

NATAŠA PRŽULJ: CURRICULUM VITÆ

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RESEARCH INTERESTS

Molecular and clinical data integration for precision medicine: patient stratification, biomarker discovery, drug re-purposing, disease re-classification
Data analytics, modeling, fusion, dynamics, applied to clinical, molecular and biological data
Algorithms for uncovering molecular mechanisms of disease from systems-level “omics” data
Molecular networks: interactome evolution, dynamics, alignment, function prediction
Large-scale economic data analysis, fusion and modeling the dynamics of economic systems
Computational graph theory, algorithms, models

EDUCATION

Ph.D. Computer Science, University of Toronto, Canada, 2005

TITLE: *Analyzing Large Biological Networks: Protein-Protein Interactions Example*

ADVISORY COMMITTEE: Derek G. Corneil (CS, co-supervisor), Igor Jurisica (CS, co-supervisor), Rudi Mathon (CS), Gil Prive (Medical Biophysics)

M.Sc. Computer Science, University of Toronto, Canada, 2000

TITLE: *Minimal Hereditary Dominating Pair Graphs*

SUPERVISOR: Derek G. Corneil (CS)

B.Sc. Computer Science and Math., Simon Fraser University, Canada, 1997

FIRST CLASS HONORS

CGPA 3.85 out of 4

PROFESSIONAL POSITIONS

April 1, 2016 – present: Full Professor, Computer Science, University College London
2012 – March 31, 2016: Assoc. Professor, Dept. Computing, Imperial College London
2009–2012: Assistant Professor, Dept. of Computing, Imperial College London
2009–2016: Member of the Center for Integrative Systems Biology (CISBIC), Imperial
2009–2016: Member of the Institute for Systems and Synthetic Biology, Imperial College
2009–2016: Member of the Centre for Bioinformatics, Imperial College London
2010–2016: Visiting Research Scientist (20%), California Institute for Telecommunications and Information Technology, Irvine, CA, USA
2013–present: Professor (0%), School of Computing (RAF), Union University, Belgrade
2005–2009: Assistant Professor, Computer Sci. Dept., University of California, Irvine
2008–2009: Member of the University of California Irvine (UCI) Cancer Center
2006–2009: Member of the UCI Center for Complex Biological Systems (CCBS)
2005–2009: Member of the UCI Institute for Genomics and Bioinformatics (IGB)
2005: Post-doctoral Fellow, Samuel Lunenfeld Research Institute, U of Toronto, Canada
2002–2003: Research Assistant, Banting and Best Institute, University of Toronto
1999–2002: Substitute Instructor and Teaching Assistant, University of Toronto

2000: Visiting PhD Student, The Fields Institute for Research in Math. Sciences, Toronto
1997–1998: Programming Consultant, Westech Information Systems, Vancouver, Canada
1996–1997: Research Assistant, Simon Fraser University, Canada
1996: Teaching Assistant, Simon Fraser University, Canada
1995: Quality Assurance Engineer, Hughes Aircraft of Canada Ltd., Richmond, BC, Canada

AWARDS AND DISTINCTIONS

ERC Consolidator Grant (PI), €2,000,000, University College London, 2018-2023

These grants are awarded by The European Research Council (ERC) to support the next generation of research leaders in Europe.

Elected into **Academia Europaea, The Academy of Europe**, in 2017

Academia Europaea promotes the advancement and propagation of excellence in scholarship in the humanities, law, the economic, social, and political sciences, mathematics, medicine, and all branches of natural and technological sciences anywhere in the world for the public benefit and for the advancement of the education of the public of all ages in the aforesaid subjects in Europe. It is a European, non-governmental association acting as an Academy.

BCS Roger Needham Award for 2014, sponsored by **Microsoft Research**, Cambridge

The award is given annually to for a distinguished research contribution in computer science by a UK based researcher within ten years of his/her PhD. The award has been made in recognition of the potential Prof. Przulj's research and work have to revolutionise health and pharmaceuticals. Dr Przulj gave her award public lecture at **The Royal Society** in London, on November 19, 2014.

Fellow of **The British Computer Society (BCS)** Academy of Computing since 2013

The BCS Academy of Computing is a learned society dedicated to advancing computing as an academic discipline.

Elected into **The Young Academy of Europe (YAE)** in 2013

The European Research Council (ERC) has manifested its support to YAE as a bottom-up initiative of a dynamic and innovative group of recognized European young scientists with outspoken views about science and science policy. YAE also has a close association with The Academy of Europe (Academia Europaea), a functioning European Academy of Humanities, Letters and Sciences.

ERC Starting Independent Researcher Grant (PI), €1,638,175, Imperial College London and University College London, 2012-2017

These grants are awarded by The European Research Council (ERC) to support the next generation of research leaders in Europe.

USA NSF CDI-Type II Award (co-PI), \$1,999,503, UC Irvine, 10/01/2010-30/09/2016

GlaxoSmithKline Ph.D. studentships, £80,000, Imperial College London, 2010-2013

NVIDIA Academic Partnership Program, Imperial College London, 2013

Google EMEA AndroidEDU Teaching Award, Imperial College London, 2012

USA NSF CAREER Award (PI), \$569,905, UC Irvine, 2007-2011

The Faculty Early Career Development (CAREER) Program is a Foundation-wide activity that offers the USA National Science Foundation's (NSF) most prestigious awards in support of junior faculty who exemplify the role of teacher-scholars through outstanding research, excellent education and the integration of education and research within the context of the mission of their organizations.

Council on Research, Computing and Library Resources (co-PI), \$11,803, UCI, 2008-09

Center for Complex Biological Systems Annual Retreat Prizes (PI), \$20,000, UCI, 2008

Nominated for 2008 **SIAM Dénes König Prize** (SIAG/Discrete Math) for paper J-9 below

Awarded biennially to a junior researcher for outstanding research in an area of discrete mathematics, based on a publication by the candidate in a peer-reviewed

journal published in the three calendar years prior to the year of the award.

The Society for Industrial and Applied Mathematics (SIAM) is an international community fostering the development of applied mathematical and computational methodologies needed in various application areas.

Council on Research, Computing and Library Resources (CORCLR), \$5,400, UCI, 2006-2007

U of T Arts and Sciences Fellowship, University of Toronto, Winter 2004

OGS (Ontario Graduate Scholarship), University of Toronto, Jan - Dec 2004

The Ontario Graduate Scholarship Program recognizes academic excellence in graduate studies at the master's and doctoral levels in all disciplines.

IBM CAS (Center for Advanced Studies) Ph.D. Fellowship, U of Toronto, Jan - Dec 2003

NSERC Postgraduate Scholarship A, University of Toronto, 1999-2001

The Natural Sciences and Engineering Research Council of Canada (NSERC) Postgraduate Scholarships Doctoral Program provides financial support to high-calibre students who are engaged in doctoral programs in the natural sciences or engineering.

OGS (Ontario Graduate Scholarship), University of Toronto, 1998-1999

Computer Science Graduate Entrance Award, University of Toronto, 1998-1999

SFU Undergraduate Open Scholarship, Simon Fraser University, Fall 1995 – Spring 1997

SFU Alumni Scholarship, Simon Fraser University, Spring 1997

India Club Scholarship, Simon Fraser University, Spring 1997

SFU Alumni Scholarship, Simon Fraser University, Spring 1996

Motorola Wireless Data Group Scholarship, Simon Fraser University, Fall 1995

NSERC Industrial Undergraduate Student Research Award, Hughes Aircraft, Summer 1995

SFU Alumni Scholarship, Simon Fraser University, Spring 1995

Hughes Aircraft of Canada Scholarship, Simon Fraser University, Fall 1994

Ministry of Education Scholarship, University of Belgrade, Yugoslavia, 1992-1993

CONTRIBUTIONS TO RESEARCH AND DEVELOPMENT

ORCID ID: orcid.org/0000-0002-1290-853X

SCOPUS AUTHOR ID: 6603832221

SEMANTIC SCHOLAR citations on September 8, 2017: 10,057 citations, 106 highly influential
See: <https://www.semanticscholar.org/search?q=Natasa%20Przulj&sort=relevance&ae=false>

Citation indices from Google Scholar on February 8, 2018		
	All	Since 2013
Citations	6232	3852
h-index	36	32
i10-index	55	51

REFEREED JOURNAL PAPERS:

Note: the last author on a paper in this research area is the senior author, who led all aspects of the work and obtained funding for the research.

J-63 N. Malod-Dognin, J. Petschnigg and N. Przulj, "Precision medicine – A promising, yet challenging road lies ahead," *Current Opinion in Systems Biology*, Available online October 28, 2017

J-62 N. Malod-Dognin and N. Przulj, "Omics data complementarity underlines functional cross-communication in yeast", *Journal of Integrative Bioinformatics*, 14(3), 2017
Journal Impact Factor = 1.4

- J-61 N. Malod-Dognin, K. Ban and **N. Przulj**, “Unified Alignment of Protein-Protein Interaction Networks”, *Scientific Reports - Nature*, 7:953, 2017
Journal Impact Factor = 5.228
- J-60 K. Sokolina, S. Kittanakom, J. Snider, M. Kotlyar, P. Maurice, J. Ganda, A. Benleulmi-Chaachoua, K. Tadagaki, V. Wong, R. H. Maly, V. Deineko, H. Aoki, S. Amin, L. Riley, Z. Yao, X. Morato, S. Rahmati, H. Kobayashi, J. Menendez, D. Auerbach, S. Angers, **N. Przulj**, M. Bouvier, M. Babu, F. Ciruela, R. Jockers, I. Jurisica, and I. Stagljär, “Systematic protein-protein interaction mapping for clinically-relevant human GPCRs,” *Molecular Systems Biology*, 13:918, 2017
Journal Impact Factor = 10.872
- J-59 O. Yaveroglu, N. Malod-Dognin, T. Milenkovic, and N. Przulj, “Rebuttal to the Letter to the Editor in response to the paper: Proper evaluation of alignment-free network comparison methods,” *Bioinformatics*, 33 (7): 1107-1109, 2017
Journal Impact Factor = 7.307
- J-58 M. Costanzo, B. VanderSluis, E. N. Koch, A. Baryshnikova, C. Pons, G. Tan, W. Wang, M. Usaj, J. Hanchard, S. D. Lee, V. Pelechano, E. B. Styles, M. Billmann, J. van Leeuwen, N. van Dyk, Z.-Y. Lin, E. Kuzmin1, J. Nelson, J. S. Piotrowski, T. Srikumar, S. Bahr, Y. Chen, R. Deshpande, C. F. Kurat, S. C. Li, Z. Li, M. Mattiazzi Usaj, H. Okada, N. Pascoe, B.-J. San Luis, S. Sharifpoor, E. Shuteriqi, S. W. Simpkins, J. Snider, H. G. Suresh, Y. Tan, H. Zhu, N. Malod-Dognin, V. Janjic, **N. Przulj**, O. G. Troyanskaya, I. Stagljär, T. Xia, Y. Ohya, A.-C. Gingras, B. Raught, M. Boutros, L. M. Steinmetz, C. L. Moore, A. P. Rosebrock, A. A. Caudy, C. L. Myers, B. Andrews, C. Boone, “A global genetic interaction network maps a wiring diagram of cellular function,” *Science*, 353(6306):1381-1396, 2016 (**Cited 117 times**)
Journal Impact Factor = 34.661
- J-57 **N. Przulj** and N. Malod-Dognin, “Network analytics in the age of big data,” *Science*, 353(6295):123-124, 2016 (**Cited 11 times**)
Journal Impact Factor = 34.661
- J-56 A. Sarajlic, N. Malod-Dognin, O. Yaveroglu, and **N. Przulj**, “Graphlet-based Characterization of Directed Networks,” *Scientific Reports - Nature* 6, Article number: 35098, doi:10.1038/srep35098, 2016
Journal Impact Factor = 5.228
- J-55 V. Gligorijevic, N. Malod-Dognin and **N. Przulj**, “Integrative Methods for Analysing Big Data in Precision Medicine,” *Proteomics*, 16(5):741-58, 2016 (**Cited 39 times**)
Journal Impact Factor = 3.807
- J-54 V. Gligorijevic, N. Malod-Dognin and **N. Przulj**, “Fuse: Multiple Network Alignment via Data Fusion,” *Bioinformatics*, 32(8):1195-203, 2016 (**Cited 13 times**)
Journal Impact Factor = 7.307
- J-53 V. Gligorijevic and **N. Przulj**, “Methods for Biological Data Integration: Perspectives and Challenges,” *Journal of the Royal Society Interface*, 12 (112): 20150571, 2015 (**Cited 41 times**)
Journal Impact Factor = 3.917
- J-52 O. N. Yaveroglu, S. M. Fitzhugh, M. Kurant, A. Markopoulou, C. T. Butts and **N. Przulj**, “ergm.graphlets: A Package for ERG Modeling Based on Graphlet Statistics,” *Journal of Statistical Software*, 65(12), June 2015 (**Cited 3 times**)
Journal Impact Factor = 4.91
- J-51 O. N. Yaveroglu, T. Milenkovic and **N. Przulj**, “Proper evaluation of alignment-free network comparison methods,” *Bioinformatics*, 31(16):2697-2704, 2015 (**Cited 25 times**)
Journal Impact Factor = 7.307

- J-50 N. Malod-Dognin and **N. Przulj**, “L-GRAAL: Lagrangian Graphlet-based Network Aligner,” *Bioinformatics*, 31(13): 2182-2189, 2015 (**Cited 36 times**)
Journal Impact Factor = 7.307
- J-49 D. Davis, O. Yaveroglu, N. Malod-Dognin, A. Stojmirovic, and **N. Przulj**, “Topology-Function Conservation in Protein-Protein Interaction Networks,” *Bioinformatics*, 31(10): 1632-1639, 2015 (**Cited 28 times**)
Journal Impact Factor = 7.307
- J-48 A. Filipovic, Y. Lombardo, M. Fronato, J. Abrahams, E. Aboagye, Q.-D. Nguyen, B. Borda d’Aqua, A. Ridley, A. Green, E. Rahka, I. Ellis, C. Recchi, **N. Przulj**, A. Sarajlic, J.-R. Alattia, P. Fraering, M. Deonarain and R. Charles Coombes, “Anti-nicestrin monoclonal antibodies elicit pleiotropic anti-tumor pharmacological effects in invasive breast cancer cells,” *Breast Cancer Research and Treatment*, 148(2):455-62, 2014 (**Cited 13 times**)
Journal Impact Factor = 4.198
- J-47 V. Gligorijevic, V. Janjic and **N. Przulj**, “Integration of molecular network data reconstructs Gene Ontology,” Vol. 30 ECCB 2014, pages i594-i600 (14% acceptance rate), *Bioinformatics*, 30(17):i594-i600, 2014 (**Cited 23 times**)
Journal Impact Factor = 7.307
- J-46 A. Sarajlic, V. Gligorijevic, D. Radak and **N. Przulj**, “Network wiring of pleiotropic kinases yields insight into protective role of diabetes on aneurysm,” *Integrative Biology*, DOI: 10.1039/C4IB00125G, 2014
5-Year Impact Factor = 4.455
- J-45 K. Sun, N. Buchan, C. Larminie and **N. Przulj**, “The integrated disease network,” *Integrative Biology*, DOI: 10.1039/C4IB00122B, 2014 (**Cited 12 times**)
5-Year Impact Factor = 4.455
- J-44 K. Sun, J. P. Goncalves, C. Larminie and **N. Przulj**, “Predicting disease associations via biological network analysis,” *BMC Bioinformatics*, 15:304, 2014¹ (**Cited 31 times**)
Journal Impact Factor = 2.67
- J-43 V. Janjic and **N. Przulj**, “Evolution of the Topology of the Human Interactome,” *Journal of Integrative Bioinformatics*, 11(2):238, 2014
Journal Impact Factor = 1.4
- J-42 M. Cvijovic, J. Almquist, J. Hagmar, S. Hohmann, H.-M. Kaltenbach, E. Klipp, M. Krantz, P. Mendes, S. Nelander, J. Nielsen, A. Pagnani, **N. Przulj**, A. Raue, J. Stelling, S. Stoma, F. Tobin, J. A. H. Wodke, R. Zecchina, and M. Jirstrand, “Bridging the Gaps in Systems Biology,” *Molecular Genetics and Genomics*, DOI 10.1007/s00438-014-0843-3, April 13, 2014 (**Cited 22 times**)
Journal Impact Factor = 2.831
- J-41 O. Yaveroglu, N. Malod-Dognin, D. Davis, Z. Levnajic, V. Janjic, R. Karapandza, A. Stojmirovic and **N. Przulj**, “Revealing the Hidden Language of Complex Networks,” *Scientific Reports - Nature*, 4:4547, 2014 (**Cited 56 times**)²
Journal Impact Factor = 5.228
- J-40 A. Sarajlic and **N. Przulj**, “Survey of Network-Based Approaches to Research of Cardiovascular Diseases,” *BioMed Research International*, doi:10.1155/2014/527029, 2014 (**Cited 8 times**)
- J-39 V. Janjic, R. Sharan, and **N. Przulj**, “Modelling the Yeast Interactome,” *Scientific Reports - Nature*, 4:4273, 2014 (**Cited 12 times**)
Journal Impact Factor = 5.228

¹Reported as “Highly Accessed” by *BMC Bioinformatics*.

²All citations are from Google Scholar.

- J-38 N. Malod-Dognin and **N. Pržulj**, “GR-Align: Fast and Flexible Alignment of Protein 3D Structures Using Graphlet Degree Similarity,” *Bioinformatics*, 30(9):1259-65. doi:10.1093/bioinformatics/btu020, 2014 (**Cited 35 times**)
Journal Impact Factor = 7.307
- J-37 A. Sarajlic, A. Filipovic, V. Janjic, R.C. Coombes, and **N. Pržulj**, “The Role of Genes Co-Amplified with Nicastrin in Breast Invasive Carcinoma,” *Breast Cancer Research and Treatment*, DOI:10.1007/s10549-013-2805-6, 2013 (**Cited 6 times**)
Journal Impact Factor = 4.198
- J-36 M. Zitnik, V. Janjic, C. Larminie, B. Zupan, and **N. Pržulj**, “Discovering disease-disease associations by fusing systems-level molecular data,” *Scientific Reports - Nature*, 3:3202, 2013 (**Cited 53 times**)
Journal Impact Factor = 5.228
- J-35 A. Sarajlic, V. Janjic, N. Stojkovic, D. Radak, and **N. Pržulj**, “Network Topology Reveals Key Cardiovascular Disease Genes,” *PLoS ONE*, 8(8):e71537, 2013 (**Cited 29 times**)
5-Year Impact Factor = 4.24
- J-34 W. Hayes, K. Sun, and **N. Pržulj**, “Graphlet-based measures are suitable for biological network comparison,” *Bioinformatics*, 29(4): 483-491, 2013 (**Cited 51 times**)
Journal Impact Factor = 7.307
- J-33 V. Janjić, and **N. Pržulj**, “Biological function through network topology: a survey of the human diseasome,” *Briefings in Functional Genomics*, 11(6):522-532, 2012 (**Cited 37 times**)
Journal Impact Factor: 3.427
5-Year Impact Factor: 3.586
- J-32 V. Janjić, and **N. Pržulj**, “The Core Diseasome,” a special issue on **Emerging Investigators**, *Molecular BioSystems*, 8:2614-2625, July 4, 2012 (**Cited 32 times**)
Journal Impact Factor = 3.183
- J-31 V. Memisevic, and **N. Pržulj**, “C-GRAAL: Common-neighbors-based Global Graph Alignment of Biological Networks,” *Integrative Biology*, DOI:10.1039/c2ib00140c, January 10, 2012 (**Cited 77 times**)
5-Year Impact Factor = 4.455
- J-30 T. Milenkovic, V. Memisevic, and **N. Pržulj**, “Dominating Biological Networks,” *PLoS ONE*, 6(8):e23106, 2011 (**Cited 86 times**)
5-Year Impact Factor = 4.24
- J-29 Arabidopsis Interactome Mapping Consortium, “Evidence for Network Evolution in an Arabidopsis Interactome Map,” *Science*, 333:601-607, July 29, 2011 (**Cited 533 times**)
Journal Impact Factor = 34.661
- J-28 O. Kuchaiev and **N. Pržulj**, “Integrative Network Alignment Reveals Large Regions of Global Network Similarity in Yeast and Human,” *Bioinformatics*, 27(10):1390-1396, 2011 (**Cited 189 times**)
Journal Impact Factor = 7.307
- J-27 **N. Pržulj**, “Protein-protein interactions: making sense of networks via graph-theoretic modeling,” *Bioessays*, 33(2):115-123, February, 2011 (**Cited 54 times**)
Journal Impact Factor = 4.838
- J-26 O. Kuchaiev, A. Stevanovic, W. Hayes, and **N. Pržulj**, “GraphCrunch 2: Software tool for network modeling, alignment and clustering,” *BMC Bioinformatics*, 12(24):1-13,

- January 19, 2011 (**Cited 68 times**)³
Journal Impact Factor = 2.67
- J-25 T. Milenkovic, W.L. Wong, W. Hayes, and **N. Pržulj**, “Optimal network alignment with graphlet degree vectors,” *Cancer Informatics*, 9:121-37, June 30, 2010 (**Cited 151 times**)⁴
Journal Impact Factor = 1.6406
- J-24 H. Ho, T. Milenkovic, V. Memisevic, J. Aruri, **N. Pržulj** and A. K. Ganesan, “Protein Interaction Network Topology Uncovers Melanogenesis Regulatory Network Components Within Functional Genomics Datasets,” *BMC Systems Biology*, 4:84, June 15, 2010 (**Cited 45 times**)
Journal Impact Factor = 2.85
- J-23 O. Kuchaiev, T. Milenkovic, V. Memisevic, W. Hayes, and **N. Pržulj**, “Topological network alignment uncovers biological function and phylogeny,” *Journal of the Royal Society Interface*, 7:1341-1354, March 17, 2010 (**Cited 251 times**)
Journal Impact Factor = 4.907
- J-22 R. Kaake, T. Milenkovic, **N. Pržulj**, P. Kaiser, L. Huang, “Characterization of Cell Cycle Specific Interaction Network of the Yeast 26S Proteasome Complex by QTAX Strategy,” *Journal of Proteome Research*, 9(4):2016-2029, 2010 (**Cited 52 times**)
Journal Impact Factor = 5.001
- J-21 V. Memisevic, T. Milenkovic, and **N. Pržulj**, “An integrative approach to modelling biological networks,” *Journal of Integrative Bioinformatics*, 7(3):120, 2010 (**Cited 29 times**)
Journal Impact Factor = 1.4
- J-20 V. Memisevic, T. Milenkovic, and **N. Pržulj**, “Complementarity of network and sequence information in homologous proteins,” *Journal of Integrative Bioinformatics*, 7(3):135, 2010 (**Cited 58 times**)
Journal Impact Factor = 1.4
- J-19 T. Milenkovic, V. Memisevic, A. K. Ganesan, and **N. Pržulj**, “Systems-level cancer gene identification from protein interaction network topology applied to melanogenesis-related functional genomics data,” *Journal of the Royal Society Interface*, 7(44):423-437, March 6, 2010 (**Cited 92 times**)
Journal Impact Factor = 4.907
- J-18 **N. Pržulj**, “Biological Network Comparison Using Graphlet Degree Distribution,” Erratum, *Bioinformatics*, 26(6):853-854, 2010
Journal Impact Factor = 7.307
- J-17 O. Kuchaiev, M. Rasajski, D. J. Higham, and **N. Pržulj**, “Geometric de-noising of protein-protein interaction networks,” *PLoS Computational Biology*, 5(8):e1000454, August 2009 (**Cited 110 times**)
Journal Impact Factor = 4.87
5-Year Impact Factor = 5.94
- J-16 T. Milenkovic, I. Filippis, M. Lappe, and **N. Pržulj**, “Optimized Null Model of Protein Structure Networks,” *PLoS ONE*, 4(6):e5967, June 2009 (**Cited 39 times**)
Journal Impact Factor = 4.24
- J-15 C. Guerrero, T. Milenkovic, **N. Pržulj**, P. Kaiser, L. Huang, “Characterization of the proteasome interaction network using a QTAX-based tag-team strategy and protein

³Reported as “Highly Accessed” by *BMC Bioinformatics*. Software downloaded >7,000 times since November 2010.

⁴Reported as “Highly Visible” by *Cancer Informatics*.

- interaction network analysis,” *PNAS*, 105(36):13333-13338, 2008 (**Cited 121 times**)
Journal Impact Factor = 9.809
- J-14 T. Milenkovic and **N. Pržulj**, “Uncovering Biological Network Function via Graphlet Degree Signatures,” *Cancer Informatics*, 2008(6):257-273, 2008 (**Cited 248 times**)³
Journal Impact Factor = 1.6406
- J-13 D. J. Higham, M. Rasajski, and **N. Pržulj**, “Fitting a Geometric Graph to a Protein-Protein Interaction Network,” *Bioinformatics*, 24(8):1093-1099, 2008 (**Cited 102 times**)
Journal Impact Factor = 7.307
- J-12 T. Milenkovic, J. Lai, and **N. Pržulj**, “GraphCrunch: A Tool for Large Network Analyses,” *BMC Bioinformatics*, 9:70, January 30, 2008 (**Cited 115 times**)²
Journal Impact Factor = 2.67
- J-11 F. Hormozdiari, P. Berenbrink, **N. Pržulj**, and C. Sahinalp, “Not All Scale Free Networks are Born Equal: the Role of the Seed Graph in PPI Network Emulation,” *PLoS Computational Biology*, 3(7):e118, July 2007 (**Cited 73 times**)
Journal Impact Factor = 4.87
5-Year Impact Factor = 5.94
- J-10 **N. Pržulj** and D. J. Higham, “Modelling Protein-Protein Interaction Networks via a Stickiness Index,” *Journal of the Royal Society Interface*, 3(10):711-716, 2006 (**Cited 83 times**)
Journal Impact Factor = 4.907
- J-9 **N. Pržulj**, “Biological Network Comparison Using Graphlet Degree Distribution,” Proceedings of the 2006 European Conference on Computational Biology (ECCB 2006), Eilat, Israel, January 21-24, 2007, acceptance rate 18%. *Bioinformatics*, 23:e177-e183, 2007 (**Cited 462 times**)
Journal Impact Factor = 7.307
- J-8 **N. Pržulj**, D. G. Corneil, and I. Jurisica, “Efficient estimation of graphlet frequency distributions in protein-protein interaction networks,” *Bioinformatics*, 22(8):974-980, 2006 (**Cited 102 times**)
Journal Impact Factor = 7.307
- J-7 M. Barrios-Rodiles, K. R. Brown, B. Ozdamar, Z. Liu, R. S. Donovan, F. Shinjo, Y. Liu, R. Bose, J. Dembowy, I. W. Taylor, V. Luga, **N. Pržulj**, M. Robinson, H. Suzuki, Y. Hayashizaki, I. Jurisica, and J. L. Wrana, “High-Throughput Mapping of a Dynamic Signaling Network in Mammalian Cells,” *Science*, 307(5715):1621-1625, 2005 (**Cited 676 times**)
Journal Impact Factor = 34.661
- J-6 **N. Pržulj** and D. G. Corneil, “2-tree Probe Interval Graphs Have a Large Obstruction Set,” *Discrete Applied Mathematics*, 150(1-3):216-231, 2005 (**Cited 17 times**)
Journal Impact Factor = 0.677
5-Year Impact Factor = 0.838
- J-5 **N. Pržulj**, D. G. Corneil, and I. Jurisica, “Modeling Interactome: Scale-Free or Geometric?,” *Bioinformatics*, 20(18):3508-3515, 2004 (**Cited 480 times**)
Journal Impact Factor = 7.307
- J-4 A. D. King, **N. Pržulj**, and I. Jurisica, “Protein complex prediction via cost-based clustering,” *Bioinformatics*, 20(17):3013 - 3020, 2004 (**Cited 615 times**)
Journal Impact Factor = 7.307
- J-3 **N. Pržulj**, D. Wigle, and I. Jurisica, “Functional Topology in a Network of Protein Interactions,” *Bioinformatics*, 20(3):340-348, 2004 (**Cited 351 times**)
Journal Impact Factor = 7.307

- J-2 **N. Pržulj**, D. G. Corneil, and E. Koehler, “Hereditary Dominating Pair Graphs,” *Discrete Applied Mathematics*, 134:239-261, 2004 (**Cited 5 times**)
 Journal Impact Factor = 0.677
 5-Year Impact Factor = 0.838
- J-1 A. L. Liestman and **N. Pržulj**, “Minimum Average Time Broadcast Graphs,” *Par. Proc. Lett.*, 8:139-147, 1998 (**Cited 2 times**)
 Journal Impact Factor = 0.57

REFEREED CONFERENCE PAPERS:

Intelligent Systems for Molecular Biology (ISBM) and **European Conference on Computational Biology (ECCB)** are the top conferences in the field of computational biology with acceptance rates of about 15%. Every other year they are organized as one conference. Their proceedings are published as a special issue of *Bioinformatics*, the top journal in the research area. The **Pacific Symposium on Biocomputing (PSB)** is an international, multidisciplinary conference bringing together top researchers from the US, the Asian Pacific nations, and around the world to address open issues in all aspects of computational biology. PSB has an emphasis on applications in data-rich areas of molecular biology and is organized by leaders in the emerging areas and targeted to provide a forum for publication and discussion of research in biocomputing’s “hot topics.”

- C-15 V. Gligorijevic, N. Malod-Dognin and **N. Pržulj**, “Patient-Specific Data Fusion for Cancer Stratification and Personalized Treatment,” Proceedings of the 2016 *Pacific Symposium on Biocomputing (PSB)*, 21:321-332(2016), Big Island, Hawaii, USA, January 4-9, 2016 (**Cited 7 times**)
- C-14 V. Gligorijevic, V. Janjic and **N. Pržulj**, “Integration of molecular network data reconstructs Gene Ontology,” *European Conference on Computational Biology (ECCB) 2014*, Strasbourg, France, September 7-10, 2014. Acceptance rate 14% (Journal version is J-47 above)
- C-13 A. Sarajlic, V. Gligorijevic, D. Radak and **N. Pržulj**, “Network wiring of pleiotropic kinases yields insight into protective role of diabetes on aneurysm,” Drug Development workshop of ECCB’14, Strasbourg, France, September 6-10, 2014. Also in *Integrative Biology*, DOI: 10.1039/C4IB00125G, 2014 (Journal version is J-46 above)
- C-12 K. Sun, N. Buchan, C. Larminie and **N. Pržulj**, “The integrated disease network,” Drug Development workshop of ECCB’14, Strasbourg, France, September 6-10, 2014. Also in *Integrative Biology*, DOI: 10.1039/C4IB00122B, 2014 (Journal version is J-45 above)
- C-11 V. Janjic and **N. Pržulj**, Evolution of the Topology of the Human Interactome, International Symposium on Integrative Bioinformatics, Newcastle, UK, May 12-14, 2014 (Journal version is J-43 above)
- C-10 S. Drezgić, I. Grudenić, A. Ionescu, and **N. Pržulj**, “A technical approach to local government amalgamation,” Proceedings of 18th Dubrovnik Economic Conference, Croatian National Bank, Dubrovnik, Croatia, June 27-30, 2012
- C-9 B. Betkaoui, D. B. Thomas, W. Luk, and **N. Pržulj**, “A Framework for FPGA Acceleration of Large Graph Problems: Graphlet Counting Case Study,” Proceedings of International Conference on Field Programmable Technology (FPT’11), New Delhi, India, December 12-14, 2011 (**Cited 27 times**)
- C-8 V. Memisevic, T. Milenkovic, and **N. Pržulj**, “An integrative approach to modelling biological networks,” 6th Annual International Symposium on Integrative Bioinformatics, Cambridge, UK, March 22-24, 2010 (Journal version is J-21 above)

- C-7 V. Memisevic, T. Milenkovic, and **N. Pržulj**, “Complementarity of network and sequence information in homologous proteins,” 6th Annual International Symposium on Integrative Bioinformatics, Cambridge, UK, March 22-24, 2010 (Journal version is J-20 above)
- C-6 **N. Pržulj**, O. Kuchaiev, A. Stevanovic, and W. Hayes, “Geometric Evolutionary Dynamics of Protein Interaction Networks,” Proceedings of the 2010 Pacific Symposium on Biocomputing (PSB), Big Island, Hawaii, January 4-8, 2010 (**Cited 42 times**)
- C-5 O. Kuchaiev, P. T. Wang, Z. Nenadic, and **N. Pržulj**, “Structure of Brain Functional Networks,” 31st Annual International Conference of the *IEEE Engineering in Medicine and Biology Society (EMBC’09)*, Minneapolis, Minnesota, USA, September 2-6, 2009 (**Cited 15 times**)
- C-4 O. Kuchaiev and **N. Pržulj**, “Learning the structure of protein-protein interaction networks,” Proceedings of the 2009 *Pacific Symposium on Biocomputing (PSB 2009)*, Big Island, Hawaii, January 5-9, 2009 (**Cited 23 times**)
- C-3 **N. Pržulj**, “Geometric local structure in biological networks,” IEEE Xplore digital library, **Invited Paper**, Proceedings of the 2007 *IEEE Information Theory Workshop (ITW 2007)*, Lake Tahoe, California, September 2-6, 2007
- C-2 F. Hormozdiari, P. Berenbrink, **N. Pržulj**, and C. Sahinalp, “Not All Scale Free Networks are Born Equal: the Role of the Seed Graph in PPI Network Emulation,” in Proceedings of *Research in Computational Molecular Biology (RECOMB) Satellite Conferences on Systems Biology and Computational Proteomics*, UC San Diego, December 1-3, 2006, acceptance rate 26%; *Lecture Notes in Computer Science*, volume 4532/2007, pages 1-13, September 19, 2007 (Journal version is J-11 above)
- C-1 **N. Pržulj**, “Biological Network Comparison Using Graphlet Degree Distribution,” Proceedings of the 2006 European Conference on Computational Biology (ECCB 2006), Eilat, Israel, January 21-24, 2007, acceptance rate 18% (Journal version is J-9 above)

REFEREED BOOK CHAPTERS:

Prof. Przulj’s chapters are in books published by the top publishers, including Springer, Cambridge University Press, and Wiley.

- B-13 N. Malod-Dognin, S. Windels and N. Przulj, “Machine Learning for Data Integration in Cancer Precision Medicine: Matrix Factorization Approaches,” a chapter in *Analyzing Network Data in Biology and Medicine*, edited by Natasa Przulj, Cambridge University Press, to appear, 2018
- B-12 L. Leal, R. Kosir and N. Przulj, “From Genetic Data to Medicine: from DNA samples to disease risk prediction in personalized genetic tests,” a chapter in *Analyzing Network Data in Biology and Medicine*, edited by Natasa Przulj, Cambridge University Press, to appear, 2018
- B-11 N. Malod-Dognin and N. Przulj, “Network Alignment,” a chapter in *Analyzing Network Data in Biology and Medicine*, edited by Natasa Przulj, Cambridge University Press, to appear, 2018
- B-10 T. Gaudelet and N. Przulj, “Introduction to graph and network theory,” a chapter in *Analyzing Network Data in Biology and Medicine*, edited by Natasa Przulj, Cambridge University Press, to appear, 2018
- B-9 K. Pavelic, M. Klobucar, D. Kuzelj, N. Przulj, and S. Kraljevic Pavelic, “Analysis of the signatures of cancer stem cells in malignant tumours using protein interactomes and STRING database,” a chapter in *Analyzing Network Data in Biology and Medicine*, edited by Natasa Przulj, Cambridge University Press, to appear, 2018

- B-8 V. Gligorijevic and **N. Pržulj**, “Computational Methods for Integration of Biological Data,” a chapter in *Personalised Medicine: A New Medical and Social Challenge*, edited by N. Bodiřoga-Vukobrat, K. Pavelic, D. Rukavina, and G. G. Sander, Springer Verlag, ISBN 978-3-319-39349-0, 2016
- B-7 T. Milenkovic and **N. Pržulj**, “Topological Characteristics of Molecular Networks,” a chapter in *Functional Coherence of Molecular Networks in Bioinformatics*, edited by M. Koyuturk, S. Subramaniam, and A. Grama, Springer, 2012
- B-6 D. J. Higham and **N. Pržulj**, “Random graph models and their application to protein-protein interaction networks,” a chapter in *Handbook of Statistical Systems Biology*, edited by D. Balding, M. Girolami and M. Stumpf, Wiley, 2011
- B-5 **N. Pržulj**, “Biological networks uncover evolution, disease and gene functions,” a chapter in *Bioinformatics for Biologists*, edited by Pavel Pevzner and Ron Shamir, Cambridge University Press, 2011
- B-4 A. D. King, **N. Pržulj**, and I. Jurisica, “Protein Complex Prediction with RNSC,” a chapter in the special volume of *Methods in Molecular Biology* dedicated to *Bacterial Molecular Networks*, edited by J. van Helden, A. Toussaint, and D. Thieffry, Humana Press, USA (part of the Springer publishing group), 2011
- B-3 **N. Pržulj**, “From Topology to Phenotype in Protein-Protein Interaction Networks,” a chapter in *Complex Networks across the Natural and Technological Sciences*, edited by Des Higham, Ernesto Estrada, Maria Fox, and Gian-Luca Oppo, Springer, pp 31-49, DOI: 10.1007/978-1-84996-396-1_3, 2010
- B-2 **N. Pržulj** and T. Milenkovic, “Computational Methods for Analyzing and Modeling Biological Networks,” a chapter in *Biological Data Mining*, edited by Jake Chen and Stefano Lonardi, CRC Press, 2010
- B-1 **N. Pržulj**, “Graph Theory Analysis of Protein-Protein Interactions,” a chapter in *Knowledge Discovery in Proteomics*, edited by Igor Jurisica and Dennis Wigle, CRC Press, 2006 (**Cited 27 times**)²

BOOK:

N. Pržulj, “Analyzing Network Data in Biology and Medicine: A textbook for training biological, medical and computational inter-disciplinary scientists,” Cambridge University Press, to appear, 2018

REFEREED POSTERS:

58 refereed posters since 2003

RESEARCH SOFTWARE:

1. GraphCrunch^{5,6}, published in refereed journal papers J-26 and J-12 listed above and downloaded 7,000 times since November, 2010.
2. ergm.graphlets R package that enables the use of graphlet properties within the exponential random graph modeling, ergm, package of R (paper J-49 above).

PRESS COVERAGE:

⁵<http://bio-nets.doc.ic.ac.uk/graphcrunch2/>

⁶<http://bio-nets.doc.ic.ac.uk/graphcrunch/>

- PC-10 “Conquering Cancer,” by Mike Hall, ITNOW (Autumn 2016) 58 (3): 40-41
doi:10.1093/itnow/bww076 (Oxford Journals; The British Computer Society), September 2016
- PC-9 “Computing Versus Prostate Cancer,” by Mike Hall, MBCS CITP, who explains how Natasaa Przulj’s BCS Needham Lecture on data mining has led to a potentially groundbreaking research project that could transform prostate cancer diagnosis and treatment. ITNOW (Autumn 2015) 57 (3): 54-55 doi:10.1093/itnow/bwv080 (Oxford Journals; The British Computer Society), September 2015
- PC-8 Vecernje Novosti, Belgrade, Serbia: Srpkinja najbolji racunarski istrazivac u Britaniji. March 24, 2014
- PC-7 The British Computer Society (BCS) Academy of Computing Press Release, “Mining Biological Networks - Dr Nataša Pržulj,”⁷ Needham Lecture on 19 November 2014 at The Royal Society in London
- PC-6 45-minute video interview with Henry Tucker, The British Computer Society (BCS), about my work, what it means for pharmaceuticals, health informatics and women in IT, 2014⁸
- PC-5 The British Computer Society (BCS) Academy of Computing Press Release, “Nataša Pržulj announced as BCS Roger Needham Award 2014 Award,”⁹ March 7, 2014
- PC-4 An interview for BioTechniques Journal of Life Sciences Methods, titled “Finding Connections Between Genes and Diseases,”¹⁰ December 12, 2013
- PC-3 An interview for European Commission Community Research and Development Information Service (CORDIS) News, titled “Beyond genetics: mining biological networks for new treatments for disease,”¹¹ October 11, 2013
- PC-2 A television interview about my scientific work was shown on *Enter TV*, Belgrade, Serbia, on September 28, 2007
- PC-1 An interview about my scientific work was published in the daily newspaper *Borba*, Belgrade, Serbia, on September 24, 2007

INVITED TALKS:

- IT-134 **N. Pržulj**, “Heuristic Algorithms for Data-Driven Biomedicine,” AlgoUK Workshop, King’s College London, UK, February 6, 2018
- IT-133 **N. Pržulj**, “Data-Driven Medicine,” MCM/WS Conference on Systems Medicine, Valletta, Malta, September 13, 2017
- IT-132 **N. Pržulj**, “Data-Driven Medicine,” the Department of Biosystems Science and Engineering, ETH Zurich, Switzerland, August 30, 2017
- IT-131 **N. Pržulj**, “Data-Driven Biomedical Science,” International Signalling Workshop, Visegrad, Hungary, July 16-20, 2017
- IT-130 **N. Pržulj**, “Data-Driven Medicine,” Biomedical Engineering, University of Calgary, Canada, July 10, 2017
- IT-129 **N. Pržulj**, “Data-Driven Medicine,” Institute of Mathematics of the Serbian Academy of Sciences and Arts, Belgrade, Serbia, June 27, 2017

⁷<http://www.bcs.org/content/conWebDoc/53611>

⁸<http://www.bcs.org/content/conWebDoc/52305>

⁹<http://academy.bcs.org/news/nataša-przulj-announced-bcs-roger-needham-award-2014-award>

¹⁰<http://www.biotechniques.com/news/Finding-Connections-Between-Genes-and-Diseases/biotechniques-348720.html#.UqsQX-KMRuZ>

¹¹http://cordis.europa.eu/fetch?CALLER=EN_NEWS&ACTION=D&RCN=36151

- IT-128 **N. Pržulj**, “Data-Driven Medicine,” **Keynote talk** at Integrative Bioinformatics 2017, Odense, Denmark, June 22-24, 2017
- IT-127 **N. Pržulj**, “Mining Biological Networks,” The European Human Genetics Conference (ESHG) 2017, session on “Network Medicine,” Copenhagen, Denmark, May 27-30, 2017
- IT-126 **N. Pržulj**, “Data-Driven Medicine,” Inaugural Lecture, University College London, UK, April 5, 2017
- IT-125 **N. Pržulj**, “Predictive Integration of Networked Big Data: From Biology to Economics,” Seminar at the Department of Computing, Simon Fraser University, Vancouver, Canada, February 17, 2017
- IT-124 **N. Pržulj**, “Predictive Integration of Networked Big Data,” Banff International Research Station for Mathematical Innovation and Discovery (BIRS) Workshop on Statistical and Computational Challenges in Large Scale Molecular Biology, Canada, March 26-31, 2017
- IT-123 **N. Pržulj**, “Data-Driven Medicine,” School of Biological Sciences Seminar, University of Essex, UK, March 15, 2017
- IT-122 **N. Pržulj**, “Data-Driven Medicine,” **Keynote talk** at the celebration of the 20th anniversary of the Pacific Institute for the Mathematical Sciences (PIMS) at Simon Fraser University (SFU), Vancouver, Canada, November 25, 2016
- IT-121 **N. Pržulj**, “Data-Driven Medicine,” CSH Workshop on Future directions in medical data science, Vienna, Austria, October 10-11, 2016
- IT-120 **N. Pržulj**, “Data-Driven Medicine,” MGMS Big Data in Biomolecular Systems, London at School of Pharmacy, UCL, London, UK, September 9, 2016
- IT-119 **N. Pržulj**, “Patient-Specific Network Data Fusion for Stratification, Biomarker Discovery and Personalized Treatment,” NetBio/SysMod COSI Session, Intelligent Systems for Molecular Biology (ISMB), Orlando, FL, USA, July 10-12, 2016
- IT-118 **N. Pržulj**, “Patient-Specific Network Data Fusion for Stratification, Biomarker Discovery and Personalized Treatment,” **Keynote Talk**, Network Biology SIG at Intelligent Systems for Molecular Biology (ISMB), Orlando, FL, USA, July 8, 2016
- IT-117 **N. Pržulj**, “Data-Driven Medicine,” Symposium on Medical Informatics, University of Zurich, Switzerland, July 7, 2016
- IT-116 **N. Pržulj**, “Network Data Integration Enables Precision Medicine,” **Plenary Talk**, From Solid State to BioPhysics VIII: From Basic to Life Sciences, Cavtat, Croatia, June 4-11, 2016
- IT-115 **N. Pržulj**, “Real-World Data Analytics: from Biomedical to Economic Networked Data,” Public Lecture at The Real Time Club, London, UK, April 19, 2016
- IT-114 **N. Pržulj**, “Network Data Integration Enables Precision Medicine,” Network Biology Workshop, Simons Institute for the Theory of Computing, UC Berkeley, CA, USA, April 11-15, 2016
- IT-113 **N. Pržulj**, “Predictive Integration of Networked Big Data: From Biology to Economics,” Generalized Network Structures and Dynamics Workshop, Mathematical Biosciences Institute, Columbus, OH, USA, March 21-25, 2016
- IT-112 **N. Pržulj**, “Network Data Integration Enables Precision Medicine and Furthers Economics,” Public Lecture at OSSA Celebration of 160th Anniversary of Nikola Tesla’s Birth, Cambridge University, UK, February 19, 2016
- IT-111 **N. Pržulj**, “Network Data Integration Enables Precision Medicine,” Theodore L. Badger Lecture in Network Medicine, Channing Division of Network Medicine at Brigham and Women’s Hospital, Harvard University, USA, December 15, 2015

- IT-110 **N. Pržulj**, “Mining Real-World Networks: from Biology to Economics,” Institute for Complex Systems Simulations (ICSS), Complex Systems Seminar Series, University of Southampton, UK, December 10, 2015
- IT-109 **N. Pržulj**, Distinguished Lecture at Computer Science Department, University College London, UK, October 9, 2015
- IT-108 **N. Pržulj**, “Predictive Integration of Networked Big Data: From Biology to Economics,” Workshop on Mathematical Data Science, Serbian Academy of Sciences and Art (SASA), Belgrade, Serbia, June 22, 2015
- IT-107 **N. Pržulj**, “Network Data Integration Enables Precision Medicine,” Odense eScience Symposium on Computational Biology, Odense, Denmark, June 11, 2015
- IT-106 **N. Pržulj**, “Mining real-world networks: from biology to economics,” **Keynote Talk** at NetSci 2015, International School and Conference on Network Science, Zaragoza, Spain, June 1-5, 2015
- NetSci** is the leading conference on Network Science bringing together leading researchers, practitioners, and teachers in network science.
- IT-105 **N. Pržulj**, “Network Data Integration Enables Precision Medicine,” Network-enabled Personalized Medicine (NetMed) workshop at NetSci 2015, Zaragoza, Spain, June 1-5, 2015
- IT-104 **N. Pržulj**, “Vision of Data Science,” Faculty of Science Seminar, University of British Columbia, Canada, May 26, 2015
- IT-103 **N. Pržulj**, “Real-World Data Analytics: from Biology to Economics,” Research Seminar at the Computer Science Department, University of British Columbia, Canada, May 25, 2015
- IT-102 **N. Pržulj**, “Mining real-world networks: from biology to economics,” Research Seminar at the Computer Science Department, University of Leeds, UK, March 25, 2015
- IT-101 **N. Pržulj**, “Mining real-world networks: from biology to economics,” School Research Seminar at Computer Science, University of Manchester, UK, February 17, 2015
- IT-100 **N. Pržulj**, **Roger Needham lecture**¹², “Mining biological networks,” **The Royal Society**, 6-9 Carlton House Terrace, London, UK, November 19, 2014
- IT-99 **N. Pržulj**, “Mining network data” **Keynote Talk** at ITIS 2014, Smarjeske toplice, Slovenia, November 6, 2014
- IT-98 **N. Pržulj**, **Keynote Talk** at ECCB’14 workshop on *Drug Development 2.0 – Computational drug repurposing, target discovery and translational research*, Strasbourg, France, September 7, 2014
- IT-97 **N. Pržulj**, “Mining real-world networks: from biology to economics,” Microsoft Research, Redmond, WA, USA, August 14, 2014
- IT-96 **N. Pržulj**, “Revealing the Hidden Language of Complex Networks,” Young Academy of Europe Annual Meeting, Barcelona, Spain, July 15, 2014
- IT-95 **N. Pržulj**, “Mining Biological Networks,” **Plenary Talk** at From Solid State To Bio Physics 2014, Cavtat, Croatia, June 7-14, 2014
- IT-94 **N. Pržulj**, “Mining Biological Networks: Network Integration,” Quantitative Biology Conference, The Francis Crick Institute, London, UK, June 5, 2014
- IT-93 **N. Pržulj**, “Mining Biological Networks,” Johnson & Johnson, Spring House, PA, USA, May 21, 2014

¹²<http://academy.bcs.org/content/roger-needham-lecture>

- IT-92 **N. Pržulj**, **Colloquium Lecture** “Revealing the Hidden Language of Complex Networks,” Computer and Information Sciences Department, Temple University, Philadelphia, USA, May 20, 2014
- IT-91 **N. Pržulj**, “Revealing the Hidden Language of Complex Networks,” **Keynote Talk** at Integrative Bioinformatics Conference 2014, Newcastle University, Newcastle upon Tyne, UK, May 12-14, 2014
- IT-90 **N. Pržulj**, “Mining real-world networks,” Computer Science, Tel Aviv University, Israel, April 10, 2014
- IT-89 **N. Pržulj**, “Mining real-world networks: from biology to economics,” Cambridge Networks Network seminar series, University of Cambridge, UK, February 11, 2014
- IT-88 **N. Pržulj**, “Mining real-world networks: from biology to economics,” Computing Science Department, Simon Fraser University, Canada, December 20, 2013
- IT-87 **N. Pržulj**, “Mining real-world networks: from biology to economics,” Theoretical Approaches to Bioinformation Systems (TABIS 2013), Belgrade, Serbia, September 17-22, 2013
- IT-86 **N. Pržulj**, “Network topology as a source of biological information,” **Keynote Talk** at Network Biology SIG of ISMB/ECCB 2013, Berlin, Germany, July 19, 2013
- IT-85 **N. Pržulj**, “Analysing Large Networked data,” SASS Winter Camp 2013, Piran, Slovenia, March 15-17, 2013
- IT-84 **N. Pržulj**, “Network topology as a source of biological information,” Department of Social, Genetic and Developmental Psychiatry, King’s College London, UK, January 29, 2013
- IT-83 **N. Pržulj**, “Network topology as a source of information in biological and economic networks,” Scientific Colloquium of University of Rijeka, Croatia, November 12, 2012
- IT-82 **N. Pržulj**, “Network topology as a source of biological information,” Faculty of Computer and Information Science, University of Ljubljana, Slovenia, November 6, 2012
- IT-81 **N. Pržulj**, “Network topology as a source of information,” Institute Jozef Stefan, Ljubljana, Slovenia, November 6, 2012
- IT-80 **N. Pržulj**, “Network topology complements sequence as a source of biological information,” IUBMB-FEBS 2012 Congress, Sevilla, Spain, September 4-9, 2012
- IT-79 **N. Pržulj**, “ERC experience,” ERC Session at IUBMB-FEBS 2012 Congress, Sevilla, Spain, September 4-9, 2012
- IT-78 **N. Pržulj**, “Networks of protein interactions,” Petnica International Seminar, Petnica Research Station, Serbia, August 11, 2012
- IT-77 **N. Pržulj**, “Network topology as a source of biological information,” International Meeting on Data Mining in Bioinformatics, Belgrade, Serbia, June 26-28, 2012
- IT-76 **N. Pržulj**, “Topology versus function,” Function Prediction in Complex Networks, Kavli Royal Society International Scientific Centre, UK, May 28-29, 2012
- IT-75 **N. Pržulj**, “Network topology as a source of biological information,” 6th conference From Solid State to BioPhysics VI: From Physics to Life Sciences, Dubrovnik, Croatia, June 9-16, 2012
- IT-74 **N. Pržulj**, “Network topology as a source of biological information,” Department of Computer Science, University College London, April 4, 2012
- IT-73 **N. Pržulj**, “Network topology complements sequence: insights into human disease,” Workshop on Network Links: Connecting Social, Communication and Biological Network Analysis, Institute for Mathematics and Its Applications, University of Minnesota, USA, Feb 28, 2012

- IT-72 **N. Pržulj**, “Network topology complements sequence: insights into human disease,” Institute of Cancer Research, London, UK, February 15, 2012
- IT-71 **N. Pržulj**, “Network topology as a source of biological information,” Workshop on Group Testing Designs, Algorithms, and Applications to Biology, Institute for Mathematics and Its Applications, University of Minnesota, USA, Feb 14, 2012
- IT-70 **N. Pržulj**, “New insights into biology from analysis of biological networks,” Bioinformatics Research Group, Faculty of Mathematics, University of Belgrade, December 21, 2011
- IT-69 **N. Pržulj**, “Network topology complements sequence: insights into human disease,” ICREA Conference on Network Medicine Approaches to Human Disease: from Computers to the Clinics, Barcelona, Spain, November 21-23, 2011
- IT-68 **N. Pržulj**, “Network topology meets biological function,” Institute of Systems and Synthetic Biology - Autumn Symposium, Imperial College London, UK, November 16-17, 2011
- IT-67 **N. Pržulj**, “Network topology meets biological function,” **Plenary Talk** at ISIT’11, Dolenjske Toplice, Slovenia, November 9-11, 2011
- IT-66 **N. Pržulj**, “Network mining uncovers new biology,” Theoretical Physics, Jozef Stefan Institute, Ljubljana, Slovenia, November 8, 2011
- IT-65 **N. Pržulj**, “Network topology meets biological function,” University of Toronto, MaRS Centre, Canada, October 21, 2011
- IT-64 **N. Pržulj**, “Network topology as a source of biological information”, *EMBO/EMBL Symposium: Structure and Dynamics of Protein Networks*, EMBL Advanced Training Centre (ATC), Heidelberg, Germany, October 13 - 16, 2011
- IT-63 **N. Pržulj**, “Network mining uncovers new biology,” Physics Institute, University of Belgrade, Serbia, August 26, 2011
- IT-62 **N. Pržulj**, “Network mining uncovers new biology,” Petnica International Seminar, Petnica Research Station, Serbia, August 3, 2011.
- IT-61 **N. Pržulj**, “Network mining uncovers new biology,” Centre for Systems and Synthetic Biology, Brunel University, London, UK, June 1, 2011
- IT-60 **N. Pržulj**, “Graph-Theoretic Modeling of Biological Networks,” Physics Seminar, Petnica Research Station, Valjevo, Serbia, May 1, 2011
- IT-59 **N. Pržulj**, “Graph-Theoretic Modeling of Biological Networks,” Serbian Academy of Sciences and Art (SANU), Belgrade, Serbia, April 29, 2011
- IT-58 **N. Pržulj** and Saša Drezgić, “Graph theory, biological networks and economic systems,” Scientific Society of Economists Election Meeting, Zagreb, Croatia, February 26, 2011
- IT-57 **N. Pržulj**, “Graph-Theoretic Modeling of Biological Networks,” FutureSysBio Workshop on “Defining modelling strategies for systems biology,” Goteborg, Sweden, January 20-21, 2011
- IT-56 **N. Pržulj**, “Mathematical and computational analysis of biological networks uncovers evolution, disease, and gene functions,” School of Computing (RAF), Union University, Belgrade, Serbia, December 29, 2010
- IT-55 **N. Pržulj**, “Network Topology Uncovers Function, Disease, and Phylogeny,” Physiological Laboratory Seminar, University of Liverpool, December 3, 2010
- IT-54 **N. Pržulj**, “Biological Networks Uncover Evolution, Disease, and Gene Functions,” Complexity and Networks Programme workshop on “Complexity and Networks – Biology,” Imperial College London, December 1, 2010

- IT-53 **N. Pržulj**, “Network Topology Uncovers Function, Disease, and Phylogeny,” **Plenary Talk** at the 5th International Conference on Pattern Recognition in Bioinformatics (PRIB), Nijmegen, The Netherlands, September 22-24, 2010
- IT-52 **N. Pržulj**, “Network Topology Uncovers Function, Disease, and Phylogeny,” **Plenary Talk** at Network Dynamics and Synchronization, University of Manchester, sponsored by The London Mathematical Society and CICADA, May 17-19, 2010
- IT-51 **N. Pržulj**, “Network Topology Uncovers Function, Disease, and Phylogeny,” Disordered Systems Group, Mathematics Seminar, King’s College London, April 21, 2010
- IT-50 **N. Pržulj**, “Network Topology Uncovers Function, Disease, and Phylogeny,” Glaxo-SmithKline, Stevenage, UK, February 8, 2010
- IT-49 **N. Pržulj**, “From Network Topology to Biological Function and Disease,” **Plenary Talk** at 7th Georgia Tech - ORNL Conference on Bioinformatics, Atlanta, Georgia, USA, November 12-14, 2009
- IT-48 **N. Pržulj**, “Deciphering Biological Networks,” INRIA Colloquium, Paris, November 3-5, 2009
- IT-47 **N. Pržulj**, “Deciphering Biological Networks,” Statistics Seminar, University of Oxford, October 29, 2009
- IT-46 **N. Pržulj**, “From Network Topology to Biological Function and Disease” MITACS-MoMiNIS Seminar, Dalhousie University, Halifax, Nova Scotia, Canada, August 12, 2009
- IT-45 **N. Pržulj**, “From Network Topology to Biological Function and Disease,” Canadian Discrete and Algorithmic Mathematics Conference (CanaDAM) 2009, Minisymposium on Complex Real-World Networks, Montreal, Quebec, May 25-28, 2009
- IT-44 **N. Pržulj**, “From Network Topology to Biological Function and Disease,” Center for Cancer Systems Biology (CCSB) Seminar Series, Department of Cancer Biology, Dana-Farber Cancer Institute, Harvard Medical School, Boston, MA, May 21, 2009
- IT-43 **N. Pržulj**, “What can we learn from protein-protein interaction networks?” Barbados Workshop on biological and computational analysis of protein-protein interaction networks, McGill University Center for Bioinformatics, Holetown, Barbados, April 19th - 25th, 2009
- IT-42 **N. Pržulj**, “From Network Topology to Biological Function and Disease,” RECOMB Satellite Conference on Bioinformatics Education, UC San Diego, La Jolla, California, March 14-15, 2009
- IT-41 **N. Pržulj**, “From Network Topology to Biological Function and Disease,” Interdisciplinary Workshop on Complex Networks across the Natural and Technological Sciences, The Institute for Advanced Studies, Glasgow, UK, January 27-30, 2009
- IT-40 **N. Pržulj**, “From Network Topology to Biological Function and Disease,” Department of Computing, Imperial College London, UK, January 26, 2009
- IT-39 **N. Pržulj**, “Protein-protein Interaction Networks,” Workshop on Complex Networks across the Natural and Technological Sciences, The Institute for Advanced Studies, UK, January 19-23, 2009
- IT-38 **N. Pržulj**, “From Network Topology to Biological Function and Disease,” Computer Science Department, McGill University, Canada, January 15, 2009
- IT-37 **N. Pržulj**, “From Network Topology to Biological Function and Disease,” University of Edinburgh, UK, December 15, 2008
- IT-36 **N. Pržulj**, “Towards a Theory of Biological Networks,” Structural and Computational Biology Programme Seminar, Institute for Research in Biomedicine (IRB) Barcelona, Spain, October 29, 2008

- IT-35 **N. Pržulj**, “Towards a Theory of Biological Networks,” Spanish National Cancer Research Center (CNIO), Madrid, Spain, October 27, 2008
- IT-34 **N. Pržulj**, “Towards a Theory of Biological Networks,” School of Computing (RAF), Union University, Belgrade, Serbia, October 20, 2008
- IT-33 **N. Pržulj**, “Towards a Theory of Biological Networks,” Petnica Research Station, Valjevo, Serbia, October 19, 2008
- IT-32 **N. Pržulj**, “Towards a Theory of Biological Networks,” Centre National de la Recherche Scientifique (CNRS), Laboratoire d’Informatique de Nantes-Atlantique (LINA), University of Nantes, France, July 16, 2008
- IT-31 **N. Pržulj**, “Examining Biological Networks via Graphlet Degree Signatures,” a minisymposium on “Networks: Biological, Social and Internet” at the SIAM Annual Meeting, San Diego, California, July 7-11, 2008
- IT-30 **N. Pržulj**, “Towards a Theory of Biological Networks,” Imperial College London, June 30, 2008
- IT-29 **N. Pržulj**, “Towards a Theory of Biological Networks,” University of Southampton, UK, June 27, 2008
- IT-28 **N. Pržulj**, “Towards a Theory of Biological Networks,” University of Helsinki, Finland, June 24, 2008
- IT-27 **N. Pržulj**, “From Structure to Function in Biological Networks,” 2008 UCI Center for Complex Biological Systems Retreat, Pasadena, California, March 28-30, 2008
- IT-26 **N. Pržulj**, “From Structure to Function in Biological Networks,” 2007 UCI Cancer Center Conference, Rancho Mirage, California, November 9-11, 2007
- IT-25 **N. Pržulj**, “Protein-Protein Interaction and Other Biological Networks,” Dept. of Biological Chemistry, UC Irvine, September 21, 2007
- IT-24 **N. Pržulj**, “Geometric Local Structure in Biological Networks,” 2007 IEEE Information Theory Workshop (ITW 2007), Lake Tahoe, California, September 2-6, 2007
- IT-23 **N. Pržulj**, “Graphs, Proteins, and Simulations,” Petnica Research Station, Valjevo, Serbia, August 11, 2007
- IT-22 **N. Pržulj**, “Geometric Local Structure in Biological Networks,” 39th Symposium on the Interface: Computing Science and Statistics (Theme: Systems Biology), Philadelphia, Pennsylvania, May 23-26, 2007
- IT-21 **N. Pržulj**, “Geometric Local Structure in Biological Networks,” Department of Defense Biotechnology HPC Software Applications Institute, Fort Detrick, Frederick, MD, May, 23, 2007
- IT-20 **N. Pržulj**, “Modeling Large Biological Networks,” Center for Complex Biological Systems at UC Irvine, CCBS/MCB/MCSB Retreat, Redondo Beach, March 23-25, 2007
- IT-19 **N. Pržulj**, “Protein-Protein Interaction Networks: Issues, Models, and Comparisons,” Institute for Mathematical Behavioral Sciences, UC Irvine, Human Complex Systems Conference, December 8, 2006
- IT-18 **N. Pržulj**, “Comparing and Modeling Protein-Protein Interaction Networks,” University of Glasgow, Computing Science Seminar, Glasgow, UK, October 20, 2006
- IT-17 **N. Pržulj**, “Comparing and Modeling Protein-Protein Interaction Networks,” University of Strathclyde, Mathematics Colloquium, Glasgow, UK, October 18, 2006
- IT-16 **N. Pržulj**, “Comparing and Modeling Protein-Protein Interaction Networks,” Max Planck Institute for Molecular Genetics, Berlin, Germany, September 28, 2006
- IT-15 **N. Pržulj**, “Comparing and Modeling Protein-Protein Interaction Networks,” University of Bremen, Germany, September 26, 2006

- IT-14 **N. Pržulj**, “Protein-Protein Interaction Networks: Issues, Models, and Comparisons,” The Foundation for Research and Technology – Hellas (FORTH) Research Center, Heraklion, Greece, September 14, 2006
- IT-13 **N. Pržulj**, “Protein-Protein Interaction Networks: Issues, Models, and Comparisons,” International mathematical conference: *Topics in Mathematical Analysis and Graph Theory (MAGT’06)*, Belgrade, Serbia, September 1-4, 2006
- IT-12 **N. Pržulj**, “Comparing and Modeling Protein-Protein Interaction Networks,” The Institute of Physics, University of Belgrade, Belgrade, Serbia, August 29, 2006
- IT-11 **N. Pržulj**, “Comparing and Modeling Protein-Protein Interaction Networks,” Petnica Research Station, Valjevo, Serbia, August 26, 2006
- IT-10 **N. Pržulj**, “Comparing and Modeling Protein-Protein Interaction Networks,” Workshop on *Algorithms in Bioinformatics (AlBio’06)*, Moscow, Russia, July 11-13, 2006
- IT-9 **N. Pržulj**, “Analyzing Large Biological Networks: Protein-Protein Interaction Example,” *Simon Fraser University*, Vancouver, Canada, December 14, 2005
- IT-8 **N. Pržulj**, “Analyzing Large Biological Networks: Protein-Protein Interaction Example,” *University of Victoria*, Victoria, Canada, December 13, 2005
- IT-7 **N. Pržulj**, “Analyzing Large Biological Networks: Protein-Protein Interaction Example,” *University of British Columbia*, Vancouver, Canada, December 12, 2005
- IT-6 **N. Pržulj**, “Analyzing Large Biological Networks: Protein-Protein Interaction Example,” *Institute of Physics, University of Belgrade*, Zemun, Serbia and Montenegro, September 14, 2005
- IT-5 **N. Pržulj**, “Analyzing Large Biological Networks: Protein-Protein Interaction Example,” *BMC Research Center, RIKEN*, Nagoya, Japan, May 24, 2005
- IT-4 **N. Pržulj**, “Analyzing Large Biological Networks: Protein-Protein Interaction Example”, *Computer Science Department, UC Riverside*, Riverside, CA, April 25, 2005
- IT-3 **N. Pržulj**, “Analyzing Large Biological Networks: Protein-Protein Interaction Example”, *Computer Science Department, UC Irvine*, Irvine, CA, March 17, 2005
- IT-2 **N. Pržulj**, “Analyzing Software Call Graphs,” *Microsoft Research, Redmond*, WA, August 22, 2003
- IT-1 **N. Pržulj**, D. Wigle, and I. Jurisica, “Functional Topology in a Network of Protein Interactions,” *BioPathways, ISMB’03*, Brisbane, Australia, June 27 - 28, 2003

CONTRIBUTED TALKS:

Recall that **Intelligent Systems for Molecular Biology (ISBM)** and **European Conference on Computational Biology (ECCB)** are the top conferences in the field of computational biology with acceptance rates of about 15%. Every other year they are organized as one conference. Their proceedings are published as a special issue of *Bioinformatics*, the top journal in the research area. **Network Biology Special Interest Group Meeting (NetBio SIG)** is the top meeting in the field of biological networks, organized yearly as a pre-conference of ISMB.

- CT-32 V. Gligorijevic, N. Malod-Dognin and **N. Pržulj**, “Patient-Specific Data Fusion for Cancer Stratification and Personalized Treatment,” Proceedings of the 2016 *Pacific Symposium on Biocomputing (PSB)*, 21:321-332(2016), Big Island, Hawaii, USA, January 4-9, 2016
- CT-31 V. Gligorijevic, V. Janjic and **N. Pržulj**, “Integration of molecular network data reconstructs Gene Ontology,” *European Conference on Computational Biology (ECCB) 2014*, Strasbourg, France, September 7 to 10, 2014

- CT-30 A. Sarajlic, V. Gligorijevic, D. Radak and **N. Pržulj**, “Network wiring of pleiotropic kinases yields insight into protective role of diabetes on aneurysm,” Drug Development workshop of ECCB’14, Strasbourg, France, September 6-10, 2014
- CT-29 K. Sun, N. Buchan, C. Larminie and **N. Pržulj**, “The integrated disease network,” Drug Development workshop of ECCB’14, Strasbourg, France, September 6-10, 2014
- CT-28 V. Janjic and **N. Pržulj**, Evolution of the Topology of the Human Interactome, International Symposium on Integrative Bioinformatics, Newcastle, UK, May 12-14, 2014
- CT-27 S. Drezgić, I. Grudenić, A. Ionescu, and **N. Pržulj**, “A technical approach to local government amalgamation,” Proceedings of 18th Dubrovnik Economic Conference, Croatian National Bank, Dubrovnik, Croatia, June 27-30, 2012
- CT-26 B. Betkaoui, D. B. Thomas, W. Luk, and **N. Pržulj**, “A Framework for FPGA Acceleration of Large Graph Problems: Graphlet Counting Case Study,” Proceedings of International Conference on Field Programmable Technology (FPT’11), New Delhi, India, December 12-14, 2011
- CT-25 **N. Pržulj**, “Topological network alignment uncovers biological function and phylogeny,” *Highlights Track, ISMB/ECCB 2011*, Vienna, Austria, July 17-19, 2011
- CT-24 **N. Pržulj**, “Integrative Network Alignment and Analysis: MI-GRAAL and GraphCrunch,” *Network Biology Special Interest Group (SIG) of ISMB/ECCB 2011*, Vienna, Austria, July 15, 2011
- CT-23 **N. Pržulj**, “Geometric Evolutionary Dynamics of Protein Interaction Networks,” School and Conference on Computational Methods in Dynamics, Trieste, Italy, July 6, 2011
- CT-22 **N. Pržulj**, “Protein-Protein Interaction Network Topology Uncovers Evolution, Disease, and Gene Functions,” *ESF EMBO Symposium on “Molecular Perspectives on Protein-Protein Interactions,”* Sant Feliu de Guixols, Spain, November 14-19, 2010
- CT-21 **N. Pržulj**, “From biological networks to phylogeny and disease,” *Cold Spring Harbor Laboratory Meeting on Systems Biology: Networks*, Hinxton, UK, August 11-15, 2010
- CT-20 **N. Pržulj**, “Uncovering melanogenesis regulatory pathways from protein-protein interaction networks: the computational method and software tool,” *RECOMB Computational Cancer Biology 2010*, Oslo, Norway, June 24-25, 2010
- CT-19 V. Memisevic, T. Milenkovic, and **N. Pržulj**, “An integrative approach to modelling biological networks,” 6th Annual International Symposium on Integrative Bioinformatics, Cambridge, UK, March 22-24, 2010
- CT-18 V. Memisevic, T. Milenkovic, and **N. Pržulj**, “Complementarity of network and sequence information in homologous proteins,” 6th Annual International Symposium on Integrative Bioinformatics, Cambridge, UK, March 22-24, 2010
- CT-17 O. Kuchaiev, P. T. Wang, Z. Nenadic, and **N. Pržulj**, “Structure of Brain Functional Networks,” 31st Annual International Conference of the *IEEE Engineering in Medicine and Biology Society (EMBC’09)*, Minneapolis, Minnesota, USA, September 2-6, 2009
- CT-16 O. Kuchaiev, T. Milenkovic, V. Memisevic, W. Hayes, and **N. Pržulj**, “Topological network alignment uncovers biological function and phylogeny,” *BioPathways*, a Satellite Conference of *Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB’09)*, Stockholm, Sweden, June 27 - July 2, 2009
- CT-15 O. Kuchaiev and **N. Pržulj**, “Learning the structure of protein-protein interaction networks,” *Pacific Symposium on Biocomputing (PSB 2009)*, Big Island, Hawaii, January 5-9, 2009
- CT-14 **N. Pržulj**, “Biological Network Comparison Using Graphlet Degree Distribution,” *12th Serbian Mathematical Congress*, Novi Sad, Serbia, August 28 - September 2, 2008

- CT-13 T. Milenkovic and **N. Pržulj**, “Uncovering Biological Network Function via Graphlet Degree Signatures,” *12th Serbian Mathematical Congress*, Novi Sad, Serbia, August 28 - September 2, 2008
- CT-12 T. Milenkovic and **N. Pržulj**, “From network structure to biological function in protein-protein interaction networks,” *BioPathways*, a Satellite Conference of *Intelligent Systems for Molecular Biology (ISMB’08)*, Toronto, Canada, July 18-19, 2008
- CT-11 T. Milenkovic and **N. Pržulj**, “Uncovering Biological Network Function via Graphlet Degree Signatures,” *BioPathways*, a Satellite Conference of *Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB’07)*, Vienna, Austria, July 19-20, 2007
- CT-10 **N. Pržulj**, “Biological Network Comparison Using Graphlet Degree Distributions”, *European Conference on Computational Biology (ECCB’06)*, acceptance rate 18%, Eilat, Israel, January 21-24, 2007
- CT-9 Fereydoun Hormozdiari, Petra Berenbrink, **N. Pržulj**, and Cenk Sahinalp, “Not All Scale Free Networks are Born Equal: the Role of the Seed Graph in PPI Network Emulation”, *Research in Computational Molecular Biology (RECOMB’06) Satellite Conferences on Systems Biology and Computational Proteomics*, UC San Diego, December 1-3, 2006
- CT-8 **N. Pržulj** and Wayne Hayes, “Biological network comparison using graphlet degree distributions,” *3rd International Symposium on Networks in Bioinformatics (ISNB’06)*, acceptance rate 20%, Amsterdam, the Netherlands, May 29-31, 2006
- CT-7 **N. Pržulj**, “Uncovering Structure in Protein-Protein Interaction Networks,” *BioPathways*, a Satellite Conference of *Intelligent Systems for Molecular Biology (ISMB’05)*, Detroit, Michigan, June 23 - 24, 2005
- CT-6 **N. Pržulj**, D. G. Corneil, and I. Jurisica, “Geometric Model of Protein Interaction Networks,” *CNET 2004*, University of Aveiro, Portugal, August 29 - September 2, 2004
- CT-5 **N. Pržulj** and D. G. Corneil, “2-tree probe interval graphs have a large obstruction set,” *12th Ontario Combinatorics Workshop*, University of Ottawa, May 1-2, 2003
- CT-4 **N. Pržulj**, G. Lee, and I. Jurisica, “Functional Analysis of Large Software Networks,” *IBM Academy: Proactive Problem Prediction, Avoidance and Diagnosis*, IBM T.J. Watson Research Center, Yorktown, NY, April 28-29, 2003
- CT-3 **N. Pržulj**, “Minimal Hereditary Dominating Pair Graphs,” *Workshop on Structured Families of Graphs*, The Fields Institute, May 8-13, 2000
- CT-2 **N. Pržulj**, “Minimal Hereditary Dominating Pair Graphs,” *Special Year on Graph Theory and Combinatorial Optimization Program Seminar Series*, The Fields Institute, March 22, 2000
- CT-1 A. L. Liestman and **N. Pržulj**, “Minimum Average Time Broadcast Graphs,” *27th SE International Conference on Combinatorics, Graph Theory, and Computing*, Boca Raton, Florida, March, 1997

ACADEMIC SERVICE

SCIENTIFIC ADVISORY BOARD MEMBER:

- Helmholtz Centre for Infection Research (HZI / Braunschweig, Germany)

ASSOCIATE EDITOR:

- Systems Medicine: Journal of Medical Systems Biology and Network Medicine (Libert)

- * The premier open access, peer reviewed journal focused on interdisciplinary approaches to exploiting the power of big data by applying systems biology and network medicine. Systems Medicine yields major breakthroughs towards mechanism-based re-definitions of diseases for high-precision diagnostics and treatments.
- * Associate editors are by invitation only
- BMC Bioinformatics (BioMed Central)
 - * An open access, peer-reviewed journal that considers articles on all aspects of the development, testing and novel application of computational and statistical methods for the modeling and analysis of all kinds of biological data, as well as other areas of computational biology.
 - * Impact factor: 2.67
 - * Associate editors are by invitation only
- Journal of Complex Networks (Oxford Academic)
 - * Publishes original articles and reviews with a significant contribution to the analysis and understanding of complex networks and its applications in diverse fields
 - * Associate editors are by invitation only

EDITORIAL BOARD MEMBER:

- Bioinformatics (Oxford Journals)
 - * A leading journal in its field, Bioinformatics publishes the highest quality scientific papers and review articles of interest to academic and industrial researchers. Its main focus is on new developments in genome bioinformatics and computational biology.
 - * Impact factor: 7.307
 - * Editorial board members are by invitation only
- Scientific Reports - Nature (Nature Publishing Group)
 - * Scientific Reports is an online, open access journal from the publishers of *Nature*. It publishes scientifically valid primary research from all areas of the natural and clinical sciences. According to the 2013 Journal Citation Reports Science Edition (Thomson Reuters, 2014), Scientific Reports is the 5th among all multidisciplinary science primary research journals.
 - * Impact factor: 5.078
 - * Editorial board members are by invitation only
- Frontiers in Genetics (Frontiers)
 - * Open-access, publishes reviews, opinions, and commentaries across the full spectrum of genetic and genomic inquiry, from the most basic to the most applied, across all branches of the tree of life, embracing methodology, applications and implications.
- International Journal of Knowledge Discovery in Bioinformatics (IJKDB) (IGI Global)
 - * Published quarterly since being established in 2010
 - * Collects the most significant research and latest practices in computational knowledge discovery approaches to bioinformatics
 - * Outstanding editorial board, by invitation only

GUEST EDITOR:

- Internet Mathematics (A K Peters Ltd)
 - * Internet Mathematics publishes research papers that address fundamental problems, both conceptual and algorithmic, that arise in dealing with large complex information networks such as the Internet

* Impact factor: 2014 evaluation pending

CONFERENCE ORGANIZING:

Recall that **Intelligent Systems for Molecular Biology (ISBM)** and **European Conference on Computational Biology (ECCB)** are the top conferences in the field of computational biology with acceptance rates of about 15%. Every other year they are organized as one conference. Their proceedings are published as a special issue of *Bioinformatics*, the top journal in the research area. **Network Biology Special Interest Group Meeting (NetBio SIG)** is the top meeting in the field of biological networks, organized yearly as a pre-conference of ISMB, Prof. Przulj has been a co-organizer.

15. **Senior Program Committee** member of **ISMB 2018, co-Chair of all tracks, representing NetBio COSI**, Chicago, USA, July 6-10, 2018
14. **Proceedings Area Chair** of Network Biology track at **ISMB/ECCB 2017**, Prague, CZ, July 21-25, 2017
13. **Proceedings Area Chair** of Protein Interactions and Molecular Networks track at **ISMB 2016**, Orlando, FL, USA, July 8-12, 2016
12. Network Biology Special Interest Group Meeting (NetBio SIG) at ISMB 2016, Orlando, FL, USA, July 8-12, 2016
11. “Challenges and approaches in comprehensive and informative complex network analysis for precision medicine,” Workshop at ECCB 2016, co-organized with Prof. Igor Jurisica and Prof. Tijana Milenkovic, The Hague, Netherlands, September 3-7, 2016
10. **Proceedings Area Chair** of Protein Interactions and Molecular Networks track at **ISMB/ECCB 2015**, Dublin, Ireland, July 10-14, 2015
9. Network Biology Special Interest Group Meeting (NetBio SIG) at ISMB/ECCB 2015, Dublin, Ireland, July 10-14, 2015
8. “Challenges and approaches in comprehensive and informative complex network analysis for precision medicine”, co-organized with Igor Jurisica and Tijana Milenkovic, The [BC]² Basel Computational Biology Conference, Switzerland, June 9, 2015
7. “Integrative Dynamic Analyses of Large Biomedical Network Data,” Workshop at ECCB 2014, co-organized with Prof. Tijana Milenkovic, Strasbourg, France, September 7-10, 2014
6. Network Biology Special Interest Group Meeting (NetBio SIG) at ISMB 2014, Boston, USA, July 11-12, 2014
5. ACM Conference on Bioinformatics, Computational Biology, and Biomedicine (ACM BCB 2013), **Area Chair of System Biology** track, Washington, DC, USA, Sep 22-25, 2013
 - ACM-BCB is the main flagship conference of the ACM SIGBio (ACM Special Interest Group on Bioinformatics, Computational Biology and Biomedical Informatics).
 - Association for Computing Machinery (ACM) is the world’s largest educational and scientific computing society, it delivers resources that advance computing as a science and a profession, provides the computing field’s premier Digital Library and serves its members and the computing profession with leading-edge publications, conferences, and career resources.
4. Network Biology Special Interest Group Meeting (NetBio SIG) at ISMB/ECCB 2013, Berlin, Germany, July 19-23, 2013
3. Network Biology Special Interest Group Meeting (NetBio SIG) at ISMB 2012, Long Beach, CA, USA, July 15-17, 2012

2. “Network Links: Connecting Social, Communication and Biological Network Analysis,” Institute for Mathematics and Its Applications, University of Minnesota, USA, Feb 27 - March 2, 2012
 - Co-organized with: Prof. Mathieu Blanchette, McGill University, Canada; Dr. Graham Cormode AT&T Laboratories - Research, USA; Prof. Ben Raphael, Brown University, USA; and Prof. S. Cenk Sahinalp, Simon Fraser University, Canada.
 - Founded in 1982, the Institute for Mathematics and its Applications (IMA) is an NSF-funded visitors’ institute that has grown to become among the most influential math institutes in the world. Located on the University of Minnesota campus in the USA, it is one of eight NSF Mathematical Sciences Research Institutes.
1. “Biological Networks: Analyses, Models, Functions, and Disease,” Tutorial at the 9th International Conference on Systems Biology (ICSB’08), Gothenburg, Sweden, August 22-28, 2008
 - Co-organized with Prof. Tijana Milenkovic, University of Notre Dame, USA.
 - International Conference on Systems Biology (ICSB) is the highly-anticipated main event for the global systems biology community. It attracts top system biologists from all over the world to an environment that encourages integration of biology, computer science, engineering and chemistry, and that spans leading areas of biomedical research.

GOVERNMENT GRANT PROPOSAL REVIEWING:

23. Expert reviewer and panelist for the Research Council of Norway, 2017
22. Expert reviewer and panelist for the Research Council of Norway, 2016
21. Expert reviewer for Horizon 2020, EU, 2016
20. Expert reviewer and panelist for the Research Council of Norway, 2015
19. Expert reviewer for Horizon 2020, EU, 2015
18. Reviewed proposals for Engineering and Physical Sciences Research Council (EPSRC), UK, 2015
17. Expert reviewer and panellist for Horizon 2020, EU, 2014
16. Reviewed proposals for EPSRC, UK, 2014
15. Reviewed proposals for French Aix-Marseille excellence initiative A*MIDEX, 2014
14. Reviewed proposals for Medical Research Council (MRC), UK, 2013
13. Reviewed proposals for the Agency for Science, Research and Technology (A*STAR) in Singapore, 2013
12. Reviewed proposals for University of Southern Denmark strategic research fund, 2013
11. Reviewed proposals for EPSRC, UK, 2012
10. Reviewed proposals for the Defense Threat Reduction Agency (DTRA), DoD, USA 2011
9. Reviewed proposals for Canada Foundation for Innovation, 2010
8. Reviewed proposals for the Netherlands Genomics Initiative, 2010
7. Reviewed proposals for the Medical Research Council (MRC), UK, 2009
6. Reviewed proposals for the Israel Science Foundation (ISF), Israel, 2009
5. A panelist for the Academy of Finland Research Council for Natural Sciences and Engineering, Helsinki, Finland, 2008
4. Reviewed proposals for the Biotechnology and Biological Sciences Research Council (BBSRC), UK, 2007

3. Reviewed proposals for the US NSF (National Science Foundation) DMS Applied Mathematics Program, 2007
2. US NSF (National Science Foundation) panelist at a Panel of CISE IIS program, Arlington, VA, USA, 2007
1. US NSF (National Science Foundation) panelist at a Panel of CISE SEII program, Arlington, VA, USA, 2006

PROGRAM COMMITTEE MEMBER:

35. COMPLEX NETWORKS 2018, Cambridge, UK, December 11 - 13, 2018
34. ISMB 2018, Chicago, USA, July 6-10, 2018
33. RECOMB 2018, Paris, France, April 21-24, 2018
32. COMPLEX NETWORKS 2017, Lyon, France, November 29 - December 1, 2017
31. ISMB/ECCB 2017, Prague, CZ, July 21-25, 2017
30. European Conference on Computational Biology (ECCB) 2016, The Hague, Netherlands, September 3-7, 2016
29. Intelligent Systems for Molecular Biology (ISMB) 2016, Orlando, FL, USA, July 8 - July 12, 2016
28. Network Biology Special Interest Group Meeting (NetBio SIG) of Intelligent Systems for Molecular Biology (ISMB) 2016, Orlando, Florida, USA, July 8-12, 2016
27. Research in Computational Molecular Biology (RECOMB) 2016, Los Angeles, CA, USA, April 17-21, 2016
26. ACM International Conference on Bioinformatics and Computational Biology (ACM-BCB) 2015, Atlanta, GA, USA, September 9-12, 2015
25. Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB) 2015, Dublin, Ireland, July 10 - July 14, 2015
24. NetBio SIG of ISMB/ECCB 2015, Dublin, Ireland, July 10, 2015
23. Brazilian Symposium on Bioinformatics (BSB) 2014, Belo Horizonte, MG, Brazil, October 28-30, 2014
22. ECCB 2014 satellite workshop on Computational Integrative Biology Methods for Drug Development, Strasbourg, France, September 7, 2014
21. ISMB 2014, Boston, USA, July 11-15, 2014
20. NetBio SIG of ISMB 2014, Boston, USA, July 11, 2014
19. IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), Miami Beach, FL, USA, June 2-4, 2014
18. ACM-BCB 2013, Washington DC, Sep 22-25, 2013
17. ISMB/ECCB 2013, Berlin, Germany, July 19-23, 2013
16. NetBio SIG of ISMB/ECCB 2013, Berlin, Germany, July 19, 2013
15. ACM-BCB 2012, Orlando, Florida, October 7-10, 2012
14. ECCB 2012, Basel, Switzerland, September 9 - 12, 2012
13. Brazilian Symposium on Bioinformatics (BSB & EBB), Campo Grande, Mato Grosso do Sul, Brazil, August 13-17, 2012
12. ISMB 2012, Long Beach, California, USA, July 15-17, 2012
11. NetBio SIG at ISMB 2012, Long Beach, CA, USA, July 15-17, 2012
10. ISMB/ECCB 2011, Vienna, Austria, July 15 - July 19, 2011

9. ACM-BCB 2011, Chicago, USA, August 1-3, 2011
8. ISMB 2010, Boston, USA, July 11 - July 13, 2010
7. ACM-BCB, Niagara Falls, NY, USA, August 2-4, 2010
6. Immunoinformatics and Computational Immunology Workshop (ICIW 2010), in conjunction with ACM International Conference on Bioinformatics and Computational Biology (ACM-BCB), Niagara Falls, NY, USA, August 2-4, 2010
5. Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB) 2009, Stockholm, Sweden, June 27 - July 2, 2009
4. 16th International Symposium on Graph Drawing, Crete, Greece, September 21-24, 2008
3. International Workshop on Data Mining in Bioinformatics (BIOKDD '08) at the ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (SIGKDD'08), Las Vegas, NV, USA, August 24-27, 2008
2. International Workshop on Data Mining in Bioinformatics (BIOKDD '07) at the ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (SIGKDD'07), San Jose, CA, USA, August 12th, 2007
1. Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB) 2007, Vienna, Austria, July 21-25, 2007

SESSION CHAIR:

14. COMPLEX NETWORKS 2017, Lyon, France, November 29 - December 1, 2017
13. ECCB 2016, The Hague, NL, Sep 3 - 7, 2016
12. ECCB 2016 Workshop on Challenges and approaches in comprehensive and informative complex network analysis for precision medicine, Sep 3, 2016
11. ISMB 2016, Orlando, FL, USA, July 10 - July 12, 2016
10. ISMB/ECCB 2015, Dublin, Ireland, July 10 - July 14, 2015
9. NetSci 2015, International School and Conference on Network Science, Zaragoza, Spain, June 1-5, 2015
8. "Integrative Dynamic Analyses of Large Biomedical Network Data," Workshop at ECCB 2014, Strasbourg, France, September 7-10, 2014
7. Plenary Session 2, From Solid State To Bio Physics 2014, Cavtat, Croatia, June 7-14, 2014
6. Network Biology Special Interest Group Meeting (NetBio SIG) at ISMB/ECCB 2013, Berlin, Germany, July 19-23, 2013
5. "Network Links: Connecting Social, Communication and Biological Network Analysis," Institute for Mathematics and Its Applications, University of Minnesota, USA, Feb 27 - March 2, 2012
4. RECOMB Satellite Conference on Bioinformatics Education (RECOMB-BE) 2009, UC San Diego, La Jolla, California, March 14-15, 2009
3. Invited session, Center for Algorithmic and Systems Biology, CASB-20, UC San Diego, La Jolla, California, March 14-15, 2009
2. Invited session on *Networks in Society and Technology* at the *Complex Networks Across the Technological and Natural Sciences*, Institute for Advanced Studies, Glasgow, UK, January 27-30, 2009
1. Invited session on *Biological Networks* at the *39th Symposium on the Interface: Computing Science and Statistics – Systems Biology*, Philadelphia, PA, May 23-26, 2007

JOURNAL PAPER REVIEWER:

24. *Algorithms for Molecular Biology* (BioMed Central)
23. *Bioinformatics* (Oxford Journals)
22. *BMC Bioinformatics* (BioMed Central)
21. *Briefings in Functional Genomics* (Oxford Journals)
20. *Cancer Informatics* (Libertas Academica)
19. *Cell Systems* (Cell Press)
18. *Cell Death and Disease* (Nature Publishing Group)
17. *Data Mining and Knowledge Discovery*
16. *Discrete Mathematics* (Elsevier)
15. *Discrete Applied Mathematics* (Elsevier)
14. *FEBS Letters* (Elsevier)
13. *Genome Biology* (BioMed Central)
12. *IEEE Transactions on Computational Biology and Bioinformatics* (IEEE Computer Society)
11. *IEEE Transactions on Neural Networks and Learning Systems* (IEEE Computer Society)
10. *Journal of Complex Networks* (Oxford Journals)
9. *Nature Biotechnology* (Nature Publishing Group)
8. *Nature Communications* (Nature Publishing Group)
7. *Nature Methods* (Nature Publishing Group)
6. *Nature Protocols* (Nature Publishing Group)
5. *Nucleic Acids Research* (Oxford Journals)
4. *PLoS Computational Biology* (Public Library of Science)
3. *PLoS One* (Public Library of Science)
2. *Proteins: Structure, Function, and Bioinformatics* (Wiley)
1. *Science* (AAAS)

CONFERENCE PAPER REVIEWER:

32. COMPLEX NETWORKS 2018, Cambridge, UK, December 11 - 13, 2018
31. ISMB 2018, Chicago, USA, July 6-10, 2018
30. RECOMB 2018, Paris, France, April 21-24, 2018
29. COMPLEX NETWORKS 2017, Lyon, France, November 29 - December 1, 2017
28. ISMB/ECCB 2017, Prague, CZ, July 21-25, 2017
27. Research in Computational Molecular Biology (RECOMB) 2016, Los Angeles, CA, USA, April 17-21, 2016
26. ACM-BCB 2015, Atlanta, GA, USA, September 9-12, 2015
25. ISMB/ECCB 2015, Dublin, Ireland, July 10 - July 14, 2015
24. Brazilian Symposium on Bioinformatics (BSB) 2014, Belo Horizonte, MG, Brazil, October 28-30, 2014
23. ECCB 2014 satellite workshop on Computational Integrative Biology Methods for Drug Development, Strasbourg, France, September 7, 2014

22. ISMB 2014, Boston, USA, July 11-15, 2014
21. IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), Miami Beach, FL, USA, June 2-4, 2014
20. ACM-BCB 2013, Washington DC, Sep 22-25, 2013
19. ISMB/ECCB 2013, Berlin, Germany, July 19-23, 2013
18. ECCB 2012, Basel, Switzerland, September 9 - 12, 2012
17. Brazilian Symposium on Bioinformatics (BSB & EBB), Campo Grande, Mato Grosso do Sul, Brazil, August 13-17, 2012
16. ISMB 2012, Long Beach, California, USA, July 15-17, 2012
15. RECOMB 2012, Barcelona, Spain, April 21-24, 2012
14. ISMB/ECCB 2011, Vienna, Austria, July 15 - July 19, 2011
13. ACM-BCB 2011, Chicago, USA, August 1-3, 2011
12. Intelligent Systems for Molecular Biology (ISMB) 2010, Boston, USA, July 11 - July 13, 2010
11. ACM International Conference on Bioinformatics and Computational Biology (ACM-BCB), Niagara Falls, NY, USA, August 2-4, 2010
10. Immunoinformatics and Computational Immunology Workshop (ICIW 2010), in conjunction with ACM International Conference on Bioinformatics and Computational Biology (ACM-BCB), Niagara Falls, NY, USA, August 2-4, 2010
9. Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB) 2009, Stockholm, Sweden, June 27 - July 2, 2009
8. 2009 American Medical Informatics Association (AMIA) Summit on Translational Bioinformatics (STB 2009), San Francisco, CA, March 15-17, 2009
7. International Workshop on Data Mining in Bioinformatics (BIOKDD '08) at the ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (SIGKDD'08), Las Vegas, NV, USA, August 24-27, 2008
6. Computational Systems Bioinformatics (CSB '08), Stanford, CA, August 25-29, 2008
5. Combinatorial Pattern Matching (CPM '08), Pisa, Italy, June 18-20, 2008
4. International Workshop on Data Mining in Bioinformatics (BIOKDD '07) at the ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (SIGKDD '07), San Jose, CA, USA, August 12, 2007
3. Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB '07), Vienna, Austria, July 21-25, 2007
2. Pacific Symposium on Biocomputing (PSB '07), Maui, Hawaii, January 3-7, 2007
1. Intelligent Systems for Molecular Biology (ISMB '06), Fortaleza, Brazil, August 6-10, 2006

UNIVERSITY SERVICE:

5. Member of the Project Board for the Data Storage Improvement Project, University College London, 2017-present
4. MSc in in Bioinformatics and Theoretical Systems Biology Coordinator, Department of Computing, Imperial College London, 2009–2016
3. School of Information and Computer Sciences (ICS) representative to the UC Irvine Senate Assembly, 2008-2009
2. Graduate Committee, Information and Computer Science (ICS), UCI, 2006–2008

1. Computing Committee, Information and Computer Science (ICS), UCI, 2005–2006

SERVICE AS A STUDENT:

4. President: Computer Science Graduate Student Society, U of T, 2000-2002
3. Executive member: Computer Science Graduate Student Society, U of T, 1998-2004
2. Graduate Student Representative: Graduate Committee, Department of Computer Science, U of T, 1998-2001
1. President: International Students' Club, Simon Fraser University, 1995-1996

TEACHING

TAUGHT GRADUATE COURSES:

18. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2016
– Enrollment: 123 students
17. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2015
– Enrollment: 93 students
16. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2014
– Enrollment: 84 students
15. Bioinformatics II, MSc in Bioinformatics and Theoretical Systems Biology, Imperial College London, Fall 2013
– Enrollment: 18 students
14. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2013
– Enrollment: 87 students
13. Bioinformatics II, MSc in Bioinformatics and Theoretical Systems Biology, Imperial College London, Fall 2012
– Enrollment: 16 students
12. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2012
– Enrollment: 65 students
11. Bioinformatics II, MSc in Bioinformatics and Theoretical Systems Biology, Imperial College London, Fall 2011
– Enrollment: 24 students
10. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2011
– Enrollment: 80 students
9. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2010
– Enrollment: 27 students
8. COMPSCI 265 Graph Algorithms, ICS, UCI, Winter 2009
– Enrollment: 12 students
– Student Evaluations – Overall Median: 7 (on 0-9 scale); 8 students responded
7. COMPSCI 288A Biological Networks, ICS, UCI, Winter 2009
– Enrollment: 3 students
– Student Evaluations – Overall Median: 9 (on 0-9 scale); 2 students responded
6. ICS 288A Biological Networks, ICS, UCI, Winter 2007

- Enrollment: 6 students
- Student Evaluations – Overall Median: 9 (on 0-9 scale); 3 students responded
- 5. I&C SCI 280 Biological Networks, ICS, UCI, Winter 2006
 - Enrollment: 7 students
 - Student Evaluations – Overall Median: 7.71 (on 0-9 scale); 7 students responded
- 4. I&C SCI 265 Graph Algorithms, ICS, UCI, Winter 2006
 - Enrollment: 7 students
 - Student Evaluations – Overall Median: 6.33 (on 0-9 scale); 3 students responded
- 3. ICS 298 Thesis Supervision ICS, UCI, Winter-Spring 2008
 - Enrollment: 3 students
- 2. I&C SCI 299: Individual Study, ICS, UCI, 2006-2009
 - Enrollment: 5 students
- 1. I&C SCI 290: Research Project, ICS, UCI, 2006-2009
 - Enrollment: 4 students

TAUGHT UNDERGRADUATE COURSES:

- 15. 3096: Research Group Project, Comp. Sci., University College London, Winter 2018
- 14. 3095: Research Methods, Computer Science, University College London, Fall 2017
- 13. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2016
 - Enrollment: 123 students
- 12. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2015
 - Enrollment: 93 students
- 11. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2014
 - Enrollment: 84 students
- 10. Bioinformatics II, MSc in Bioinformatics and Theoretical Systems Biology, Imperial College London, Fall 2013
 - Enrollment: 18 students
- 9. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2013
 - Enrollment: 87 students
- 8. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2012
 - Enrollment: 65 students
- 7. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2011
 - Enrollment: 80 students
- 6. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2010
 - Enrollment: 27 students
- 5. ICS 139W: Critical Writing, ICS, UCI, Winter 2009
 - Enrollment: 58 students
 - Student Evaluations – Overall Median: 7 (on 0-9 scale); 19 students responded
- 4. CS 163: Graph Algorithms, ICS, UCI, Spring 2008
 - Enrollment: 49 students
 - Student Evaluations–Overall Median: 6.65 (on 0-9 scale); 17 students responded
- 3. ICS 139W: Technical Writing, ICS, UCI, Winter 2007

- Enrollment: 53 students
 - Student Evaluations–Overall Median: 8.50 (on 0-9 scale); 16 students responded
2. ICS 139W: Technical Writing, ICS, UCI, Winter 2007
 - Enrollment: 30 students
 - Student Evaluations–Overall Median: 7 (on 0-9 scale); 9 students responded
 1. I&C SCI 199: Individual Study, ICS, UCI, Spring and Fall 2006
 - Enrollment: 2 students

DEVELOPED A NEW UNDERGRADUATE/GRADUATE COURSE:

1. 341: Introduction to Bioinformatics, Department of Computing, Imperial College, first offered in Spring 2010

DEVELOPED A NEW GRADUATE COURSE:

1. I&C SCI 288A Biological Networks, ICS, UCI, first offered in Winter 2007

STUDENT SUPERVISION

PH.D. ALUMNI:

7. Anida Sarajlic, Ph.D., 2016, Department of Computing, Imperial College London
Thesis title: “Analysing Directed Network Data”
– Defended on October 13, 2015
6. Vuk Janjic, Ph.D, 2015, Department of Computing, Imperial College London.
Thesis title: “Mining real-world networks in systems biology and economics”
– Now working in a bank in London City
5. Kai Sun, Ph.D., 2014, Department of Computing, Imperial College London
Thesis title: “Uncovering Disease Associations via Integration of Biological Networks”
– Now a post-doc at Imperial College London
4. Omer Yaveroglu, Ph.D., 2014, Department of Computing, Imperial College London
Thesis title: “Graphlet Correlations for Network Comparison and Modelling: World Trade Network Example”
– Now at Google, London, UK; previously a post-doc at UC Irvine
3. Tijana Milenkovic, Ph.D., 2010, Computer Science, UC Irvine
Thesis title: “From Topological Network Analyses and Alignments to Biological Function, Disease, and Evolution”
– Now an Assistant Professor in Computer Science, University of Notre Dame, USA
2. Oleksii Kuchaiev, Ph.D., 2010, Computer Science, UC Irvine
Thesis title: “Modeling and Alignment of Biological Networks”
– Since December 2013, a Senior Applied Researcher, Apple, USA
– Previously a Research Engineer, Microsoft, Redmond, USA
1. Vesna Memisevic, Ph.D., 2010, Computer Science, UC Irvine
Thesis title: “Uncovering Biological Knowledge from Network Structure”
– Now a Scientist at Biotechnology HPC Software Application Institute, US Army, Frederick, USA

M.Sc. ALUMNI:

10. Sam Windels, M.Sc. Computing, 2015, Imperial College London

9. Varun Verma, M.Eng. Computing, 2015, Computing, Imperial College London
8. Vasileios Smyrlis, M.Eng. Bioengineering, 2015, Imperial College London
7. Javier Tapial, M.Sc. Bioinformatics and Theoretical Systems Biology, 2014, Imperial College London
6. Razvan Marinescu, M.Eng. Computing, 2014, Imperial College London
5. Miles Mulholland, M.Eng. Computing, 2011, Imperial College London
4. Aleksandar Stevanovic, M.Sc., 2010, Computer Science, UC Irvine. Thesis title: “Models of Biological Networks and a Software Tool for Network Analysis”
3. Oleksii Kuchaiev, M.Sc., 2009, Computer Science, UC Irvine. Thesis title: “Geometric graphs in biological networks”
2. Tijana Milenkovic, M.Sc., 2008, Computer Science, UC Irvine. Thesis title: “Interplay of topology and biology in protein-protein interaction networks”
1. Hania El Ayoubi, M.Sc., 2007, Computer Science, University of Toronto. Co-supervised by Prof. D. G. Corneil. Project title: “Proposing new protein-protein interaction network models validated by emerging data and network-characterizing metrics”

SUPERVISED POST-DOCTORAL FELLOWS:

7. Remi Momo, Computer Science Department, University College London, Dec 2017 – present
6. Chhedi Gupta, Computer Science Department, University College London, Nov 2017 – present
5. Noel Malod-Dognin, Computer Science Department, University College London (previously also at Imperial College), September 2012 – present
4. Julia Petschnigg, Computer Science Department, University College London, June–November 2017
3. Omer Nebil Yaveroglu, Calit2, UC Irvine, January 2014 – September 2015
2. Joana P. Goncalves, Department of Computing, Imperial College, April – December 2012
1. Marija Rasajski, Information and Computer Science (ICS), UCI, May 2007 – May 2008

EXTERNAL REVIEWER / EXAMINER OF PH.D. THESES:

4. Jonathan Cardoso Silva, King’s College London, UK, February, 2018
3. Josch Konstantin Pauling, University of Southern Denmark, August 1, 2016
2. Eudes Guilherme Vieira Barbosa, University of Southern Denmark, July 29, 2016
1. Richard Rottger, Naturwissenschaftlich-Technischen Fakultät I, Saarbrücken, Germany, February 2014

SUPERVISED PH.D. STUDENTS:

14. Amine Kaddioui, Ph.D. student, UCL, September 2017 – present
13. Sam Windels, Ph.D. student, UCL, September 2016 – present
12. Thomas Gaudet, Ph.D. student, UCL, September 2016 – present
11. Luis Leal, Ph.D. student, Imperial College, October 2015 – March 2016
10. Domagoj Margan, Ph.D. student, Imperial College, October 2015 – March 2016
9. Vladimir Gligorijevic, Ph.D. student, Imperial College, December 2013 – March 2016

8. Anida Sarajlic, Ph.D., Imperial College, September 2012 – December 2015
7. Vuk Janjic, Ph.D., Imperial College, April 2011 – February 2015
6. Kai Sun, Ph.D., Imperial College, October 2010 – June 2014
5. Omer Nebil Yaveroglu, Ph.D., Imperial College London, October 2010 – December 2013
4. Tijana Milenkovic, Ph.D., ICS, UCI, September 2006 – March 2010
3. Vesna Memisevic, Ph.D., ICS, UCI, September 2007 – June 2010
2. Oleksii Kuchaiev, Ph.D., ICS, UCI, September 2007 – June 2010
1. Jingjing Li, Ph.D. student, ICS UCI, September–December, 2006

SERVED ON PH.D. COMMITTEES OF:

16. Vladimir Gligorijevic, Ph.D. transfer, Imperial College, December 2014
15. Anida Sarajlic, Ph.D. transfer, Imperial College, June 2013
14. Vuk Janjic, Ph.D. transfer, Imperial College, February 2012
13. Kai Sun, Ph.D. transfer, Imperial College, June 2011
12. Omer Nebil Yaveroglu, Ph.D. transfer, Imperial College, June 2011
11. Vesna Memisevic, Ph.D., Computer Science, UCI. May 28, 2010, Ph.D. Defence, Ph.D. Advisor
10. Oleksii Kuchaiev, Ph.D., Computer Science, UCI. May 27, 2010, Ph.D. Defence, Ph.D. Advisor
9. Tijana Milenkovic, Ph.D., Computer Science, UCI. Dec. 3, 2009, Ph.D. Defence, Ph.D. Advisor
8. Weng Leong Ng, Ph.D. candidate, Computer Science, UCI. Sept. 11, 2009, Ph.D. Candidacy Exam, Committee member
7. Oleksii Kuchaiev, Ph.D. candidate, Computer Science, UCI. June 12, 2009, Ph.D. Candidacy Exam, Ph.D. Advisor
6. Vesna Memisevic, Ph.D. candidate, Computer Science, UCI. June 11, 2009, Ph.D. Candidacy Exam, Ph.D. Advisor
5. Tijana Milenkovic, Ph.D. candidate, Computer Science, UCI. July 3, 2008, Ph.D. Candidacy Exam, Ph.D. Advisor
4. Martin Brandon, Ph.D. candidate, Information and Computer Science (ICS), UCI. December 13, 2006, Ph.D. Topic Defense, Committee member
3. Harindar Keer, Ph.D. candidate, Chemistry, UCI. March 21, 2007, Ph.D. Candidacy Exam, Committee member
2. Shyam Srinivasan, Ph.D. candidate, Information and Computer Science (ICS), UCI. 2006, Ph.D. Candidacy Exam, Committee member
1. David Joshua Dibble, Ph.D. candidate, Organic Chemistry, UCI. 2006, Ph.D. Candidacy Exam, Committee member

UNDERGRADUATE STUDENTS:

6. Razvan Marinescu, Computing, Imperial College London, May 2012 – June 2014
5. Brigitta Devenyi, Computing, Imperial College London, Oct. 2010 – June 2011
4. Vitaliy Kozak, Math and Computing, Imperial College London, Oct. 2009 – June 2010
3. Naveen Nathan, ICS, UCI, June 2007 – December 2007

2. David Hubin, ICS, UCI, March 2006 – June 2007. Recipient of a SURP UCI award for Summer 2006 and a UROP UCI award for 2006/07
1. Jason Lai, ICS, UCI, October 2005 – June 2007

HIGH-SCHOOL STUDENT:

1. Stefan Covic, May 2006

RESEARCH SUPPORT

16. ERC Consolidator Grant
 Title: Integrated Connectedness for a New Representation of Biology
 PI: Nataša Pržulj, University College London
 Funding Organization: European Research Council
 Funding period: 2018 – 2023
 Funds received: €2,000,000
15. The Prostate Project Charity, UK
 PI: Nataša Pržulj, University College London
 Funding period: 2017–2019
 Funds received: £50,000
14. Slovenian Research Agency (ARRS): Biomedical Data Fusion Using a Non-Negative Matrix Tri-Factorization
 PI: Nataša Pržulj, Institute of Mathematics, Physics and Mechanics (IMFM), Ljubljana, Slovenia
 Funding Organization: Slovenian Research Agency (ARRS)
 Funding period: 01/06/2017 – 1/06/2020
 Funds received: €300,000
13. University College London, Computer Science Department, Start-up:
 PI: Nataša Pržulj, University College London
 Two Ph.D. studentships
 Funding period: 2016–2020
12. The Farr Institute for Health Informatics Research, UK:
 PI: Nataša Pržulj, University College London
 Two post-doctoral fellowships
 Funding period: 2016–2018
 Funds received: £140,572.48
11. ERC Starting Independent Researcher Grant
 Title: Network Topology Complements Genome as a Source of Biological Information
 PI: Nataša Pržulj, Imperial College and University College London
 Funding Organization: European Research Council
 Funding period: 01/01/2012 – 31/12/2017
 Funds received: €1,638,175
10. NSF CDI-Type II: Topology and Function in Computer, Social and Biological Networks
 PI: Athina Markopoulou, UC Irvine
 Co-PIs: Carter Butts and Nataša Pržulj, UC Irvine
 Funding Organization: National Science Foundation
 Funding period: 10/01/2010 – 09/30/2016
 Funds received: \$1,999,503

9. Slovenian Research Agency (ARRS) J1-5454: Unravelling Biological Networks
 PI: Nataša Pržulj, Faculty of Information Studies
 Funding Organization: Slovenian Research Agency (ARRS)
 Funding period: 01/08/2013 – 31/07/2016
 Funds received: €150,000
8. Serbian Ministry of Education and Science III44006: Algorithms, combinatorics and optimization with applications in internet technologies, social networks, wireless networks and mobile communications, biological networks, optical networks and supply chain management
 PI: Zoran Ognjanovic, Mathematics Institute of the Serbian Academy of Arts and Sciences
 Funding Organization: Serbian Ministry of Education and Science
 Funding period: 01/01/2011 – present
 Funds received: €21,600
7. GlaxoSmithKline Ph.D. studentships
 PI: Nataša Pržulj, Imperial College London
 Funding period: 2010–2014
 Funds received: £80,000
6. Imperial College London, Dept. of Computing, Start-up:
 PI: Nataša Pržulj, Imperial College London
 One Ph.D. studentship
 Research and travel support
 Funding period: 2009–2013
5. NSF CAREER: Tools for Analyzing, Modeling, and Comparing Protein-Protein Interaction Networks
 PI: Nataša Pržulj, UC Irvine
 Funding Organization: National Science Foundation
 Funding period: 2007–2011
 Funds received: \$569,905
4. UCI Set-up:
 PI: Nataša Pržulj, UC Irvine
 Funding Organization: UC Irvine, School of Information and Computer Sciences
 Funding period: 2005–2011
 Funds received: \$200,000
3. UCI Council on Research, Computing and Library Resources (CORCLR):
 PI: Zoran Nenadic, Biomedical Engineering, UC Irvine
 co-PI: Nataša Pržulj, Computer Science, UC Irvine
 Funding Organization: Council on Research, Computing and Library Resources, UCI
 Funding period: 2008–2009
 Funds received: \$11,800
2. UCI Center for Complex Biological Systems (CCBS):
 PI: Nataša Pržulj, Computer Science, UC Irvine
 co-PI: Zoran Nenadic, Biomed. Engineering, UCI
 Funding Organization: Center for Complex Biological Systems (CCBS), UCI
 Funding period: 2008
 Funds received: \$10,000
1. UCI Center for Complex Biological Systems (CCBS):
 PI: Nataša Pržulj, Computer Science, UC Irvine
 co-PI: Anand Ganesan, Dermatology, UCI

Funding Organization: Center for Complex Biological Systems (CCBS), UCI
Funding period: 2008
Funds received: \$10,000

EXPERIENCE DETAILS

Full Professor, Computer Science Department, University College London, UK
April 2016 – present

Associate Professor (Reader), Dept. of Computing, Imperial College London, UK
August 2012 – March 2016

Assistant Professor, Dept. of Computing, Imperial College London, UK
October 2009 – July 2012

Visiting Research Scientist (20% time) California Institute for Telecommunications and Information Technology
October 2010–2016

Professor (0% appointment), School of Computing (RAF), Union University, Belgrade
June 2013–present
Previously Associate Professor (0%), from October 2008 to June 2013

Assistant Professor, Department of Computer Science, UC Irvine, Irvine, CA, USA
July 2005 – July 2010
On leave from October 2009 to Imperial College London

Postdoctoral Fellow, Samuel Lunenfeld Research Institute, Toronto, ON, Canada
March 2005 – June 2005
SUPERVISOR: Jeff Wrana

- Prof. Przulj analyzed and modeled protein-protein interaction networks. Her models were used to guide biological experiments for identifying protein-protein interactions.

Research Assistant, Banting and Best Institute, University of Toronto, ON, Canada
September 2002 - May 2003
- Analyzed large networks of protein interactions using novel graph-theoretic approaches.

Teaching Assistant and Substitute Instructor, University of Toronto, ON, Canada
May 1999 - May 2002
- Gave lectures, tutorials, and office hours, marked assignments, supervised and marked exams for the following courses:

First year course:

Teaching Assistant and Substitute Instructor: CSC 199 Beautiful Algorithms, Fall 2001 and Spring 2002.

Second year course:

Teaching Assistant: CSC 238 Discrete Mathematics, Summer 1999 and Summer 2001.

Third year course:

Teaching Assistant: MATC32 Graph Theory and Algorithms, University of Toronto at Scarborough, Fall 2000.

Graduate course:

Teaching Assistant: CSC 2414 Topics in Applied Discrete Mathematics: Analysis of Algorithms, Spring 2002.

Visiting Ph.D. Student, The Fields Institute, Toronto, ON, Canada
January 2000 - December 2000

Programming Consultant, Westech Information Systems, Vancouver, BC, Canada
May 1997 - August 1998

- Prof. Przulj worked full-time as a programming consultant on the GIS Smallworld team, and provided programming services for object oriented AM/FM/GIS systems on the Windows NT platform. She developed Object Oriented GUI GIS utility applications in Smallworld Magik, translated data from GFIS to Smallworld, installed an Oracle Server and made an interface between Oracle and Smallworld applications. She also performed System Administration GIS tasks such as image building and maintenance.

Research Assistant, Simon Fraser University, Burnaby, BC, Canada
September 1996 - December 1996 and September 1997 - December 1997

- Worked under the supervision of Prof. A. Liestman on network broadcasting problems. The research resulted in the paper J-1 listed above, and the talk CT-1 listed above.

Teaching Assistant, Simon Fraser University, Burnaby, BC, Canada
January 1996 - April 1996

- MAT 154, 155, 157, 158 Applied Calculus Courses. Held office hours, explained mathematical problems to students, marked homework, supervised and marked exams.

Quality Assurance Engineer, Hughes Aircraft of Canada Ltd., Richmond, BC, Canada
May 1995 - Aug 1995

- Prof. Przulj reviewed and approved documents of all phases of software development, participated in meetings conducted to approve software development phases, and wrote a proprietary document entitled "Metrics Collections Instructions" for monitoring the progress of the Canadian Automated Air Traffic Control System project as part of her Natural Sciences and Engineering Research Council of Canada (NSERC) Industrial Undergraduate Student Research Award. The document was approved by Dr. K. Toth, the Quality Assurance Director, and subsequently included in the company's formal procedures. It has been used by Quality Assurance Engineers both weekly and monthly as a guide for metrics collections on the Canadian Automated Air Traffic Control System project.

AFFILIATIONS

Elected into Academia Europaea, The Academy of Europe, since 2017

The International Society for Computational Biology (ISCB), since 2003

Fellow of The British Computer Society (BCS), since 2013

Elected into The Young Academy of Europe (YAE), since 2013

The Association for Computing Machinery (ACM), since 2013

REFERENCES

Available upon request