

Predrag Radivojac, Ph.D.

Associate Professor of Informatics and Computing
Adjunct Associate Professor of Statistics
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Education

2003	Temple University	Ph.D.	Computer and Information Sciences	(Artificial Intelligence)
1997	University of Belgrade, Serbia	M.S.	Electrical Engineering	(Information Theory)
1994	University of Novi Sad, Serbia	B.S.	Electrical Engineering	(Signal Communications)

Professional Experience

2010-	Adjunct Associate Professor, Department of Statistics, Indiana University, Bloomington, IN
2010-	Associate Professor, School of Informatics and Computing, Indiana University, Bloomington, IN
2009-2010	Adjunct Assistant Professor, Department of Statistics, Indiana University, Bloomington, IN
2005-2010	Assistant Professor, School of Informatics, Indiana University, Bloomington, IN
2004-2005	Visiting Assistant Professor, School of Informatics, Indiana University, Bloomington, IN
2004-2005	Consultant, Molecular Kinetics Inc., Indianapolis, IN
2004	Post-doctoral fellow, School of Medicine, Indiana University, Indianapolis, IN
2002 Summer	Visiting Researcher, Molecular Kinetics Inc., Pullman, WA
2001 Summer	Software Design Engineer, Natural Language Group, Microsoft Corp., Redmond, WA
2000-2003	Teaching and Research Assistant (half-time position), Temple University, Philadelphia, PA
1994-1999	Associate Instructor and Research Associate (full-time position; 12/1997-12/1998 – military service) School of Engineering, University of Novi Sad, Serbia

Teaching Experience

CSCI-B555: Machine Learning (Fall 2010, Fall 2011)
INFO-I211: Information Infrastructure II (Spring 2008, Spring 2009, Spring 2010)
INFO-I500: Fundamental Computer Concepts of Informatics (Fall 2005, Fall 2006, Fall 2007, Fall 2008, Fall 2009)
INFO-I619: Structural Bioinformatics (Spring 2006, Spring 2008)
INFO-I400: Topics in Informatics: Data Mining (Spring 2005)
INFO-I400: Topics in Informatics: Genes and Blue Genes (Fall 2004)

Awards and Honors

- Nominated two times by students and recognized for exemplar support of women in informatics. Women In Computing (WIC) Banquet 2009-2010, Bloomington, IN.
- National Science Foundation CAREER Award (2007-2012)
- \$500 graduate student award, Temple University (2002)
- Outstanding young researcher, fully subsidized university housing (400 ft² apt.) for 3 years, University of Novi Sad (1998-1999)
- Travel grant, International Symposium on Information Theory, Ulm Germany (1997)

Student Awards

- Fuxiao Xin, 2011, Full Travel Award for Grace Hopper Conference, Portland, OR, Women in Informatics and Computing, Indiana University
- Fuxiao Xin, 2011, \$25,000 Don Brown Bioinformatics Fellowship, School of Informatics and Computing, Indiana University
- Wyatt Clark, 2011, \$1,500 Travel Award for AFP/CAFA SIG at ISMB 2011, National Institutes of Health
- Chantel Mikiska, 2011, \$1000, Hutton Honors College Professional Experience Internship Award
- Jose Lugo-Martinez, 2010-2013, \$66,000 Ford Foundation Predoctoral Diversity Fellowship
- Shuyan Li, 2010, \$1,250 Travel Award for PSB 2010, National Library of Medicine, National Institutes of Health
- Amrita Mohan, 2007-2009, \$38,750 Lilly Fellowship, Eli Lilly and Company Foundation
- Pedro Alves, 2007, \$1,250 Travel Award for PSB 2007, National Institutes of Health
- Amrita Mohan, 2007, Teaching Award, School of Informatics, Indiana University
- Amrita Mohan, 2007, \$600 Travel Award from NSF to attend Academic Workshop for Underrepresented Assistant Professors, Associate Professors, and Senior Doctoral Students, organized by the Coalition to Diversify Computing ([CDC](#))
- Wyatt Clark, 2006, \$750 Travel Award for SDM 2006, Lawrence Livermore National Laboratory
- James Costello, 2006, \$750 Travel Award for SDM 2006, Lawrence Livermore National Laboratory
- Narmada Jayasankar; \$100, Best Poster Award, InWIC 2006
- Kenneth Daily; 2005, \$400, Travel Award for CIBCB 2005, IEEE Computational Intelligence Society
- Stuart Young, 2004; \$3000, McNair Fellowship, Indiana University

Professional Memberships

- 2004- Member, International Society for Computational Biology (ISCB)
- 2007- Member, American Society for Mass Spectrometry (ASMS)
- 2004- AGEP Professor (Alliances for Graduate and Professoriate Program). AGEP is an alliance addressing national minority education challenge and promoting participation of minorities.

Professional Service

- Editorial Board member: Bioinformatics (2010-2012)
- Board of Directors: International Society for Computational Biology (2012-)
- Ad-hoc Associate Editor: PLoS Computational Biology
- Vice Chair: ACM Conference on Bioinformatics, Computational Biology and Biomedicine 2011; Scientific Program Committee member: AMIA Summit on Translational Bioinformatics 2009-2010; Program Committee: PRIB 2005-2007, ECCB 2008, SDM 2009, ECML 2009-2010, CIBCB 2007, CSB 2010, RECOMB 2011.
- Session Chair: AMIA Summit on Translational Bioinformatics 2009 (Computations underpinning molecular mechanisms of disease), 2010 (Late breaking presentations), PSB 2006-2009 (Protein interactions and disease; Molecular bioinformatics for diseases); Area Chair and Session Chair: ISMB 2006-2007 (Human health; Bioinformatics of disease), 2011 (Highlights, Late Breaking Research)
- Reviewer (journals): Bioinformatics, PLoS Comput Biol, PLoS Pathog, Nat Protoc, PLoS ONE, BMC Bioinformatics, J Biomed Inform, Hum Genet, J Proteome Res, J Mol Biol, Mol Biol Evol, Proteins, Genome Biol, Genomics, IEEE Trans Comp Biol Bioinformatics, J Bioinform Comput Biol, J Chem Inf Model...
- Reviewer (conferences): PSB 2004-2005, PSB 2010, SDM 2003-2004, CSB 2004, 2007, BioKDD 2003, RECOMB 2008, AMIA STB 2010, AMIA STB 2011 ...
- NSF grant panelist (2008, 2011); ad-hoc NSF and NIH grant reviewer

Summary of Interests

The research of Prof. Radivojac focuses on the development and application of computational approaches towards understanding of protein function at the residue and whole-molecule level. Current and future projects are also oriented towards understanding whether and how amino acid substitutions lead to human disease and inferring gene-disease relationships. Of particular interests are protein post-translational modifications and ways in which they regulate protein function and lead to a disease state. Another direction of Prof. Radivojac's research is computational mass spectrometry-based proteomics, i.e. algorithm development for peptide/protein identification and label-free quantification from tandem mass spectrometry (MS/MS) data. The eventual goal is

biomarker discovery and diagnostics from MS/MS data. Prof. Radivojac also studies/develops classification algorithms in the supervised and semi-supervised scenarios and is interested in statistical inference from large, biased, and high-dimensional data.

M.S. Thesis Advisor:	Vojin Senk	School of Engineering, University of Novi Sad, Serbia
Ph.D. Thesis Advisor:	Zoran Obradovic	Dept. of Computer and Information Sciences, Temple University
Post-doc Advisor:	A. Keith Dunker	Dept. of Biochemistry, School of Medicine, Indiana University

Selected Talks, Tutorials, Guest Lectures

1. The Critical Assessment of Function Annotation (CAFA) experiment: a community-wide effort towards a better functional annotation of genes and genomes, Rocky 2011, Snowmass Village, Colorado, December 2011
2. Protein function: characterization, methods, challenges, AFP SIG at ISMB 2011, Vienna, Austria, July 2011
3. Towards predicting molecular cause of disease from amino acid substitutions, Post-Genome Wide Association Initiative Meeting, Bethesda, Maryland, January 2011 (invited talk by the National Cancer Institute)
4. Testing the ortholog conjecture with comparative and functional genomics data, Buck Institute for Age Research, Novato, California, December 2010 (invited talk)
5. Towards predicting molecular cause of disease from amino acid substitutions, Department of Computer and Information Sciences, Temple University, Philadelphia, Pennsylvania, October 2010 (invited talk)
6. Towards predicting molecular cause of disease from amino acid substitutions, Department of Computer and Information Science, Delaware State University, Dover, Delaware, October 2010 (invited talk)
7. Protein function: prediction, evolution, and future informatics challenges, Department of Bioengineering and Therapeutic Sciences, University of California – San Francisco, San Francisco, California, March 2010 (invited talk)
8. Towards predicting molecular cause of disease from amino acid substitutions, Department of Biological Sciences, University of Maryland – Baltimore County, Baltimore, Maryland, October 2009 (invited talk)
9. Protein function: prediction, evolution, and future informatics challenges, Department of Microbiology, Miami University, Oxford, Ohio, September 2009 (invited talk)
10. Methods towards characterizing amino acid substitutions in human disease, Genentech Inc., San Francisco, California, March 2009 (invited talk)
11. Graph kernels for predicting functionally important residues in proteins, Department of Computer Science and Engineering, University of Notre Dame, South Bend, Indiana, January 2009 (invited talk)
12. Networks in bioinformatics, Department of Computer Science and Engineering, University of Notre Dame, South Bend, Indiana, January 2009 (guest lecture)
13. Molecular bioinformatics for disease, Pacific Symposium on Biocomputing, Big Island, Hawaii, January 2009 (tutorial)
14. Methods for protein identification and quantification from MS/MS data, Department of Statistics, Purdue University, March 2008 (invited talk)
15. Gain and loss of phosphorylation sites in human cancer, European Conference on Computational Biology (ECCB), Cagliari, Italy, September 2008
16. Methods for protein identification from mass spectrometry data, School of Engineering, University of Novi Sad, Novi Sad, Serbia, September 2008 (invited talk)
17. Predicting protein-disease relationships, Automated Function Prediction SIG Meeting at ISMB, Toronto, Canada, July 2008 (conference talk)
18. Prediction of protein function: a journey from molecular to phenotypic level, Automated Function Prediction SIG Meeting at ISMB, Toronto, Canada, July 2008 (tutorial, with Prof. Yanay Ofran, Bar-Ilan University, Israel)
19. Methods for protein identification and quantification from tandem mass spectrometry data. 39th Symposium on Interface: Computing Science and Statistics. Theme: Systems Biology. Philadelphia, Pennsylvania, May 2007 (invited talk)
20. Informatics approaches to protein post-translational modifications, Methods for Protein Structure Analysis (MPSA), Lille, France, September 2006 (conference talk)
21. A machine learning approach to predicting peptide fragmentation spectra, The 3rd Annual Indiana Bioinformatics Conference, Indianapolis, Indiana, May 2006 (invited talk)
22. Computational approaches to protein identification and quantification, Indiana Centers for Applied Protein Sciences (INCAPS), Indianapolis, Indiana, June 2006 (invited talk)
23. What is Bioinformatics? School of Engineering, University of Novi Sad, Serbia, August 2005 (invited talk)
24. Bioinformatics: major tasks and methods for predicting protein function, Department of Computer Science and Engineering, University of Notre Dame, South Bend, Indiana, April 2005 (guest lecture)

Panels

1. Panelist. Biomolecular networks: from analysis to synthesis. Pacific Symposium on Biocomputing (PSB 2009). Big Island, Hawaii, January 2009.
2. Panel co-chairperson. Molecular bioinformatics for diseases: protein interactions and phenomics. Pacific Symposium on Biocomputing (PSB 2008). Big Island, Hawaii, January 2008.
3. Panelist. Prediction of intrinsically disordered protein regions. 7th community wide experiment on the Critical Assessment of Techniques for Protein Structure Prediction (CASP7). Pacific Grove, California, November 2006.
4. Panel chairperson. Protein interactions in disease. Pacific Symposium on Biocomputing (PSB 2006). Maui, Hawaii, January 2006.

Active Funding

Informatic profiling of clinically relevant mutation

- PI: Sean Mooney, Buck Institute for Research on Ageing
- National Institute of Health, 2 R01 LM009722-06A1
- 09/30/11-08/31/15
- Role: co-Investigator
- 2 students per year

Automated function prediction (AFP 2011)

- PI: Predrag Radivojac
- National Institutes of Health, R13 HG006079-01A1
- 01/01/11-12/31/11
- \$20,000

Computational approaches to protein identification and quantification using MS/MS

- PI: Predrag Radivojac
- National Institutes of Health, R01 RR024236-01A1
- 09/15/08-08/31/11 (extension 2012)
- \$813,146 (total award; 1 post-doc, 3 students per year)

CAREER: Bioinformatics of protein post-translational modifications

- PI: Predrag Radivojac
- National Science Foundation, DBI-0644017
- 07/01/07-06/30/12 (extension 2013)
- \$595,948 (total award; 2 students per year)
- \$12,500 REU Supplement awarded as of 07/2009 for one additional undergraduate student

Recently Completed Funding

The center of excellence in systems microbiology

- PI: Yves Brun, Indiana University, Dept. of Biology
- MetaCyt, Indiana University Award
- 01/01/08-12/31/10
- \$1,895,385 (total award; 1 student per year)
- Role: co-PI

APT: the analytical proteomics team

- PI: Fred Regnier, Purdue University, Dept. of Chemistry
- National Cancer Institute, U24 CA126480-01
- 10/01/06-08/31/11
- \$5,959,801 (total award; 1 student per year)
- Role: co-PI

Informatic profiling of clinically relevant mutation

- PI: Sean Mooney, Buck Institute for Age Research
- National Institute of Health, R01 LM009722-01
- 10/01/07-09/30/11
- \$1,314,515 (total award; 1 post-doc per year)
- Role: co-Investigator

Current Group Members

Ph.D. students:

Wyatt Clark (Informatics; exp. grad. 2012)
 Jose Lugo-Martinez (Computer Science)
 Vikas Pejaver (Informatics)
 Fuxiao Xin (Informatics; exp. grad. 2012)

Xin He (Informatics; unofficial advising)
 Chao Ji (Informatics; unofficial advising)
 Kymberleigh Pagel (Informatics; unofficial advising)

Undergraduate students:

Joseph Mikiska

Ph.D. Theses Advised

Amrita Mohan

Thesis title: A systematic study of intrinsic disorder and its roles in functional proteomics

Program: Informatics

Defense: October 23, 2009

Next position: Post-doctoral research fellow in cancer systems biology, OSI Pharmaceuticals, Melville, New York

Yong Li

Thesis title: Statistical learning algorithms for protein inference and quantification in proteomics

Program: Informatics

Defense: August 11, 2011

Next position: Senior Biologist, Dow AgroSciences LLC, Indianapolis, Indiana

Department/School Service

- Director of the Computer Science Ph.D. Studies (2010-2012)
 - Proposed a new Ph.D. curriculum; Approved by the University Graduate School
- Graduate Admissions Committee (2004-2006, 2007-2008)
- Undergraduate Education Committee (2006)
- Strategic Research Committee (2007)
- Colloquium Committee (2007-2008)
- Hiring Committee(s) (2008, 2010, 2011 as chair)
- Space Committee (2010)
- Web Steering Committee (2010-2011)

Miscellaneous, Trivia

- H-index: 19 (ISI Web of Knowledge), 24 (Google Scholar)
- CASP7 – second best predictor of protein function; category of difficult-to-infer functions (team: IUBInfo)
- CASP5, CASP6, CASP7 – best predictor for intrinsically disordered proteins (team: ISTZoran)
- Paper "Intrinsic disorder and functional proteomics" by Radivojac et al. in 2007 was the first review article ever in the Biophysical Journal
- According to the Mathematics Genealogy Project (MGP), maintained at the North Dakota State University, some of my famous scientific (great)ⁿ grandfathers are Alonzo Church (6th generation), Simeon Lagrange, Leonard Euler, and Jacob Bernoulli.
- My name in the Serbian Cyrillic alphabet: Предраг Радивојац

[CASP](#) stands for "Critical Assessment of techniques for protein Structure Prediction" and is the major meeting for world-wide assessment of computational methods for predicting protein structure and function. CASP is held bi-yearly.

Complete Publication List

Reviews

1. Xin F, Radivojac P. Computational methods for identification of functional residues in protein structures. *Curr. Prot. Pept. Sci.* (2011) 12(6): 456-469.
2. Dalkilic MM, Costello JC, Clark WT, Radivojac P. From protein-disease associations to disease informatics. *Front. Biosci.* (2008) 13: 3391-3407.
3. Radivojac P, Iakoucheva LM, Oldfield CJ, Obradovic Z, Uversky VN, Dunker AK. Intrinsic disorder and functional proteomics. *Biophys. J.* (2007) 92(5): 1439-1456.
4. Senk V, Radivojac P, Stanojevic I. An overview of decoding procedures for trellis codes. *Proc. Telecommunication Forum, TELFOR 1999*, pp. 257-264, Belgrade, Serbia, November 1999.

Research Papers

5. Li YF, Arnold RJ, Radivojac P, Tang H. Protein identification problem from a Bayesian point of view. Accepted in *Statistics and Its Interface*.
6. Zhao Y, Clark WT, Mort M, Cooper DN, Radivojac P, Mooney SD. Prediction of functional regulatory SNPs in monogenic and complex disease. *Hum. Mutat.* (2011) 32(10): 1183-1190.
7. Liu X, Li YF, Bohrer BC, Arnold RJ, Radivojac P, Tang H, Reilly JP. Investigation of VUV photodissociation propensities using peptide libraries. *Int. J. Mass Spectrom.* (2011) 308(2-3): 142-154.
8. Nehrt NL, Clark WT, Radivojac P, Hahn MW. Testing the ortholog conjecture with comparative functional genomics data from mammals. *PLoS Comput. Biol.* (2011) 7(6): e1002073.
9. Clark WT, Radivojac P. Analysis of protein function and its prediction from amino acid sequence. *Proteins* (2011) 79(7): 2086-2096.
10. Pereira L, Soares P, Radivojac P, Li B, Samuels DC. Comparing phylogeny and the predicted pathogenicity of protein variations reveals equal purifying selection across the global human mtDNA diversity. *Am. J. Hum. Genet.* (2011) 88(4): 433-439.
11. Li S, Arnold RJ, Tang H, Radivojac P. On the accuracy and limits of peptide fragmentation spectrum prediction. *Anal. Chem.* (2011) 83(3): 790-796.
12. Li YF, Arnold RJ, Tang H, Radivojac P. The importance of peptide detectability for protein identification, quantification, and experiment design in MS/MS proteomics. *J. Proteome Res.* (2010) 9(12): 6288-6297.
13. Bohrer BC, Li YF, Reilly JP, Clemmer DE, DiMarchi RD, Radivojac P, Tang H, Arnold RJ. Combinatorial libraries of synthetic peptides as a model for shotgun proteomics. *Anal. Chem.* (2010) 82(15): 6559-6568.
14. Xin F, Myers S, Li YF, Cooper DN, Mooney SD, Radivojac P. Structure-based kernels for the prediction of catalytic residues and their involvement in human inherited disease. *Bioinformatics* (2010) 26(16): 1975-1982.
15. Mort M, Evani US, Krishnan VG, Kamati KK, Baenziger PH, Bagchi A, Peters BJ, Sathyesh R, Li B, Sun Y, Xue B, Shah NH, Kann MG, Cooper DN, Radivojac P, Mooney SD. *In silico* functional profiling of human disease-associated and polymorphic amino acid substitutions. *Hum. Mutat.* (2010) 31(3): 335-346.
16. Vacic V, Iakoucheva LM, Lonardi S, Radivojac P. Graphlet kernels for prediction of functional residues in protein structures. *J. Comput. Biol.* (2010) 17(1): 55-72.
17. Radivojac P, Vacic V, Haynes C, Cocklin RR, Mohan A, Heyen JW, Goebel MG, Iakoucheva LM. Identification, analysis and prediction of protein ubiquitination sites. *Proteins* (2010) 78(2): 365-380.
18. Li S, Iakoucheva LM, Mooney SD, Radivojac P. Loss of post-translational modification sites in disease. *Pac. Symp. Biocomput.* (2010) 337-347.
19. Li B, Krishnan VG, Mort ME, Xin F, Kamati KK, Cooper DN, Mooney SD, Radivojac P. Automated inference of molecular mechanisms of disease from amino acid substitutions. *Bioinformatics* (2009) 25(21): 2744-2750.
20. Mohan A, Uversky VN, Radivojac P. Influence of sequence changes and environment on intrinsically disordered proteins. *PLoS Comput. Biol.* (2009) 5(9): e1000497.
21. Li YF, Arnold RJ, Li Y, Radivojac P, Sheng Q, Tang H. A Bayesian approach to protein inference problem in shotgun proteomics. *J. Comput. Biol.* (2009) 16(8): 1183-1193.
 - 21.1. Li YF, Arnold RJ, Li Y, Radivojac P, Sheng Q, Tang H. A Bayesian approach to protein inference problem in shotgun proteomics. *The 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB 2008*, pp. 167-180, Singapore, 2008.
22. Lee E, Jung H, Radivojac P, Kim J-W, Lee D. Analysis of AML genes in dysregulated molecular networks. *BMC Bioinformatics* (2009) 10 (Suppl 9): S2.

- 22.1. Lee E, Jung H, Radivojac P, Kim J-W, Lee D. Analysis of AML genes in dysregulated molecular networks. *AMIA Summit on Translational Bioinformatics* (2009), San Francisco, California, March 2009.
23. Radivojac P, Baenziger PH, Kann MG, Mort ME, Hahn MW, Mooney SD. Gain and loss of phosphorylation sites in human cancer. *Bioinformatics* (2008) 24(16): i241-i247.
24. Mohan A, Sullivan WJ Jr, Radivojac P, Dunker AK, Uversky VN. Intrinsic disorder in pathogenic and non-pathogenic microbes: discovering and analyzing the unfoldomes of early-branching eukaryotes. *Mol. Biosyst.* (2008) 4(4): 328-340.
25. Radivojac P, Peng K, Clark WT, Peters BJ, Mohan A, Boyle SM, Mooney SD. An integrated approach to inferring gene-disease associations in humans. *Proteins* (2008) 72(3): 1030-1037.
26. Saha S, Harrison SH, Shen C, Tang H, Radivojac P, Arnold RJ, Zhang X, Chen JY. HIP2: An online database of human plasma proteins from healthy individuals. *BMC Med. Genomics* (2008), 1(1): 12.
27. Singh A, Olowoyeye A, Baenziger PH, Dantzer J, Kann MG, Radivojac P, Heiland R, Mooney SD. MutDB: update on development of tools for the biochemical analysis of genetic variation. *Nucleic Acids Res.* (2008) 36(Database issue): D815-819.
28. Abi-Haidar A, Kaur J, Maguitman A, Radivojac P, Rechtsteiner A, Verspoor K, Wang Z, Rocha LM. Uncovering protein interaction in abstracts and text using a novel linear model and word proximity networks. *Genome Biol* (2008) 9(S2): S11.
- 28.1. Abi-Haidar A, Kaur J, Maguitman A, Radivojac P, Rechtsteiner A, Verspoor K, Wang Z, Rocha LM. Uncovering protein-protein interactions in the bibliome. *Proceedings of the Second BioCreative Challenge Evaluation Workshop*, 2007.
29. Alves P, Arnold RJ, Clemmer DE, Li Y, Reilly JP, Sheng Q, Tang H, Xun Z, Zeng R, Radivojac P. Fast and accurate identification of semi-tryptic peptides in shotgun proteomics. *Bioinformatics* (2008) 24(1): 102-109.
30. Vacic V, Oldfield CJ, Mohan A, Radivojac P, Cortese MS, Uversky VN, Dunker AK. Characterization of molecular recognition features, MoRFs, and their binding partners. *J. Proteome Res.* (2007) 6(6): 2351-66.
31. Youn E, Peters BJ, Radivojac P, Mooney SD. Evaluation of features for catalytic residue prediction in novel folds. *Protein Sci.* (2007) 16(2): 216-226.
32. Alves P, Arnold RJ, Novotny MV, Radivojac P, Reilly JP, Tang H. Advancement in protein inference from shotgun proteomics using peptide detectability. *Pac. Symp. Biocomput.* (2007) 409-420.
33. Tang H, Arnold RJ, Alves P, Xun Z, Clemmer DE, Novotny MV, Reilly JP, Radivojac P. A computational approach toward label-free protein quantification using predicted peptide detectability. *Bioinformatics* (2006) 22(14): e481-e488.
34. Mohan A, Oldfield CJ, Radivojac P, Vacic V, Cortese MS, Dunker AK, Uversky VN. Analysis of molecular recognition features (MoRFs). *J. Mol. Biol.* (2006) 362(5): 1043-1059.
35. Haynes C, Oldfield CJ, Ji F, Klitgord N, Cusick ME, Radivojac P, Uversky VN, Vidal M, Iakoucheva LM. Intrinsic disorder is a common feature of hub proteins from four eukaryotic interactomes. *PLoS Comput. Biol.* (2006) 2(8): e100.
36. Dalkilic MM, Clark WT, Costello JC, Radivojac P. Using compression to detect classes of inauthentic texts. *SIAM International Conference on Data Mining, SDM 2006*, pp. 604-608, Bethesda, Maryland, U.S.A., April 2006.
37. Roy S, Schnell S, Radivojac P. Unraveling the nature of the segmentation clock: intrinsic disorder of clock proteins and their interaction map. *Comput. Biol. Chem.* (2006) 30(4): 241-248.
38. Vacic V, Iakoucheva LM, Radivojac P. Two Sample Logo: a graphical representation of the differences between two sets of sequence alignments. *Bioinformatics* (2006) 22(12): 1536-1537.
39. Romero PR, Zaidi S, Fang YY, Uversky VN, Radivojac P, Oldfield CJ, Cortese MS, Sickmeier M, LeGall T, Obradovic Z, Dunker AK. Alternative splicing in concert with protein intrinsic disorder enables increased functional diversity in multicellular organisms. *Proc. Natl. Acad. Sci. USA* (2006) 103(22): 8390-8395.
40. Peng K, Radivojac P, Vucetic S, Dunker AK, Obradovic Z. Length-dependent prediction of protein intrinsic disorder. *BMC Bioinformatics* (2006) 7(1): 208.
41. Radivojac P, Vucetic S, O'Connor TR, Uversky VN, Obradovic Z, Dunker AK. Calmodulin signaling: analysis and prediction of a disorder-dependent molecular recognition. *Proteins* (2006) 63(2): 398-410.
42. Arnold RJ, Jayasankar N, Aggarwal D, Tang H, Radivojac P. A machine learning approach to predicting peptide fragmentation spectra. *Pac. Symp. Biocomput.* (2006) 219-230.
43. Daily KM, Radivojac P, Dunker AK. Intrinsic disorder and protein modifications: building an SVM predictor for methylation. *IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology, CIBCB 2005*, pp. 475-481, San Diego, California, U.S.A., November 2005.
44. Obradovic Z, Peng K, Vucetic S, Radivojac P, Dunker AK. Exploiting heterogeneous sequence properties improves prediction of protein disorder. *Proteins* (2005) 61(S7): 176-182.
45. Peng K, Vucetic S, Radivojac P, Brown CJ, Dunker AK, Obradovic Z. Optimizing long intrinsic disorder predictors with protein evolutionary information. *J. Bioinform. Comput. Biol.* (2005) 3(1): 35-60.
46. Vucetic S, Obradovic Z, Vacic V, Radivojac P, Peng K, Iakoucheva LM, Cortese MS, Lawson JD, Brown CJ, Sikes JG, Newton CD, Dunker AK. DisProt: A database of protein disorder. *Bioinformatics* (2005) 21(1): 137-140.

47. Radivojac P, Obradovic Z, Dunker AK, Vucetic S. Feature selection filters based on the permutation test. *European Conference on Machine Learning, ECML 2004*, pp. 334-346, Pisa, Italy, September 2004.
48. Radivojac P, Chawla NV, Dunker AK, Obradovic Z. Classification and knowledge discovery in protein databases. *J. Biomed. Inform.* (2004) 37(4): 224-239.
49. Iakoucheva LM, Radivojac P, Brown CJ, O'Connor TR, Sikes JG, Obradovic Z, Dunker AK. The importance of intrinsic disorder for protein phosphorylation. *Nucleic Acids Res.* (2004) 32(3): 1037-1049.
50. Radivojac P, Obradovic Z, Smith DK, Zhu G, Vucetic S, Brown CJ, Lawson JD, Dunker AK. Protein flexibility and intrinsic disorder. *Protein Sci.* (2004) 13(1): 71-80.
51. Obradovic Z, Peng K, Vucetic S, Radivojac P, Brown CJ, Dunker AK. Predicting intrinsic disorder from amino acid sequence. *Proteins* (2003) 53(S6): 566-572.
52. Smith DK, Radivojac P, Obradovic Z, Dunker AK, Zhu G. Improved amino acid flexibility parameters. *Protein Sci.* (2003), 12(5):1060-1072.
53. Radivojac P, Korad U, Sivalingam KM, Obradovic Z. Learning from class-imbalanced data in wireless sensor networks. *IEEE Semiannual Vehicular Technology Conference, VTC-Fall 2003*, Vol. 5, pp. 3030-3034, Orlando, Florida, U.S.A., October 2003.
54. Radivojac P, Obradovic Z, Brown CJ, Dunker AK. Prediction of boundaries between intrinsically ordered and disordered protein regions. *Pac. Symp. Biocomput.* (2003) 216-227.
55. Senk V, Radivojac P, Radujkov I. The systolic bidirectional algorithm for decoding trellis codes. *IEEE International Symposium on Information Theory, ISIT 2002*, p. 260, Lausanne, Switzerland, July 2002.
- 55.1. Senk V, Radivojac P. A new bidirectional algorithm for decoding trellis codes. *IEEE International Conference on Trends in Communications, EUROCON 2001*, pp. 34-36, Bratislava, Slovak Republic, July 2001.
56. Radivojac P, Obradovic Z, Brown CJ, Dunker AK. Improving sequence alignments for intrinsically disordered proteins. *Pac. Symp. Biocomput.* (2002) 589-600.
57. Vucetic S, Radivojac P, Dunker AK, Brown CJ, Obradovic Z. Methods for improving protein disorder prediction. *International Joint INNS-IEEE Conference on Neural Networks*, Vol. 4, pp. 2718-2723, Washington DC, U.S.A., July 2001.
58. Senk V, Radivojac P, Todic O. An application of the bidirectional stack algorithm to speech coding. *IEEE International Conference on Telecommunications in Modern Satellite, Cable, and Broadcasting Services, TELSIKS 1999*, Vol. I, pp. 259-262, Nis, Serbia, October 1999.
59. Senk V, Radivojac P. Universal trellis coding of speech. *International Conference on Telecommunications, ICT 1998*, Vol. II, pp. 273-277, Porto Carras, Greece, June 1998.
- 59.1. Radivojac P, Senk V, Savic M. Filter bank based trellis coding of speech. *Australian Workshop on Signal Processing Applications, WoSPA 1997*, pp. 51-54, Brisbane, Australia, November 1997.
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