

UČNI NAČRT PREDMETA / COURSE SYLLABUS

Predmet:	Bioinformacijski algoritmi
Course title:	Bioinformatics Algorithms

Študijski program in stopnja Study programme and level	Študijska smer Study field	Letnik Academic year	Semester Semester
Interdisciplinarni doktorski študijski program BIOZNANOSTI 3. stopnja	Bionformatika	1,2	1,2,3,4
Interdisciplinary Doctoral Study Programme in BIOSCIENCES 3rd cycle	Bioinformatics	1,2	1,2,3,4

Vrsta predmeta / Course type

individualno raziskovalni predmet / individual research course

Univerzitetna koda predmeta / University course code:

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Predavanja Lectures	Seminar Seminar	Vaje Tutorial	Klinične vaje work	Druge oblike študija	Samost. delo Individ. work	ECTS
/	15	5	/	5	100	5

Nosilec predmeta / Lecturer:

Nosilec: doc. dr. Tomaž Curk

Jeziki / Languages:

Predavanja / Lectures:	slovenski / angleški Slovene / English
Vaje / Tutorial:	slovenski / angleški Slovene / English

Pogoji za vključitev v delo oz. za opravljanje študijskih obveznosti:

Osnovna znanja programiranja, verjetnosti in statistike.

Prerequisites:

Basics of computer programming in any language, basic knowledge of probability and statistics.

Vsebina:

Content (Syllabus outline):

- Algoritmi za analizo zaporedij, iskanje podzaporedij, iskanje motivov.
- Določanje zaporedja genomov, algoritmi na grafih.
- Primerjava zaporedij, dinamično programiranje.
- Algoritmi za filogenetsko analizo.
- Skriti markovski modeli, analiza strukture genoma.
- Analiza genskih izrazov, razvrščanje v skupine, klasifikacija, analiza obogatnosti genskih skupin.
- Rekonstrukcija in analiza genskih mrež.
- Vizualizacija podatkov.

- Sequence analysis, search for subsequences, motif search.
- Genome assembly, graph algorithms.
- Comparison of biological sequences, dynamic programming.
- Phylogeny algorithms.
- Hidden Markov Models and gene prediction.
- Gene expression analysis, clustering and supervised data mining, enrichment analysis.
- Gene network reconstruction and analysis.
- Data visualization.

Temeljni literatura in viri / Readings:

- Durbin R, Eddy SR, Krogh A, Mitchison G (1998) Biological sequence analysis: probabilistic models of proteins and nucleic acids, Cambridge University Press.
- Jones NC, Pevzner PA (2004) An introduction to bioinformatics algorithms, The MIT Press.

Ostalo: revijalni članki s področja, tekoča periodika in druga učna gradiva.

Cilji in kompetence:

Študentje se bodo pri predmetu naučili implementirati vrsto algoritmov, ki jih lahko uporabimo na področju bioinformatike in sistemske biologije. Znali bodo razbrati, na kater tip biološki vprašanj lahko odgovorimo z razvojem in uporabo računskih pristopov.

Objectives and competences:

Students completing the course should be able to implement a variety of bioinformatics and systems biology algorithms, and learn which type of biological questions can be answered by means of computational approaches.

Predvideni študijski rezultati:

Študentje se bodo seznanili z glavnimi razredi algoritmov, ki so uporabljajo na področju bioinformatike in lahko z njimi analiziramo zaporedja, grafe in podatke o meritvah iz molekularne biologije. Na praktičnih primerih analize velike množice podatkov bodo spoznali probleme pri razvoju teh algoritmov, ki so vezani na hitrost izvajanja in uporabo spomina. Izpopolnili bodo svoje predznanje programiranja in v praksi uporabili predznanja s področja verjetnosti in statistike.

Intended learning outcomes:

Students will become familiar with main classes of computational approaches and algorithms in bioinformatics. The algorithms that they will design in a class are those from sequence and graph analysis and analysis of data coming from experimental measurements in molecular biology. In practical cases of analysis of large data sets they will need to cope with problems of computational efficiency and limited data storage (computer memory). They will advance their knowledge of programming, and use their previously developed skills in probability and statistics in practical problems from systems biology.

Metode poučevanja in učenja:

Praktične vaje, domače naloge, seminar, konzultacije. Reševanje problemov na učnih spletnih straneh <http://rosalind.info> in <http://stepic.org>.

Learning and teaching methods:

Workshops, homeworks, consultations, seminar. Solving problems on learning portals such as <http://rosalind.info> and <http://stepic.org>.

Načini ocenjevanja:

Seminar
Domače naloge

Delež (v %) /
Weight (in %)

80 %
20 %

Assessment:

Seminar
Homeworks

Reference nosilca / izvajalcev / Lecturer's references:**Tomaž Curk:**

1. Yoichiro Sugimoto, Julian König, Shobbir Hussain, Blaž Zupan, Tomaž Curk, Michaela Frye, Jernej Ule (2012) Analysis of CLIP and iCLIP methods for nucleotide-resolution studies of protein-RNA interactions, *Genome Biology* 13(8): 1-33. [COBISS.SI-ID 9319764]
2. Tomaž Curk, Gregor Rot, Blaž Zupan (2011) SNPsyn : detection and exploration of SNP-SNP interactions, *Nucleic Acids Research* 39(2): 444-449. [COBISS.SI-ID 8352596]
3. James R. Tollervey*, Tomaž Curk*, Boris Rogelj*, Michael Briese, Matteo Cereda, Melis Kayikci, Julian König, Tibor Hortobágyi, Agnes L. Nishimura, Vera Župunski, Rickie Patani, Siddharthan Chandran, Gregor Rot, Blaž Zupan, Christopher E. Shaw, Jernej Ule (2011) Characterizing the RNA targets and position - dependent splicing regulation by TDP-43, *Nature Neuroscience* 14(4): 452-459. [COBISS.SI-ID 8278100]
4. Julian König, Kathi Zarnack, Gregor Rot, Tomaž Curk, Melis Kayikci, Blaž Zupan, Daniel J. Turner, Nicholas M. Luscombe, Jernej Ule (2010) ICLIP reveals the function of hnRNP particles in splicing at individual nucleotide resolution, *Nature Structural and Molecular Biology* 17(7): 909-916. [COBISS.SI-ID 7800916]
5. Tomaž Curk, Uroš Petrovič, Gad Shaulsky, Blaž Zupan (2009) Rule-based clustering for gene promoter structure discovery, *Methods of Information in Medicine* 48(3): 229-235. [COBISS.SI-ID 22605095]
6. Petra Fey, Pascale Gaudet, Tomaž Curk, Blaž Zupan, Eric M. Just, Basu Siddhartha, Soheli N. Merchant, Yulia A. Bushmanova, Gad Shaulsky, Warren A. Kibbe, Rex L. Chisholm (2009) DictyBase - a Dictyostelium bioinformatics resource update, *Nucleic Acids Research* 37: 515-519. [COBISS.SI-ID 6916180]