UČNI NAČRT PREDMETA / COURSE SYLLABUS	
Predmet:	BIOKEMIJSKA INFORMATIKA
Course Title:	BIOCHEMICAL INFORMATICS

Študijski program in stopnja Study Programme and Level	Študijska smer Study Field	Letnik Academic Year	Semester Semester
UN Biokemija, 1. stopnja	**/**	**2.**	**4.**
USP Biochemistry, 1st Cycle	**/**	**2nd**	**4th**

Vrsta predmeta / Course Type: obvezni / Mandatory

Univerzitetna koda predmeta / University Course Code: BK122

Predavanja Lectures	Seminar Seminar	Vaje Tutorial	Klinične vaje Work	Druge oblike študija	Samost. delo Individual Work	ECTS
30	**10**	**35 LV**	**/**	**/**	**75**	**5**

Nosilec predmeta / Lecturer: doc. dr. Miha Pavšič / Dr. Miha Pavšič, Assistant Professor

Jeziki / Languages:

Predavanja / Lectures:	**slovenski / Slovenian**
Vaje / Tutorial:	**slovenski / Slovenian**

Pogoji za vključitev v delo oz. za opravljanje študijskih obveznosti:	**Prerequisites:**
Študent oz. kandidat mora imeti predmet opredeljen kot študijsko obveznost.	The course has to be assigned to the student.

Vsebina:	**Content (Syllabus outline):**
Obdelava biokemijskih podatkov ter njihova statistična obravnava. Biokemijske in biološke podatkovne baze: bibliografske baze, kemijske spojine, nukleotidna in aminokislinska zaporedja, geni in njihovo izražanje, genom, bolezni, taksonomija, metabolične poti in strukture makromolekul. Nukleotidna zaporedja: sekvenciranje, analiza nukleotidnih zaporedij (restrikcijska mesta, odprti bralni okviri in prevajanje v aminokislinsko zaporedje, geni in regulatorne regije, eksoni in introni) in verižna reakcija s polimerazo in načrtovanje začetnih oligonukleotidov.	Analysis of biochemical data and application of statistical methods. Biochemical and biological databases: bibliographic databases, compounds, nucleotide and amino acid sequences, genes and gene expression, genome, diseases, taxonomy, metabolic pathways, and structure of macromolecules. Nucleotide sequences: sequencing, analysis of nucleotide sequences (restriction sites, open reading frames, translation to an amino acid sequence, genes and regulatory regions, exons and introns), and polymerase chain reaction and construction of oligonucleotides. Amino acid sequences: calculation/prediction of

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Aminokislinska zaporedja: izračun/napoved lastnosti proteina na osnovi aminokislinskega zaporedja (molekulska masa, ekstinkcijski koeficient, izoelektrična točka, hidrofobnost in transmembranske regije), iskanje motivov (glikozilacija, mesta cepitve s peptidazami, ...) in napoved sekundarne strukture. Prileganje zaporedij: prileganje nukleotidnih in aminokislinskih zaporedij, lokalno in globalno prileganje, skupno zaporedje, iskanje podobnih zaporedij, grupiranje zaporedij in gradnja filogenetskih dreves. 3D-struktura makromolekul: 3D-struktura proteinov in nukleinskih kislin, zapis in vizualizacija strukturnih podatkov, tipi zvitja, domene, podobnost struktur, modeliranje in umestitev.	protein properties on the basis of its amino acid sequence (molecular mass, extinction coefficient, isoelectric point, hydrophobicity and transmembrane regions), motif search (glycosylation, peptidase cleavage sites, etc.), and secondary structure prediction. Sequence alignment: alignment of nucleotide and amino acid sequences, local and global alignment, consensus sequence, search for similar sequences, sequence grouping and construction of phylogenetic trees. 3D structure of macromolecules: 3D structure of proteins and nucleic acids, format and visualization of structural data, folds, domains, structure similarity, modeling, and docking.

Temeljna literatura in viri / Readings:

Arthur M. Lesk: Introduction to Bioinformatics. 4. izdaja, Oxford University Press, 2014.
Michael Agostino: Practical Bioinformatics. 1. izdaja, Garland Science, 2012.
Dodatna literatura/ Additional literature: navodila za spletna orodja.

Cilji in kompetence:	**Objectives and Competences:**
Študenti bodo spoznali orodja in pristope pri računalniško podprti analizi biokemijskih podatkov. Po uspešno opravljenih obveznostih bodo sposobni samostojnega pridobivanja podatkov iz podatkovnih baz, njihove analize, povezovanja in interpretacije.	Students will familiarize themselves with tools and approaches in computer aided biochemical data analysis. Upon successful completion of the course they will be able to independently perform data collection from databases, its analysis, integration and interpretation.

Predvideni študijski rezultati:	**Intended Learning Outcomes:**
<u>Znanje in razumevanje</u> Študenti bodo spoznali osnove iskanja, zbiranja in analize podatkov ter njihove in interpretacije. Preko poznavanja algoritmov, na katerih ti računalniški pristopi temeljijo, bodo postopke tudi razumeli in jih tako znali ustrezno uporabiti.	<u>Knowledge and Comprehension</u> Knowledge of modern computer approaches in data collection and analysis is critical for every biochemist. Students will apply the acquired knowledge and skills in other courses during their study as well as during their independent research work.
<u>Uporaba</u> Znanje biokemijske informatike je danes pomembno na vseh področjih biokemije. V okviru vaj in seminarske naloge študent pridobi tudi praktična znanja.	<u>Application</u> Knowledge of biochemical informatics and its tools is important in all fields of biochemistry. Applicable knowledge is achieved through practical exercises and project work.

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Refleksija Študenti bodo pridobili pregled biokemijskih podatkovnih baz in računalniških orodij, ob poznavanju uporabnosti pa se bodo zavedali tudi njihovih omejitev.	Analysis Students will get an overview of the biochemical databases and computer tools, their functionality and, importantly, their limitations.
Prenosljive spretnosti Izkušnje pri reševanju problemov in projektnem delu. Principi računalniških algoritmov. Zbiranje podatkov, njihova analiza, povezovanje, interpretacija ter predstavitev.	Skill-transference Ability Skills in problem solving and project work. Principles of computer algorithms. Data collection, its analysis, integration, interpretation, and presentation.

Metode poučevanja in učenja:	**Learning and Teaching Methods:**
Predavanja. Laboratorijske vaje.	Lectures. Computer exercises.

Načini ocenjevanja:	Delež (v %) / Weight (in %)	**Assessment:**
Kolokvij iz vaj. 40 % Pisni izpit in seminarska naloga. 60 % Ocene: 6-10 (pozitivno), 1-5 (negativno).	**40%** **60%**	Practical exam. Written exam and seminar work. Grades: 6-10 (positive), 1-5 (negative).

Reference nosilca / Lecturer's references:

- Tsaktanis T, Kremling H, **Pavšič M**, von Stackelberg R, Mack B, Fukumori A, Steiner H, Vielmuth F, Spindler V, Huang Z, Jakubowski J, Stoecklein NH, Luxenburger E, Lauber K, Lenarčič B, Gires O. Cleavage and Cell Adhesion Properties of Human Epithelial Cell Adhesion Molecule (HEPCAM). Journal of Biological Chemistry 2015 Oct 2;290(40):24574-91. doi: 10.1074/jbc.M115.662700
- **Pavšič M**, Ilc G, Vidmar T, Plavec J, Lenarčič B. The cytosolic tail of the tumor marker protein Trop2--a structural switch triggered by phosphorylation. Sci Rep. 2015 May 18;5:10324. doi: 10.1038/srep10324
- **Pavšič M**, Gunčar G, Djinović-Carugo K, Lenarčič B. Crystal structure and its bearing towards an understanding of key biological functions of EpCAM. Nature Communications 2014 Aug 28;5:4764. doi: 10.1038/ncomms5764

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