MINISTRY OF SCIENCE AND HIGHER EDUCATION OF RUSSIAN FEDERATION
Federal State Autonomous Educational Institution of Higher Education
Far Eastern Federal University
(FEFU)
SCHOOL OF BIOMEDICINE

AGREED
Head of OP

_____
(Signed)   (Full name)

CLAIM
Director of the Department of Medical Biology and
Biotechnology

_____
(Signed)   (Acting Name)
December 06, 2022

WORK PROGRAM OF THE DISCIPLINE
Bioinformatics
Direction of training 06.04.01 Biology
Master's Programme in Molecular and Cell Biology
Form of training: full-time

Course 1 semester 2
Lectures - hour.
Practical classes – 36 hours.
Including with the use of MAE - an hour.
The total hours of classroom load are 36 hours.
Including with the use of MAE - an hour.
Independent work – 72 hours.
Abstract works are provided
Coursework is not provided
Credit 2 semester

The work program is drawn up in accordance with the requirements of the Federal State Educational Standard in the direction of training 06.04.01 Biology, approved by the order of the Ministry of Education and Science of Russia dated 11.08.2020 No. 934

The work program was discussed at the meeting of the Department of Medical Biology and Biotechnology Protocol dated December 06, 2022 No. 2

Director of the Department of Medical Biology and Biotechnology , *Ph.D.V.V. Kumeiko*

Vladivostok
2022

Reverse side of the RPD cover page

1. The work program was revised at the meeting of the Department / department / department (implementing the discipline) and approved at the meeting of the Department / department / department (issuing structural unit), the protocol from "_____ __ № _____

2.The work program was revised at the meeting of the Department / department / department (implementing the discipline) and approved at the meeting of the Department / department / department (issuing structural unit), the protocol from "__ № _____

3.The work program was revised at the meeting of the Department / Department / Department (implementing the discipline) and approved at the meeting of the Department / Department / Department (issuing structural unit), the protocol from "____ № _____

4.The work program was revised at the meeting of the Department / Department / Department (implementing the discipline) and approved at the meeting of the Department / Department / Department (issuing structural unit), the protocol from "_____ __ № _____

5.The work program was revised at the meeting of the Department / Department / Department (implementing the discipline) and approved at the meeting of the Department / Department / Department (issuing structural unit), the protocol from "_____ __ № _____

Abstract of the work program of the discipline
«Bioinformatics»

The working program of the academic discipline B1.O.06 "Bioinformatics" is compiled for students in the educational program of the magistracy 06.04.01 Biology "Molecular and cellular biology (together with the NSCMB FEB RAS)" in accordance with the requirements of the Federal State Educational Standard in the direction of training 06.04.01 Biology, approved by the order of the Ministry of Education and Science of Russia dated 11.08.2020 No. 934.

Discipline B1.O.06 "Bioinformatics" is compiled for students in the educational program of the magistracy 06.04.01 Biology, is included in the basic part of the compulsory disciplines of the master's program "Molecular and Cell Biology (together with the NSCMB FEB RAS)".

The total labor intensity of mastering the discipline is 2 z.u. (72 hours). The curriculum provides for practical classes (36 hours) and independent work (72 hours). Evaluation of learning outcomes: credit.

The course "Bioinformatics" has a general biological significance. To fully master the material of the course, basic knowledge of general biology, cell biology, chemistry, genetics and molecular biology is necessary. This course touches upon the basic fundamental principles of modern molecular biology, the theory of indexing and information retrieval, the principles of storage and retrieval of scientific information in computer networks, the alignment of primary sequences of biological molecules, the basics of proteomics and modeling of the three-dimensional structure of biomolecules.

The purpose of studying the discipline: to teach the student to apply methods based on modern information technologies to solve biological scientific problems.

Tasks:

− to acquaint the student with the current state of bioinformatics as a science and identify its actual tasks, main successes and prospects to date;

− to explain the basic principles of storage and retrieval of scientific information;

− to teach the student to use information resources to solve problems of molecular biology and evolutionary genetics.

General professional competencies of graduates and indicators of their achievement:

Name of the category (group) of general professional competencies	Code and name of general professional competence (the result of mastery)	Code and name of the competency achievement indicator
	OPK-6 Is able to	OPK-6.1 Develops ways and prospects

	creatively apply and modify modern computer technologies, work with professional databases, professionally design and present the results of new developments.	for the application of modern computer technologies in biological sciences and education. OPK-6.2 Uses with professional databases and data banks in the chosen field of professional activity, the necessary mathematical apparatus, analysis and algorithm for storing electronic images, has experience in modifying computer technologies for the purpose of professional research. OPK-6.3 Uses modern computer technologies, works with professional databases, draws up and presents the results of new developments.

Code and name of the competency achievement indicator	Name of the assessment indicator (the result of training in the discipline)
OPK-6.1 Develops ways and prospects for the application of modern computer technologies in biological sciences and education.	Knows the methods of modern computer technologies in biological sciences and education Able to apply in practice the knowledge of modern computer technologies in biological sciences and education Has the skills to work on modern computer equipment using methods
OPK-6.2 Uses with professional databases and data banks in the chosen field of professional activity, the necessary mathematical apparatus, analysis and algorithm for storing electronic images, has experience in modifying computer technologies for the purpose of professional research.	Knows professional databases and data banks in his professional activities, Able to use professional databases and data banks in the chosen field of professional activity, the necessary mathematical apparatus, analysis and algorithm for storing electronic images He has the skill of applying the mathematical apparatus in his professional field, the skill of working with databases, modifying computer technologies for the purpose of professional research.
OPK-6.3 Uses modern computer technologies, works with professional databases, draws up and presents the results of new developments.	Knows the tools of modern computer technology Able to apply modern computer technologies, work with professional databases, design and present the results of new developments. Own the skill of working on modern computer equipment

1.   Labor intensity of discipline and types of training sessions in the discipline

The total labor intensity of the discipline is 3 z.u. (108 academic hours), (1 credit corresponds to 36 academic hours).

Types of training sessions and work of the student in the discipline are:

Designation	Types of training sessions and work of the student

Ave	Practical exercises
Pr electr.	
WED:	Independent work of the student during the period of theoretical training
including control	Independent work of the student and contact work of the student with the teacher during the period of intermediate certification
	And other types of work

Structure of the discipline:

The form of training is full-time.

№	Name of the section Discipline	Se me ster	Number of hours by types of training sessions and work of the student						Intermediate attestation forms
			Lek	Lab	Av e	OK	WE D	Cont rol	
1	Topic 1. Tasks and methods of bioinformatics (2 h)	2			6		12		UO-1 vpr. to the beginning NoNo 1,2
2	Topic 2. Fundamental Principles of Molecular Biology (2 h)				6		12		UO-1 vpr. to the zach. №№ 3-9
3	Topic 3. Information retrieval theory (3 h)				6		12		UO-1 vpr. to the zach. №№ 10-12
4	Topic 4. Access to the archives of scientific information (3 hours)				6		12		UO-1 vpr. to the zach. №№ 13-15
5	Topic 5. Alignment of primary sequences of biomolecules (4 h)				6		12		UO-1 vpr. to the zach. №№ 16-33
	Topic 6. Proteomics and modeling of the three-dimensional structure of biomolecules (4 hours)				6		12		UO-1 vpr. to the zach. №№ 34-39
	Total:	2			36		72		Credit

THE STRUCTURE AND CONTENT OF THE THEORETICAL PART OF THE COURSE

Lecture classes are not provided for in the curriculum.

IV. STRUCTURE AND CONTENT OF THE PRACTICAL PART OF THE COURSE AND INDEPENDENT WORK

Practical training (36 hours)

Topic 1. Problems and methods of bioinformatics (6 has.)
1) History of the emergence and development of bioinformatics.
a. The emergence of the term "bioinformatics".
b. History of the development of methods in biological science.
c. Human Genome Project. The role of bioinformatics in its promotion.
d. Tendency of formation of biology as an exact science.
The current state of bioinformatics: successes, prospects, actual and unsolved tasks.
2) Areas of interest, tasks and methods of bioinformatics.
a. Relevance of bioinformatics.
b. Relationship of bioinformatics with other modern branches of biology.
c. Related and related disciplines: computational biology, mathematical biology; differences from "biological computations".
d. Goals and objectives of bioinformatics.
e. Areas of interest of bioinformatics:
− Biomedical text mining (automated development of scientific texts).
− Analysis of primary sequences of biological molecules (sequences), alignment.
− Molecular phylogenetics.
− Gene annotation, gene ontology, expression profiles.
− Biology of gene regulatory networks and signaling pathways. The concept of an interactome.
− Bioinformatics of structures. Folding.
− Image analysis. Pattern recognition.
Problematic issues:
1. The range of unsolved problems facing bioinformatics in the modern scientific world.
2. An attempt to predict: what new tasks can bioinformatics face, taking into account the vector of development of modern biological science?

Topic 2. Fundamental Principles of Molecular Biology (6 has.)

1) Biological classification and nomenclature.

a. History of the formation of modern taxonomy.

b. Use of sequences to determine phylogenetic relationships.

c. Molecular phylogenetics. Cladistics.

2) Central dogma of molecular biology. Genetic code

a. Molecular-genetic level of life organization. The fundamental basis of life.

b. Central Dogma of Molecular Biology. The meaning, meaning, and realization of biological information.

c. Transcription. Translation.

d. The concept of the genome and the organization of the genome. Differences in the organization of the genome of prokaryotes and eukaryotes.

e. Genetic code. Code properties: universality, triplet, degeneracy. Features of the genetic code in different groups of living organisms.

e. Extended genetic code and protein engineering.

3) Genomics and sequencing.

a. A brief history and essence of the sequencing method.

b. Assembling sequences.

c. Sequencing of entire genomes of organisms.

d. Identification, prediction and annotation of genes.

4) Variability, mutations, nucleotide substitutions.

a. Mutagenesis. The causes of mutations and the mechanisms of their fixation in the genome.

b. Transients and transversions.

c. Synonymous and non-synonymous substitutions.

d. Inserts (insertions), deletions, inversions.

e. Genome reorganization.

e. Evolution of the nucleotide sequence.

g. Epigenetic factors of variability.

5) Principles of molecular evolution.

a. Natural selection and neo-Darwinism.

b. Fixation of mutations in the population.

c. The concept of molecular clocks.

d. Neutral theory of molecular evolution.

e. Contradiction and complementary of the concept of molecular clock and neutral theory of molecular evolution.

e. Evolutionary systematics. Evolutionary analysis.

6) Homologous and similar signs; divergence and convergence.

Examples of convergence in nature.

b. Idioadaptations and Ecological Radiation.

Problematic issues:

1) The problem of the need to update the evolutionary paradigm in connection with the development of evolutionary molecular phylogenetics and new data from the field of molecular evolution and epigenetics.

2) Synthetic theory of evolution and its current state.

3) The problem of the conflict between cladistics and classical taxonomy.

Topic 3. Theory of information retrieval (6 has.)

1) Theory of search indexing of information.

a. The main forms of organization of information in computer networks.

b. The concept of "metadata". Varieties and forms of presentation of metadata.

2) Search operators, advanced search methods.

a. Boolean operators.

b. The main varieties of logical operators for constructing advanced search queries.

c. Search syntax. Interpretation of queries by search engines.

d. Regular expressions.

e. Stop words (noise words).

3) Search engines.

a. How the search engine works.

b. The work of search robots ("spiders", crawlers).

c. Methods of optimization of the work of search robots.

d. Sitemaps, keywords, robot access restriction file (exclusion standard for search engine crawlers).

e. Policy of search robots (selectivity, repeated attendance, "conscientiousness", coordination).

e. Other varieties of auxiliary search programs.

g. Indexing.

h. Search. Search results of information. Ranking in search results.

i. Metasearch systems.

j. Directed (focused) search engines. Academic search robots. Use of reinforcement machine learning by search robots.

4) Organization of databases, database access systems.

a. Organization of databases.

b. Database Management Systems (DBMS).

c. The difference between a classic database and a "knowledge base".

d. Expert systems. Automatic inferences (reasoning).

e. Automatic proofs (interactive proof of theorems).

f. Artificial intelligence in the system of functioning of knowledge bases.

g. Knowledge Base Systems. Output systems (construction of logical inference).

Problematic issues:

1) The problem of combining classical logic, fuzzy logic and higher-order logic in the operation of knowledge base systems.

2) Application of artificial intelligence and machine learning in the work of knowledge base systems.

3) Differences in the recognition of different search operators by different search engines.

4) Comparison of features and functionality of different search engines.

Topic 4. Access to the archives of scientific information (6 h)

1) Nucleic acid sequence databases.

2) Genomic databases.

3) Proteomic databases

a. Protein sequence databases.

b. Structure Databases.

c. Databases on Expression and Proteomics.

4) Metabolic pathway data banks.

5) Basic databases of scientific literature and systems of access to them.

a. Hierarchy of the most popular bibliographic databases and information organizations: who is who.

b. The largest scientific publishing houses. Springer. Thompson Reuters, Elsevier.

c. PubMed. Highwire.

d. Russian-language resources.

6) Databases for citation of academic literature.

a. Scopus.

b. Web of Knowledge.

c. Citation indices of scientific literature. Impact factor of articles and journals.

7) Citation managers (bibliographic information management systems).

Relevance of use and scope of bibliographic information management systems.

b. Local programs for managing bibliographic information.

c. Online bibliographic information management systems.

Problematic issues:

1) The problem of confusion in the hierarchy of different databases and search engines. Who owns whom and who controls whom?

2) The problem of mutual integration of various databases in different areas of molecular biological knowledge.

3) The problem of access to full-text versions of scientific articles.

4) "Cabinet research": aggregation, compilation, analysis and synthesis of scientific information. How to make a scientific discovery without leaving the computer?

Topic 5. Alignment of primary sequences of biomolecules (6 has.)

1) Dynamic programming. Build and use point affinity matrices.

a. Algorithms for aligning two sequences. General principles of dynamic programming in sequence alignment.

b. The principle of the matrix of points (point matrix of similarity).

c. Needleman–Wunsch and Smith–Waterman algorithms.

d. Global and local alignment.

e. Measure of sequence similarity. Scoring and equalization penalty system: scoring schemes.

f. Preparation of amino acid substitution matrices.

g. Weighing insertions and deletions. Accounting for missing information.

h. Multiple alignments.

i. Variations and generalizations of alignments.

k. Approximate methods for quickly searching databases.

2) Use of computer programs to align amino acid and nucleotide sequences.

a. Programs for constructing point similarity matrices.

b. Programs for multiple alignment of amino acid and nucleotide sequences in databases.

c. BLAST (Basic Local Alignment Search Tool).

d. Profiles and hidden Markov models.

3) Molecular phylogenetics. Phylogenetic analysis.

4) Evaluation of genetic distances. Evolutionary models. Construction of phylogenetic trees.

a. Observed, true and calculated distances.

b. Evolutionary models and distances between nucleotide sequences:

c. Jux-Cantor model.

g. Kimura model.

e. Tajdima-Nei model.

e. Other evolutionary models.

g. Gamma distances.

h. Comparative analysis of different models.

i. Amino acid distances, probability matrices of amino acid substitutions.

5) Phylogenetic analysis in taxonomy. Cladistics.

a. Remote methods of constructing phylogenetic trees.

b. Methods of analysis of discrete features.

c. Statistical evaluation of the tree, bootstrep analysis.

d. Phenetics and Cladistics.

Problematic issues:

1) The problem of the ratio of calculated and true evolutionary distances. Is it possible to determine the true evolutionary distance?

2) Experiments on artificial evolution and their role in molecular phylogenetics.

Topic 6. Proteomics and modeling of the three-dimensional structure of biomolecules (6 h.)

1) Formation of proteins of three-dimensional structure, folding (folding of proteins).

a. Primary structure of proteins and secondary structure of proteins.

b. Tertiary and Quaternary structure of proteins.

c. Stabilization of the tertiary structure of proteins: hydrophobicity and hydrophilicity.

2) Stability of protein structure. Denaturation. Isoforms of proteins.

a. Graphical representations to describe the permitted conformations of the main chain.

3) Structural alignments.

4) Prediction and modeling of the three-dimensional structure of proteins.

a. Homology Modeling.

b. Recognition of folding pattern.

c. Calculation of conformational energy and molecular dynamics.

d. Prediction of protein functions.

Problematic issues:

1) The problem of folding proteins as one of the urgent tasks of modern biology.

2) Inverse problem of deciphering the structure of proteins.

3) Alternative splicing: the ratio of the number of protein-coding genes in the genome and the true diversity of proteins and their isoforms.

V. EDUCATIONAL AND METHODOLOGICAL SUPPORT OF INDEPENDENT WORK OF STUDENTS

Educational and methodological support for the independent work of students in the discipline "Bioinformatics" includes:

- a schedule for the implementation of independent work in the discipline, including approximate norms of time for each task;

- characteristics of tasks for independent work of students and methodological recommendations for their implementation;

- requirements for the presentation and design of the results of independent work;
- criteria for evaluating the performance of independent work.

Calendar-thematic plan of the discipline "Bioinformatics"

Semester and week	**Lecture**	**Practical works. Testing.**
2 semester 1 week	Topic 1. Tasks and methods of bioinformatics (12 h)	Theory and practice of information retrieval.
2 semester 2-3 weeks	Topic 2. Fundamental Principles of Molecular Biology (12 h)	(continued).
2 semester 4-5 weeks	Topic 3. Information retrieval theory (12 h)	(continued). Testing No. 1.
2 semester 6-7 weeks	Topic 4. Access to the archives of scientific information (6 h)	Test work on the topic "Theory and practice of information retrieval and indexing"
2 semester 8-9 weeks	Topic 4. Access to the archives of scientific information (continued) (6 hours)	Bibliographic information management systems
2 semester 10-11 weeks	Topic 5. Alignment of primary sequences of biomolecules (6 h)	Bibliographic information management systems (continued).
2 semester 12-13 weeks	Topic 5. Alignment of primary sequences of biomolecules (continued) (6 h)	Bibliographic information management systems (continued).
2 semester 14-15 weeks	Topic 6. Proteomics and modeling of three-dimensional structure of biomolecules (6 h)	Bibliographic information management systems (continued).
2 semester 16-18 weeks	Topic 6. Proteomics and modeling of the three-dimensional structure of biomolecules (continued) (6 h)	Bibliographic management systems

Schedule for the implementation of independent work in the discipline "Bioinformatics"

№ p/n	Due Date/Deadlines	Type of independent work	Approximate norms of execution time	Form of control
2 semester				
1	1 week	Work with literature and lecture notes, preparation for the test work	4 hours	Work in a practical lesson, oral answer
2	Week 2	Work with literature and lecture notes, preparation for laboratory classes. Independent study of individual sections of the discipline.	4 hours	Work in a practical lesson, oral answer.
3	Week 3	Work with literature and lecture notes, preparation for practical classes, control work	4 hours	Work in a practical lesson, oral answer.
4	Week 4	Work with literature and lecture notes. Preparation for practical exercises.	4 hours	Work in a practical lesson, oral answer
5	Week 5	Work with literature and lecture notes Preparation for the test work	4 hours	Work in a practical lesson, oral answer.

6	Week 6	Work with literature and lecture notes	4 hours	Work in a practical lesson, oral answer.
7	Week 7	Work with literature and lecture notes	4 hours	Work in a practical lesson, oral answer.
8	Week 8	Work with literature and lecture notes,	4 hours	Work in a practical lesson, oral answer.
9	Week 9	Work with literature and lecture notes. Independent study of individual sections of the discipline.	4 hours	Work in a practical lesson, oral answer.
10	Week 10	Work with literature and lecture notes.	4 hours	Work in a practical lesson, oral answer.
11	Week 11	Work with literature and lecture notes	4 hours	Work in a practical lesson, oral answer.
12	Week 12	Work with literature and lecture notes, preparation of homework	4 hours	Work in a practical lesson, oral answer.
13	Week 13	Independent study of individual sections of the discipline. Preparation for practical exercises. Preparation of homework.	4 hours	Work in a practical lesson, oral answer.
14	Week 14	Work with literature and lecture notes. Preparation for practical exercises. Preparation of homework.	4 hours	Work in a practical lesson, oral answer. Homework assessment. Performance of control work
15	Week 15	Work with literature and lecture notes. Independent study of individual sections of the discipline. Preparation of homework.	4 hours	Work in a practical lesson, oral answer.
16	16week	Work with literature and lecture notes. Preparation for practical exercises. Preparation of homework.	4 hours	Work in a practical lesson, oral answer. Homework assessment.
17	Week 17	Work with literature and lecture notes. Preparation of homework.	4 hours	Work in a practical lesson, oral answer, performance of control and practical work
18	Week 18	Preparation for the test.	4 hours	Homework assessment. Final interview / credit
		Total per semester	72 hours	

Current monitoring of the results of independent work is carried out during oral interviews, interviews at lectures, checking homework and testing. Based on these results, the student receives current and examination grades, according to which the final grade is derived. Intermediate (semester) certification is carried out in the form of a test. Based on these results, the student receives current grades, according to which the final grade is derived.

Methodical instructions for preparation for tests

On individual topics, tests, control and practical work or testing can be carried out at practical classes. The student should prepare for the test work (testing) especially

carefully, since the received assessment goes to the rating. It is necessary to repeat the lecture material once again, read the necessary section in the textbook, recall the seminar discussion. For a good memorization of formulas, schemes, terms, they need to be written several times on paper. If you intend to solve problems, it is useful to work out similar ones in advance.

In the test work, theoretical issues should be covered briefly, but quite fully. The answer should contain a definition of the phenomenon, process, structure, enumeration of the most characteristic features or properties of the phenomenon, process, structure. Schematization of the answer in the form of a figure indicating the details and connections is welcomed. Control and practical tasks, as a rule, are performed on a computer and consist in performing tasks similar to those analyzed in practical classes.

Methodical instructions for working with literature

Students are asked to compile an initial list of sources. Also, the list can be provided by the teacher, if necessary, the set of literature can be limited to this list. The basis may be the list of references recommended in the work program of the course. For the convenience of work, you can compile your own file cabinet of selected sources (surname of the authors, title, characteristics of the publication) in the form of an electronic database in a librarian program, for example, Mendeley. Such a file cabinet has an advantage, because it allows you to add sources, replace one with another if necessary, make a quick search of the database, perform bibliometric analysis, etc. The initial list of references can be supplemented using the electronic catalog of the FEFU library and information systems from the resource catalog of the FEFU library.

Working with literature on a particular topic, it is necessary not only to read, but also to learn the method of its study: make a brief summary, an algorithm, a scheme of the material read, which allows you to quickly understand it, remember it. It is not recommended to rewrite the text verbatim.

Examples ofadaniy for self-execution

Task No. 1: Compilation and organization of a thematic personal database on scientific literature in the citation manager program (librarian program).

Students are asked to compile their own database of scientific literature from 20 (or more) records in one of the reference management software. By default, mendeley is offered.

Methodical instructions for homework No. 1:

Students receive the skills necessary to perform this homework in practical classes, where a number of examples demonstrate the order of work and the functionality of the corresponding programs. To use the Mendeley program, you must

register on the http://www.mendeley.com/ website, download and install the program (free of charge).

Literature on the subject can be searched in the main databases on the scientific literature of the biological direction, for example, MEDLINE through PubMed (http://www.ncbi.nlm.nih.gov/pubmed/), Scopus (http://www.scopus.com/) or Web of Science (http://wokinfo.com/). Access to the search in the Scopus and Web of Science databases is non-free (by subscription) and can be carried out from FEFU computers or when connected through the University's network. Access to MEDLINE is free.

The easiest way to add articles to the Mendeley database is possible when you install the official add-on for the web browser, which adds a button to the bookmarks bar (http://www.mendeley.com/import/). It is recommended to use Mozilla Firefox or Google Chrome browsers for this. As a result, a locally installed copy of Mendeley receives integration with the main sites of publishers, databases and search engines for scientific literature (Scopus, Web of Science, ScienceDirect, PubMed, Springer, etc.). If you find the desired article, you need to open its card in a separate tab/window and click the Mendeley add-ons button in the browser bookmarks bar. As a result, An individual article card will be created in Mendeley with all the bibliographic information about the article.

Task #2: Identification of proposed amino acid or nucleotide sequences by alignment.

Students are offered nucleotide or amino acid sequences; it is necessary to determine which gene or protein they belong to with the greatest probability. It is also required to indicate to which organism this sequence belongs, and which sequences are most homologous to this one. A number of substitutions, deletions, or insertions may be randomly added to the proposed sequences.

Examples of sequences for identification:

gccttcaggtggcagccgtcagggcacgggggcttcggcgacaaccgcaaggcaccctcafagkqledgrtlsd yniqkestlhlvlrlrggviepslrilaqykynqdkicrkcyartttggcctcztcctggctcaagaagtggccagtgcccaac catccttatccagggcttatccagggctgactgaacacmritlkvggqpvtflvdtgaqhsvltqnaapgplksawvqgatg gkryrwttdrkvhlatgkvthsflhfhvpdcpypllggrdllklkaqihfegsgvgpmgqplqwltlniedeyrlh

Methodical instructions for homework No2.

To align the resulting sequence with others from the gene bank, you need to use the BLAST (Basic Local Alignment Search Tool, http://blast.ncbi.nlm.nih.gov/Blast.cgi). It is necessary to select the desired type of program corresponding to the resulting sequence (amino acid or nucleotide, blastp or blastn, respectively). It is also required to apply different algorithms for alignment and compare the result obtained, which may be necessary in the event that the student

received a sequence with a sufficiently large number of substitutions. The student presents the result of the work in the form of a copy of the graphic representation of the evolutionary element built by the BLAST program indicating the gene / protein with which the alignment was made and its affiliation, as well as the sequence identification number in the NCBI databases. Therefore, you must select the first five records from

issuing BLAST (with the highest number of alignment points). In this case, it is necessary to omit the records marked as "Predicted", which are open reading frames predicted by the results of the analysis of the sequence of the entire genome of the organism, and therefore these sequences may turn out to be pseudogenes.

Task No. 3: Compilation of a phylogenetic tree for the proposed nucleotide sequences using software tools.

Students are required to construct a phylogenetic tree for the proposed nucleotide sequences. Examples of nucleotide sequences are given below:

AGGGTGGCCTAAATGTGCCTCACACGTTACCCGATATCGATAATCGCAC AGGGTGGCCTAATGTGCCTCACACTTACGCGATATCGATAATCGCAC CGGGTGGCCTAGGCGTGCCTCACACGTTGCCCGATATCGATAATCGCCAGG TTGGCCTAAATGTGCCCCACGTTACCCGATATCGATAATCGCACCGGGTGGC CTAGGCGTGCCTCACACGTTGCCCGATATCGATAATCGCACAGCGTGGCCT AATGTGCCTCACACTTACGCGATATCGATAATCGAC

Methodical instructions for homework No. 3:

To build a tree, students are asked to calculate distances using evolutionary models, for example, the Tajima-Nei model or the Kimura model, and then build an evolutionary tree using the maximum parsimony method and assess the reliability of the construction by the bootstrap analysis method. As a software tool for building and visualizing a phylogenetic tree, it is proposed to use the MEGA program, but other programs can also be used.

VI. MONITORING THE ACHIEVEMENT OF COURSE OBJECTIVES

The following assessment tools are used for monitoring:
UO-1 – individual interview;
PR-1 – written (or computer) test;
PR-2 - control works.

No p/n	Supervised sections / topics of the discipline	Achievement indicator code and name	Learning outcomes	Assessment tools	
				current control	Intermediate-accurate certification

			Knows Can Owns	UO-1	UO-1 vpr. to the beginning NoNo 1,2
1.	Topic 1. Tasks and methods of bioinformatics	OPK-6.1; OPK-6.2; OPK-6.3	Knows Can Owns	UO-1	UO-1 vpr. to the beginning NoNo 1,2
2.	Topic 2. Fundamental Principles of Molecular Biology	OPK-6.1; OPK-6.2; OPK-6.3	Knows Can Owns	PR-1 PR-2	UO-1 vpr. to the zach. №№ 3-9
3.	Topic 3. Information retrieval theory	OPK-6.1; OPK-6.2; OPK-6.3	Knows Can Owns	PR-1 PR-2	UO-1 vpr. to the zach. №№ 10-12
4.	Topic 4. Access to archives of scientific information	OPK-6.1; OPK-6.2; OPK-6.3	Knows Can Owns	PR-1 PR-2	UO-1 vpr. to the zach. №№ 13-15
5.	Topic 5. Alignment of primary sequences of biomolecules	OPK-6.1; OPK-6.2; OPK-6.3	Knows Can Owns	PR-1 PR-2	UO-1 vpr. to the zach. №№ 16-33
6.	Topic 6. Proteomics and modeling of the three-dimensional structure of biomolecules	OPK-6.1; OPK-6.2; OPK-6.3	Knows Can Owns	PR-1 PR-2	UO-1 vpr. to the zach. №№ 34-39

Criteria for scoring on the test

The "credit" grade is given when the student is fluent in the theoretical material of the discipline being studied, does not make mistakes when answering the questions asked, using visual tables, or admits some inaccuracies in the answers, but quickly corrects errors when asking him leading questions. In addition, the student is guided in the collection of histological preparations in their determination.

The grade "not counted" is given when the student does not own the materials of the discipline being studied, does not answer additional questions of the teacher and does not navigate the collection of histological preparations when determining them.

Questions for the test in the discipline "Bioinformatics"

1. History of the development of molecular biology and bioinformatics.

2. Central dogma of molecular biology. Principles of storage and implementation of genetic information.

3. Properties of the genetic code.

4. Types of nucleotide substitutions and mutations.

5. Transpositions and transversions.

6. Insertions/deletions.

7. Basic principles of the evolutionary process. Homology, analogy/convergence.

8. Natural selection and neo-Darwinism.

9. The concept of molecular clocks.

10. Principles of indexing information in databases. Metadata.

11. Fundamental search operators. Boolean operators.

12. Search engines. Focused search engines.

13. Databases on scientific literature and citations.

14. Citation indexes. Bibliometrics.

15. Programs - bibliographic information management systems.

16. Alignment of primary sequences of biological macromolecules.

17. Point sequence similarity matrices.

18. Global and Local Alignment. Dynamic programming.

19. Multiple alignments.

20. Genetic distances.

21. Phylogenetic evolutionary models: Jux–Cantor model.

22. Kimura's model.

23. Tajima model – Nei.

24. Gamma distances.

25. Amino acid distances. Amino acid substitution matrices.

26. Methods of analysis of discrete features.

27. Phylogenetic trees.

28. Construction of phylogenetic trees by UPGMA method.

29. Construction of phylogenetic trees by the method of transformed distance.

30. The method of minimum evolution. The method of joining neighbors.

31. Maximum savings method.

32. Methods of maximum plausibility.

33. Bootstrap support for phylogenetic trees.

34. Levels of organization of protein molecules. Primary, secondary, tertiary, quaternary structure.

35. Factors that stabilize the three-dimensional structure of proteins.

36. Folding proteins.

37. Levinthal's paradox. The problem of folding forecasting.

38. Isoforms of proteins. Classification of protein structures.

39. Structural alignment of biomolecules.

VII. LIST OF REFERENCES AND INFORMATION AND METHODOLOGICAL SUPPORT OF THE DISCIPLINE

Main literature

1. Lesk, A. Vvedenie v bioinformatika (per. s eng.), 2-e izdanie // – Moskva: BINOM. Knowledge Lab. 2015. – 318 p. Access mode: http://lib.dvfu.ru:8080/lib/item?id=chamo:797691&theme=FEFU

2. Lukashov, V.V. Molecular evolution and phylogenetic analysis. Uchebnoe posobie // M.: Binom, 2009. 256 s. Access mode: http://lib.dvfu.ru:8080/lib/item?id=chamo:299205&theme=FEFU

3. Informatics and medical statistics / [G. N. Tsarik, V. M. Ivoilov, I. A. Polyanskaya et al.]; ed. by G. N. Tsarik. Moscow: GEOTAR-Media, 2017. 302 s.

4. Medical informatics: a textbook for universities on basic medical specialties / V. P. Omelchenko, A. A. Demidova. Moscow: GEOTAR-Media, 2016. 527 s.

Stefanov, V. E. Bioinformatics : a textbook for universities / V. E. Stefanov, A. A. Tulub, G. R. Mavropulo-Stolyarenko. — Moscow : Izdatelstvo Yurait, 2020. — 252 p. — (Higher education). — ISBN 978-5-534-00860-9. — Text : electronic // Educational platform Yurait [site]. — URL: https://urait.ru/bcode/450856

Further reading

1. Karetin, Yu.A. Synergetics. Course of lectures for biologists // Publishing House of the Far Eastern University, 2008. 259 s. Access mode: http://lib.dvfu.ru:8080/lib/item?id=chamo:262992&theme=FEFU

2. Kartavtsev, Yu.F. Molecular evolution and population genetics textbook for universities // Izd-vo Dalnevostochnogo universiteta, 2009. 277 s. Access mode: http://ini-.dvgu.ru/scripts/refget.php?ref=/ukazatel/kartavtsev/kartavtsev54.pdf

3. Marri, R., Grenner, D., Meyes, P. Biochemistry of Man (trans. with English M. D. Gvozdovoy, R. B. Kapner, A. L. Ostermana) // M: Mir BINOM. Laboratory of Knowledge, 2009. 414 s. Access mode: http://lib.dvfu.ru:8080/lib/item?id=chamo:277694&theme=FEFU

4. Petri A., Sabin K.. Visual medical statistics [textbook for universities] (per. s eng. V. P. Leonova.) // Moscow : GEOTAR-Media, 2015. 215 s. Access mode: http://lib.dvfu.ru:8080/lib/item?id=chamo:816955&theme=FEFU

5. Spirin, A. S. Molecular biology. Ribosomes and protein biosynthesis. Textbook for universities on biological specialties // M: Akademiya, 2011. 498 s. Access Mode: http://lib.dvfu.ru:8080/lib/item?id=chamo:669007&theme=FEFU

6. Wilson, C., Walker, J. S. Principles and methods of biochemistry and molecular biology (trans. from English Mosolova, T. P., Bozelek-Reshetnyak, E. Yu.) // (editor-in-chief Gilyarov, M.S.). M.: Binom, 2012. 848 s. Access mode: http://lib.dvfu.ru:8080/lib/item?id=chamo:705602&theme=FEFU

7. Haubald, B., Vie, T. Introduction to Computational Biology: An Evolutionary Approach (trans. from The English Chudov, S. V.) / M.: Izd-vo Instituta Computer Research "Regular and Chaotic Dynamics", 2011. 455 s. Access mode: http://lib.dvfu.ru:8080/lib/item?id=chamo:673149&theme=FEFU

8. Tsarik, G. N., Ivoilov, V. M., Polyanskaya, I. A. Informatika i medicinskaya statistica / Moscow : GEOTAR-Media, 2017. 302 sec. Access Mode: http://lib.dvfu.ru:8080/lib/item?id=chamo:842407&theme=FEFU

9. Online Resourse Centre: Lesk: Introduction to Bioinformatics // Internet: http://global.oup.com/uk/orc/biosciences/bioinf/leskbioinf3e/

10. Bioinformatics: a textbook for use in educational institutions that implement the main professional educational programs of higher education in the areas of training 30.05.01 "Medical biochemistry", 30.05.02 "Medical biophysics", 30.05.03 "Medical

cybernetics" / N. Y. Chasskikh.- Moscow : GEOTAR-Media, 2020.- 346 p.
https://lib.dvfu.ru/lib/item?id=chamo:885734&theme=FEFU

11. Information biology : uchebnoe posobie dlya vuzov / M. A. Kamenskaya ; pod redaktsii A. A. Kamenskogo.- Moskva : Akademiya, 2006.- 360, [1] p. -
https://lib.dvfu.ru/lib/item?id=chamo:245392&theme=FEFU

12. Introduction to bioinformatics : per. s eng. / A. Lesk.- Moskva : BINOM. Laboratory of Knowledge, 2009.- 318 p., [2] l. ill.
https://lib.dvfu.ru/lib/item?id=chamo:288426&theme=FEFU

List of resources of the information and telecommunication network "Internet"

1. http://rosalind.info/problems/locations/ is a resource for self-study of Bioinformatics Rosalind.

2. http://bioinformatics.ru/ - website of the Bioinformatics.ru "Bioinformatics, Programming and Data Analysis".

3. http://www.ncbi.nlm.nih.gov/ - website of the National Center for Biotechnological Information NCBI.

4. http://blast.ncbi.nlm.nih.gov/Blast.cgi - BLAST: Basic Local Alignment Search Tool.

5. http://www.mendeley.com/ - *Mendeley*: Free reference manager and PDF organizer; librarian program.

6. http://www.ebi.ac.uk - website of the European Institute of Bioinformatics.

7. http://www.scopus.com – bibliographic database and Scopus citation index.

8. http://thomsonreuters.com/thomson-reuters-web-of-science /bibliographic database and Web of Science citation index.

List of information technologies and software

1. In the implementation of the educational process, students use software: Microsoft Office (Excel, PowerPoint, Word, etc.), Statistica, electronic resources of the FEFU website, including FEFU EBS.

2. Bibliographic database and citation index Scopus, bibliographic database and citation index Web of Science, search engine, gene bank and online software package NCBI, scientific electronic library eLIBRARY, electronic library system "Znanium", electronic library system IPRbooks, information system "SINGLE WINDOW" access to educational resources access to electronic order of books in the FEFU library.

VIII. METHODICAL INSTRUCTIONS FOR MASTERING THE DISCIPLINE

IX. MATERIAL AND TECHNICAL SUPPORT OF DISCIPLINE

Training sessions on the discipline are held in rooms equipped with appropriate equipment and software.

The list of material and technical and software of the discipline is given in the table.

Logistics and Software Discipline

Mastering the discipline "Bioinformatics" involves the use of the following logistics: Multimedia audience equipped with broadband Internet access. Computer class. All computers are connected to the FEFU corporate computer network and are in a single domain.

To perform independent work, students in fefu residential buildings are provided with Wi-Fi.

Name of equipped premises and premises for independent work	List of main equipment
Classroom for practical exercises Computer class Of the School of Biomedicine Aud. M723, 15 workplaces, area 80,3 m²	Screen with electric drive 236 * 147 cm Trim Screen Line; Projector DLP, 3000 ANSI Lm, WXGA 1280x800, 2000:1 EW330U Mitsubishi; Subsystem of specialized fasteners of equipment CORSA-2007 Tuarex; Video switching subsystem: DVI DXP 44 DVI Pro Extron matrix switch; DVI twisted pair extender DVI 201 Tx/Rx Extron; Subsystem of audio switching and sound amplification; acoustic system for ceiling mounting SI 3CT LP Extron; digital audio processor DMP 44 LC Extron; extension for IPL T CR48 management controller; Wireless LANs for trainees are provided with a system based on 802.11a/b/g/n 2x2 MIMO(2SS) access points.
Reading rooms of the FEFU Scientific Library with open access to the fund (building A - level 10)	HP All-in-One 400 All-in-One 19,5 (1600x900), Core i3-4150T, 4GB DDR3-1600 (1x4GB), 1TB HDD 7200 SATA, DVD+/-RW,GigEth,Wi-Fi,WT,usb kbd/mse,Win7Pro (64-bit)+Win8.1Pro(64-bit),1-1-1 Wty Internet access speed 500 Mbps. Workplaces for people with disabilities are equipped with Braille displays and printers; equipped with: portable devices for reading flat-printed texts, scanning and reading machines video magnifier with the ability to regulate color spectra; magnifying electronic magnifiers and ultrasonic markers
Auditorium for independent work of students Vladivostok, Russky, Ajax, 10, Building 25.1, Oud. M621 Area 44.5 m²	Computer Lab: Monoblock Lenovo C360G-i34164G500UDK 19.5" Intel Core i3-4160T 4GB DDR3-1600 SODIMM (1x4GB)500GB Windows Seven Enterprise - 17 pieces; Wired LAN - Cisco 800 series; wireless LANs for students are provided with a system based on access points 802.11a / b / g / n 2x2 MIMO (2SS).
Auditorium for lectures Vladivostok, Russky Island, Ajax village, FEFU campus, korp. M, aud. M 422, area 158,6 m²	Multimedia audience: Monoblock Lenovo C360G-i34164G500UDK; Projection screen Projecta Elpro Electrol, 300x173 cm; Multimedia projector, Mitsubishi FD630U, 4000 ANSI Lumen, 1920x1080; Mortise interface with TLS TAM 201 Stan automatic cable retraction system; Avervision CP355AF Visualizer; Microphone cordless radio system UHF band Sennheiser EW 122 G3 consisting of a wireless microphone and receiver; LifeSizeExpress 220- Codeconly- Non-AES video conferencing codec; Network video camera Multipix MP-HD718; Two 47" LCD panels, Full HD, LG M4716CCBA; Subsystem of audio switching and sound amplification; centralized uninterrupted power supply

In order to provide special conditions for the education of disabled people and persons with disabilities at FEFU, all buildings are equipped with ramps, elevators, lifts, specialized places equipped with toilets, signs of information and navigation support.

X.   VALUATION FUNDS

FOS Passport

General professional competencies of graduates and indicators of their achievement:

Name of the category (group) of general professional competencies	Code and name of general professional competence (the result of mastery)	Code and name of the competency achievement indicator
	OPK-6 Is able to creatively apply and modify modern computer technologies, work with professional databases, professionally design and present the results of new developments.	OPK-6.1 Develops ways and prospects for the application of modern computer technologies in biological sciences and education. OPK-6.2 Uses with professional databases and data banks in the chosen field of professional activity, the necessary mathematical apparatus, analysis and algorithm for storing electronic images, has experience in modifying computer technologies for the purpose of professional research. OPK-6.3 Uses modern computer technologies, works with professional databases, draws up and presents the results of new developments.

Code and name of the competency achievement indicator	Name of the assessment indicator (the result of training in the discipline)
OPK-6.1 Develops ways and prospects for the application of modern computer technologies in biological sciences and education.	Knows the methods of modern computer technologies in biological sciences and education Able to apply in practice the knowledge of modern computer technologies in biological sciences and education Has the skills to work on modern computer equipment using methods
OPK-6.2 Uses with professional databases and data banks in the chosen field of professional activity, the necessary mathematical apparatus, analysis and algorithm for storing electronic images, has experience in modifying computer technologies for the purpose of professional research.	Knows professional databases and data banks in his professional activities, Able to use professional databases and data banks in the chosen field of professional activity, the necessary mathematical apparatus, analysis and algorithm for storing electronic images He has the skill of applying the mathematical apparatus in his professional field, the skill of working with databases, modifying computer technologies for the purpose of professional research.
OPK-6.3 Uses modern computer technologies, works with professional	Knows the tools of modern computer technology Able to apply modern computer technologies, work with

	databases, draws up and presents the results of new developments.	professional databases, design and present the results of new developments. Own the skill of working on modern computer equipment

No p/n	Supervised sections / topics of the discipline	Achievement indicator code and name	Learning outcomes	Assessment tools	
				current control	Intermediate-accurate certification
7.	Topic 1. Tasks and methods of bioinformatics	OPK-6.1; OPK-6.2; OPK-6.3	Knows Can Owns	UO-1	UO-1 vpr. to the beginning NoNo 1,2
8.	Topic 2. Fundamental Principles of Molecular Biology	OPK-6.1; OPK-6.2; OPK-6.3	Knows Can Owns	PR-1 PR-2	UO-1 vpr. to the zach. №№ 3-9
9.	Topic 3. Information retrieval theory	OPK-6.1; OPK-6.2; OPK-6.3	Knows Can Owns	PR-1 PR-2	UO-1 vpr. to the zach. №№ 10-12
10	Topic 4. Access to archives of scientific information	OPK-6.1; OPK-6.2; OPK-6.3	Knows Can Owns	PR-1 PR-2	UO-1 vpr. to the zach. №№ 13-15
11	Topic 5. Alignment of primary sequences of biomolecules	OPK-6.1; OPK-6.2; OPK-6.3	Knows Can Owns	PR-1 PR-2	UO-1 vpr. to the zach. №№ 16-33
12	Topic 6. Proteomics and modeling of the three-dimensional structure of biomolecules	OPK-6.1; OPK-6.2; OPK-6.3	Knows Can Owns	PR-1 PR-2	UO-1 vpr. to the zach. №№ 34-39

Scale of assessment of the level of formation of competencies

Competence code and wording	Stages of competence formation		criteria	Indicators
OPK-6.1 Develops ways and prospects for the application of modern computer technologies in biological sciences and education.	knows (threshold level)	methods and methodological methods of scientific research, methods of modern computer technologies in biological sciences and education	knowledge of problems in the study area	the ability to argue the choice of methods of scientific research on the topic, to characterize the problems in the field under study in accordance with the topic of the master's thesis

	can (advanced)	apply in practice the knowledge of modern computer technologies in biological sciences and education	ability to master new subject areas	the ability to master a new subject area for solving problems in scientific research on the topic of the master's thesis and to lead to the defense of the justification of the selected solutions
	owns (high)	skills in mastering new subject areas, identifying problems in their own research and solving them, skills in working on modern computer equipment	possession of skills in mastering new subject areas, identifying problems in their own research and solving them	the ability to give comparisons of alternative options and give arguments to justify the advantages of the selected in the performance of research
OPK-6.2 Uses with professional databases and data banks in the chosen field of professional activity, the necessary mathematical apparatus, analysis and algorithm for storing electronic images, has experience in modifying computer technologies for the purpose of professional research.	knows (threshold level)	modern achievements of theoretical biology, professional databases and data banks in their professional activities	knowledge of professional databases, data banks Main	ability to work in professional databases/data banks
	can (advanced)	creatively apply proven methods and techniques in a specific professional activity, use professional databases and data banks in the selected field of professional activity, the necessary mathematical apparatus, analysis and algorithm for storing electronic images	the ability to apply the basic provisions, laws and patterns of theoretical biology in scientific and professional activities, to use professional databases and data banks in the chosen field of professional activity	Ability to apply the necessary knowledge of fundamental and applied biological disciplines in scientific research on the topic of the master's thesis, to compare the results of research work with general provisions and draw conclusions
	owns (high)	creative approach to solving professional problems, the skill of applying the mathematical apparatus in their professional sphere, the skill of working with databases,	possession of search skills, setting strategic and tactical tasks for solving professional problems, the ability to work with databases, information retrieval	the ability to creatively approach the solution of problems in the professional field, to determine the direction of scientific research

		modifying computer technologies for the purpose of professional research.		
OPK-6.3 Uses modern computer technologies, works with professional databases, draws up and presents the results of new developments.	knows (threshold level)	tools of modern computer technologies	Methods and means of modern computer technologies	the ability to independently plan and carry out scientific research, select adequate methods of collecting and processing material for solving scientific problems; the ability to conduct a comparative analysis of the results of the study with the literature data
	can (advanced)	apply modern computer technologies, work with professional databases, design and present the results of new developments.	possession of basic professional skills in the application of modern computer technology in their professional field	the ability to receive, design and present the results of their developments
	owns (high)	the skill of working on modern computer equipment	ability to work on modern computer equipment	the ability to work on modern computer equipment to demonstrate on the defense the ability to set goals and objectives, solve problems in their professional field, receive, analyze and present the information received using modern computer technologies

Methodological recommendations that determine the procedures for assessing the results of mastering the discipline

According to the discipline under study, the following are used for current control and intermediate (semester) certification

Valuation tools:

UO-1 – individual interview;

PR-1 – written (or computer) test;

PR-2 – control works.

Oral questioning is the most common method of monitoring students' knowledge. Oral questioning establishes direct contact between the teacher and students, during which the teacher receives ample opportunities to study the individual possibilities of students' assimilation of educational material. It is the most common and adequate form of monitoring students' knowledge. Includes an interview on credit.

Criteria for evaluating an oral response:

"5 points" are given to the student if he gives the right answers to the questions under discussion, which are distinguished by the depth and completeness of the disclosure of the topic, is able to draw conclusions and generalizations, give reasoned answers that are logical and consistent.

"4 points" is given to the student if he gives the right answers to the questions under discussion, which differ in the depth and completeness of the disclosure of the topic, is able to draw conclusions and generalizations, but one or two errors in the answers are allowed.

"3 points" are given to the student if he gives answers to the discussed questions that do not fully disclose it, there is no logical construction of the answer, makes several mistakes.

"2 points" are given to the student if he gives answers to the questions under discussion, which show that he does not own the material of the topic, cannot give reasoned answers, serious errors are made in the content of the answer.

A seminar session can serve as a form not only of testing, but also of increasing the knowledge of students. At colloquia, all or individual topics, issues of the course being studied can be discussed.

The criteria for evaluating speeches (reports) at seminars and practical classes are the same as for oral response.

The test is a written or computer form of control aimed at checking the possession of the terminological apparatus and specific (accurate) knowledge in the field of fundamental and applied disciplines.

Test evaluation criteria:

5 points are given to the student if he answered 86-100% of all questions.

4 points are given for the correct answer to 76-85% of all questions.

3 points are given for the correct answer to 61-75% of all questions.

2 points are given for the correct answer to 50-61% of all questions.

1 point is given for the correct answer on less than 50% of all questions.

A test work is a written or electronic form of control over the current assimilation of material on a large section (topic) of the discipline, evaluates the assimilation of terms, basic concepts, methods, the ability to solve practical problems.

Criteria for assessing the control work:

Test works are estimated by the share of work performed from the volume of the entire task.

5 points are given to a student if he has completed 86-100% of the total amount of the task.

4 points are given for the completion of 76-85% of the total volume of the task.

3 points are given for the completion of 61-75% of the total volume of the task.

2 points are given for the completion of 50-61% of the total volume of the task.

1 point is given for completing less than 50% of the total amount of the task.

Tests and tests are carried out during the hours allotted for practical exercises.

Assessment tools for intermediate attestation

As the final stage of the intermediate (semester) certification in the discipline "Bioinformatics" **, credit is provided**.

Guidelines for passing the test

Criteria for scoring on the test

The "credit" grade is given when the student is fluent in the theoretical material of the discipline being studied, does not make mistakes when answering the questions asked, using visual tables, or admits some inaccuracies in the answers, but quickly corrects errors when asking him leading questions. In addition, the student is guided in the collection of histological preparations in their determination.

The grade "not counted" is given when the student does not own the materials of the discipline being studied, does not answer additional questions of the teacher and does not navigate the collection of histological preparations when determining them.

Questions for the test in the discipline "Bioinformatics"

1. History of the development of molecular biology and bioinformatics.

2. Central dogma of molecular biology. Principles of storage and implementation of genetic information.

3. Properties of the genetic code.

4. Types of nucleotide substitutions and mutations.

5. Transpositions and transversions.

6. Insertions/deletions.

7. Basic principles of the evolutionary process. Homology, analogy/convergence.

8. Natural selection and neo-Darwinism.

9. The concept of molecular clocks.

10. Principles of indexing information in databases. Metadata.

11. Fundamental search operators. Boolean operators.

12. Search engines. Focused search engines.

13. Databases on scientific literature and citations.

14. Citation indexes. Bibliometrics.

15. Programs - bibliographic information management systems.

16. Alignment of primary sequences of biological macromolecules.

17. Point sequence similarity matrices.

18. Global and Local Alignment. Dynamic programming.

19. Multiple alignments.

20. Genetic distances.

21. Phylogenetic evolutionary models: Jux–Cantor model.

22. Kimura's model.

23. Tajima model – Nei.

24. Gamma distances.

25. Amino acid distances. Amino acid substitution matrices.

26. Methods of analysis of discrete features.

27. Phylogenetic trees.

28. Construction of phylogenetic trees by UPGMA method.

29. Construction of phylogenetic trees by the method of transformed distance.

30. The method of minimum evolution. The method of joining neighbors.

31. Maximum savings method.

32. Methods of maximum plausibility.

33. Bootstrap support for phylogenetic trees.

34. Levels of organization of protein molecules. Primary, secondary, tertiary, quaternary structure.

35. Factors that stabilize the three-dimensional structure of proteins.

36. Folding proteins.

37. Levinthal's paradox. The problem of folding forecasting.

38. Isoforms of proteins. Classification of protein structures.

39. Structural alignment of biomolecules.

Assessment tools for the current attestation

Testing on the topics covered is carried out on paper forms or in a computer lab. An example of the test is given below.

Intermediate Attestation Test Example

Test paper No1 "Basic principles of molecular biology. Central Dogma of Molecular Biology"

<p style="text-align:center">Option No1.</p>

1) Reach the complementary chain to the following single-stranded DNA molecule, indicate its direction (3' and 5' ends):

5' G – G – T – A - G – T – T – A – G – C – C – A – T – C – G 3'

2) What are the enzymes that complete the second, complementary to it, chain according to the matrix of one DNA chain?

a. Histones

b. Polymerases

c. Primemazy

Helicazy

3) Formulate the central dogma of molecular biology. What are the main synthesis processes that reflect the stages of the implementation of genetic information?

4) What is the degeneracy of the genetic code?

<p style="text-align:center">Option No2.</p>

1) Reach the complementary chain to the following single-stranded DNA molecule, indicate its direction (3' and 5' ends):

3' T – C – T – T - G – A – A – T – G – C – G – G – T – C – G 5'

2) What are the names of the enzymes that complete the DNA chain with a complementary RNA chain?

a. RNA-Helicases

b. Primemazy

c. Histones

g. RNA polymerases

3) Formulate the central dogma of molecular biology. What are the main synthesis processes that reflect the stages of the implementation of genetic information?

4) What is the triplete nature of the genetic code?

<p style="text-align:center">Test paper No2 "Theory of search for scientific information"</p>
<p style="text-align:center">Option 1</p>

1) Name the main Boolean operators. What is their purpose?

2) Name the main search operators that can limit the scope of search in the Yandex search engine.

3) What is the main functionality of Web of Science? What tasks can I use this system for?

<p style="text-align:center">Option 2</p>

1) What are regular expressions? Give examples.

2) What are the main search operators that can limit the scope of search in the Google Scholar search engine?

3) What is the main functionality of Scopus? What tasks can I use this system for?

Control and practical work No3

Task: In the GenBank database, which is accessed from the main page of the NCBI Institute (http://www.ncbi.nlm.nih.gov/), find the sequence of messenger RNA for a given gene of a certain organism.

Examples of genes:

- o   Human p53 gene
- o   Reverse transcriptase of MMLV virus
- o   Domestic cow genprion protein (PRNP)

Perform the alignment of the found nucleotide sequence using the BLAST program (http://blast.ncbi.nlm.nih.gov/Blast.cgi) with testing of various algorithms and comparing the results of their application. Determine which sequences from the gene bank are most homologous to your sequence (specify the first 10 of them). To which organisms do they belong?