

UČNI NAČRT PREDMETA/COURSE SYLLABUS

Predmet:	Bioinformatična orodja in podatkovne zbirke
Course title:	Bioinformatics Tools and Databases
Članica nosilka/UL Member:	UL FRI

Študijski programi in stopnja	Študijska smer	Letnik	Semestri
Bioznanosti, tretja stopnja, doktorski	Ni členitve (študijski program)		Celoletni

Univerzitetna koda predmeta/University course code:	0037262
Koda učne enote na članici/UL Member 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: Tomaž Curk, Cene Gostinčar, Jernej Jakše, Roman Jerala, Tanja Kunej, Uroš Petrovič, Blaž Stres

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):

- Bioinformatične 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.
- Bioinformatična orodja v proteomiki in interaktomiki.
- Integrativna genomika.
- Aplikacije: bioinformatika v okoljski genomiki, farmakogenomiki.
- Ontologije in zbirke znanj v bioinformatiki.
- Bioinformatičski pristopi v kemogenomiki.

- 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.
- Integrative genomics.
- Bioinformatics tools in proteomics and interactomics.
- Applications: Bioinformatics in environmental genomics, pharmacogenomics.
- Ontologies and knowledge databases in bioinformatics.

- Projektno delo s specifičnimi programskimi orodji med predavanji in v okviru seminarske naloge.	- Bioinformatics approaches in chemogenomics. - Project work with specific software tools during the lectures and within seminar.
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Temeljna literatura in viri/Readings:

- Jonathan Pevsner (2015) Bioinformatics and Functional Genomics, 3rd Edition, ISBN 9781118581780
- David W. Mount (2004) Bioinformatics. Sequence and Genome Analysis. Cold Spring Harbor Laboratory Press, USA, 2nd edition, ISBN 0879697121.
- pregledni in originalni znanstveni članki s širšega področja bioinformatike.

Cilji in kompetence:

Seznantitev 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 bioinformatična 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, projektno delo, praktične vaje z računalniki.

Learning and teaching methods:

Lectures, project workshops, practical work with computers.

Načini ocenjevanja:

Pisno preverjanje znanja

Delež/Weight

100,00 %

Assessment:

Written exam

Reference nosilca/Lecturer's references:

Jernej Jakše

1. PRENTOUT, Djivan, ŠTAJNER, Nataša, ČERENAK, Andreja, TRICOU, Theo, BROCHIER-ARMANET, Céline, JAKŠE, Jernej, KÄFER, Jos, MARAIS, Gabriel A. B. Plant genera Cannabis and Humulus share the same pair of well-differentiated sex chromosomes. The New phytologist, ISSN 0028-646X, 2021, vol. , iss. , str., doi: 10.1111/nph.17456. [COBISS.SI-ID 63536131]
2. GONZALEZ, Francisco, JIBIN, Johny, WALKER III, William B., GUAN, Qingtian, MFARREJ, Sara, JAKŠE, Jernej, MONTAGNÉ, Nicolas, JACQUIN-JOLY, Emmanuelle, ALQARNI, Abdulaziz A., MOHAMMED ALI, Al-Saleh, PAIN, Arnab, ANTONY, Binu. Antennal transcriptome sequencing and identification of candidate chemoreceptor proteins from an invasive pest, the American palm weevil, Rhyncophorus palmarum. Scientific reports, ISSN 2045-2322, 2021, vol. 11, str. 1-14 (8334), ilustr. <https://www.nature.com/articles/s41598-021-87348-y>, doi: 10.1038/s41598-021-87348-y. [COBISS.SI-ID 60452099]
3. ŠTAJNER, Nataša, RADIŠEK, Sebastjan, KUMAR MISHRA, Ajay, NATH, Vishnu Sukumari, MATOUŠEK, Jaroslav, JAKŠE, Jernej. Evaluation of Disease Severity and Global Transcriptome response Induced by Citrus bark cracking viroid, Hop latent viroid, and their co-infection in hop (Humulus lupulus L.). International journal of molecular sciences, ISSN 1422-0067, 2019, vol. 20, no. 13, str. 1-21 (3154), doi: 10.3390/ijms20133154. [COBISS.SI-ID 9268089]
4. JESENIČNIK, Taja, ŠTAJNER, Nataša, RADIŠEK, Sebastjan, JAKŠE, Jernej. RNA interference core components identified and characterised in Verticillium nonalfalfae, a vascular wilt pathogenic plant fungi of hops. Scientific

reports, ISSN 2045-2322, 2019, vol. 9, str. 1-12 (8651), ilustr. <https://doi.org/10.1038/s41598-019-44494-8>, doi: 10.1038/s41598-019-44494-8. [COBISS.SI-ID 9242233]

5. NATH, Vishnu Sukumari, KUMAR MISHRA, Ajay, KUMAR, Atul, MATOUŠEK, Jaroslav, JAKŠE, Jernej. Revisiting the role of transcription factors in coordinating the defense response against citrus bark cracking viroid infection in commercial hop (*Humulus Lupulus L.*). *Viruses*, ISSN 1999-4915, 2019, vol. 11, iss. 5: 419, str. 1-19. <https://doi.org/10.3390/v11050419>. [COBISS.SI-ID 9229433]
6. POKORN, Tine, RADIŠEK, Sebastjan, JAVORNIK, Branka, ŠTAJNER, Nataša, JAKŠE, Jernej. Development of hop transcriptome to support research into host-viroid interactions. *PloS one*, ISSN 1932-6203, Sep. 2017, vol. 12, iss. 9, 0184528. <https://doi.org/10.1371/journal.pone.0184528>. [COBISS.SI-ID 8793977]

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]
5. MORI, Jerneja, VRANAC, Tanja, SMREKAR, Boštjan, ČERNILEC, Maja, ČURIN-ŠERBEC, Vladka, HORVAT, Simon, IHAN, Alojz, BENČINA, Mojca, JERALA, Roman. Chimeric flagellin as the self-adjuvanting antigen for the activation of immune response against *Helicobacter pylori*. *Vaccine*, ISSN 0264-410X. [Print ed.], 2012, vol. 30, issue 40, str. 5856-5863. <http://www.sciencedirect.com/science/article/pii/S0264410X12010134>, doi: 10.1016/j.vaccine.2012.07.011. [COBISS.SI-ID 5023770]
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. ŠKRLJ, Blaž, ERŽEN, Nika, LAVRAČ, Nada, KUNEJ, Tanja, KONC, Janez. CaNDis: a web server for investigation of causal relationships between diseases, drugs, and drug targets. *Bioinformatics*, ISSN 1367-4803, 2021, vol. 36, no. 6, str. 885-887. doi: 10.1093/bioinformatics/btaa762. [COBISS.SI-ID 27212035]
2. ŠKRLJ, Blaž, KUNEJ, Tanja, KONC, Janez. Insights from ion binding site network analysis into evolution and functions of proteins. *Molecular informatics*, ISSN 1868-1743, 2018, vol. 37, 1700144, str. 1-11. doi: 10.1002/minf.201700144. [COBISS.SI-ID 4043912]
3. ROZMAN, Vita, KUNEJ, Tanja. Harnessing omics big data in nine vertebrate species by genome-wide prioritization of sequence variants with the highest predicted deleterious effect on protein function. *Omics: a journal of integrative biology*, ISSN 1536-2310, 2018, vol. 22, no. 6, str. 410-421. doi: 10.1089/omi.2018.0046. [COBISS.SI-ID 4072584]
4. URH, Kristian, KUNEJ, Tanja. Genome-wide screening for smallest regions of overlaps in cryptorchidism. *Reproductive biomedicine online*, ISSN 1472-6491, 2018, vol. 37, no. 1, str. 85-99. doi: 10.1016/j.rbmo.2018.02.008. [COBISS.SI-ID 4061320]
5. ŠKRLJ, Blaž, KONC, Janez, KUNEJ, Tanja. Identification of sequence variants within experimentally validated protein interaction sites provides new insights into molecular mechanisms of disease development. *Molecular informatics*, ISSN 1868-1743, 2017, vol. 36, no. 9, str. 1-8. doi: 10.1002/minf.201700017. [COBISS.SI-ID 3888008]
6. KONC, Janez, ŠKRLJ, Blaž, ERŽEN, Nika, KUNEJ, Tanja, JANEŽIČ, Dušana. GenProBiS: web server for mapping of sequence variants to protein binding sites. *Nucleic acids research*, ISSN 0305-1048, 2017, vol. 45, no. W1, str. W253-W259. doi: 10.1093/nar/gkx420. [COBISS.SI-ID 3897736]

Uroš Petrovič:

1. GODEC, Primož, PANČUR, Matjaž, ILENIČ, Nejc, ČOPAR, Andrej, STRAŽAR, Martin, ERJAVEC, Aleš, PRETNAR, Ajda, DEMŠAR, Janez, STARIČ, Anže, TOPLAK, Marko, ŽAGAR, Lan, HARTMAN, Jan, HAMILTON, Wang, BELLAZZI, Riccardo, PETROVIČ, Uroš, GARAGNA, Silvia, ZUCCOTTI, Maurizio, PARK, Dongsu, SHAULSKY, Gad, ZUPAN, Blaž. Democratized image analytics by visual programming through integration of deep models and small-scale machine learning. *Nature communications*. 2019, vol. 10, str. 4551-1-4551-7. ISSN 2041-1723. DOI: 10.1038/s41467-019-12397-x. [COBISS.SI-ID 32755751]
2. ARHAR, Simon, GOGG-FASSOLTER, Gabriela, BRLOŽNIK, Mojca, PAČNIK, Klavdija, SCHWAIGER, Katharina, ŽGANJAR, Mia, PETROVIČ, Uroš, NATTER, Klaus. Engineering of *Saccharomyces cerevisiae* for the accumulation of high amounts of triacylglycerol. *Microbial cell factories*. 2021, no. 20, issue 1, str. 147-1-147-15. ISSN 1475-2859. DOI: 10.1186/s12934-021-01640-0. [COBISS.SI-ID 71619331]
3. MEIJNEN, Jean-Paul, RANDAZZO, Paola, FOULQUIÉ-MORENO, María R., BRINK, Joost van den, VANDECRUYS, Paul, STOJILJKOVIĆ, Marija, DUMORTIER, Françoise, ZALAR, Polona, BOEKHOUT, Teun, GUNDE-CIMERMAN, Nina, KOKOŠAR, Janez, ŠTAJDOHAR, Miha, CURK, Tomaž, PETROVIČ, Uroš, THEVELEIN, Johan M. Polygenic analysis and targeted improvement of the complex trait of high acetic acid tolerance in the yeast *Saccharomyces cerevisiae*. *Biotechnology for biofuels*. 2016, vol. 9, str. 1-18. ISSN 1754-6834. DOI: 10.1186/s13068-015-0421-x. [COBISS.SI-ID 29140775]
4. MATTIAZZI, Mojca, BRLOŽNIK, Mojca, KAFERLE, Petra, ŽITNIK, Marinka, WOLINSKI, Heimo, LEITNER, F., KOHLWEIN, Sepp D., ZUPAN, Blaž, PETROVIČ, Uroš. Genome-wide localization study of yeast Pex11 identifies peroxisome-mitochondria interactions through the ERMES complex. *Journal of molecular biology*. Jun. 2015, vol. 427, no. 11, str. 2072-2087, ilustr. ISSN 0022-2836. DOI: 10.1016/j.jmb.2015.03.004. [COBISS.SI-ID 28442663]
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. MATTIAZZI, Mojca, PRELEC, Metod, BRLOŽNIK, Mojca, PRIMO, Cecilia, CURK, Tomaž, ŠČANČAR, Janez, YENUSH, Lynne, PETROVIČ, Uroš. Yeast *Saccharomyces cerevisiae* adiponectin receptor homolog *Izh2* is involved in the regulation of zinc, phospholipid and pH homeostasis. *Metallomics*. 2015, vol. 7, iss. 9, str. 1338-1351. ISSN 1756-5901. DOI: 10.1039/C5MT00095E. [COBISS.SI-ID 28620583]

Cene Gostinčar:

1. CONLON, Benjamin H., GOSTINČAR, Cene, FRICKE, Janis, KREUZENBECK, Nina B., DANIEL, Jan-Martin, SCHLOSSER, Malte S.L., PEEREBOOM, Nils, AANEN, Duur K., DE BEER, Z. Wilhelm, BEEMELMANNNS, Christine, GUNDE-CIMERMAN, Nina, POULSEN, Michael. Genome reduction and relaxed selection is associated with the transition to symbiosis in the basidiomycete genus *Podaxis*. *iScience*. 2021, vol. 24, iss. 6, str. 1-20, ilustr. ISSN 2589-0042. <https://www.sciencedirect.com/science/article/pii/S2589004221006489?via%3Dihub>, DOI: 10.1016/j.isci.202102680. [COBISS.SI-ID 68516099], [JCR, SNIP, WoS, Scopus]
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3. GOSTINČAR, Cene, STAJICH, Jason Eric, KEJŽAR, Anja, SINHA, Sunita, NISLOW, Corey, LENASSI, Metka, GUNDE-CIMERMAN, Nina. Seven years at high salinity - experimental evolution of the extremely halotolerant black yeast *Hortaea werneckii*. *Journal of fungi*. 2021, vol. 7, iss. 9, str. 1-22. ISSN 2309-608X. <https://www.mdpi.com/2309-608X/7/9/723>, DOI: 10.3390/jof709072 [COBISS.SI-ID 76085763], [JCR, SNIP, WoS, Scopus]
4. SCHALK, Felix, GOSTINČAR, Cene, KREUZENBECK, Nina B., CONLON, Benjamin H., SOMMERWERK, Elisabeth, RABE, Patrick, BURKHARDT, Immo, KRÜGER, Thomas, KNIEMEYER, Olaf, BRAKHAGE, Axel A., GUNDE-CIMERMAN, Nina, DE BEER, Z. Wilhelm, DICKSCHAT, Jeroen S., POULSEN, Michael, BEEMELMANNNS, Christine. The termite fungal cultivar *Termitomyces* combines diverse enzymes and oxidative reactions for plant biomass conversion. *mBio*. 2021, vol. 12, iss. 3, str. 1-17. ISSN 2150-7511. DOI: 10.1128/mBio.03551-20. [COBISS.SI-ID 68499459], [JCR, SNIP, WoS, Scopus]
5. GOSTINČAR, Cene, TURK, Martina, ZAJC, Janja, GUNDE-CIMERMAN, Nina. Fifty *Aureobasidium pullulans* genomes reveal a recombining polyextremotolerant generalist. *Environmental microbiology*. [Print ed.]. 2019, vol. 21, iss. 10, str. 3638-3652. ISSN 1462-2912. <https://doi.org/10.1111/1462-2920.14693>, DOI: 10.1111/1462-2920.14693. [COBISS.SI-ID 5158991], [JCR, SNIP, WoS do 24. 9. 2021: št. citatov (TC): 7, čistih citatov (CI): 4, čistih citatov na avtorja (CIAu): 1,00, Scopus do 26. 10. 2021: št. citatov (TC): 8, čistih citatov (CI): 6, čistih citatov na avtorja (CIAu): 1,50]

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Tomaž Curk:

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3. EHRMANN, Ingrid, CRICHTON, James H., GAZZARA, Matthew R., JAMES, Katherine, LIU, Yilei, GRELLSCHEID, Sushma N., CURK, Tomaž, ROOIJ, Dirk de, STEYN, Jannetta S., COCKELL, Simon, ADAMS, Ian R., BARASH, Yoseph, ELLIOTT, David J. An ancient germ cell-specific RNA-binding protein protects the germline from cryptic splice site poisoning. *eLife*, ISSN 2050-084X, Jan. 2019, vol. 8, str. 1-26, ilustr. <https://www.ncbi.nlm.nih.gov/pubmed/30674417>, doi: 10.7554/eLife.39304. [COBISS.SI-ID 1538163395]
4. BRIESE, Michael, HABERMAN, Nejc, SIBLEY, Christopher R., FARAWAY, Rupert, ELSEY, Andrea S., CHAKRABARTI, Anob M., WANG, Zhen, KÖNIG, Julian, PERERA, David, WICKRAMASINGHE, Vihandha O., VENKITARAMAN, Ashok R., LUSCOMBE, Nicholas M., SAIEVA, Luciano, PELLIZZONI, Livio, SMITH, Christopher W. J., CURK, Tomaž, ULE, Jernej. A systems view of spliceosomal assembly and branchpoints with iCLIP. *Nature structural & molecular biology*, ISSN 1545-9985. Online ed., Oct. 2019, vol. 26, no. 10, str. 930-940, ilustr. <https://www.nature.com/articles/s41594-019-0300-4>, doi: 10.1038/s41594-019-0300- [COBISS.SI-ID 1538384323]
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6. ROT, Gregor, WANG, Zhen, HUPPERTZ, Ina, MODIC, Miha, LENČE, Tina, HALLEGGGER, Martina, HABERMAN, Nejc, CURK, Tomaž, MERING, Christian von, ULE, Jernej. High-resolution RNA maps suggest common principles of splicing and polyadenylation regulation by TDP-43. *Cell reports*, ISSN 2211-1247, May 2017, vol. 19, iss. 5, str. 1056-1067, graf. prikazi. [http://www.cell.com/cell-reports/fulltext/S2211-1247\(17\)30522-3](http://www.cell.com/cell-reports/fulltext/S2211-1247(17)30522-3), doi: 10.1016/j.celrep.2017.04.028. [COBISS.SI-ID 1537665475]

Blaž Stres:

1. MUROVEC, Boštjan, DEUTSCH, Leon, STRES, Blaž. General Unified Microbiome Profiling Pipeline (GUMPP) for large scale, streamlined and reproducible analysis of bacterial 16S rRNA data to predicted microbial metagenomes, enzymatic reactions and metabolic pathways. *Metabolites*. 2021, vol. 11, no. 6, str. 1-15, 336, ilustr. ISSN 2218-1989. <https://www.mdpi.com/2218-1989/11/6/336>, DOI: 10.3390/metabo11060336.
2. MUROVEC, Boštjan, DEUTSCH, Leon, STRES, Blaž. Computational framework for high-quality production and large-scale evolutionary analysis of metagenome assembled genomes. *Molecular biology and evolution*, ISSN 0737-4038, 2020, doi: 10.1093/molbev/msz237
3. ŠKET, Robert, DEBEVEC, Tadej, KUBLIK, Susanne, SCHLOTTER, Michael, SCHOELLER, Anne, MUROVEC, Boštjan, VOGEL-MIKUŠ, Katarina, MAKUC, Damjan, PEČNIK, Klemen, PLAVEC, Janez, MEKJAVIČ, Igor B., EIKEN, Ola, PREVORŠEK, Zala, STRES, Blaž. Intestinal metagenomes and metabolomes in healthy young males : inactivity and hypoxia generated negative physiological symptoms precede microbial dysbiosis. *Frontiers in physiology*, ISSN 1664-042X, 2018, doi: 10.3389/fphys.2018.00198.
4. ŠKET, Robert, DEBEVEC, Tadej, MEKJAVIČ, Igor B., MUROVEC, Boštjan, PREVORŠEK, Zala, STRES, Blaž, et al. Hypoxia and inactivity related physiological changes (constipation, inflammation) are not reflected at the level of gut metabolites and butyrate producing microbial community : the PlanHab study. *Frontiers in physiology*. 2017, vol. 8, art. no. 250, str. 1-16. ISSN 1664-042X. DOI: 10.3389/fphys.2017.00250.
5. ŠKET, Robert, TREICHEL, Nicole S., KUBLIK, Susanne, DEBEVEC, Tadej, EIKEN, Ola, MEKJAVIČ, Igor B., SCHLOTTER, Michael, VITAL, Marius, CHANDLER, Jenna, TIEDJE, James M., MUROVEC, Boštjan, PREVORŠEK, Zala, LIKAR, Matevž, STRES, Blaž. Hypoxia and inactivity related physiological changes precede or take place in absence of

significant rearrangements in bacterial community structure : the PlanHab randomized trial pilot study. PLoS one. 2017, vol. 12, no. 12, str.1-26, e0188556. ISSN 1932-6203.

<http://journals.plos.org/plosone/article/file?id=10.1371/journal.pone.0188556&type=printable>, DOI: 10.1371/journal.pone.0188556.

6. NICOLA, Lidia, INSAM, Heribert, PERTOT, Ilaria, STRES, Blaž. Reanalysis of microbiomes in soils affected by apple replant disease (ARD) : old foes and novel suspects lead to the proposal of extended model of disease development. Applied soil ecology. avg. 2018, vol. 129, str. 24-33, ilustr. ISSN 0929-1393.
<https://www.sciencedirect.com/science/article/pii/S0929139317312556>, DOI: 10.1016/j.apsoil.2018.04.010.

UČNI NAČRT PREDMETA/COURSE SYLLABUS

Predmet: Uvod v znanost o podatkih
Course title: Introduction to data science
Članica nosilka/UL Member:

Študijski programi in stopnja	Študijska smer	Letnik	Semestri
Bioznanosti, tretja stopnja, doktorski	Ni členitve (študijski program)		Celoletni
Bioznanosti, tretja stopnja, doktorski	Ni členitve (študijski program)		Celoletni

Univerzitetna koda predmeta/University course code: 0041833
Koda učne enote na članici/UL Member 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:

splošni pogoji za vpis na doktorski študij

Prerequisites:

general conditions for enrollment into doctoral studies

Vsebina:

- Uvod v vizualno programiranje in razvoj shem za podatkovno analitiko. Branje podatkov, vizualizacija, izbor. Razsevni diagrami, izbor projekcije podatkov.
- Klasifikacija. Klasifikacijska drevesa. Ocenjevanje napovedne točnosti (klasifikacijska točnost, AUC). Pregled ostalih metod, vključno z logistično regresijo, SVM in naključnimi gozdovi. Statistična primerjava klasifikacijskih metod.
- Regresija. Metoda linearne in polinomske regresije. Vpliv regularizacije na uspešnost napovedi na učni in testni množici. Določanje parametrov učnih algoritmov.
- Razvrščanje v skupine. Tehnika hierarhičnega razvrščanja v skupine, metoda voditeljev in metoda

Content (Syllabus outline):

- Introduction to visual programming and data mining workflows. Data input, visualization, data selection and interactive data exploration. Scatterplot visualization, choice of projection.
- Classification. Classification trees. Confusion matrix. Scoring of classification models. Classification accuracy and AUC. Data sampling, training and test sets. Cross-validation. A glimpse into logistic regression, random forests, and SVM. Statistical comparison of classifiers.
- Regression. Linear and polynomial regression. Regularization. Effects of regularization on accuracy in training and test sets. Parameter search. Other regression techniques (random forests).
- Clustering. Hierarchical clustering. Explorative data analysis with clustering and data projections. k-

<p>DBSCAN. Računske in prostorske kompleksnosti posameznih metod.</p> <p>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.</p>	<p>means clustering. DBSCAN clustering. Time and space complexity. Cluster scoring and selection of number of clusters.</p> <p>5. Data projections. Principal component analysis. Multi-dimensional scaling. TSNE. Analysis of unstructured data, like images and sequences. Data embedding. Deep models.</p>
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Temeljna literatura in viri/Readings:

Video tečajji za programski paket Orange na YouTube-u (<http://bit.ly/21E8Vt8>).
Delovna skripta Zupan B, Demšar J: Introduction to Data Science.

Cilji in kompetence:

Cilj predmeta je spoznati osnovne tehnike strojnega učenja in odkrivanja znanj iz podatkov ter njihovo uporabo v biomedicini. Tehnike bodo predstavljene intuitivno preko praktičnega dela z orodjem za podatkovno rudarjenje; tečaj ne bo vključeval predstavitev matematičnih oziroma formalnih podlag za algoritme. Po uspešnem zaključku predmeta bodo študenti znali urediti in z osnovnimi tehnikami podatkovnega rudarjenja analizirati svoje podatke. Tehnike bodo spoznali v obsegu, ki jim bo olajšal komunikacijo s statistiki in eksperti s področja znanosti o podatkih.

Objectives and competences:

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 techniques 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:

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.

Refleksija: Spoznavanje osnov algoritmičnega razmišljanja.

Prenosljive spretnosti: Poznavanje in učinkovita uporaba vizualnega programiranja in konstrukcije shem za podatkovno analitiko.

Intended learning outcomes:

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.

Transferable skills: Understanding and use of visual programming and data analysis workflows.

Metode poučevanja in učenja:

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.

Learning and teaching methods:

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:

Sprotno preverjanje (domače naloge, kolokviji in projektno delo). Ocene: 6-10 pozitivno, 1-5 negativno (v skladu s Statutom UL)

Delež/Weight

100,00 %

Assessment:

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:	Zajem in računalniško podprta analiza slik
Course title:	Image Acquisition and Computer-Assisted Analysis
Članica nosilka/UL Member:	UL FRI

Študijski programi in stopnja	Študijska smer	Letnik	Semestri
Bioznanosti, tretja stopnja, doktorski	Ni členitve (študijski program)		Celoletni

Univerzitetna koda predmeta/University course code:	0037266
Koda učne enote na članici/UL Member 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, Žiga Špiclin, Tomaž Vrtovec
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:

- 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: upragovanje, opisovanje s poravnavo topoloških, fizikalnih ali statističnih modelov, regresija in razvrščanje slik z globokimi samoučečimi modeli, izločanje značilnic objektov zanimanja, analiza rasti in gibanja.
- Načrtovanje in uporaba slikovnih informacijskih sistemov: programska orodja za pridobivanje in analizo

Content (Syllabus outline):

- 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, registration-driven (physical, topological, statistical) model based description, regression and analysis based on deep learning models, region-of-interest description and measurement, growth and motion analysis.

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).	- 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.).
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Temeljna literatura in viri/Readings:

<ul style="list-style-type: none"> - Thomas M. Deserno. Biomedical Image Processing. Springer, 2011. - Klaus D. Tonnies. Guide to Medical Image Analysis: Methods and Algorithms. Springer, 2012. - Deep Learning (Ian J. Goodfellow, Yoshua Bengio and Aaron Courville), MIT Press, 2016. - Boštjan Likar. Biomedicinska slikovna informatika in diagnostika, 1. izdaja, Založba FE in FRI, Ljubljana: Fakulteta za elektrotehniko, 2008.
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Cilji in kompetence:

<p>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; posredovati znanje o strojnem in globokem strojnem učenju in uporabo teh orodij za regresijo in razvrščanje na podlagi biomedicinskih slik ter njihovo analizo; seznanjanje s pristopi k načrtovanju in uporabi slikovnih informacijskih sistemov v biotehniških raziskavah in aplikacijah.</p>	<p>Objectives and competences:</p> <p>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; to develop basic understanding of machine and deep learning based tools for digital image regression, classification and 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.</p>
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Predvideni študijski rezultati:

<p>Študenti, ki bodo izbrali ta predmet, bodo pridobili znanja o zajemanju digitalnih slik; znali prikazovati, manipulirati in zgoščevati slike; znali izbrati in uporabljati obstoječe postopke; digitalne analize slik; znali načrtovati, učiti in vrednotiti globoke samoučeče modele za regresijo in razvrščanje na podlagi slikovne informacije; znali načrtovati in uporabljati slikovne informacijske sisteme v bioznanostih.</p>	<p>Intended learning outcomes:</p> <p>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, and design, train and validate deep learning based models for image-based regression and classification tasks in the field of biosciences.</p>
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Metode poučevanja in učenja:

<p>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.</p>	<p>Learning and teaching methods:</p> <p>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.</p>
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Načini ocenjevanja:

Načini ocenjevanja:	Delež/Weight	Assessment:
Pisno poročilo o projektu	70,00 %	Written report on assigned project
Predstavitev (PPT) projekta	30,00 %	Oral (PPT) presentation

Reference nosilca/Lecturer's references:

<p>Žiga Špiclin</p> <p>1. BIZJAK, Žiga, PERNUŠ, Franjo, ŠPICLIN, Žiga. Deep shape features for predicting future intracranial aneurysm growth. <i>Frontiers in physiology</i>, vol. 12, article 644349, str. 1-10, 202</p>

2. SAVŠEK, Lina, STERGAR, Tamara, STROJNIK, Vojko, IHAN, Alojz, KOREN, Aleš, ŠPICLIN, Žiga, ŠEGA, Saša. Impact of aerobic exercise on clinical and magnetic resonance imaging biomarkers in persons with multiple sclerosis : an exploratory randomized controlled trial. *Journal of rehabilitation medicine*, vol. 53, iss. 4, str. 1-9, 2021.
3. MADAN, Hennadii, BERLOT, Rok, RAY, Nicola J., PERNUŠ, Franjo, ŠPICLIN, Žiga. Practical priors for Bayesian inference of latent biomarkers. *IEEE journal of biomedical and health informatics*, vol. 24, no. 2, str. 396-406, 2020.
4. JERMAN, Tim, CHIEN, Aichi, PERNUŠ, Franjo, LIKAR, Boštjan, ŠPICLIN, Žiga. Automated cutting plane positioning for intracranial aneurysm quantification. *IEEE transactions on bio-medical engineering*, vol. 67, no. 2, str. 577-587, 2020.
5. MADAN, Hennadii, PERNUŠ, Franjo, ŠPICLIN, Žiga. Reference-free error estimation for multiple measurement methods. *Statistical methods in medical research*, vol. 28, issue 7, str. 2196-2209, 2019.
6. MITROVIĆ, Uroš, LIKAR, Boštjan, PERNUŠ, Franjo, ŠPICLIN, Žiga. 3D-2D registration in endovascular image-guided surgery : evaluation of state-of-the-art methods on cerebral angiograms. *International journal of computer assisted radiology and surgery : a journal for interdisciplinary research, developemnt and applications of image guided diagnosis and therapy*, vol. 13, no. 2, str. 193-202, 2018.

Tomaž Vrtovec

1. KOREZ, Robert, PUTZIER, Michael, VRTOVEC, Tomaž. A deep learning tool for fully automated measurements of sagittal spinopelvic balance from X-ray images : performance evaluation. *European spine journal*, vol. 29, no. 9, str. 2295-2305, 2020.
2. KHOLIIVCHENKO, M., SIRAZITDINOV, I., KUBRAK, K., BADRUTDINOVA, R., KULEEV, R., YUAN, Y., VRTOVEC, Tomaž, IBRAGIMOV, Bulat. Contour-aware multi-label chest X-ray organ segmentation. *International journal of computer assisted radiology and surgery : a journal for interdisciplinary research, developemnt and applications of image guided diagnosis and therapy*, vol. 15, iss. 4, str. 425-436, 2020.
3. BRINK, Rob C., VAVRUCH, Ludvig, SCHLÖSSER, Tom P. C., ABUL-KASIM, Kasim, OHLIN, Acke, TROPP, Hans, CASTELEIN, René M., VRTOVEC, Tomaž. Three-dimensional pelvic incidence is much higher in (thoraco)lumbar scoliosis than in controls. *European spine journal*, vol. 28, no. 3, str. 544-550, 2019.
4. KNEZ, Dejan, NAHLE, Imad S., VRTOVEC, Tomaž, PARENT, Stefan, KADOURY, Samuel. Computer-assisted pedicle screw trajectory planning using CT-inferred bone density : a demonstration against surgical outcomes. *Medical Physics*, vol. 46, no. 8, str. 3543-3554, 2019.
5. PINHEIRO, Alan Petrônio, COELHO, Júlio César, PASCHOARELLI VEIGA, Antônio C., VRTOVEC, Tomaž. A computerized method for evaluating scoliotic deformities using elliptical pattern recognition in X-ray spine images. *Computer methods and programs in biomedicine*, vol. 161, str. 85-92, 2018.
6. MOČNIK, Domen, IBRAGIMOV, Bulat, XING, Lei, STROJAN, Primož, LIKAR, Boštjan, PERNUŠ, Franjo, VRTOVEC, Tomaž. Segmentation of parotid glands from registered CT and MR images. *Physica medica*, vol. 52, str. 33-41, 2018.

Boštjan Likar

1. ZELINSKYI, Yevhen, NAGLIČ, Peter, PERNUŠ, Franjo, LIKAR, Boštjan, BÜRMEIN, Miran. Fast and accurate Monte Carlo simulations of subdiffusive spatially resolved reflectance for a realistic optical fiber probe tip model aided by a deep neural network. *Biomedical optics express*, vol. 11, no. 7, str. 3875-3889, 2020.
2. MEHLE, Andraž, KITAK, Domen, PODREKAR, Gregor, LIKAR, Boštjan, TOMAŽEVIČ, Dejan. In-line agglomeration degree estimation in fluidized bed pellet coating processes using visual imaging. *International journal of pharmaceuticals*, vol. 546, no. 1/2, str. 78-85, 2018.
3. NAGLIČ, Peter, PERNUŠ, Franjo, LIKAR, Boštjan, BÜRMEIN, Miran. Lookup table-based sampling of the phase function for Monte Carlo simulations of light propagation in turbid media. *Biomedical optics express*, vol. 8, no. 3, str. 1895-1910, 2017.
4. IVANČIČ, Matic, NAGLIČ, Peter, PERNUŠ, Franjo, LIKAR, Boštjan, BÜRMEIN, Miran. Virtually increased acceptance angle for efficient estimation of spatially resolved reflectance in the subdiffusive regime : a Monte Carlo study. *Biomedical optics express*, vol. 8, no. 11, str. 4872-4886, 2017.
5. MEHLE, Andraž, LIKAR, Boštjan, TOMAŽEVIČ, Dejan. In-line recognition of agglomerated pharmaceutical pellets with density-based clustering and convolutional neural network. *IPSI transactions on computer vision and applications*, vol. 9, 7, str. 1-6, 2017.
6. JEMEC, Jurij, PERNUŠ, Franjo, LIKAR, Boštjan, BÜRMEIN, Miran. Three-dimensional point spread function measurements of imaging spectrometers. *Journal of optics*, no. 9, 095002, str. 1-7, 2017.

Franjo Pernuš

1. IVANČIČ, Matic, NAGLIČ, Peter, PERNUŠ, Franjo, LIKAR, Boštjan, BÜRMEIN, Miran. Efficient estimation of subdiffusive optical parameters in real time from spatially resolved reflectance by artificial neural networks. *Optics letters*, vol. 43, no. 12, str. 2901-2904, 2018.

2. LESJAK, Žiga, GALIMZIANOVA, Alfiia, KOREN, Aleš, LUKIN, Matej, PERNUŠ, Franjo, LIKAR, Boštjan, ŠPICLIN, Žiga. A novel public MR image dataset of multiple sclerosis patients with lesion segmentations based on multi-rater consensus. *Neuroinformatics*, vol. 16, no. 1, str. 51-63, 2018.
3. IBRAGIMOV, Bulat, KOREZ, Robert, LIKAR, Boštjan, PERNUŠ, Franjo, XING, Lei, VRTOVEC, Tomaž. Segmentation of pathological structures by landmark-assisted deformable models. *IEEE transactions on medical imaging*, vol. 36, no. 7, str. 1457-1469, 2017.
4. JEMEC, Jurij, PERNUŠ, Franjo, LIKAR, Boštjan, BÜRMENT, Miran. 2D sub-pixel point spread function measurement using a virtual point-like source. *International journal of computer vision*, vol. 121, no. 3, str. 391-402, 2017.
5. MADAN, Hennadii, PERNUŠ, Franjo, LIKAR, Boštjan, ŠPICLIN, Žiga. A framework for automatic creation of gold-standard rigid 3D-2D registration datasets. *International journal of computer assisted radiology and surgery : a journal for interdisciplinary research, development and applications of image guided diagnosis and therapy*, vol. 12, no. 2, str. 263-275, 2017.
6. AKSOY, T., ŠPICLIN, Žiga, PERNUŠ, Franjo, UNAL, Gozde. Monoplane 3D-2D registration of cerebral angiograms based on multi-objective stratified optimization. *Physics in Medicine & Biology*, vol. 62, no. 24, str. 9377-9394, 2017.