

UČNI NAČRT PREDMETA / COURSE SYLLABUS	
Predmet:	Bioinformacijska orodja in podatkovne zbirke
Course title:	Bioinformatics Tools and Databases

Študijski program in stopnja Study programme and level	Študijska smer Study field	Letnik Academic year	Semester Semester
Interdisciplinarni doktorski študijski program BIOZNANOSTI 3. stopnja	Bioinformatika	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

teoretični predmet / theoretical course

Univerzitetna koda predmeta / University course code:

Predavanja Lectures	Seminar Seminar	Vaje Tutorial	Klinične vaje work	Druge oblike študija	Samost. delo Individ. work	ECTS
20	40	/	/	/	190	10

Nosilec predmeta / Lecturer:

Nosilec: prof. dr. Jernej Jakše

**Jeziki /
Languages:**

**Predavanja /
Lectures:**
Vaje / Tutorial:

slovenski / angleški
Slovene / English
slovenski / angleški
Slovene / English

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

Splošni pogoji za vpis na doktorski študij.

Prerequisites:

General conditions for enrolment in doctoral studies.

Vsebina:

- Bioinformacijske podatkovne zbirke: zaporedja nukleinskih kislin, proteinov, strukturne podatkovne zbirke, bibliografske podatkovne zbirke. Orodja za analizo zaporedij in struktur.
- Genomski projekti modelnih organizmov, primerjalna genomika, določevanje genov in regulatornih regij v genomih, SNP analize, genske mreže.
- Orodja v transkriptomiki in visoko-zmogljivostni genetiki.
- Bioinformacijska orodja v proteomiki in

Content (Syllabus outline):

- Databases in bioinformatics, nucleic acid sequences, protein sequences, 3D structures, bibliographic information. Tools for analysis of sequences and structures.
- Genomic projects of model organisms, comparative genomics, identifying genes and regulatory regions of genomes, SNP analysis, gene networks.
- Bioinformatics tools in transcriptomics and high-throughput genetics.
- Bio-informatics tools in proteomics and interactomics.

interaktomiki.

- Aplikacije: bioinformatika v okoljski genomiki, farmakogenomiki.
- Ontologije in zbirke znanj v bioinformatiki.
- Bioinformacijski pristopi v kemogenomiki.
- Projektno delo s specifičnimi programskimi orodji med predavanji in v okviru seminarske naloge.

- Applications: Bioinformatics in environmental genomics, pharmacogenomics.

- Ontologies and knowledge databases in bioinformatics.
- Bioinformatics approaches in chemogenomics.
- Project work with specific software tools during the lectures and within seminar.

Temeljni literatura in viri / Readings:

- David W. Mount (2004) Bioinformatics. Sequence and Genome Analysis. Cold Spring Harbor Laboratory Press, USA.
- Klipp E. Et al. (2005) Systems Biology in Practice. Wiley-VCH, Weinheim, Germany
- Knudsen S. (2004) Guide to analysis of DNA microarray data, 2nd edition. A John Wiley & Sons, Inc. Publications.
- Caroline St. Clair, Jonathan E. Visick. (2013) Exploring Bioinformatics, Second Edition, A Project-Based Approach. Jones & Bartlett Publishers.
- pregledni in originalni znanstveni članki s širšega področja bioinformatike.

Cilji in kompetence:

Seznanitev s celotnim področjem bioinformatike in trenutnimi trendi v razvoju bioinformatike. Predmet daje študentu pregled nad celotnim področjem bioinformatike in ga uvaja v raziskovalno delo na glavnih toriščih raziskav v bioinformatiki.

Objectives and competences:

Students will become familiar with the entire area of bioinformatics and current trends in the development of bioinformatics. The subject gives students an overview of the field and introduces the research work on the main spheres of research in bioinformatics.

Predvideni študijski rezultati:

Znanje in razumevanje:
Študenti bodo spoznali specifična bioinformacijska orodja, njihove omejitve in potrebe po njihovem izboljšanju glede na razvoj raziskav v genetiki, genomiki, proteomiki, sistemski in strukturni biologiji ter v evolucijskih študijah. Študenti se bodo tudi seznanili z naravo podatkov v bioloških raziskavah in z najpomembnejšimi biološkimi podatkovnimi zbirkami ter njihovo uporabo.

Intended learning outcomes:

Knowledge and understanding:
Students will learn specific bioinformatics tools, their limitations and their need for improvement in relation to the development of research in genetics, genomics, proteomics, systems and structural biology and in evolutionary studies. Students will also learn about the nature of the data in biological research and the most important biological databases and their use.

Metode poučevanja in učenja:

Predavanja, praktične vaje z računalniki, samostojna priprava seminarjev in predstavitev.

V okviru seminarske naloge bo vsak študent z uporabo bioinformacijskih orodij rešil praktični

Learning and teaching methods:

Lectures, seminars, project workshops, practical work with computers.

In the context of seminar, each student will have to use bioinformatics tools to solve a practical problem. He will then present the results in

problem in ga predstavil pisno v obliki znanstvenega članka in ustno v obliki dvajsetminutne predstavitve.	writing in the form of a scientific paper and orally in the form of a twenty-minute presentation.
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Načini ocenjevanja:		Delež (v %) / Weight (in %)	Assessment:
Seminar s predstavitvijo		50 %	Seminar with public presentation
Pisno preverjanje znanja		50 %	Written exam

Reference nosilca / Lecturer's references:

Jernej Jakše:

1. ANTONY, Binu, SOFFAN, Alan, JAKŠE, Jernej, ALFAIFI, Sulieman, SUTANTO, Koko D., ALDOSARI, Saleh A., ALDAWOOD, Abdulrahman S., PAIN, Arnab. Genes involved in sex pheromone biosynthesis of *Ephestia cautella*, an important food storage pest, are determined by transcriptome sequencing. *BMC genomics*, 2015, vol. 16, July, str. 1-26.
2. CREGEEN, Sara, RADIŠEK, Sebastjan, MANDELIC, Stanislav, TURK, Boris, ŠTAJNER, Nataša, JAKŠE, Jernej, JAVORNIK, Branka. Different gene expressions of resistant and susceptible hop cultivars in response to infection with a highly aggressive strain of *Verticillium albo-atrum*. *Plant molecular biology reporter*, 2015, vol. 33, iss. 3, str. 689-704.
3. JAKŠE, Jernej, RADIŠEK, Sebastjan, POKORN, Tine, MATOUŠEK, Jaroslav, JAVORNIK, Branka. Deep-sequencing revealed Citrus bark cracking viroid (CBCVd) as a highly aggressive pathogen on hop. *Plant Pathology*, 2015, vol. 64, iss. 4, str. 831-842.
4. MAJER, Aljaž, JAVORNIK, Branka, ČERENAK, Andreja, JAKŠE, Jernej. Development of novel EST-derived resistance gene markers in hop (*Humulus lupulus* L.). *Molecular breeding*, 2014, vol. 33, issue 1, str. 61-74.
5. REŠETIČ, Tjaša, ŠTAJNER, Nataša, BANDELJ, Dunja, JAVORNIK, Branka, JAKŠE, Jernej. Validation of candidate reference genes in RT-qPCR studies of developing olive fruit and expression analysis of four genes involved in fatty acids metabolism. *Molecular breeding*, 2013, vol. 32, issue 1, str. 211-222.
6. MCMANUS, Michael T., JOSHI, Srishti, SEARLE, Bruce, PITHER-JOYCE, Meeghan, SHAW, Martin, LEUNG, Susanna, ALBERT, Nick, SHIGYO, Masayoshi, JAKŠE, Jernej, HAVEY, Michael J., MCCALLUM, A. John. Genotypic variation in sulfur assimilation and metabolism of onion (*Allium cepa* L.). III, Characterization of sulfite reductase. *Phytochemistry*, 2012, vol. 83, str. 34-42.
7. JAKŠE, Jernej, ŠTAJNER, Nataša, LUTHAR, Zlata, JELTSCH, Jean-Marc, JAVORNIK, Branka. Development of transcript-associated microsatellite markers for diversity and linkage mapping studies in hop (*Humulus lupulus* L.). *Molecular breeding*, 2011, vol. 28, no. 2, str. 227-239.
8. JAKŠE, Jernej, TELGMANN, Alexa, JUNG, Christian, KHAR, Anil, MELGAR, Sergio, CHEUNG, Foo, TOWN, Christopher, HAVEY, Michael J. Comparative sequence and genetic analyses of asparagus BACs reveal no microsynteny with onion or rice. *Theoretical and Applied Genetics*, 2006, vol. 114, str. 31-39.
9. MARTIN, William J., MCCALLUM, John, SHIGYO, Masayoshi, JAKŠE, Jernej, KUHL, Joseph C., YAMANE, Naoko, PITHER-JOYCE, Meeghan, GOKCE, Ali Fuat, SINK, Kenneth C., TOWN, Christopher, HAVEY, Michael J. Genetic mapping of expressed sequences in onion and in silico comparisons with rice show scant colinearity. *Molecular genetics and genomics*, 2005, vol. 274, str. 197-204.

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

teoretični predmet / theoretical course

Univerzitetna koda predmeta / University course code:

Predavanja Lectures	Seminar Seminar	Vaje Tutorial	Klinične vaje work	Druge oblike študija	Samost. delo Individ. work	ECTS
10	/	20	/	/	95	5

Nosilec predmeta / Lecturer:

Nosilec: prof. dr. Blaž Zupan

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 obogatenosti 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. Znalci bodo razbrali, 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 classess 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 thier previously developed skills in probability and statistics in practical problems from systems biology.

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Metode poučevanja in učenja:

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

Learning and teaching methods:

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

Načini ocenjevanja:

Domače naloge

Delež (v %) /

Weight (in %)

Assessment:

Homeworks

Reference nosilca / izvajalcev / Lecturer's references:
Blaž Zupan:

1. Toplak M, Močnik R, Polajnar M, Bosnić Z, Carlsson L, Hasselgren C, Demšar J, Boyer S, Zupan B, Ståhring J (2014) Assessment of Machine Learning Reliability Methods for Quantifying the Applicability Domain of QSAR Regression Models, J Chem Inf Model 54(2):431-41.
2. Žitnik M, Janjić V, Larminie C, Zupan B, Pržulj N (2013) Discovering disease-disease associations by fusing systems-level molecular data, Scientific Reports, 13:3202. [COBISS.SI-ID 10253396]
3. Demšar J, Curk T, Erjavec A, Gorup C, Hocevar T, Milutinovic M, Mozina M, Polajnar M, Toplak M, Staric A, Stajdohar M, Umek L, Zagar L, Zbontar J, Zitnik M, Zupan B (2013) Orange: data mining toolbox in Python, Journal of Machine Learning Research, 14:2349-2353. [COBISS.SI-ID 10118740]
4. Nasser W, Santhanam B, Miranda ER, Parikh A, Juneja K, Rot G, Dinh C, Chen R, Zupan B, Shaulsky G, Kuspa A (2013) Bacterial discrimination by dictyostelid amoebae reveals the complexity of ancient interspecies interactions, Current Biology, 23(10):862-872. [COBISS.SI-ID 9921108]
5. Miranda ER, Zhuchenko O, Toplak M, Santhanam B, Zupan B, Kuspa A, Shaulsky G (2013) ABC transporters in Dictyostelium discoideum development, PLoS One, 8 (8). e70040. [COBISS.SI-ID 10035284]
6. Mendes M, Franco-Duarte R, Umek L, Fonseca E, Drumonde-Neves J, Dequin S, Zupan B, Schuller D (2013) Computational models for prediction of yeast strain potential for winemaking from phenotypic profiles, PLoS One, 8 (7). e66523. [COBISS.SI-ID 10005844]

UČNI NAČRT PREDMETA / COURSE SYLLABUS	
Predmet:	Biološke teme za nebiologe
Course title:	Topics in Biology for Non-Biologists

Študijski program in stopnja Study programme and level	Študijska smer Study field	Letnik Academic year	Semester Semester
Interdisciplinarni doktorski študijski program BIOZNANOSTI 3. stopnja	Bioinformatika	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

teoretični predmet / theoretical course

Univerzitetna koda predmeta / University course code:

Predavanja Lectures	Seminar Seminar	Vaje Tutorial	Klinične vaje work	Druge oblike študija	Samost. delo Individ. work	ECTS
10	30	/	/	10	75	5

Nosilec predmeta / Lecturer:

Nosilec: prof. dr. Marina Dermastia

Jeziki /
Languages:

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

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

Splošni pogoji za vpis na doktorski študij.

Prerequisites:

General conditions for enrolment in doctoral studies.

Vsebina:

Content (Syllabus outline):

Kjer bo le mogoče, bodo predpisane vsebine prilagojene in predstavljene v povezavi z osnovnimi področji vsakoletno vpisanih študentov.

V predmetu bodo študenti na primerih modelnih organizmov z vseh kraljestev spoznali celico kot strukturno in funkcionalno enoto vseh živih organizmov, s poudarkom na razlikah med prokariotskimi, rastlinskimi in živalskimi celicami. Razumeli bodo osnove molekulske biologije gena in osnovne energetske celične procese (dihanje, fotosinteza). Na osnovi skupnega evolucijskega izvora organizmov bo predstavljena uporabnost rezultatov raziskovanja modelnih organizmov pri razumevanju splošnih bioloških pojavov, ohranjanju dednine in ohranjanju metabolnih ter razvojnih poti.

Predstavljena bo organizacija rasti rastlin in živali, s poudarkom na evolucijski razvojni biologiji na osnovi izražanja genov in genske regulacije.

Študenti bodo spoznali tudi osnove ekologije.

Whenever possible, the contents will be adapted and presented in association with the knowledge backgrounds of students.

Suitable model organism from all kingdoms of living organisms will be selected in order to understand that cells are structural and functional units of all organisms. The differences between prokaryotic, plant and animal cells will be emphasized. The applicability of the model organism research for understanding of general biological phenomena, including common principles in genetics, metabolism and development.

The organization of the growth of plants and animals will be presented, with emphasize on the evolutionary developmental biology based on gene expression and gene regulation.

The principles of ecology will be also introduced.

Temeljni literatura in viri / Readings:

- Spellman F. R. Biology for Nonbiologists, Government Institutes; 1 edition (2007), 292 strani, ISBN-10: 0865874212

- Dermastia M. Pogled v rastline, Nacionalni inštitut za biologijo (2007), ISBN 978-961-90363-7-2, str. 1-76

- Alberts B. Molecular Biology of the Cell, Garland Science (2007); ISBN-10: 0815341067, izbrane vsebine iz knjige glede na področje predizobrazbe in zanimanje študentov v tekočem letniku

Cilji in kompetence:

Predmet je namenjen študentom, ki so končali drugostopenjske magistrske programe orientirane v fiziko, kemijo, matematiko, računalništvo ipd., z izraženim interesom, da povežejo svoje znanje z biološkimi disciplinami.

Izobraževalni cilji: Cilj predmeta je, da študenti razumejo koncepte biologije. Z usvojenim znanjem se bodo bolj zavedali pomena in motivov njim manj znanega biološkega področja.

Objectives and competences:

The course is intended for students who have completed any 2nd level masters related to physics, chemistry or mathematics, with an explicit interest in linking their knowledge with biological disciplines.

Educational aims are to understand the main concepts in biology. The gained knowledge will increase their awareness of the field of biology that is less familiar to them.

Predvideni študijski rezultati:

Intended learning outcomes:

Študenti se bodo s pridobljenim znanjem lahko enakopravno vključevali v znanstvene razprave s študenti z biološkim predznanjem v času študija in skupaj z njimi kasneje oblikovali interaktivno mrežo področnih sodelovanj.

With the gained knowledge, students will be able to equally participate on scientific discussions with students with previous biological education and together with them form interactive networks of cooperation between the fields.

Metode poučevanja in učenja:

Teoretična znanja v obliki interaktivnih predavanj s poudarkom na povezanosti biologije z drugimi naravoslovnimi znanostmi; vodeno samoučenje; razprave o specifičnih temah zbranih iz temeljnih študijskih virov ali dodatnih virov z aktualnimi tematikami in konzultacije pri pripravi in predstavitvi seminarske naloge iz izbranih preglednih vsebin v znanstveni literaturi.

Learning and teaching methods:

Interactive lectures with emphasize on the linkage of biology with other natural sciences, guided self-learning; discussions on specific selected themes; and consultation for preparation and presentation of seminar tasks from selected review contents in the scientific literature.

Načini ocenjevanja:

- Prisotnost pri kontaktnih urah
- Sprotna izdelava in oddaja krajših nalog
- Izdelava in predstavitev seminarja

Delež (v %) /
Weight (in %)

15 %
25 %
60 %

Assessment:

- Presence at contact hours
- Concurrent preparation and handing of shorter tasks
- Preparation and presentation of a seminar

Reference nosilca / Lecturer's references:

Marina Dermastia

1. MILJKOVIĆ, Dragana, STARE, Tjaša, MOZETIČ, Igor, PODPEČAN, Vid, PETEK, Marko, WITEK, Kamil, DERMASTIA, Marina, LAVRAČ, Nada, GRUDEN, Kristina. Signalling network construction for modelling plant defence response. *PloS one*, ISSN 1932-6203, 2012, 7(12) e51822-1e51822-18. [COBISS.SI-ID 26363431]
2. KOGOVŠEK, Polona, KLADNIK, Aleš, MLAKAR, Jana, TUŠEK-ŽNIDARIČ, Magda, DERMASTIA, Marina, RAVNIKAR, Maja, POMPE NOVAK, Maruša. Distribution of Potato virus Y in potato plant organs, tissues and cells. *Phytopathology*, ISSN 0031-949X. [Print ed.], 2011, 101(11): 1292-1300. [COBISS.SI-ID 2401359]
3. DERMASTIA, Marina, KLADNIK, Aleš, DOLENC KOCE, Jasna, CHOUREY, Prem S. A cellular study of teosinte *Zea mays* subsp. *parviglumis* (Poaceae) caryopsis development showing several processes conserved in maize. *Am. j. bot.*, 2009, 96(10):1798-1807. [COBISS.SI-ID 2075215]
4. VIDIC, Tatjana, GREILHUBER, J., VILHAR, Barbara, DERMASTIA, Marina. Selective significance of genome size in a plant community with heavy metal pollution. *Ecol. appl.*, 2009, 19(6): 1515-1521. [COBISS.SI-ID 2075471]
5. DOLENC KOCE, Jasna, ŠKONDRIČ, Siniša, BAČIČ, Martina, DERMASTIA, Marina, et al. Amounts of nuclear DNA in marine halophytes. *Aquatic botany*, ISSN 0304-3770. [Print ed.],

2008, 89(4): 385-389. [COBISS.SI-ID 1877327]

6. RAZINGER, Jaka, DERMASTIA, Marina, DOLENC KOCE, Jasna, ZRIMEC, Alexis. Oxidative stress in duckweed (*Lemna minor* L.) caused by short-term cadmium exposure. *Environmental pollution*, ISSN 0269-7491. [Print ed.], 2008, 153: 687-694. [COBISS.SI-ID 1850447]

UČNI NAČRT PREDMETA / COURSE SYLLABUS	
Predmet:	Računska biologija
Course title:	Computational Biology

Študijski program in stopnja Study programme and level	Študijska smer Study field	Letnik Academic year	Semester Semester
Interdisciplinarni doktorski študijski program BIOZNANOSTI 3. stopnja	Bioinformatika	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

teoretični predmet / theoretical course

Univerzitetna koda predmeta / University course code:

Predavanja Lectures	Seminar Seminar	Vaje Tutorial	Klinične vaje work	Druge oblike študija	Samost. delo Individ. work	ECTS
10	15	15	/	5	80	5

Nosilec predmeta / Lecturer:

Nosilec: prof. dr. Miha Mraz

Jeziki / Languages:

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

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

- Splošni pogoji za vpis na doktorski študij

Prerequisites:

- General prerequisites for the enrolment in the doctoral programme

Vsebina:

- Biološki sistemi kot preklopno procesni, pomnilni in oscilatorni gradniki.
- Modelirni pristopi za potrebe računske biologije: kvalitativno in kvantitativno modeliranje, deterministično in stohastično modeliranje, agentno modeliranje, razvoj novih pristopov k modeliranju.
- Kvalitativna in kvantitativna analiza bioloških sistemov (analiza stabilnosti, robustnosti, občutljivosti itd.).
- Avtomatizirano in računalniško podprto načrtovanje bioloških sistemov.
- Metode za vrednotenje parametrov, ki opisujejo dinamiko v bioloških sistemih.
- Principi modularnosti pri gradnji kompleksnejših bioloških sistemov.
- Povratna zanka v bioloških sistemih.

Content (Syllabus outline):

- Biological systems as information processing, memory and oscillatory structures.
- Modelling approaches: general approaches, differentiation of approaches (e.g. deterministic modelling, stochastic modelling, agent based modelling), establishment of computational models.
- Qualitative and quantitative analysis of biological systems; stability, sensitivity and robustness.
- Computational design of biological systems: automatic design, computer aided design.
- Parameter estimation techniques, tuning the modelled behaviour with the experimental behaviour.
- Biological systems as information processing platforms, logic gates, oscillators, complex information processing systems.
- Feedback loop in biological systems.

Temeljni literatura in viri / Readings:

- U.Alon: Introduction to systems biology, Hal/CRC, 2006
- Control Theory and systems biology (Ur. A.Iglesias, B.P.Ingalss), MIT Press 2010
- B.Palsson: Systems biology - simulation of dynamic network systems, Cambridge University Press, 2011

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

Cilji in kompetence:**Objectives and competences:**

Poznavanje metod modeliranja bioloških procesov. Razumevanje in uporaba rezultatov dobljenih z analizo modela. Sposobnost samostojne gradnje enostavnih modelov. Sposobnost načrtovanja novih bioloških sistemov z uporabo računalniških pristopov.

Overview of methods for modelling of biological processes. Understanding and use of model analysis results. Ability to design and implement simple models. Ability to design novel biological systems with computational approaches.

Predvideni študijski rezultati:

Znanje in razumevanje računalniškega modeliranja, analize in načrtovanja bioloških sistemov.

Intended learning outcomes:

Knowledge and understanding of computational modelling, analysis and design of biological systems.

Metode poučevanja in učenja:

Predavanja, seminarske naloge in praktične vaje iz uporabe programske opreme.

Learning and teaching methods:

Lectures, seminars, and hands-on exercises with various computer software.

Načini ocenjevanja:

Domače naloge	Delež (v %) / Weight (in %)	50 %
Seminarsko delo		50 %

Assessment:

Homework assignments
Seminal work

Reference nosilca / izvajalcev / Lecturer's references:

Miha Mraz:

1. MOŠKON, Miha, MRAZ, Miha. Systematic approach to computational design of gene regulatory networks with information processing capabilities. *IEEE/ACM transactions on computational biology and bioinformatics*, ISSN 1545-5963. [Print ed.], 2014, 11(1):431-440. [COBISS.SI-ID 10323028]
2. PETRONI, Mattia, ZIMIC, Nikolaj, MRAZ, Miha, MOŠKON, Miha. Stochastic simulation algorithm for gene regulatory networks with multiple binding sites. *Journal of computational biology*, ISSN 1557-8666. [Online ed.], 2014, 21: 1-9. [COBISS.SI-ID 10671956]
3. STRAŽAR, Martin, MRAZ, Miha, ZIMIC, Nikolaj, MOŠKON, Miha. An adaptive genetic algorithm for parameter estimation of biological oscillator models to achieve target quantitative system response. *Natural computing*, ISSN 1567-7818, Mar. 2014, 13(1): 119-127. [COBISS.SI-ID 9950804]
4. MOŠKON, Miha, NOVAK, Štefan, MEDEOT, Marino, LEBAR BAJEC, Iztok, ZIMIC, Nikolaj, MRAZ, Miha. Solving the logistic problems with optimal resource assignment using fuzzy logic methods. *Journal of advanced transportation*, ISSN 0197-6729, June 2013, 47(4): 447-460. [COBISS.SI-ID 8198740]
5. MOŠKON, Miha, MRAZ, Miha. Modelling and analysing the information processing capabilities of simple biological systems. *Mathematical modelling and analysis*, ISSN 1392-6292, Sep. 2012, 17(4): 467-484. [COBISS.SI-ID 9330004]
6. JANEŽ, Miha, PEČAR, Primož, MRAZ, Miha. Layout design of manufacturable quantum-dot cellular automata. *Microelectronics journal*, ISSN 0959-8324. [Print ed.], Jul. 2012, 43(7): 501-513. [COBISS.SI-ID 9040468]

UČNI NAČRT PREDMETA / COURSE SYLLABUS	
Predmet:	Zajem in računalniško podprta analiza slik
Course title:	Image Acquisition and Computer-Assisted Analysis

Študijski program in stopnja Study programme and level	Študijska smer Study field	Letnik Academic year	Semester Semester
Interdisciplinarni doktorski študijski program BIOZNANOSTI 3. stopnja	Bioinformatika	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

teoretični predmet / theoretical course

Univerzitetna koda predmeta / University course code:

Predavanja Lectures	Seminar Seminar	Vaje Tutorial	Klinične vaje work	Druge oblike študija	Samost. delo Individ. work	ECTS
10	/	20	/	/	95	5

Nosilec predmeta / Lecturer:

Nosilec: prof. dr. Franjo Pernuš

Jeziki /
Languages:

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

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

Splošni pogoji za vpis na doktorski študij.

Prerequisites:

General conditions for enrolment in doctoral studies.

Vsebina:

Content (Syllabus outline):

- Zajemanje digitalnih slik: optično-zaznavne lastnosti človeškega vida, vrste in definicije digitalnih slik, predstavitev barv in barvni prostori, parametri kakovosti, tehnologije zajemanja vizualnih podatkov na makro in mikroskopski ravni z digitalnimi fotoaparati in kamerami, osnove rentgenskega slikanja, računalniške tomografije, magnetne resonance in ultrazvoka, razumevanje vsebine slik.
- Prikazovanje, manipulacija in zgoščevanje sivinskih, barvnih in večdimenzionalnih slik
- Analiza slik: upravljanje, razgradnja na osnovi robov, širjenja, združevanja in razdruževanja področij, opisovanje s poravnavo modelov, predstavitev in štetje objektov, opisovanje in merjenje mej in področij, analiza rasti in gibanja.
- Načrtovanje in uporaba slikovnih informacijskih sistemov: programska orodja za pridobivanje in analizo slik, načrtovanje, integracija in uporaba slikovnih informacijskih sistemov v biotehniških raziskavah in aplikacijah (mikroskopija, kontrola kakovosti živil, spremljanje rasti in gibanja živali, rastlin in mikroorganizmov, itn).

- Acquisition of digital images: optical and perceptual characteristics of human vision, types and definitions of digital images and videos, color representation and color spaces, quality parameters, technologies for image acquisition with digital photography and cameras for visible and invisible light, on macro- and microscopic levels, fundamentals of radiographic imaging, computed tomography, magnetic resonance imaging and ultrasound, image content understanding.
- Visualization, manipulation and compression of grayscale, color and multidimensional images.
- Image analysis: thresholding, edge based segmentation, region growing, merging and splitting, model based description, object representation and counting, border and region description and measurement, growth and motion analysis.
- Design and implementation of imaging information systems: software tools for image acquisition and analysis, design, integration and implementation of imaging information systems in bioengineering research and applications (microscopy, food quality control, monitoring of growth and motion of animals, plants and microorganisms, etc.).

Temeljni literatura in viri / Readings:

- Boštjan Likar. Biomedicinska slikovna informatika in diagnostika, 1. izdaja, Založba FE in FRI, Ljubljana: Fakulteta za elektrotehniko, 2008.
- John C. Russ. The Image Processing Handbook, 6th edition, CRC Press, 2011.
- Jerry L. Prince, Jonathan Links. Medical Imaging Signals and Systems, 2nd Revised edition, Prentice Hall, 2014
- Erik Reinhard, Erum Arif Khan, Ahmet Oguz Akyüz, Garrett M. Johnson. Color Imaging: Fundamentals and Applications, A K Peters/CRC Press, 2008.

Cilji in kompetence:

Seznani študente s področjem zajemanja in računalniško podprte analize biomedicinskih slik; posredovati znanje o sodobnih postopkih za zajemanje biomedicinskih slik, za njihovo prikazovanje, manipulacijo, zgoščevanje, ter kvantitativno analizo; seznanjanje s pristopi k načrtovanju in uporabi slikovnih informacijskih sistemov v biotehniških raziskavah in aplikacijah.

Objectives and competences:

To provide an introduction to biomedical image acquisition, computer-assisted image analysis; to develop basic understanding of digital image processing, restoration, calibration and quantitative analysis; and to develop understanding of image processing and analysis methods, which enable objective and quantitative evaluation of the environment, space, objects and subjects in bioengineering.

Predvideni študijski rezultati:

Intended learning outcomes:

Študenti, ki bodo izbrali ta predmet, bodo pridobili znanja o zajemanju digitalnih slik; znali prikazovati, manipulirati in zgoščevati slike; znali izbrati in uporabljati osnovne postopke digitalne analize slik; znali načrtovati in uporabljati slikovne informacijske sisteme v bioznanostih.

Students completing this course will gain a fundamental understanding of biomedical image acquisition and computer-assisted image processing and analysis; will gain hands-on knowledge of applications of image processing and analysis and be able to apply existing image processing algorithms to analyse images from the field of biosciences.

Metode poučevanja in učenja:

Teoretične osnove in širši pregled nad področjem predmeta študentje pridobijo na predavanjih, praktična znanja in izkušnje pa pri laboratorijskih vajah in izdelavi izbrane projektne ali seminarske naloge z njihovega področja zanimanja.

Learning and teaching methods:

An overview of the area and basic theory will be provided through lectures, while practical knowledge and experience will be provided through lab work and projects or seminars, selected by the students to best match their specific interests.

Načini ocenjevanja:

Pisno poročilo o projektu
Predstavitev (PPT) projekta

Delež (v %) /

Weight (in %)

Assessment:

Written report on assigned project
Oral (PPT) presentation

Reference nosilca / izvajalcev / Lecturer's references:

Franjo Pernuš

Uroš Mitrović, Žiga Špiclin, **Boštjan Likar** in **Franjo Pernuš**. 3D-2D registration of cerebral angiograms: a method and evaluation on clinical images. IEEE Transactions on Medical Imaging, 32(8):1550-1563, 2013

Jaka Katrašnik, **Franjo Pernuš** in **Boštjan Likar**. A method for characterizing illumination systems for hyperspectral imaging. Optics Express, 21(4):4841-4853, 2013

Darko Štern, Vesna Njagulj, **Boštjan Likar**, **Franjo Pernuš** in Tomaž Vrtovec. Quantitative vertebral morphometry based on parametric modeling of vertebral bodies in 3D Osteoporosis International, 24(4):1357-1368, 2013

Peter Usenik, Miran Bürmen, Aleš Fidler, **Franjo Pernuš** in **Boštjan Likar**. Automated classification and visualization of healthy and diseased hard dental tissues by near-infrared hyperspectral imaging. Applied Spectroscopy, 66(9):1067-1074, 2012

Primož Markelj, Dejan Tomaževič, **Boštjan Likar** in **Franjo Pernuš**. A review of 3D/2D registration methods for image-guided interventions. Medical Image Analysis, 16(3):642-661, 2012

Peter Usenik, Tomaž Vrtovec, **Franjo Pernuš** in **Boštjan Likar**. Automated tracking and analysis of phospholipid vesicle contours in phase contrast microscopy images. Medical & Biological

