BIOINFORMATIKA – TEORETIČNI PREDMETI

UČNI NAČRT PREDMETA/COURSE SYLLABUS

Predmet:	Bioinformacijska orodja in podatkovne zbirke
Course title:	Bioinformatics Tools and Databases

Študijski programi in stopnja	Študijska smer	Letnik	Semestri
Bioznanosti, tretja stopnja, doktorski	bioinformatika		Celoletni

Univerzitetna koda predmeta/University course code:	3764

Predavanja	Seminar	Vaje	Klinične vaje	Druge oblike študija	Samostojno delo	ECTS
20	40	0	0	0	190	10

Nosilec predmeta/Lecturer:	Jernej Jakše

Izvajalci predavanj:	Jernej Jakše, Roman Jerala, Tanja Kunej, Uroš Petrovič
Izvajalci seminarjev:	
Izvajalci vaj:	
Izvajalci kliničnih vaj:	
Izvajalci drugih oblik:	
Izvajalci praktičnega usposabljanja:	

Vrsta predmeta/Course type:	teoretični/theoretical

Jeziki/Languages:	Predavanja/Lectures:	Angleščina, Slovenščina
	Vaje/Tutorial:	Angleščina, Slovenščina

Pogoji za vključitev v delo oz. za opravljanje študijskih obveznosti:	Prerequisites:
Splošni pogoji za vpis na doktorski študij.	General conditions for enrolment in doctoral studies.

Vsebina:	Content (Syllabus outline):
- Bioinformacijske podatkovne zbirke: zaporedja nukleinskih kislin, proteinov, strukturne podatkovne zbirke, bibliografske podatkovne zbirke. Orodja za analizo zaporedij in struktur.	- 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.
- Genomski projekti modelnih organizmov, primerjalna genomika, določevanje genov in regulatornih regij v genomih, SNP analize, genske mreže.	- Bioinformatics tools in transcriptomics and high-throughput genetics.
- Orodja v transkriptomiki in visoko-zmogljivostni genetiki.	- Bio-informatics tools in proteomics and interactomics.
- Bioinformacijska orodja v proteomiki in interaktomiki.	- Applications: Bioinformatics in environmental genomics, pharmacogenomics.
- Aplikacije: bioinformatika v okoljski genomiki, farmakogenomiki.	- Ontologies and knowledge databases in bioinformatics.
- Ontologije in zbirke znanj v bioinformatiki.	- Bioinformatics approaches in chemogenomics.
- Bioinformacijski pristopi v kemogenomiki.	- Project work with specific software tools during the lectures and within seminar.
- Projektno delo s specifičnimi programskimi orodji med predavanji in v okviru seminarske naloge.	

Temeljna 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. - pregledni in originalni znanstveni članki s širšega področja bioinformatike.

Cilji in kompetence:	Objectives and competences:
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.	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:	Intended learning outcomes:
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.	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:	Learning and teaching methods:
Predavanja, praktične vaje z računalniki, samostojna priprava seminarjev in predstavitev.	Lectures, seminars, project workshops, practical work with computers.

V okviru seminarske naloge bo vsak študent z uporabo bioinformacijskih orodij rešil praktični problem in ga predstavil pisno v obliki znanstvenega članka in ustno v obliki dvajsetminutne predstavitve.	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 writing in the form of a scientific paper and orally in the form of a twenty-minute presentation.

Načini ocenjevanja:	Delež/Weight	Assessment:
Seminar s predstavitvijo	50,00 %	Seminar with public presentation
Pisno preverjanje znanja	50,00 %	Written exam

Reference nosilca/Lecturer's references:

Gregor Anderluh:

1. KOVAČIČ, Lidija, PAULIČ, Nejc, LEONARDI, Adrijana, HODNIK, Vesna, ANDERLUH, Gregor, PODLESEK, Zdravko, ŽGUR-BERTOK, Darja, KRIŽAJ, Igor, BUTALA, Matej. Structural insight into LexARecA interaction. Nucleic acids research, ISSN 0305-1048, 2013, vol. 42, issue 21, str. 9901-9910, doi: 10.1093/nar/gkt744. [COBISS.SI-ID 26953767]

2. GILBERT, Robert J., MIKELJ, Miha, DALLA SERRA, Mauro, FROELICH, Christopher J., ANDERLUH, Gregor. Effects of MACPF/CDC proteins on lipid membranes. Cellular and molecular life sciences, ISSN 1420-682X, 2013, vol. 70, issue 12, str. 2083-2098, doi: 10.1007/s00018-012-1153-8. [COBISS.SI-ID 5056026]

3. YACHI, Rieko, UCHIDA, Yasunori, BALAKRISHNA, Bhat Hema, ANDERLUH, Gregor, KOBAYASHI, Toshihide, TAGUCHI, Tomohiko, ARAI, Hiroyuki. Subcellular localization of sphingomyelin revealed by two toxin-based probes in mammalian cells : Elektronski vir. Genes to cells, ISSN 1365-2443, 2012, vol. 17, iss. 8, str. 720-727, ilustr., doi: 10.1111/j.1365-2443.2012.01621.x. [COBISS.SI-ID 5025562]

4. CONRADO, Robert J., LEBAR, Tina, TURNŠEK, Jernej, TOMŠIČ, Nejc, AVBELJ, Monika, GABER, Rok, KOPRIVNJAK, Tomaž, MORI, Jerneja, GLAVNIK, Vesna, VOVK, Irena, BENČINA, Mojca, HODNIK, Vesna, ANDERLUH, Gregor, JERALA, Roman, et al. DNA-guided assembly of biosynthetic pathways promotes improved catalytic efficiency. Nucleic acids research, ISSN 0305-1048, 2012, vol. 40, no. 4, str. 1879-1889, ilustr. http://nar.oxfordjournals.org/content/early/2011/10/22/nar.gkr888.full.pdf+html, doi: 10.1093/nar/gkr888. [COBISS.SI-ID 4824602]

5. MATTIAZZI, Mojca, SUN, Yidi, WOLINSKI, Heimo, BAVDEK, Andrej, PETAN, Toni, ANDERLUH, Gregor, KOHLWEIN, Sepp D., DRUBIN, David, KRIŽAJ, Igor, PETROVIČ, Uroš. A neurotoxic phospholipase A [sub] 2 impairs yeast amphiphysin activity and reduces endocytosis. PloS one, ISSN 1932-6203, 2012, vol. 7, iss. 7, str. 1-13, e40931, doi: 10.1371/journal.pone.0040931. [COBISS.SI-ID 5026074]

6. ŠKEDELJ, Veronika, ARSOVSKA, Emilija, TOMAŠIČ, Tihomir, KROFLIČ, Ana, HODNIK, Vesna, HRAST, Martina, BEŠTER-ROGAČ, Marija, ANDERLUH, Gregor, GOBEC, Stanislav, BOSTOCK, Julieanne M., CHOPRA, Ian, O'NEILL, Alex, RANDALL, Christopher, ZEGA, Anamarija. 6-arylpyrido[2,3-d]pyrimidines as novel ATP-competitive inhibitors of bacterial D-alanine: D-alanine ligase. PloS one, ISSN 1932-6203, 2012, vol. 7, no. 8, str. e39922-1-e39922-14, ilustr. http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0039922. [COBISS.SI-ID 3286897]

7. BUTALA, Matej, KLOSE, Daniel, HODNIK, Vesna, REMS, Ana, PODLESEK, Zdravko, KLARE, Johann P., ANDERLUH, Gregor, BUSBY, Steve J. W., STEINHOFF, Heinz-Jürgen, ŽGUR-BERTOK, Darja. Interconversion between bound and free conformations of LexA orchestrates the bacterial SOS response. Nucleic acids research, ISSN 0305-1048, 2011, vol. 39, issue 15, str. 6546-6557. http://dx.doi.org/10.1093/nar/gkr265, doi: 10.1093/nar/gkr265. [COBISS.SI-ID 2368847]

8. PRAPER, Tilen, KLADNIK, Aleš, ANDERLUH, Gregor, et al. Perforin activity at membranes leads to invaginations and vesicle formation. Proceedings of the National Academy of Sciences of the United States of America, ISSN 0027-8424, 2011, vol. 108, no. 52, str. 21016-21021. http://dx.doi.org/10.1073/pnas.1107473108, doi: 10.1073/pnas.1107473108. [COBISS.SI-ID 2493519]

9. BAKRAČ, Biserka, KLADNIK, Aleš, MAČEK, Peter, MCHAFFIE, Gavin, WERNER, Andreas, LAKEY, Jeremy H., ANDERLUH, Gregor. A toxin-based probe reveals cytoplasmic exposure of golgi sphingomyelin. The Journal of biological chemistry, ISSN 0021-9258, 2010, issue 29, vol. 285, str. 22186-22195.

http://www.jbc.org/doi/10.1074/jbc.M110.105122, doi: 10.1074/jbc.M110.105122. [COBISS.SI-ID 2219855]

10. OTTMANN, Christian, LUBERACKI, Borries, KÜFNER, Isabell, KOCH, Wolfgang, BRUNNER, Frédéric, WEYAND, Michael, MATTINEN, Laura, PIRHONEN, Minna (umetnik), ANDERLUH, Gregor, SEITZ, Hanns Ulrich, NÜRNBERGER, Thorsten, OECKING, Claudia. A common toxin fold mediates microbial attack and plant defense. Proceedings of the National Academy of Sciences of the United States of America, ISSN 0027-8424, 2009, no. 25, vol. 106, str. 10359-10364. [COBISS.SI-ID 2010191]

Roman Jerala:

1. GRADIŠAR, Helena, BOŽIČ, Sabina, DOLES, Tibor, VENGUST, Damjan, HAFNER BRATKOVIČ, Iva, MERTELJ, Alenka, WEBB, Ben, ŠALI, Andrej, KLAVŽAR, Sandi, JERALA, Roman. Design of a single-chain polypeptide tetrahedron assembled from coiled-coil segments. Nature chemical biology, ISSN 1552-4450, 2013, vol. 9, issue 6, str. 362-366, doi: 10.1038/nCHeMBIO.1248. [COBISS.SI-ID 5222682

2. FEKONJA, Ota, AVBELJ, Monika, JERALA, Roman. Suppression of TLR signaling by targeting TIR domain-containing proteins. Current protein and peptide science, ISSN 1389-2037, 2012, vol. 13, no. 8, str. 776-788, doi: 10.2174/1389203711213080007. [COBISS.SI-ID 5167898]

3. MANČEK KEBER, Mateja, BENČINA, Mojca, JAPELJ, Boštjan, PANTER, Gabriela, ANDRÄ, Jörg, BRANDENBURG, Klaus, TRIANTAFILOU, Martha, TRIANTAFILOU, Kathy, JERALA, Roman. MARCKS as a negative regulator of lipopolysaccharide signaling. The journal of immunology, ISSN 0022-1767, 2012, vol. 188, no. 8, str. 3893-3902. http://www.jimmunol.org/content/early/2012/03/16/jimmunol.1003605.abstract, doi: 10.4049/jimmunol.1003605. [COBISS.SI-ID 4930586]

4. CONRADO, Robert J., LEBAR, Tina, TURNŠEK, Jernej, TOMŠIČ, Nejc, AVBELJ, Monika, GABER, Rok, KOPRIVNJAK, Tomaž, MORI, Jerneja, GLAVNIK, Vesna, VOVK, Irena, BENČINA, Mojca, HODNIK, Vesna, ANDERLUH, Gregor, JERALA, Roman, et al. DNA-guided assembly of biosynthetic pathways promotes improved catalytic efficiency. Nucleic acids research, ISSN 0305-1048, 2012, vol. 40, no. 4, str. 1879-1889, ilustr. http://nar.oxfordjournals.org/content/early/2011/10/22/nar.gkr888.full.pdf+html, doi: 10.1093/nar/gkr888. [COBISS.SI-ID 4824602]

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6. PANTER, Gabriela, JERALA, Roman. Ectodomain of the toll-like receptor 4 prevents constitutive receptor activation. The Journal of biological chemistry, ISSN 0021-9258, 2011, vol. 286, no. 26, str. 23334-23344, doi: 10.1074/jbc.M110.205419. [COBISS.SI-ID 4652570]

Tanja Kunej:

1. JEVŠINEK SKOK, Daša, GODNIČ, Irena, ZORC, Minja, HORVAT, Simon, DOVČ, Peter, KOVAČ, Milena, KUNEJ, Tanja. Genome-wide in silico screening for microRNA genetic variability in livestock species. Animal genetics, ISSN 0268-9146, 2013, vol. 44, no. 6, str. 669-677. http://onlinelibrary.wiley.com/doi/10.1111/age.12072/pdf, doi: 10.1111/age.12072. [COBISS.SI-ID 3249544]

2. CANNISTRACI, C.V., OGOREVC, Jernej, ZORC, Minja, RAVASI, Timothy, DOVČ, Peter, KUNEJ, Tanja. Pivotal role of the muscle-contraction pathway in cryptorchidism and evidence for genomic connections with cardiomyopathy pathways in RASopathies. BMC medical genomics, ISSN 1755-8794, 2013, vol. 6, no. 5, str. 1-16. http://www.biomedcentral.com/content/pdf/1755-8794-6-5.pdf, doi: 10.1186/1755-8794-6-5. [COBISS.SI-ID 3189640]

3. GODNIČ, Irena, ZORC, Minja, JEVŠINEK SKOK, Daša, CALIN, George Adrian, HORVAT, Simon, DOVČ, Peter, KOVAČ, Milena, KUNEJ, Tanja. Genome-wide and species-wide in silico screening for intragenic microRNAs in human, mouse and chicken. PloS one, ISSN 1932-6203, 2013, vol. 8, no. 6, str. 1-14, e-65165. http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0065165, doi: 10.1371/journal.pone.0065165. [COBISS.SI-ID 3234696]

4. ZORC, Minja, JEVŠINEK SKOK, Daša, GODNIČ, Irena, CALIN, George Adrian, HORVAT, Simon, JIANG, Zhihua, DOVČ, Peter, KUNEJ, Tanja. Catalog of MicroRNA seed polymorphisms in vertebrates. PloS one,

ISSN 1932-6203, 2012, vol. 7, no. 1, str. 1-8, e30737. http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0030737, doi: 10.1371/journal.pone.0030737. [COBISS.SI-ID 3003528]

5. OGOREVC, Jernej, DOVČ, Peter, KUNEJ, Tanja. Comparative genomics approach to identify candidate genetic loci for male fertility. Reproduction in domestic animals, ISSN 0936-6768, 2011, vol. 46, str. 229-239, doi: 10.1111/j.1439-0531.2010.01648.x. [COBISS.SI-ID 2645384]

6. OGOREVC, Jernej, KUNEJ, Tanja, RAZPET, Andrej, DOVČ, Peter. Database of cattle candidate genes and genetic markers for milk production and mastitis. Animal genetics, ISSN 0268-9146, 2009, vol. 40, str. 832-851, doi: 10.1111/j.1365-2052.2009.01921.x. [COBISS.SI-ID 2462344]

Uroš Petrovič:

1. MATTIAZZI, Mojca, KAFERLE, Petra, TOPLAK, Alenka, TREBŠE, Polonca, PETROVIČ, Uroš. Determination of toxicity of neonicotinoids on the genome level using chemogenomics in yeast. Chemosphere, ISSN 0045-6535. [Print ed.], [in press] 2013, 6 str., doi: 10.1016/j.chemosphere.2013.10.063. [COBISS.SI-ID 27258407]

2. MATTIAZZI, Mojca, SUN, Yidi, WOLINSKI, Heimo, BAVDEK, Andrej, PETAN, Toni, ANDERLUH, Gregor, KOHLWEIN, Sepp D., DRUBIN, David, KRIŽAJ, Igor, PETROVIČ, Uroš. A neurotoxic phospholipase A [sub] 2 impairs yeast amphiphysin activity and reduces endocytosis. PloS one, ISSN 1932-6203, 2012, vol. 7, iss. 7, str. 1-13, e40931, doi: 10.1371/journal.pone.0040931. [COBISS.SI-ID 5026074]

3. MATTIAZZI, Mojca, CURK, Tomaž, KRIŽAJ, Igor, ZUPAN, Blaž, PETROVIČ, Uroš. Inference of the molecular mechanism of action from genetic interaction and gene expression data. Omics. , ISSN 1536-2310, 2010, vol. 14, no. 4, 1str. 357-367, doi: 10.1089/omi.2009.0144. [COBISS.SI-ID 23789607]

4. MATTIAZZI, Mojca, JAMBHEKAR, Ashwini, KAFERLE, Petra, DERISI, Joseph, KRIŽAJ, Igor, PETROVIČ, Uroš. Genetic interactions between a phospholipase A[sub]2 and the Rim101 pathway components in S. cerevisiae reveal a role for this pathway in response to changes in membrane composition and shape. Molecular genetics and genomics, ISSN 1617-4615, 2010, vol. 283, no. 6, str. 519-530, doi: 10.1007/s00438-010-0533-8. [COBISS.SI-ID 23541287]

5. CURK, Tomaž, PETROVIČ, Uroš, SHAULSKY, Gad, ZUPAN, Blaž. Rule-based clustering for gene promoter structure discovery. Methods of information in medicine, ISSN 0026-1270, 2009, vol. 48, no. 3, str. 229-235. http://eprints.fri.uni-lj.si/897/. [COBISS.SI-ID 22605095]

6. WOLINSKI, Heimo, PETROVIČ, Uroš, MATTIAZZI, Mojca, PETSCHNIGG, Julia, HEISE, Bettina, NATTER, Klaus, KOHLWEIN, Sepp D. Imaging-based live cell yeast screen identifies novel factors involved in peroxisome assembly. Journal of proteome research, ISSN 1535-3893, 2009, vol. 8, no. 1, str. 20-27. [COBISS.SI-ID 22360871]

UČNI NAČRT PREDMETA/COURSE SYLLABUS

Predmet:	Uvod v znanost o podatkih
Course title:	Introduction to data science

Študijski programi in stopnja	Študijska smer	Letnik	Semestri
Bioznanosti, tretja stopnja, doktorski	bioinformatika		Celoletni

Univerzitetna koda predmeta/University course code:	3948

Predavanja	Seminar	Vaje	Klinične vaje	Druge oblike študija	Samostojno delo	ECTS
10	0	20	0	0	95	5

Nosilec predmeta/Lecturer:	Blaž Zupan

Izvajalci predavanj:	Janez Demšar, Blaž Zupan
Izvajalci seminarjev:	
Izvajalci vaj:	
Izvajalci kliničnih vaj:	
Izvajalci drugih oblik:	
Izvajalci praktičnega usposabljanja:	

Vrsta predmeta/Course type:	teoretični/theoretical course

Jeziki/Languages:	Predavanja/Lectures:	Slovenščina
	Vaje/Tutorial:	Slovenščina

Pogoji za vključitev v delo oz. za opravljanje študijskih obveznosti:	Prerequisites:
splošni pogoji za vpis na doktorski študij	general conditions for enrollment into doctoral studies

Vsebina:	Content (Syllabus outline):
1. Uvod v vizualno programiranje in razvoj shem za podatkovno analitiko. Branje podatkov, vizualizacija, izbor. Razsevni diagrami, izbor projekcije podatkov. 2. Klasifikacija. Klasifikacijska drevesa. Ocenjevanje napovedne točnosti (klasifikacijska točnost, AUC). Pregled ostalih metod, vključno z logistično regresijo, SVM in naključnimi gozdovi. Statistična primerjava klasifikacijskih metod.	1. Introduction to visual programming and data mining workflows. Data input, visualization, data selection and interactive data exploration. Scatterplot visualization, choice of projection. 2. Classification. Classification trees. Confusion matrix. Scoring of classification models. Classification accuracy and AUC. Data sampling, training and test sets. Cross-validation. A

3. Regresija. Metoda linearne in polinomske regresije. Vpliv regularizacije na uspešnost napovedi na učni in testni množici. Določanje parametrov učnih algoritmov.	glimpse into logistic regression, random forests, and SVM. Statistical comparison of classifiers.
4. Razvrščanje v skupine. Tehnika hierarhičnega razvrščanja v skupine, metoda voditeljev in metoda DBSCAN. Računske in prostorske kompleksnosti posameznih metod.	3. Regression. Linear and polynomial regression. Regularization. Effects of regularization on accuracy in training and test sets. Parameter search. Other regression techniques (random forests).
5. Projekcije podatkov. Metoda glavnih komponent, večrazredno lestvičenje in metoda TSNE. Analiza nestrukturiranih podatkovnih virov, kot so slike in zaporedja. Vložitev objektov v vektorskih prostor. Globoki modeli.	4. Clustering. Hierarchical clustering. Explorative data analysis with clustering and data projections. k-means clustering. DBSCAN clustering. Time and space complexity. Cluster scoring and selection of number of clusters. 5. Data projections. Principal component analysis. Multi-dimensional scaling. TSNE. Analysis of unstructured data, like images and sequences. Data embedding. Deep models.

Temeljna literatura in viri/Readings:
Video tečaji za programski paket Orange na YouTube-u (http://bit.ly/21E8Vt8). Delovna skripta Zupan B, Demšar J: Introduction to Data Science.

Cilji in kompetence:	Objectives and competences:
Cilj predmeta je spoznati osnovne tehnike strojnega učenja in odkrivanja znanj iz podatkov ternjihovo uporabo v biomedicini. Tehnike bodo predstavljene intuitivno preko praktičnega dela z orodjem za podatkovno rudarjenje; tečaj ne bo vključeval predstavitve matematičnih oziroma formalnih podlag za algoritme. Po uspešnem zaključku predmeta bodo študenti znali urediti in z osnovnimi tehnikami podatkovnega rudarjenja analizati svoje podatke. Tehnike bodo spoznali v obsegu, ki jim bo olajšal komunikacijo s statistiki in eksperti s področja znanosti o podatkih.	The course will familiarize graduate students with basic techniques in machine learning and data mining and will illustrate their utility on a range of case studies from biomedicine. Teaching will present data mining techiques on the intuitive level, and will not venture into mathematical foundations. After completing the course, students should be able to gain insight into their own data, access and use key public bioinformatics databases, and creatively collaborate with statisticians and expert bioinformaticians on advanced data analysis projects.

Predvideni študijski rezultati:	Intended learning outcomes:
Znanje in razumevanje: Poznavanje osnovnih tehnik s področja znanosti o podatkih in analize biomedicinskih podatkov. Konstrukcija shem za podatkovno analitiko. Razumevanje ustreznosti posameznih postopkov v podatkovnem rudarjenju za izbran problem oziroma podatkovni nabor. **Uporaba:** Predmet bo potekal praktično, v obliki delavnice; študenti bodo med spoznavanjem metod reševali probleme iz analitike podatkov iz biomedicine. Pridobljena znanja bodo po zaključku predmeta lahko uporabili pri svojem raziskovalnem delu.	**Knowledge and understanding:** Understanding of basic data science methods and their utility on analysis of biomedical data sets. Design of data mining workflows. Understanding of which type of data mining is appropriate for specific data analysis problem. **Application:** The course will be carried out as a hands-on tutorial; students will apply data mining procedures on real data sets. They will gain knowledge on application of data analytics methods in their own research. **Reflection:** Understanding of basics of analytical thinking.

Refleksija: Spoznavanje osnov algoritmičnega razmišljanja.	Transferable skills: Understanding and use of visual programming and data analysis workflows.
Prenosljive spretnosti: Poznavanje in učinkovita uporaba vizualnega programiranje in konstrukcije shem za podatkovno analitiko.	

Metode poučevanja in učenja:	Learning and teaching methods:
Predavanja bodo izvedena v obliki praktičnih delavnic. Študenti bodo na predavanjih spoznavali tehnike podatkovnega rudarjenja preko praktične uporabe orodja Orange (http://orange.biolab.si), ki za razvoj shem podatkovne analitike uporablja vizualno programiranje.	This is a hands-on workshop style course. The students will learn about data mining procedures through designing data analysis workflows in a visual programming environment Orange (http://orange.biolab.si).

Načini ocenjevanja:	Delež/Weight	Assessment:
Sprotno preverjanje (domače naloge, kolokviji in projektno delo). Ocene: 6-10 pozitivno, 1-5 negativno (v skladu s Statutom UL)	100,00 %	Continuing work (homeworks) Grading: 6-10 pass, 1-5 fail.

Reference nosilca/Lecturer's references:

Blaž Zupan
1. Zitnik M, Zupan B (2016) Jumping across biomedical contexts using compressive data fusion, *Bioinformatics* 15;32(12):i90-i100.
2. Li CL, Santhanam B, Webb AN, Zupan B, Shaulsky G (2016) Gene discovery by chemical mutagenesis and whole-genome sequencing in Dictyostelium, *Genome Res* 26(9): i90-i100.
3. Stražar M, Žitnik M, Zupan B, Ule J, Curk T (2016) Orthogonal matrix factorization enables integrative analysis of multiple RNA binding proteins, *Bioinformatics* 32(10): 1527-35.
4. Zitnik M, Nam EA, Dinh C, Kuspa A, Shaulsky G, Zupan B (2015) Gene prioritization by compressive data fusion and chaining, *PLoS Computational Biology* 11(10):e1004552.
5. Staric A, Demsar J, Zupan B (2015) Concurrent software architectures for exploratory data analysis. *WIREs Data Mining and Knowledge Discovery* 5(4):165-180.
6. Zitnik M, Zupan B (2015) Gene network inference by fusing data from diverse distributions. *Bioinformatics* 31(12):i230-i239.

Janez Demšar
1. Hočevar T, Demšar J (2017) Combinatorial algorithm for counting small induced graphs and orbits. *PloS One* 12(2): 1-17.
2. Corani G, Benavoli A, Demšar J, Mangili F, Zaffalon M (2017) Statistical comparison of classifiers through Bayesian hierarchical modelling. *Machine Learning* 1-21.
3. Žabkar J, Bratko I, Demšar J (2016) Extracting qualitative relations from categorical data. *Artificial Intelligence* 239:54-69.
4. Hočevar T, Demšar J (2016) Computation of graphlet orbits for nodes and edges in sparse graphs. *Journal of Statistical Software* 71(10):1-24.
5. Staric A, Demsar J, Zupan B (2015) Concurrent software architectures for exploratory data analysis. *WIREs Data Mining and Knowledge Discovery* 5(4):165-180.

Demsar J, Curk T, Erjavec A, …, Zupan B (2013) Orange: data mining toolbox in Python, *Journal of Machine Learning Research* 14:2349-2353.

UČNI NAČRT PREDMETA/COURSE SYLLABUS

Predmet:	Biološke teme za nebiologe
Course title:	Topics in Biology for Non-Biologists

Študijski programi in stopnja	Študijska smer	Letnik	Semestri
Bioznanosti, tretja stopnja, doktorski	bioinformatika		Celoletni

Univerzitetna koda predmeta/University course code:	3766

Predavanja	Seminar	Vaje	Klinične vaje	Druge oblike študija	Samostojno delo	ECTS
10	30	0	0	10	75	5

Nosilec predmeta/Lecturer:	Marina Dermastia

Izvajalci predavanj:	Marina Dermastia, Tom Turk
Izvajalci seminarjev:	
Izvajalci vaj:	
Izvajalci kliničnih vaj:	
Izvajalci drugih oblik:	
Izvajalci praktičnega usposabljanja:	

Vrsta predmeta/Course type:	teoretični/theoretical

Jeziki/Languages:	Predavanja/Lectures:	Angleščina, Slovenščina
	Vaje/Tutorial:	Angleščina, Slovenščina

Pogoji za vključitev v delo oz. za opravljanje študijskih obveznosti:	Prerequisites:
Splošni pogoji za vpis na doktorski študij.	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 prokariontskimi, rastlinskimi in živalskimi	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

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.	applicability of the model organism research for understanding of general biological phenomena, including common principles in gentecs, 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.

Temeljna 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:	Objectives and competences:
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.	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:
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.	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:	Learning and teaching methods:

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.	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:	Delež/Weight	Assessment:
• Prisotnost pri kontaktnih urah	15,00 %	• Presence at contact hours
• Sprotna izdelava in oddaja krajših nalog	25,00 %	• Concurrent preparation and handing of shorter tasks
• Izdelava in predstavitev seminarja	60,00 %	• 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, ŠKONDRIĆ, 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]

Tom Turk

7. ANDERLUH, Gregor, SEPČIĆ, Kristina, TURK, Tom, MAČEK, Peter. Cytolytic proteins from cnidarians - an overview. Acta chimica slovenica, ISSN 1318-0207. [Tiskana izd.], 2011, 58(4):724-729. [COBISS.SI-ID 2493007]
8. GARAVENTA, Francesca, PIAZZA, Veronica, ZOVKO, Ana, TURK, Tom, CHELOSSI, E., FALUGI, C., ALUIGI, M. G., ANGELINI, Corrado, TROMBINO, S., GALLUS, L., FERRANDO, S., ALBINI, Angelo, PALEARI, L., SEPČIĆ, Kristina, FAIMALI, Marco. Multiple functions of the cholinesterase inhibiting polyalkylpyridinium salts extracted from the marine sponge, Haliclona sarai. WSEAS Transactions on Biology and Biomedicine, ISSN 1109-9518, 2010, 7(3): 103-113. [COBISS.SI-ID 27130329]
9. TURK, Tom, KEM, William R. The phylum Cnidaria and investigations of its toxins and venoms until 1990. Toxicon, ISSN 0041-0101. [Print ed.], 2009, 54(8): 1031-1037. [COBISS.SI-ID 2205263]

10. BERNE, Sabina, POHLEVEN, Franc, TURK, Tom, SEPČIĆ, Kristina. Induction of fruiting in oyster mushroom (Pleurotus ostratus) by polymeric 3-alkylpyridinium salts. Mycological research, ISSN 0953-7562, 2008, 112(9): 1085-1087. [COBISS.SI-ID 1856847]
11. RAZPOTNIK, Andrej, KRIŽAJ, Igor, KEM, William R., MAČEK, Peter, TURK, Tom. A new cytolytic protein from the sea anemone Urticina crassicornis that binds to cholesterol- and sphingomyelin-rich membranes. Toxicon, ISSN 0041-0101. [Print ed.], 2009, 53(7/8):762-769. [COBISS.SI-ID 1956175]
12. TURK, Tom, FURLAN, Borut. New records of Indo-Pacific and Atlantic mollusc species (Opisthobranchia) in the Eastern Mediterranean and Adriatic Sea. Annales, Series historia naturalis, ISSN 1408-533X, 2011, 21(1):5-10. [COBISS.SI-ID 2074067]

UČNI NAČRT PREDMETA/COURSE SYLLABUS

Predmet:	Računska biologija
Course title:	Computational Biology

Študijski programi in stopnja	Študijska smer	Letnik	Semestri
Bioznanosti, tretja stopnja, doktorski	bioinformatika		Celoletni

Univerzitetna koda predmeta/University course code:	3767

Predavanja	Seminar	Vaje	Klinične vaje	Druge oblike študija	Samostojno delo	ECTS
10	15	15	0	5	80	5

Nosilec predmeta/Lecturer:	Miha Mraz

Izvajalci predavanj:	Aleš Belič, Miha Moškon, Miha Mraz
Izvajalci seminarjev:	
Izvajalci vaj:	
Izvajalci kliničnih vaj:	
Izvajalci drugih oblik:	
Izvajalci praktičnega usposabljanja:	

Vrsta predmeta/Course type:	teoretični/theoretical

Jeziki/Languages:	Predavanja/Lectures:	Angleščina, Slovenščina
	Vaje/Tutorial:	Angleščina, Slovenščina

Pogoji za vključitev v delo oz. za opravljanje študijskih obveznosti:	Prerequisites:
• Splošni pogoji za vpis na doktorski študij	General prerequisites for the enrolment in the doctoral programme

Vsebina:	Content (Syllabus outline):
• 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.	• 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.

• 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.	• 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.

Temeljna 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:	Intended learning outcomes:
Znanje in razumevanje računalniškega modeliranja, analize in načrtovanja bioloških sistemov.	Knowledge and understanding of computational modelling, analysis and design of biological systems.

Metode poučevanja in učenja:	Learning and teaching methods:
Predavanja, seminarske naloge in praktične vaje iz uporabe programske opreme.	Lectures, seminars, and hands-on exercises with various computer software.

Načini ocenjevanja:	Delež/Weight	Assessment:
Domače naloge	50,00 %	Homework assignments
Seminarsko delo	50,00 %	Seminal work

Reference nosilca/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]

Aleš Belič:

1. BELIČ, Aleš, TÓTH, Katalin, VRZAL, Radim, TEMESVÁRY, Manna, PORROGI, Pálma, ORBÁN, Erika, ROZMAN, Damjana, DVORAK, Zdenek, MONOSTORY, Katalin. Dehydroepiandrosterone post-transcriptionally modifies CYP1A2 induction involving androgen receptor. Chemico-biological interactions, ISSN 0009-2797. [Print ed.], 2013, 203(3): 597-603.
2. BELIČ, Aleš, POMPON, Denis, MONOSTORY, Katalin, KELLY, Diane E., KELLY, Steven Lewis, ROZMAN, Damjana. An algorithm for rapid computational construction of metabolic networks : a cholesterol biosynthesis example. Computers in Biology and Medicine, ISSN 0010-4825. [Print ed.], Jun. 2013, 43(5): 471-480.
3. BELIČ, Aleš, AČIMOVIČ, Jure, NAIK, Adviti, GOLIČNIK, Marko. Analysis of the steady-state relations and control-algorithm characterisation in a mathematical model of cholesterol biosynthesis. V: ALEXÍK, Mikuláš (ur.), ŠNOREK, Miroslav (ur.), CEPEK, Miroslav (ur.). EUROSIM 2010 : special issue, (Simulation modelling practice and theory (Print), ISSN 1569-190X, vol. 33). [Amsterdam]: Elsevier, 2013, 18-27.
4. TEMESVÁRI, Manna, KÓBORI, László, PAULIK, József, SÁRVÁRY, E., BELIČ, Aleš, MONOSTORY, Katalin. Estimation of drug-metabolizing capacity by cytochrome P450 genotyping and expression. The Journal of pharmacology and experimental therapeutics, ISSN 0022-3565, 2012, 341(1): 294-305.
5. AČIMOVIČ, Jure, KOROŠEC, Tina, SELIŠKAR, Matej, BJORKHEM, Ingemar, MONOSTORY, Katalin, SZABO, Pal, PASCUSSI, Jean-Marc, BELIČ, Aleš, KOCJAN, Darko, URLEB, Uroš, ROZMAN, Damjana. Inhibition of human sterol delta 7-reductase and other post-lanosterol enzymesby 2-(4-phenethylpiperazin-1-yl)-1-(pyridine-3-yl)ethanol (LK-980), a novel inhibitor of cholesterol synthesis. Drug metabolism and disposition, ISSN 0090-9556, 2011, 39(1): 39-46.
6. BELIČ, Aleš, ŠKRJANC, Igor, ZUPANČIČ-BOŽIČ, Damjana, VREČER, Franc. Tableting process optimisation with the application of fuzzy models. International journal of pharmaceutics, ISSN 0378-5173. [Print ed.], 2010, 389(1/2): 86-93.

Miha Moškon:

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(2): 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. ŠOBERL, Domen, ZIMIC, Nikolaj, LEONARDIS, Aleš, KRIVIC, Jaka, MOŠKON, Miha. Hardware implementation of FAST algorithm for mobile applications. *Journal of signal processing systems for signal, image, and video technology*, ISSN 1939-8018. [Print ed.], 2013: 1-10. [COBISS.SI-ID 10041428]

6. 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]

UČNI NAČRT PREDMETA/COURSE SYLLABUS

Predmet:	Zajem in računalniško podprta analiza slik
Course title:	Image Acquisition and Computer-Assisted Analysis

Študijski programi in stopnja	Študijska smer	Letnik	Semestri
Bioznanosti, tretja stopnja, doktorski	bioinformatika		Celoletni

Univerzitetna koda predmeta/University course code:	3768

Predavanja	Seminar	Vaje	Klinične vaje	Druge oblike študija	Samostojno delo	ECTS
10	0	20	0	0	95	5

Nosilec predmeta/Lecturer:	Franjo Pernuš

Izvajalci predavanj:	Boštjan Likar, Franjo Pernuš
Izvajalci seminarjev:	
Izvajalci vaj:	
Izvajalci kliničnih vaj:	
Izvajalci drugih oblik:	
Izvajalci praktičnega usposabljanja:	

Vrsta predmeta/Course type:	teoretični/theoretical

Jeziki/Languages:	Predavanja/Lectures:	Angleščina, Slovenščina
	Vaje/Tutorial:	Angleščina, Slovenščina

Pogoji za vključitev v delo oz. za opravljanje študijskih obveznosti:	Prerequisites:
Splošni pogoji za vpis na doktorski študij.	Genaral conditions for enrolment in doctoral studies.

Vsebina:	Content (Syllabus outline):
- Zajemanje digitalnih slik: optično-zaznavne lastnosti človeškega vida, vrste in definicije digitalnih slik, predstavitve 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.	- 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,

- Prikazovanje, manipulacija in zgoščevanje sivinskih, barvnih in večdimenzionalnih slik - Analiza slik: upragovljanja, razgradnja na osnovi robov, širjenja, združevanja in razdruževanja področij, opisovanje s poravnavo modelov, predstavitve 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).	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.).

Temeljna 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:	Objectives and competences:
Seznaniti 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.	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:	Learning and teaching methods:
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.	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:	Delež/Weight	Assessment:
Pisno poročilo o projektu	70,00 %	Writen report on assigned project
Predstavitev (PPT) projekta	30,00 %	Oral (PPT) presentation

Reference nosilca/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 Engineering & Computing, 49(8):957-966, 2011