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| Specifikacija predmeta |
| Naziv predmeta | Genomska informatika |
| Studijski program | Elektrotehnika i računarstvo |
| Modul | Računarska tehnika i informatika |
| Tip studija | Master akademske studije |
| Broj ESPB | 6 | Status predmeta | izborni |
| Uslov | Predmet IR5PSZ/SI5PSZ nije preduslov za ovaj novi predmet (IR5GI/SI5GI), ali se preporučuje uzimanje IR5PSZ/SI5PSZ pre uzimanja ovog novog predmeta i zato je ovaj novi predmet smešten u proletnjem semestru, tako da se može uzeti nakon IR5PSZ/SI5PSZ,koji je smešten u jesenjem semestru. |
| Cilj predmeta | U okviru ovog predmeta predstavljeni su osnovni metodi računarske analize podataka dobijenih iz genoma, a sa ciljem izvođenja biološki značajnih zakljucaka. Biće ukazano na prednosti i mane ovih metoda i na značajne parametare koji utiču na rezultate ovih analiza. |
| Ishod predmeta | Studenti će razumeti principe dizajna algoritama za obradu bioloških podataka i kako oni rade. Biće sposobni da analiziraju probleme i primene odgovarajuće metode. |
| Sadržaj predmeta |
| Sadržaj teorijske nastave | Sequence Alignments, Hidden Markov Models, Multiple Alignment Algorithms, Gene Expression Analysis, Population Genomics, Molecular Evolution, Comparative Genomics |
| Sadržaj praktične nastave | Prakticna nastava ce tematski pratiti teorijsku nastavu. |
| Literatura |
| 1 | R. Durbin, S. Eddy, A. Krogh, G. Mitchison: Biological Sequence Analysis, Cambridge University Press |
| 2 | Neil C. Jones, Pavel A. Pevzner: An Introduction to Bioinformatics Algorithms, MIT Press |
| 3 | D. Gusfield: Alogorithms on Strings, Trees and Sequences, Cambridge University Press (lektira) |
| 4 | Najnoviji radovi po izboru predavaca |
| Broj časova aktivne nastave nedeljno tokom semestra/trimestra/godine |
| Predavanja | Vežbe | Don | Studijski i istraživački rad | Ostali časovi |
| 2 | 2 |  | 1 |  |
| Metode izvođenja nastave |
| Predavanja | Slajdovi za predavanja (na osnovu knjige: R. Durbin, S. Eddy, A. Krogh, G. Mitchison: Biological Sequence Analysis, Cambridge University Press) su, uz dozvolu autora (autori slajdova: S. Batzoglou + V.Popic), preuzeti sa portala odgovarajućeg predmeta na univerzitetu Stanford (koji koristi isti udžbenik kao ETF). |
| Auditorne vežbe | Slajdovi za auditorne vežbe (na osnovu knjige: Neil C. Jones, Pavel A. Pevzner: An Introduction to Bioinformatics Algorithms, MIT Press), su formirani na ETF (autor slajdova: N. Miletić). |
| Projekat | Projekat je baziran na alatu (Weka + Phyton) i setu podataka (AML/ALL dataset + GenBank), oba iz javnog domena.  |
| Ispit | Ispitna pitanja će biti rađena po ugledu na odgovarajući MIT predmet (koji koristi isti udžbenik kao ETF), što je takođe informacija iz javnog domena. Učesnici međunarodnih takmičenja iz Genomske informatike, koji ostvare zapažene rezultate do trenutka zaključivanja finalne ocene, dobijaju do 10 dodatnih poena (odluka o tačnom broju poena je diskreciono pravo predavača). |
| Ocena znanja (maksimalni broj poena 100) |
| Predispitne obaveze | Poena | Završni ispit | Poena |
| Aktivnosti u toku predavanja | 0 | Pismeni ispit | 50 |
| Praktična nastava | 0 |  |
| Projekti | 50 |  |
| Kolokvijumi | 0 |  |
| Seminari | 0 |  |

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| Course specification |
| Course title | Computational Genomics |
| Study programme |  |
| Module |  |
| Type of study |  |
| ESPB | 6 | Status | izborni |
| Condition | The course IR5PSZ/SI5PSZ is not a prerequisite for this new course (IR5GI/SI5GI);however, it is recommended that the course IR5GI/SI5GI, be taken after the course IR5PSZ/SI5PSZ.Cosequently, on the level of master studies, IR5PSZ/SI5PSZ is located in the Fall semestersand IR5GI in the Spring semesters. |
| The goal | This course presents some of the basic computational methods that can infer biological information from genomic data, the strengths and weaknesses of related methods, and the important parameters embedded in these analyses. Theoretical, applied, and statistical issues will be addressed.  |
| The outcome | Students should be able to understand the principles of algorithm design for biological datasets, to analyze problems, and use described methods in order to locate genes, repeat families, similarities between sequences of different organisms and several other applications. |
| Contents |
| Contents of lectures | Sequence Alignments, Hidden Markov Models, Multiple Alignment Algorithms, Gene Expression Analysis, Population Genomics, Molecular Evolution, Comparative Genomics |
| Contents of exercises | Same as for the theoretical lessons |
| Literature |
| 1 | R. Durbin, S. Eddy, A. Krogh, G. Mitchison: Biological Sequence Analysis, Cambridge University Press |
| 2 | Neil C. Jones, Pavel A. Pevzner: An Introduction to Bioinformatics Algorithms, MIT Press |
| 3 | D. Gusfield: Alogorithms on Strings, Trees and Sequences, Cambridge University Press |
| 4 | Most current research work |
| Number of hours per week during the semester / trimester / year |
| Lectures | Exercises | OTC | Study and Research | Other classes |
| 2 | 2 |  | 1 |  |
| Methods of teaching |
| Lectures | Lecture notes (based on textbook: R. Durbin, S. Eddy, A. Krogh, G. Mitchison: Biological Sequence Analysis, Cambridge University Press) are courtesy of Stanford instructors (S. Batzoglou + V.Popic, course: Computational Genomics) and are used with permission. |
| Exercises | Exercise notes (based on textbook: Neil C. Jones, Pavel A. Pevzner: An Introduction to Bioinformatics Algorithms, MIT Press) are prepared by Nevena Miletic. |
| Project | Tools (Weka + Python) and datasets (AML/ALL dataset + GenBank) used in project are both in public domain. |
| Final exam | Final exam will bi prepared based on the MIT course on Computational genomics (from public domain). Students who participiate and achieve significant results in relevant international competition will be awarded with 10 additional points maximum (decision on the exact number of points is in professor's discretionary power). |
| Knowledge score (maximum points 100) |
| Pre obligations | Points | Final exam | Points |
| Activities during lectures | 0 | Test paper | 50 |
| Practical lessons | 0 |  |
| Projects | 50 |  |
| Colloquia | 0 |  |
| Seminars | 0 |  |

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| 1. | Uvod u predavanja i vežbe | Uvod - Osnovne postavke |
| 2. | Align I + Align II + Align III | Sequence Alignment - Dynamic Programming |
| Sequence Alignment continued |
| Database Search - String Matching - Hashing |
| 3. | HMMs I + HMMs II | HMMs - Viterbi decoding |
| HMMs - Forward/Backward, Posterior Decoding, S/U Learning |
| 4. | Pair HMMs + CRF | Pair HMMs  |
| Gene Prediction - Conditional Random Fields |
| 5. | Sequence Assembly I + Sequence Assembly II |  |
| 6. | Gene Expression I + Gene Expression II | Clustering |
| Classification |
| 7. | Molecular Evolution I + Molecular Evolution II | [**Phylogenetics**](http://stellar.mit.edu/S/course/6/fa07/6.047/courseMaterial/topics/topic3/lectureNotes/Lecture11_Phylogenetics/Lecture11_Phylogenetics.pdf) |
| [**Selection**](http://stellar.mit.edu/S/course/6/fa07/6.047/courseMaterial/topics/topic3/lectureNotes/Lecture12_Selection/Lecture12_Selection.pdf) |
| 8. | Population Genomics I + Population Genomics II | [**Selection**](http://stellar.mit.edu/S/course/6/fa07/6.047/courseMaterial/topics/topic3/lectureNotes/Lecture13_PopulationGenomics/Lecture13_PopulationGenomics.pdf) |
| [**Association Studies**](http://stellar.mit.edu/S/course/6/fa07/6.047/courseMaterial/topics/topic3/lectureNotes/Lecture14_CaseStudies/Lecture14_CaseStudies.pdf) |
| 9. | Multiple Sequence Alignment + Sequencing Technologies |  |
| 10. | Comparative Genomics I + Comparative Genomics II | [**Evolutionary Signatures**](http://stellar.mit.edu/S/course/6/fa07/6.047/courseMaterial/topics/topic3/lectureNotes/Lecture18_ComparativeGeno---utionarySignatures/Lecture18_ComparativeGeno---utionarySignatures.pdf) |
| [**Protein - coding genes**](http://stellar.mit.edu/S/course/6/fa07/6.047/courseMaterial/topics/topic3/lectureNotes/Lecture19_CGII_GeneIdentification/Lecture19_CGII_GeneIdentification.pdf)**,** [**Gene Regulation**](http://stellar.mit.edu/S/course/6/fa07/6.047/courseMaterial/topics/topic3/lectureNotes/Lecture20_CGIII_GeneRegulation/Lecture20_CGIII_GeneRegulation.pdf) |
| 11. | Evolutionary Genomics + Motif Discovery | [**Genome Duplication - Phylogenomics**](http://stellar.mit.edu/S/course/6/fa07/6.047/courseMaterial/topics/topic3/lectureNotes/Lecture26_GenomeEvolution/Lecture26_GenomeEvolution.pdf) |
| Motif Discovery - Expectation Maximization - Gibbs Sampling |
| 12. | Ponavljanje gradiva |  |