

Predrag Radivojac, Ph.D.

Professor

Department of Computer Science
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EDUCATION

2003	Ph.D.	Computer and Information Sciences, Temple University, USA
1997	M.Sc.	Electrical Engineering, University of Belgrade, Serbia
1994	B.Sc.	Electrical Engineering, University of Novi Sad, Serbia

RESEARCH INTERESTS

Bioinformatics and Computational Biology

Understanding protein function and method development for function prediction. Post-translational modifications. Algorithm development for mass spectrometry (MS) and MS/MS proteomics.

Biomedical Informatics and Precision Medicine

Development of computational models for understanding, predicting and experimentally testing molecular mechanisms of disease. Candidate gene prioritization and biomarker discovery. Genome interpretation.

Machine Learning

Structured-output learning and performance evaluation. Kernel-based inference on (hyper)graphs. Learning from biased data. Semi-supervised learning. Distance metrics.

PROFESSIONAL EXPERIENCE

2015-	Professor, Department of Computer Science, Indiana University, Bloomington
2009-	Adjunct Faculty, Department of Statistics, Indiana University, Bloomington
2010-2015	Associate Professor, Department of Computer Science and Informatics, Indiana University, Bloomington
2005-2010	Assistant Professor, School of Informatics and Computing, Indiana University, Bloomington
2004-2005	Visiting Assistant Professor, School of Informatics, Indiana University, Bloomington
2004-2005	Consultant, Molecular Kinetics Inc., Indianapolis
2004	Post-doctoral fellow, School of Medicine, Indiana University, Indianapolis
2002 Summer	Visiting Researcher, Molecular Kinetics Inc., Pullman, Washington
2001 Summer	Software Design Engineer, Natural Language Group, Microsoft Corp., Redmond, Washington
2000-2003	Teaching and Research Assistant, Temple University, Philadelphia, Pennsylvania

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-P556: Applied Machine Learning (Fall 2017)
CSCI-B365: Introduction to Data Analysis and Mining (Fall 2016)
CSCI-B565: Data Mining (Spring 2016)
CSCI-B503: Algorithms Design and Analysis (Fall 2015)
CSCI-B490: Seminar in Computer Science: Data Mining (Falls 2014-2015)
CSCI-Y799: Computer Science Colloquium (Falls 2013-2014, Spring 2014)
CSCI-B555: Machine Learning (Falls 2010-2011, Springs 2013-2015)
INFO-I211: Information Infrastructure II (Springs 2008-2010)
INFO-I500: Fundamental Computer Concepts of Informatics (Falls 2005-2009)
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

August-Wilhelm Scheer Visiting Professor at Technical University of Munich, Germany, 2016-2017
Senior Member, International Society for Computational Biology, 2015
National Science Foundation CAREER Award, 2007
Graduate student award, Temple University, 2002
Outstanding young researcher, University of Novi Sad, 1998
Travel grant, International Symposium on Information Theory, Ulm, Germany, 1997

PROFESSIONAL SOCIETIES

Senior Member, International Society for Computational Biology (ISCB)
Member, American Society for Mass Spectrometry (ASMS)
Member, Association for Computing Machinery (ACM)

PROFESSIONAL ACTIVITIES

Board of Directors, International Society for Computational Biology (ISCB), 2012-

Associate Editor, PLoS Computational Biology, 2014-
Guest Associate Editor, PLoS Computational Biology, 2013-2014
Guest Editor, Human Mutation, 2016-2017
Editorial Board member, Bioinformatics, 2010-

Program Chair
Great Lakes Bioinformatics Conference, GLBIO 2015

Area Chair

Intelligent Systems for Molecular Biology and European Conference on Computational Biology,
ISMB/ECCB 2007
Intelligent Systems for Molecular Biology, ISMB 2006

Vice Chair

ACM Conference on Bioinformatics, Computational Biology and Biomedicine, ACM BCB 2011

Proceedings Chair

Intelligent Systems for Molecular Biology, ISMB 2018

Session Organizer

Pacific Symposium on Biocomputing, PSB 2017
Automated Function Prediction Special Interest Group Meeting, AFP-SIG 2011-2015
Pacific Symposium on Biocomputing, PSB 2006-2009

Program Committees:

ACM Conference on Bioinformatics, Computational Biology, and Health Informatics, ACM BCB 2015-2017
Intelligent Systems for Molecular Biology, ISMB 2016
ISCB-Asia International Conference on Genome Informatics, GIW/ISCB 2014
International Workshop on Data Mining in Bioinformatics, BioKDD 2003, 2013-2014
ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics, ACM BCB 2012-2013
Intelligent Systems for Molecular Biology and European Conference on Computational Biology, ISMB/ECCB 2013, 2017
Research in Computational Molecular Biology, RECOMB 2011
Computational Systems Bioinformatics, CSB 2010
European Conference on Machine Learning, ECML 2009-2010
AMIA Summit on Translational Bioinformatics, AMIA STB 2009-2010
SIAM International Conference on Data Mining, SDM 2009
European Conference on Computational Biology, ECCB 2008
Pattern Recognition in Bioinformatics, PRIB 2005-2007
IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology, IEEE CIBCB 2007

Session Chairing

ACM Conference on Bioinformatics, Computational Biology and Health Informatics, ACM BCB 2015
Intelligent Systems for Molecular Biology, ISMB, 2006-2007, 2013-2014, 2016
ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics, ACM BCB 2013
Intelligent Systems for Molecular Biology, ISMB, Highlights, 2011-2012
Intelligent Systems for Molecular Biology, ISMB, Late Breaking Research, 2011-2012
AMIA Summit on Translational Bioinformatics, AMIA STB, Late Breaking Research, 2010

Scientific Panels

Panelist, Junior Principal Investigators Meeting, International Conference on Intelligent Systems for Molecular Biology (ISMB 2014), Boston, Massachusetts
 Panelist, Pacific Symposium on Biocomputing (PSB 2009), Big Island, Hawaii, 2009
 Panel chairperson, Pacific Symposium on Biocomputing (PSB 2008), Big Island, Hawaii, 2008
 Panelist, Critical Assessment of Techniques for Protein Structure Prediction (CASP7), Pacific Grove, California, 2006
 Panel chairperson, Pacific Symposium on Biocomputing (PSB 2006), Maui, Hawaii, 2006

Reviewer (journals)

Bioinformatics
 Biostatistics
 BMC Bioinformatics
 Brief Bioinform
 Genome Biol
 Genomics
 Hum Genet
 IEEE-ACM Trans Comput Biol Bioinform
 J Bioinform Comput Biol
 J Biomed Inform
 J Chem Inf Model
 J Mach Learn Res
 J Mass Spectrom
 J Mol Biol
 J Proteome Res
 Mol Biol Evol
 Nat Commun
 Nat Methods
 Nat Protoc
 Nucleic Acids Res
 PeerJ
 PLoS Comput Biol
 PLoS One
 PLoS Pathog
 Proteins
 Proteomics

Reviewer (conferences)

ISIT 2015
 AMIA STB 2010, 2011
 CSB 2004, 2007
 PSB 2004-2005, 2010, 2016
 RECOMB 2008
 SDM 2003-2004

Grant panelist and reviewer

National Science Foundation, 2008, 2011, 2012
 National Institutes of Health, 2013, 2015, 2016
 Genome Canada, 2012
 Ontario Genomics Institute, 2013
 Biotechnology and Biological Sciences Research Council, 2016

EDITED VOLUMES

Selected proceedings from the Automated Function Prediction Meeting 2011. *BMC Bioinformatics*, Volume 14, Supplement 3, 2013. Editors: Iddo Friedberg and Predrag Radivojac.
 Statistical mass spectrometry-based proteomics. *BMC Bioinformatics*, Volume 13, Supplement 16, 2012. Editors: Predrag Radivojac and Olga Vitek.

ADVISEE AWARDS AND HONORS

Jose Lugo-Martinez, 2017, Lane Fellowship, Carnegie Mellon University
 Shantanu Jain, Computer Science Graduate Research Award, Indiana University
 Kimberleigh Pagel, 2017, Travel Fellowship for the Sackler Colloquium on Reproducibility of Research, Washington, DC, National Science Foundation
 Vikas Pejaver, 2016, eScience Moore/Sloan Data Science Postdoctoral Fellowship, University of Washington
 Shantanu Jain, 2016, Travel Fellowship for NIPS 2016, Barcelona, Spain
 Jose Lugo-Martinez, 2015, Travel Fellowship for the Biomedical Data Research Workshop at SHILAC 2015, San Juan, Puerto Rico
 Chao Ji, 2015, Travel Fellowship for the ACM BCB 2015 conference, Atlanta, GA, National Science Foundation
 Ruiyu Yang, 2015, Full Fellowship for the Math Modeling in Industry XIX Workshop, Institute for Mathematics and its Applications, University of Minnesota, Minneapolis, MN
 Kimberleigh Pagel, 2015, Travel Fellowship for the Sackler Colloquium on Drawing Causal Inference from Big Data, Washington, DC, National Science Foundation
 Yuxiang Jiang, 2014, Travel Fellowship for ECCB 2014
 Vikas Pejaver, 2014, Travel Fellowship for the ISCB Student Council Symposium at ISMB 2014
 Kimberleigh Pagel, 2014, Travel Fellowship for ISMB 2014, National Science Foundation
 Jacob Weimer, 2014, Best Poster Award, Research Experience for Undergraduates, School of Informatics and Computing, Indiana University
 Wyatt Clark, 2014, Travel Award for PSB 2014, National Library of Medicine, National Institutes of Health
 Wyatt Clark, 2013, Ian Lawson Van Toch Memorial Award for Outstanding Student Paper at ISMB/ECCB 2013
 Jose Lugo-Martinez, 2013, Travel Fellowship for 2013 SACNAS National Conference, SACNAS
 Jose Lugo-Martinez, 2013, Broadening Participation in Data Mining Travel Scholarship for ACM SIGKDD 2013
 Wyatt Clark, 2013, Travel Award for ISMB 2013, International Society for Computational Biology
 Wyatt Clark, 2013, Travel Award for the Phenoscape Workshop, National Science Foundation
 Kimberleigh Pagel, 2013, Travel Fellowship for CAGI 2013, National Institutes of Health
 Jose Lugo-Martinez, 2012, Travel Award for Rocky 2012, Federation of American Societies for Experimental Biology (FASEB), Maximizing Access to Research Careers (MARC) Program
 Kimberleigh Pagel, 2012, Travel Award for Rocky 2012, Federation of American Societies for Experimental Biology (FASEB), Maximizing Access to Research Careers (MARC) Program

Jose Lugo-Martinez, 2012, Best Graduate Student Oral Presentation in Computer Science, SACNAS National Conference, Seattle, Washington

Wyatt Clark, 2012, Center for Bioinformatics Research Fellowship, Indiana University

Fuxiao Xin, 2011, Travel Award for Grace Hopper Conference, Portland, Oregon, Women in Informatics and Computing, Indiana University

Fuxiao Xin, 2011, Don Brown Bioinformatics Fellowship, School of Informatics and Computing, Indiana University

Wyatt Clark, 2011, Travel Award for AFP/CAFA SIG at ISMB 2011, National Institutes of Health

Jose Lugo-Martinez, 2011-2012, Computer Packages Inc. Hispanic College Fund Scholarship

Chantel Mikiska, 2011, Hutton Honors College Professional Experience Internship Award

Jose Lugo-Martinez, 2010-2013, Ford Foundation Predoctoral Diversity Fellowship

Jose Lugo-Martinez, 2010-2011, Computer Science Corporation Hispanic College Fund Scholarship

Shuyan Li, 2010, Travel Award for PSB 2010, National Library of Medicine, National Institutes of Health

Jose Lugo-Martinez, 2009-2010, Graduate Scholars Fellowship at Indiana University

Jose Lugo-Martinez, 2009-2010, Google Hispanic College Fund Scholarship

Amrita Mohan, 2007-2009, Fellowship, Eli Lilly and Company Foundation

Pedro Alves, 2007, Travel Award for PSB 2007, National Institutes of Health

Amrita Mohan, 2007, Teaching Award, School of Informatics, Indiana University

Amrita Mohan, 2007, 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

Wyatt Clark, 2006, Travel Award for SDM 2006, Lawrence Livermore National Laboratory

Narmada Jayasankar, Best Poster Award, InWIC 2006

Kenneth Daily, 2005, Travel Award for CIBCB 2005, IEEE Computational Intelligence Society

Stuart Young, 2004, McNair Fellowship, Indiana University

TALKS AND LECTURES

2016, Challenges in Machine Learning, Workshop at Advances in Neural Information Processing Systems (NIPS 2016), Barcelona, Spain

2016, Fakultät für Informatik, Technische Universität München, Germany, invited talk

2015, International Conference on Intelligent Biology and Medicine (ICIBM 2015), invited talk

2015, School of Engineering, University of Novi Sad, invited talk

2015, School of Medicine, University of Louisville, invited talk

2015, Genomics, Bioinformatics & Systems Biology joint colloquium, University of California San Diego, invited talk

2015, Training the next generation of quantitative biologists in the era of big data, workshop at Pacific Symposium on Biocomputing (PSB 2015), Kohala Coast, Hawaii, invited talk

2014, Department of Computer Science and Informatics, University of Belgrade, Serbia, invited talk

2014, International Biocuration Meeting, Toronto, Canada, invited talk

2013, ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics (ACM BCB 2013), Bethesda, Maryland, tutorial

2013, International Workshop on Data Mining in Bioinformatics (BioKDD 2013), Chicago, Illinois, invited talk

2013, Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB 2013), Berlin, Germany, highlights talk

2013, Critical Assessment of Genome Interpretation (CAGI 2013), Berlin, Germany

2013, Department of Computer Science and Informatics, University of Belgrade, Serbia, invited talk
 2013, Biostatistics Program, Stanford University, invited talk
 2012, Department of Statistics, Indiana University, invited talk
 2012, Data Mining in Bioinformatics (DMB 2012), Belgrade, Serbia, invited talk
 2011, Rocky Mountain Bioinformatics Conference (Rocky 2011), Snowmass Village, Colorado
 2011, Automated Function Prediction Special Interest Group (AFP-SIG) Meeting at ISMB/ECCB 2011, Vienna, Austria
 2011, Post-Genome Wide Association Initiative Meeting, Bethesda, Maryland, invited talk by the National Cancer Institute
 2010, Buck Institute for Research on Aging, invited talk
 2010, Department of Computer and Information Science, Temple University, invited talk
 2010, Department of Computer and Information Science, Delaware State University, invited talk
 2010, Department of Bioengineering and Therapeutic Sciences, University of California San Francisco, invited talk
 2009, Department of Biological Sciences, University of Maryland Baltimore County, invited talk
 2009, Department of Microbiology, Miami University, invited talk
 2009, Genentech Inc., invited talk
 2009, Department of Computer Science and Engineering, University of Notre Dame, invited talk
 2009, Pacific Symposium on Biocomputing (PSB 2009), Big Island, Hawaii, tutorial
 2008, Department of Statistics, Purdue University, invited talk
 2008, European Conference on Computational Biology (ECCB 2008), Cagliari, Italy
 2008, School of Engineering, University of Novi Sad, Serbia, invited talk
 2008, Automated Function Prediction Special Interest Group (AFP-SIG) Meeting at ISMB, Toronto, Canada
 2008, Automated Function Prediction Special Interest Group (AFP-SIG) Meeting at ISMB, Toronto, Canada, tutorial, with Prof. Yanay Ofran, Bar-Ilan University, Israel
 2007, Symposium on Interface: Computing Science and Statistics. Theme: Systems Biology. Philadelphia, Pennsylvania, invited talk
 2006, Methods for Protein Structure Analysis (MPSA), Lille, France
 2006, Annual Indiana Bioinformatics Conference, Indianapolis, Indiana, invited talk
 2006, Indiana Centers for Applied Protein Sciences (INCAPS), Indianapolis, Indiana, invited talk
 2005, School of Engineering, University of Novi Sad, Serbia, invited talk

ACTIVE FUNDING

The Precision Health Initiative

PI: Anantha Shakhar, Indiana University School of Medicine

Indiana University Grand Challenge Initiative

09/01/16-08/31/20

Role: Leader for Data sciences and informatics (w/ Shaun Grannis, Lang Li)

Total award: \$120,000,000.

Computational approaches to protein identification and quantification using MS/MS

PI: Predrag Radivojac

National Institutes of Health, R01 GM103725

10/01/12-09/30/16

Total award: \$1,890,595

A computational framework for predicting the impact of mutations in autism

MPIs: Lilia Iakoucheva (UCSD) and Predrag Radivojac (Indiana)

National Institutes of Health, R01 MH105524

09/25/14-09/24/17

Total award: \$1,370,000

Bilateral BBSRC-NSF/BIO Collaborative Research: ABI Development: A Critical Assessment of Protein Function Annotation

MPIs-USA: Iddo Friedberg (Iowa State), Casey Greene (U Pennsylvania), Sean Mooney (U Washington), Predrag Radivojac (Indiana)

MPIs-UK: Maria Martin (EBI), Claire O'Donovan (EBI)

National Science Foundation, DBI-1458477

09/01/15-08/31/18

Total award: \$1,565,332 (USA) + £434,604 (UK)

COMPLETED FUNDING

Informatic profiling of clinically relevant mutation; \$1,979,307 (total award; 2 graduate students per year to IU); 09/30/11-08/31/16; National Institutes of Health, R01 LM009722; PI: Sean Mooney, Buck Institute for Research on Aging; Role: co-Investigator.

Automated function prediction (AFP 2014); \$5,000; 06/01/14-05/31/15; National Institutes of Health, R13 HG007807; PI: Predrag Radivojac.

CAREER: Bioinformatics of protein post-translational modifications; \$595,948 (total award; 2 students per year to IU); 07/01/07-06/30/13; National Science Foundation, DBI-0644017; PI: Predrag Radivojac; \$12,500 REU Supplement awarded as of 07/2009 for one additional undergraduate student.

Computational approaches to protein identification and quantification using MS/MS; \$813,146 (total award; 1 post-doc, 3 students per year to IU); 09/15/08-08/31/12; National Institutes of Health, R01 RR024236-01A1; PI: Predrag Radivojac.

Informatic profiling of clinically relevant mutation; \$1,314,515 (total award; 1 post-doc per year to IU); 10/01/07-09/30/11; National Institute of Health, R01 LM009722-01; PI: Sean Mooney, Indiana University School of Medicine; Role: co-Investigator.

Automated function prediction (AFP 2011); \$20,000; 01/01/11-12/31/11; National Institutes of Health, R13 HG006079-01A1; PI: Predrag Radivojac.

APT: the analytical proteomics team; \$5,959,801 (total award; 1 student per year to IU); 10/01/06-08/31/11; National Cancer Institute, U24 CA126480-01; PI: Fred Regnier, Purdue University; Role: co-PI.

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

A hypothesis testing approach to identification and assessment of statistical significance of peptides and proteins in shotgun proteomics; \$49,919 (total award; 1 student to IU); 01/02/07-12/31/07; CLSIR, Purdue University - Indiana University pilot grant application program; PI: Olga Vitek, Purdue University; Role: collaborator.

Development of a machine learning tool for peptide identification from tandem mass spectrometry data; \$32,408 (2 students); 06/01/05-05/31/06; Indiana University Faculty Research Support Program; PI: Randy J. Arnold; Role: co-PI.

CURRENT GROUP MEMBERS

Post-doctoral Fellows:

Sujun Li
Jose Lugo-Martinez

Ph.D. students:

Shantanu Jain	(Computer Science; co-advised with Michael Trosset)
Yuxiang Jiang	(Computer Science)
Kymberleigh Pagel	(Informatics)
Mouses Stambouliau	(Informatics)
Ruiyu Yang	(Mathematics; co-advised with Elizabeth Housworth)

Master's students:

Shawn Peng	(Computer Science)
Achal Shah	(Data Science)

Undergraduate students:

Scott Mathews	(Computer Science)
Mary Anne Smart	(Computer Science, Mathematics, Spanish)

THESES ADVISED

Jose Lugo-Martinez

Thesis title: Flexible kernel functions for learning on graphs and hypergraphs

Program: Computer Science

Defense: December 12, 2016

First Ph.D. position: Post-doctoral Fellow, Indiana University, Bloomington, Indiana

Vikas Pejaver

Thesis title: Computational methods for understanding the impact of amino acid substitutions on protein function

Program: Informatics

Defense: November 17, 2016

First Ph.D. position: Post-doctoral Fellow, University of Washington, Seattle, Washington

Chao Ji

Thesis title: Machine learning algorithms for peptide identification and protein quantification in proteomics

Program: Informatics

Defense: April 11, 2016

First Ph.D. position: Research Associate, Indiana University, Bloomington, Indiana

Wyatt Clark

Thesis title: Understanding protein function through statistical inference and evolutionary analysis

Program: Informatics

Defense: June 4, 2013

First Ph.D. position: Post-doctoral Fellow, Yale University, New Haven, Connecticut

Currently: Scientist 1, Bioinformatics, Research & Development, BioMarin Pharmaceutical Inc., Novato, California

Fuxiao Xin

Thesis title: Methods for predicting functional residues in protein structures and understanding molecular mechanisms of disease

Program: Informatics

Defense: July 12, 2012

First Ph.D. position: Lead Scientist in Machine Learning, General Electric Global Research, San Ramon, California

Yong Li

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

Program: Informatics

Defense: August 11, 2011

First Ph.D. position: Senior Biologist, Dow AgroSciences LLC, Indianapolis, Indiana

Currently: Post-doctoral Fellow, Stanford University, Stanford, California

Amrita Mohan

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

Program: Informatics

Defense: October 23, 2009

First Ph.D. position: Research Fellow in Cancer Systems Biology, OSI Pharmaceuticals, Melville, New York

Currently: Director of Bioinformatics Data Science, CHDI Management Inc., Princeton, New Jersey

SCHOOL SERVICE

Department and School of Informatics and Computing:

Director of the Computer Science Ph.D. Studies, 2010-2012

Proposed a new Ph.D. curriculum; Approved by Computer Science faculty and University Graduate School

Graduate Admissions Committee, 2004-2006, 2007-2008

Undergraduate Education Committee, 2006

Strategic Research Committee, 2007

Structure Committee, 2016

Colloquium Committee, 2007-2008, 2013-2014

Hiring Committee(s), 2008, 2010, 2011-2012 as chair, 2013-2014, 2016-2017 as chair

Space Committee, 2010

Web Steering/Oversight Committee, 2010-2011, 2013-2014

Budgetary Affairs Committee, 2014-2017

Faculty Affairs Committee, 2014-2016

Numerous other responsibilities; e.g., promotion committees, curriculum subcommittees, hiring subcommittees, etc.

Indiana University:

Department of Statistics Hiring Committee, 2014-2015

Statistics Coordination Committee, 2013-

Advisory Board member, Institute for Advanced Studies, Indiana University, 2013-2015
 AGEP* Professor, 2004-

*Alliances for Graduate and Professoriate Program (AGEP) is an alliance addressing national minority education challenge and promoting participation of minorities.

ONLINE PREPRINTS

1. Pejaver et al. MutPred2: inferring the molecular and phenotypic impact of amino acid variants. bioRxiv: 134981
2. Lugo-Martinez and Radivojac. Classification in biological networks with hypergraphlet kernels. <http://arxiv.org/abs/1703.04823>
3. Yamada M et al. Ultra high-dimensional nonlinear feature selection for big biological data. <https://arxiv.org/abs/1608.04048>
4. Yang R et al. New metrics for learning and inference on sets, ontologies, and functions. <http://arxiv.org/abs/1603.06846>
5. Jain S et al. Nonparametric semi-supervised learning of class proportions. <http://arxiv.org/abs/1601.01944>

COMPLETE PUBLICATION LIST

6. Daneshjou et al. Working towards precision medicine: predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Accepted to Human Mutation.
7. Pejaver V, Mooney SD, Radivojac P. Missense variant pathogenicity predictors generalize well across a range of function-specific prediction challenges. Accepted to Human Mutation.
8. Pagel KA, Pejaver V, Lin GN, Nam H, Mort M, Cooper DN, Sebat J, Iakoucheva LM, Mooney SD, Radivojac P. When loss-of-function is loss of function: understanding mutational signatures and impact of loss-of-function genetic variants. Accepted to ISMB/ECCB 2017.
9. Jain S, White M, Radivojac P. Recovering true classifier performance in positive-unlabeled learning. *Proceedings of the 31st AAAI Conference on Artificial Intelligence, AAAI 2017*, pp. 2066-2072, San Francisco, California, U.S.A., February 2017.
10. Friedberg I, Radivojac P. Community-wide evaluation of computational function prediction. Book Chapter in *Methods in Molecular Biology*, vol. 1446. The Gene Ontology Handbook. Edited by C. Dessimoz and N. Škunca, pp. 133-146. Springer, New York, NY. 2017.
11. Jain S, White M, Radivojac P. Estimating the class prior and posterior from noisy positives and unlabeled data. *Advances in Neural Information Processing Systems, NIPS 2016*, pp. 2693-2701, Barcelona, Spain, December 2016.
12. Ioannidis NM, Rothstein JH, Pejaver V, Middha S, McDonnell SK, Baheti S, Musolf A, Li Q, Holzinger E, Karyadi D, Cannon-Albright LA, Teerlink CC, Stanford JL, Isaacs WB, Xu J, Cooney KA, Lange EM, Schleutker J, Carpten JD, Powell IJ, Cussenot O, Cancel-Tassin G, Giles GG, MacInnis RJ, Maier C, Hsieh CL, Wiklund F, Catalona WJ, Foulkes WD, Mandal D, Eeles RA, Kote-Jarai Z, Bustamante CD, Schaid DJ, Hastie T, Ostrander EA, Bailey-Wilson JE, Radivojac P, Thibodeau SN, Whittemore AS, Sieh W. REVEL: an ensemble method for predicting the pathogenicity of rare missense variants. *Am. J. Hum. Genet.* (2016) 99(4): 877-885

13. Li S, Dabir A, Misal SA, Tang H, Radivojac P, Reilly JP. Impact of amidination on peptide fragmentation and identification in shotgun proteomics. *J. Proteome Res.* (2016) 15(10): 3656-3665.
14. Lugo-Martinez J, Pejaver V, Pagel KA, Jain S, Mort M, Cooper DN, Mooney SD, Radivojac P. The loss and gain of functional amino acid residues is a common mechanism causing human inherited disease. *PLoS Comput. Biol.* (2016) 12(8): e1005091.
15. Reddy KD, Malipeddi J, DeForte S, Pejaver V, Radivojac P, Uversky VN, Deschenes RJ. Physicochemical sequence characteristics that influence S-palmitoylation propensity. *J. Biomol. Struct. Dyn.*, Accepted.
16. Rost B, Radivojac P, Bromberg Y. Protein function in precision medicine: deep understanding with machine learning. *FEBS Lett.* (2016) 590(15): 2327-2341.
17. Jiang Y, Oron TR, Clark WT, Bankapur AR, D'Andrea D, Lepore R, Funk CS, Kahanda I, Verspoor KM, Ben-Hur A, Koo da CE, Penfold-Brown D, Shasha D, Youngs N, Bonneau R, Lin A, Sahraeian SM, Martelli PL, Profiti G, Casadio R, Cao R, Zhong Z, Cheng J, Altenhoff A, Skunca N, Dessimoz C, Dogan T, Hakala K, Kaewphan S, Mehryary F, Salakoski T, Ginter F, Fang H, Smithers B, Oates M, Gough J, Toronen P, Koskinen P, Holm L, Chen CT, Hsu WL, Bryson K, Cozzetto D, Minneci F, Jones DT, Chapman S, Bkc D, Khan IK, Kihara D, Ofer D, Rappoport N, Stern A, Cibrian-Uhalte E, Denny P, Foulger RE, Hieta R, Legge D, Lovering RC, Magrane M, Melidoni AN, Mutowo-Meullenet P, Pichler K, Shypitsyna A, Li B, Zakeri P, ElShal S, Tranchevent LC, Das S, Dawson NL, Lee D, Lees JG, Sillitoe I, Bhat P, Nepusz T, Romero AE, Sasidharan R, Yang H, Paccanaro A, Gillis J, Sedenio-Cortes AE, Pavlidis P, Feng S, Cejuela JM, Goldberg T, Hamp T, Richter L, Salamov A, Gabaldon T, Marcet-Houben M, Supek F, Gong Q, Ning W, Zhou Y, Tian W, Falda M, Fontana P, Lavezzo E, Toppo S, Ferrari C, Giollo M, Piovesan D, Tosatto SC, Del Pozo A, Fernandez JM, Maietta P, Valencia A, Tress ML, Benso A, Di Carlo S, Politano G, Savino A, Rehman HU, Re M, Mesiti M, Valentini G, Bargsten JW, van Dijk AD, Gemovic B, Glisic S, Perovic V, Veljkovic V, Veljkovic N, Almeida-e-Silva DC, Vencio RZ, Sharan M, Vogel J, Kansakar L, Zhang S, Vucetic S, Wang Z, Sternberg MJ, Wass MN, Huntley RP, Martin MJ, O'Donovan C, Robinson PN, Moreau Y, Tramontano A, Babbitt PC, Brenner SE, Linial M, Orengo CA, Rost B, Greene CS, Mooney SD, Friedberg I, Radivojac P. An expanded evaluation of protein function prediction methods shows an improvement in accuracy. *Genome Biol.* (2016) 17(1): 184.
18. Peterson TA, Mort M, Cooper DN, Radivojac P, Kann MG, Mooney SD. Regulatory single nucleotide variant predictor (RSVP) increases predictive performance of functional regulatory variants. *Hum. Mutat.* (2016) 37(11): 1137-1143.
19. Ji C, Li S, Reilly JP, Radivojac P, Tang H. XLSearch: a probabilistic database search algorithm for identifying cross-linked peptides. *J. Proteome Res.* (2016) 15(6): 1830-1841.
20. Glover MS, Dilger JM, Acton MD, Arnold RJ, Radivojac P, Clemmer DE. Examining the influence of phosphorylation on peptide ion structure by ion mobility spectrometry-mass spectrometry. *J. Am. Soc. Mass Spectrom.* (2016) 27(5): 786-794.
21. Welch L, Brooksbank C, Schwartz R, Morgan SL, Gaeta B, Kilpatrick AM, Mietchen D, Moore BL, Mulder N, Pauley M, Pearson W, Radivojac P, Rosenberg N, Rosenwald A, Rustici G, Warnow T. Applying, evaluating and refining bioinformatics core competencies (an update from the Curriculum Task Force of ISCB's Education Committee). *PLoS Comput. Biol.* (2016) 12 (5): e1004943.
22. Ramalho RF, Li S, Radivojac P, Hahn MW. Proteomic evidence for in-frame and out-of-frame alternatively spliced isoforms in mammals. *IEEE-ACM Trans. Comput. Biol. Bioinform.*, accepted.
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MISCELLANEOUS AND TRIVIA

- H-index: 30 (ISI Web of Knowledge), 35 (Scopus), 40 (Google Scholar)
- Erdos number: 3, via Stefano Lonardi and Svante Janson
- Bacon number: ∞
- 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)
- CAFA1, CAFA2 – organized the first Critical Assessment for Function Prediction in 2010-2011, 2013-2014 (with Iddo Friedberg, Sean Mooney, and Michal Linial).
- CAGI – Mooney-Radivojac group performed well in multiple CAGI challenges in CAGI 1-4.
- Paper "Intrinsic disorder and functional proteomics" by Radivojac et al. in 2007 was the first article in the Biophysical Journal labeled as "Biophysical Reviews and Perspectives" (but not the first review ever)
- 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), Joseph-Louis Lagrange, Leonhard 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.

CAFA stands for "Critical Assessment of Functional Annotation". The first CAFA meeting was held at Automated Function Prediction (AFP) Special Interest Group (SIG) meeting at ISMB/ECCB 2011, Vienna, Austria. AFP SIG was first held at ISMB 2005 in Detroit.

CAGI stands for "Critical Assessment of Genome Interpretation". The first CAGI meeting was held at University of California, Berkeley in December of 2010.