomic sequences. Primary work with sequences (alignment, correction of erroneous data), search for homologous sequences (BLAST)
5. Development of primers for amplification (Primer Blast),
6. Search for restriction sites and open reading frames within the sequence.
7. Depositing nucleotide sequences in the international GenBank database (using the Sequin program)
8. Methods for aligning sequences and constructing dendrograms, their statistical evaluation.
9. Algorithms of molecular evolution. Building a phylogenetic tree. Advantages and limitations of some methods. Interpretation of the received data.
10. Protein databases (Uniprot, PDB, TrEMBL).
11. Modeling of the three-dimensional structure of proteins based on homology, visualization of the obtained structures (RasMol program).

4.2.2. List of sample questions for the exam

not provided

5. EDUCATIONAL, METHODOLOGICAL, AND INFORMATIONAL SUPPORT

5.1. Recommended literature

5.1.1. Basic literature

1. Claverie J.-M., Notredame C. Bioinformatics for dummies. - Wiley Inc., 2006. - 436 p.
2. Bioinformatics Introduction by Mark Gerstein. – bioinfo.mbb.yale.edu/mbb452a

5.1.2. Additional literature

1. Introduction to Bioinformatics.- Esa Pitkänen esa.pitkanen@cs.helsinki.fi Autumn 2008, I period
2. www.cs.helsinki.fi/mbi/courses/08-09/itb

5.2. Methodical manuals

not provided

5.3. Software

1. Microsoft office (Word, Excel, Power point);
2. Adobe Reader.
3. Blast
4. Clustal
5. VectorNTI,
6. DNAbaser, Bioedit,
7. MEGA5,
8. Sequin,
9. Primer Blast

5.4. Databases and search systems

1. GenBank - http://www.ncbi.nlm.nih.gov/genbank/
2. PDB - http://www.wwpdb.org/
3. UniProt - www.uniprot.org/
4. PubMed - http://www.ncbi.nlm.nih.gov/pubmed/
5. Google scholar - https://scholar.google.ru/
6. Scopus - https://www.scopus.com/
7. ScienceDirect - www.sciencedirect.com
8. eLibrary - http://elibrary.ru/

5.5. Electronic learning sources

1. Zonal scientific library http://lib.urfu.ru/course/view.php7idM67
2. UrFU electronic resources http://lib.urfu.ru/mod/data/view.php7id-2802
3. Library catalogue http://lib.urfu.ru/course/view.php7idM 81.

6. MATERIAL RESOURCES AND TECHNICAL SUPPORT

6.1. Information about the auditorium and laboratory equipment for the discipline

Ural Federal University has special rooms for lecture-type classes, group and individual consultations, current control and intermediate attestation, as well as rooms for independent work, equipped with computers with the access to the Internet and electronic information educational environment, and facilities for storage and preventive maintenance of equipment. Postgraduate students of the departments are provided with special rooms for research work.