

NATAŠA PRŽULJ: CURRICULUM VITÆ

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RESEARCH INTERESTS

Systems biology: modeling, algorithms, alignment for molecular and cellular networks
Proteomics: structure and function of proteins and protein-protein interaction networks
Graph theory: computational graph theory and algorithms; structured families of graphs

EDUCATION

Ph.D. Computer Science, University of Toronto, 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, 2000

TITLE: *Minimal Hereditary Dominating Pair Graphs*

SUPERVISOR: Derek G. Corneil (CS)

B.Sc. Computer Science and Mathematics, Simon Fraser University, 1997

FIRST CLASS HONORS

CGPA 3.85 out of 4

Department of Mathematics, University of Belgrade, 1991-93

Completed 2 out of 4 years in Computer Science and Mathematics Program

CGPA 9 out of 10

AWARDS AND DISTINCTIONS

ERC Starting Independent Researcher Grant, €1,638,175, Imperial, 2012-2017

NSF CDI-Type II Award (co-PI), \$1,999,503, UC Irvine, 2010-2014

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

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

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

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

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

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

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

PROFESSIONAL POSITIONS

2009–present: Lecturer (Asst. Prof.), Dept. of Computing, Imperial College London
2009–present: Member of the Center for Integrative Systems Biology (CISBIC), Imperial
2009–present: Member of the Institute for Systems and Synthetic Biology, Imperial College
2009–present: Member of the Centre for Bioinformatics, Imperial College London
2010–present: Visiting Research Scientist, California Institute for Telecommunications
and Information Technology, Irvine, CA, USA
2008–present: Assoc. Prof. (0%), School of Computing, Union University, Belgrade
2005–2010: Assistant Professor, Computer Sci. Dept., University of California, Irvine
2008–2010: Member of the University of California Irvine (UCI) Cancer Center
2006–2010: Member of the UCI Center for Complex Biological Systems (CCBS)
2005–2010: 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

CONTRIBUTIONS TO RESEARCH AND DEVELOPMENT

REFEREED JOURNAL PAPERS:

- 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.
- J-30 T. Milenkovic, V. Memisevic, and **N. Pržulj**, “Dominating Biological Networks,” *PLoS ONE*, 6(8):e23106, 2011.
- J-29 Arabidopsis Interactome Mapping Consortium, “Evidence for Network Evolution in an Arabidopsis Interactome Map,” *Science*, 333:601-607, July 29, 2011.
- J-28 O. Kuchaiev and **N. Pržulj**, “Integrative Network Alignment Reveals Large Regions of Global Network Similarity in Yeast and Human,” *Bioinformatics*, 2011.
- J-27 **N. Pržulj**, “Protein-protein interactions: making sense of networks via graph-theoretic modeling,” *Bioessays*, 33(2):115-123, February, 2011.
- 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, 2011.¹
- 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, 2010.²

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

²Reported as “Highly Visible” by *Cancer Informatics*.

- 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.
- 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 13 times.**³
- 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.
- J-21 V. Memisevic, T. Milenkovic, and **N. Pržulj**, “An integrative approach to modelling biological networks,” *Journal of Integrative Bioinformatics*, 7(3):120, 2010.
- 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.
- 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.
- J-18 **N. Pržulj**, “Biological Network Comparison Using Graphlet Degree Distribution,” Erratum, *Bioinformatics*, 26(6):853-854, 2010.
- 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 10 times.**³
- 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.
- 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 interaction network analysis,” *PNAS*, 105(36):13333-13338, 2008. **Cited 30 times.**³
- J-14 T. Milenkovic and **N. Pržulj**, “Uncovering Biological Network Function via Graphlet Degree Signatures,” *Cancer Informatics*, 2008(6):257-273, 2008. **Cited 33 times.**^{2,3}
- 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 23 times.**³
- J-12 T. Milenkovic, J. Lai, and **N. Pržulj**, “GraphCrunch: A Tool for Large Network Analyses,” *BMC Bioinformatics*, 9:70, January 30, 2008. **Cited 28 times.**^{1,3}
- 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 35 times.**³
- 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 26 times.**³
- 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 73 times.**³
- 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 41 times.**³

³All citations are from Google Scholar.

- 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 246 times.**³
- 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 5 times.**³
- J-5 **N. Pržulj**, D. G. Corneil, and I. Jurisica, “Modeling Interactome: Scale-Free or Geometric?,” *Bioinformatics*, 20(18):3508-3515, 2004. **Cited 156 times.**³
- J-4 A. D. King, **N. Pržulj**, and I. Jurisica, “Protein complex prediction via cost-based clustering,” *Bioinformatics*, 20(17):3013 - 3020, 2004. **Cited 208 times.**³
- J-3 **N. Pržulj**, D. Wigle, and I. Jurisica, “Functional Topology in a Network of Protein Interactions,” *Bioinformatics*, 20(3):340-348, 2004. **Cited 138 times.**³
- J-2 **N. Pržulj**, D. G. Corneil, and E. Koehler, “Hereditary Dominating Pair Graphs,” *Discrete Applied Mathematics*, 134:239-261, 2004.
- J-1 A. L. Liestman and **N. Pržulj**, “Minimum Average Time Broadcast Graphs,” *Par. Proc. Lett.*, 8:139-147, 1998.

REFEREED CONFERENCE PAPERS:

- 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.
- 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.
- 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.
- 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.
- 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 *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:

- 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 11 times.**¹

REFEREED POSTERS:

- P-42 T. Milenkovic, O. Kuchaiev, W. Hayes, and **N. Pržulj**, “GraphCrunch 2 Network Analysis Tool and MI-GRAAL Network Aligner,” *Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB) 2011*, Vienna, Austria, July 17-20, 2011.
- P-41 **N. Pržulj**, “Topological network alignment uncovers biological function and phylogeny,” Highlights poster at *Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB) 2011*, Vienna, Austria, July 17-20, 2011.
- P-40 T. Milenkovic, V. Memisevic, and **N. Pržulj**, “Network topology complements sequence as a source of biological information,” *Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB) 2011*, Vienna, Austria, July 17-20, 2011.
- P-39 T. Milenkovic and **N. Pržulj**, “Network analysis uncovers key biological processes and pathways in molecular networks,” NetBio-SIG at *Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB) 2011*, Vienna, Austria, July 15, 2011.
- P-38 **N. Pržulj**, “Network topology complements sequence as a source of biological information,” *Cold Spring Harbor Laboratory Meeting on Systems Biology: Networks*, Cold Spring Harbor Laboratory, USA, March 22-26, 2011.

- P-37 **N. Pržulj**, O. Kuchaiev, A. Stevanovic, M. Rasajski, W. Hayes, and D. Higham, “Geometric evolutionary dynamics and de-noising of protein-protein interaction networks,” *RECOMB 2010*, Lisbon, Portugal, August 12-15, 2010.
- P-36 V. Memisevic, T. Milenkovic, and **N. Pržulj**, “Complementarity of network and sequence information in homologous proteins,” *RECOMB 2010*, Lisbon, Portugal, August 12-15, 2010.
- P-35 O. Kuchaiev, T. Milenkovic, V. Memisevic, W. Hayes, **N. Pržulj**, “Topological network alignment uncovers biological function and phylogeny,” *RECOMB 2010*, Lisbon, Portugal, August 12-15, 2010.
- P-34 O. Kuchaiev, T. Milenkovic, V. Memisevic, W.L. Ng, W. Hayes, and **N. Pržulj**, “Topological network alignment uncovers biological function, evolution, and disease,” *Intelligent Systems for Molecular Biology (ISMB) 2010*, Boston, USA, July 11-13, 2010.
- P-33 **N. Pržulj**, T. Milenkovic, O. Kuchaiev, V. Memisevic, W. L. Ng, W. Hayes, and A. Ganesan, “From biological networks to cancer and phylogeny,” *RECOMB Computational Cancer Biology 2010*, Oslo, Norway, June 24-25, 2010.
- P-32 O. Kuchaiev and **N. Pržulj**, “Learning the Structure of Protein-Protein Interaction Networks,” *The 10th International Conference on Systems Biology (ICSB 2009)*, Stanford, CA, August 30 - September 4, 2009.
- P-31 T. Milenkovic, V. Memisevic, O. Kuchaiev, A. K. Ganesan, and **N. Pržulj**, “Systems-level Cancer Gene Identification from Protein Interaction Network Topology Applied to Melanogenesis-Related Functional Genomics Data,” *The 10th International Conference on Systems Biology (ICSB 2009)*, Stanford, CA, August 30 - September 4, 2009.
- P-30 V. Memisevic, T. Milenkovic, O. Kuchaiev, and **N. Pržulj**, “An Integrative Approach to Modelling Biological Networks,” *The 10th International Conference on Systems Biology (ICSB 2009)*, Stanford, CA, August 30 - September 4, 2009.
- P-29 O. Kuchaiev, T. Milenkovic, V. Memisevic, W. Hayes, and **N. Pržulj**, “Topological Network Alignment Uncovers Biological Function and Phylogeny,” *The 10th International Conference on Systems Biology (ICSB 2009)*, Stanford, CA, August 30 - September 4, 2009.
- P-28 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,” *Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB) 2009*, Stockholm, Sweden, June 27 - July 2, 2009.
- P-27 R. Kaake, T. Milenkovic, **N. Pržulj**, P. Kaiser, L. Huang, “Quantifying Cell Cycle-dependent Changes in Posttranslational Modifications and Interacting Network of the Yeast 26S Proteasome,” *57th ASMS Conference on Mass Spectrometry*, Philadelphia, Pennsylvania, USA, May 31 - June 4, 2009.
- P-26 T. Milenkovic and **N. Pržulj**, “Uncovering Biological Network Function via Graphlet Degree Signatures,” *European Conference on Computational Biology (ECCB) 2008*, Cagliari, Italy, September 22-26, 2008.
- P-25 T. Milenkovic, I. Filippis, M. Lappe, and **N. Pržulj**, “Optimized Null Model for Protein Structure Networks,” *European Conference on Computational Biology (ECCB) 2008*, Cagliari, Italy, September 22-26, 2008.
- P-24 T. Milenkovic, J. Lai, and **N. Pržulj**, “GraphCrunch: A Tool for Large Network Analyses,” *European Conference on Computational Biology (ECCB) 2008*, Cagliari, Italy, September 22-26, 2008.
- P-23 D. J. Higham, M. Rasajski, and **N. Pržulj**, “Discovering Geometric Structure in Protein-Protein Interaction Networks: The Embedding Algorithm,” *European Conference on Computational Biology (ECCB) 2008*, Cagliari, Italy, September 22-26, 2008.

- P-22 T. Milenkovic and **N. Pržulj**, “Uncovering disease genes and function via graphlet degree signatures,” *International Conference on Systems Biology (ICSB) 2008*, Gothenburg, Sweden, August 22-28, 2008.
- P-21 D. J. Higham, M. Rasajski, and **N. Pržulj**, “Discovering Geometric Structure in Protein-Protein Interaction Networks: The Embedding Algorithm,” *International Conference on Systems Biology (ICSB) 2008*, Gothenburg, Sweden, August 22-28, 2008.
- P-20 T. Milenkovic, J. Lai, and **N. Pržulj**, “GraphCrunch: A Tool for Large Network Analyses,” *International Conference on Systems Biology (ICSB) 2008*, Gothenburg, Sweden, August 22-28, 2008.
- P-19 T. Milenkovic, I. Filippis, M. Lappe, and **N. Pržulj**, “Optimized Null Model for Protein Structure Networks,” *International Conference on Systems Biology (ICSB) 2008*, Gothenburg, Sweden, August 22-28, 2008.
- P-18 D. J. Higham, M. Rasajski, and **N. Pržulj**, “Discovering Geometric Structure in Protein-Protein Interaction Networks,” *Intelligent Systems for Molecular Biology (ISMB) 2008*, Toronto, Canada, July 19-23, 2008.
- P-17 T. Milenkovic and **N. Pržulj**, “Uncovering Biological Network Function via Graphlet Degree Signatures,” *Intelligent Systems for Molecular Biology (ISMB) 2008*, Toronto, Canada, July 19-23, 2008.
- P-16 T. Milenkovic, I. Filippis, M. Lappe, and **N. Pržulj**, “Optimized Null Model for Protein Structure Networks,” *Intelligent Systems for Molecular Biology (ISMB) 2008*, Toronto, Canada, July 19-23, 2008.
- P-15 C. Guerrero, T. Milenkovic, J. J. Jones, **N Pržulj**, P. Kaiser, and L. Huang, “Characterizing the 26S Proteasome Network in Yeast using a Quantitative In-Vivo Crosslinking Strategy and PPI Network Analysis,” *56th ASMS Conference on Mass Spectrometry*, Denver, Colorado, June 1 - 5, 2008.
- P-14 T. Milenkovic and **N. Pržulj**, “Protein Signatures: Interplay of Topology and Biology,” *RECOMB Satellite Conference on Systems Biology 2007*, San Diego, California, November 30 - December 1, 2007.
- P-13 T. Milenkovic, J. Lai, and **N. Pržulj**, “GraphCrunch: A Tool for Large Network Analyses,” *RECOMB Satellite Conference on Systems Biology 2007*, San Diego, California, November 30 - December 1, 2007.
- P-12 D. J. Higham, M. Rasajski, and **N. Pržulj**, “Networks as Geometric Random Graphs: A Direct Approach,” *RECOMB Satellite Conference on Systems Biology 2007*, San Diego, California, November 30 - December 1, 2007.
- P-11 T. Milenkovic, I. Filippis, M. Lappe, and **N. Pržulj**, “Optimized Null Model of Residue Interaction Graphs,” *RECOMB Satellite Conference on Systems Biology 2007*, San Diego, California, November 30 - December 1, 2007.
- P-10 T. Milenkovic, J. Lai, and **N. Pržulj**, “GraphCrunch: A Tool for Large Network Analyses,” *International Conference on Systems Biology (ICSB) 2007*, Long Beach, California, October 1-6, 2007.
- P-9 D. J. Higham, M. Rasajski, and **N. Pržulj**, “Fitting a Geometric Graph to a Protein-Protein Interaction Network,” *International Conference on Systems Biology (ICSB) 2007*, Long Beach, California, October 1-6, 2007.
- P-8 T. Milenkovic, I. Filippis, M. Lappe, and **N. Pržulj**, “Optimized Null Model of Residue Interaction Graphs,” *International Conference on Systems Biology (ICSB) 2007*, Long Beach, California, October 1-6, 2007.
- P-7 T. Milenkovic, J. Lai, and **N. Pržulj**, “GraphCrunch: A Tool for Large Network Analyses,” *Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB) 2007*, Vienna, Austria, July 21-25, 2007.

- P-6 Y. Wang and **N. Pržulj**, “Biological implications of anti-motifs in transcriptional regulation networks” *European Conference on Computational Biology (ECCB)*, Eilat, Israel, January 21-24, 2007.
- P-5 **N. Pržulj**, “Biological Network Comparison Using Graphlet Degree Distributions,” *Intelligent Systems for Molecular Biology (ISMB)* 2006, Fortaleza, Brazil, August 6-10, 2006.
- P-4 S. Zhou and **N. Pržulj**, “Do Protein-Protein Interaction Networks Look Like a Jelly-Fish?” *Intelligent Systems for Molecular Biology (ISMB)* 2006, Fortaleza, Brazil, August 6-10 2006.
- P-3 **N. Pržulj**, D. G. Corneil, and I. Jurisica, “Geometric Properties of Protein-Protein Interaction Networks,” *Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB)* 2004, Glasgow, UK, July 31 - August 4, 2004.
- P-2 **N. Pržulj** and I. Jurisica, “A Call Graph Analysis,” *CASCON 2003*, Toronto, Ontario, Canada, October 6-9, 2003.
- P-1 **N. Pržulj**, D. Wigle, and I. Jurisica, “Functional Topology in a Network of Protein Interactions,” *Intelligent Systems for Molecular Biology (ISMB)* 2003, Brisbane, Australia, June 29 - July 3, 2003.

PRESS COVERAGE:

- PC-2 A TV (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.

TUTORIAL:

- T-1 **N. Pržulj** and Tijana Milenkovic, *Biological Networks: Analyses, Models, Functions, and Disease*, 9th International Conference on Systems Biology (ICSB'08), Gothenburg, Sweden, August 22-28, 2008.

INVITED TALKS:

- 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,” a **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. Przulj**, “Network mining uncovers new biology,” Physics Institute, University of Belgrade, Serbia, August 26, 2011.
- IT-62 **N. Przulj**, “Network mining uncovers new biology,” Petnica International Seminar, Petnica Research Station, Serbia, August 3, 2011.
- IT-61 **N. Przulj**, “Network mining uncovers new biology,” Centre for Systems and Synthetic Biology, Brunel University, London, UK, June 1, 2011.
- IT-60 **N. Przulj**, “Graph-Theoretic Modeling of Biological Networks,” Physics Seminar, Petnica Research Station, Valjevo, Serbia, May 1, 2011.
- IT-59 **N. Przulj**, “Graph-Theoretic Modeling of Biological Networks,” Serbian Academy of Sciences and Art (SANU), Belgrade, Serbia, April 29, 2011.
- IT-58 **N. Przulj** and Saša Drezgić, “Graph theory, biological networks and economic systems,” Scientific Society of Economists Election Meeting, Zagreb, Croatia, February 26, 2011.
- IT-57 **N. Przulj**, “Graph-Theoretic Modeling of Biological Networks,” FutureSysBio Workshop on “Defining modelling strategies for systems biology,” Goteborg, Sweden, January 20-21, 2011.
- IT-56 **N. Przulj**, “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. Przulj**, “Network Topology Uncovers Function, Disease, and Phylogeny,” Physiological Laboratory Seminar, University of Liverpool, December 3, 2010.
- IT-54 **N. Przulj**, “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. Przulj**, “Network Topology Uncovers Function, Disease, and Phylogeny,” a **Plenary Talk** at the 5th International Conference on Pattern Recognition in Bioinformatics (PRIB), Nijmegen, The Netherlands, September 22-24, 2010.
- IT-52 **N. Przulj**, “Network Topology Uncovers Function, Disease, and Phylogeny,” a **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. Przulj**, “Network Topology Uncovers Function, Disease, and Phylogeny,” Disordered Systems Group, Mathematics Seminar, King’s College London, April 21, 2010.
- IT-50 **N. Przulj**, “Network Topology Uncovers Function, Disease, and Phylogeny,” Glaxo-SmithKline, Stevenage, UK, February 8, 2010.
- IT-49 **N. Przulj**, “From Network Topology to Biological Function and Disease,” a **Plenary Talk** at 7th Georgia Tech - ORNL Conference on Bioinformatics, Atlanta, Georgia, USA, November 12-14, 2009.
- IT-48 **N. Przulj**, “Deciphering Biological Networks,” INRIA Colloquium, Paris, November 3-5, 2009.
- IT-47 **N. Przulj**, “Deciphering Biological Networks,” Statistics Seminar, University of Oxford, October 29, 2009.
- IT-46 **N. Przulj**, “From Network Topology to Biological Function and Disease” MITACS-MoMiNIS Seminar, Dalhousie University, Halifax, Nova Scotia, Canada, August 12, 2009.
- IT-45 **N. Przulj**, “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. Przulj**, “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. Przulj**, “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. Przulj**, “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. Przulj**, “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. Przulj**, “From Network Topology to Biological Function and Disease,” Department of Computing, Imperial College London, UK, January 26, 2009.
- IT-39 **N. Przulj**, “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. Przulj**, “From Network Topology to Biological Function and Disease,” Computer Science Department, McGill University, Canada, January 15, 2009.
- IT-37 **N. Przulj**, “From Network Topology to Biological Function and Disease,” University of Edinburgh, UK, December 15, 2008.
- IT-36 **N. Przulj**, “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. Przulj**, “Towards a Theory of Biological Networks,” Spanish National Cancer Research Center (CNIO), Madrid, Spain, October 27, 2008.
- IT-34 **N. Przulj**, “Towards a Theory of Biological Networks,” School of Computing, Union University, Belgrade, Serbia, October 20, 2008.
- IT-33 **N. Przulj**, “Towards a Theory of Biological Networks,” Petnica Research Station, Valjevo, Serbia, October 19, 2008.
- IT-32 **N. Przulj**, “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. Przulj**, “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. Przulj**, “Towards a Theory of Biological Networks,” Imperial College London, June 30, 2008.
- IT-29 **N. Przulj**, “Towards a Theory of Biological Networks,” University of Southampton, UK, June 27, 2008.
- IT-28 **N. Przulj**, “Towards a Theory of Biological Networks,” University of Helsinki, Finland, June 24, 2008.
- IT-27 **N. Przulj**, “From Structure to Function in Biological Networks,” 2008 UCI Center for Complex Biological Systems Retreat, Pasadena, California, March 28-30, 2008.
- IT-26 **N. Przulj**, “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:

- 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

ASSOCIATE EDITOR: BMC Bioinformatics.

EDITORIAL REVIEW BOARD MEMBER:

International Journal of Knowledge Discovery in Bioinformatics (IJKDB) (IGI Global)

GUEST EDITOR: Internet Mathematics (A K Peters Ltd).

CONFERENCE ORGANIZING:

2. Network Biology Special Interest Group Meeting (NetBio SIG) at ISMB 2012, Long Beach, CA, USA, July 15-17, 2012.
1. “Network Links: Connecting Social, Communication and Biological Network Analysis,” Institute for Mathematics and Its Applications, University of Minnesota, USA, Feb 27 - March 2, 2012.

GOVERNMENT GRANT PROPOSAL REVIEWING:

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:

12. Brazilian Symposium on Bioinformatics (BSB & EBB), Campo Grande, Mato Grosso do Sul, Brasil, August 13-17, 2012.
11. ISMB 2012, Long Beach, California, 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. Intelligent Systems for Molecular Biology (ISMB) 2010, Boston, USA, July 11 - July 13, 2010.
7. ACM International Conference on Bioinformatics and Computational Biology (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.

TUTORIAL AUTHOR AND PRESENTER:

1. Tutorial on *Biological Networks: Analyses, Models, Functions, and Disease* at the *9th Conference on Systems Biology (ICSB)*, Gothenburg, Sweden, August 22-28, 2008.

SESSION CHAIR:

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:

11. *Algorithms for Molecular Biology* (BioMed Central).
10. *Bioinformatics* (Oxford Journals).
9. *BMC Bioinformatics* (BioMed Central).
8. *Cancer Informatics* (Libertas Academica).
7. *Discrete Mathematics* (Elsevier).
6. *Discrete Applied Mathematics* (Elsevier).
5. *Genome Biology* (BioMed Central).
4. *Nature Biotechnology* (Nature Publishing Group).
3. *Nature Protocols* (Nature Publishing Group).
2. *PLoS Computational Biology* (Public Library of Science).
1. *Proteins: Structure, Function, and Bioinformatics* (Wiley).

CONFERENCE PAPER REVIEWER:

16. Brazilian Symposium on Bioinformatics (BSB & EBB), Campo Grande, Mato Grosso do Sul, Brazil, August 13-17, 2012.
15. ISMB 2012, Long Beach, California, USA, July 15-17, 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:

4. MSc in in Bioinformatics and Systems Biology Coordinator, Department of Computing, Imperial College London, 2009–present;
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:

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:

- 8. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2012.
- 7. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2011.
- 6. 341: Introduction to Bioinformatics, Computing, Imperial College London, Winter 2010.
- 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 GRADUATE COURSE:

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

DEVELOPED A NEW UNDERGRADUATE COURSE:

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

STUDENT SUPERVISION

PH.D. ALUMNI:

3. Tijana Milenkovic, Ph.D., 2010, Computer Science, UC Irvine. Thesis title: “From Topological Network Analyses and Alignments to Biological Function, Disease, and Evolution.”
2. Oleksii Kuchaiev, Ph.D., 2010, Computer Science, UC Irvine. Thesis title: “Modeling and Alignment of Biological Networks.”
1. Vesna Memisevic, Ph.D., 2010, Computer Science, UC Irvine. Thesis title: “Uncovering Biological Knowledge from Network Structure.”

M.Sc. ALUMNI:

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:

1. Marija Rasajski, Information and Computer Science (ICS), UCI, May 2007 – May 2008.

SUPERVISED GRADUATE STUDENTS:

11. Miles Mullholand, Ph.D. student, Imperial College, October 2011 – present.
10. Yulian Ng, Ph.D. student, Imperial College, October 2011 – present.
9. Vuk Janjic, Ph.D. student, Imperial College, April 2011 – present.
8. Kai Sun, Ph.D. student, Imperial College, October 2010 – present.
7. Omer Nebil Yaveroglu, Ph.D. student, Imperial College, October 2010 – present.
6. Tijana Milenkovic, Ph.D., ICS, UCI, September 2006 – March 2010.
5. Vesna Memisevic, Ph.D., ICS, UCI, September 2007 – June 2010.
4. Oleksii Kuchaiev, Ph.D., ICS, UCI, September 2007 – June 2010.
3. Aleksandar Stevanovic, Ph.D. student, ICS, UCI, September 2008 – 2010.
2. Jingjing Li, Ph.D. student, ICS UCI, September–December, 2006.
1. Hania El Ayoubi, defended M.Sc. in 2007. Computer Science, University of Toronto. Co-supervised with Prof. D. G. Corneil, 04/2006–06/2007.

SERVED ON PH.D. COMMITTEES OF:

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. Miles Mulholland, Computing, Imperial College London, Oct. 2010 – June 2011.
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

9. ERC Starting Independent Researcher Grant
 Title: Network Topology Complements Genome as a Source of Biological Information
 PI: Natasa Przulj
 Funding Organization: European Research Council
 Funding period: 01/01/2012 – 31/12/2016
 Funds received: €1,638,175
8. NSF CDI-Type II: Topology and Function in Computer, Social and Biological Networks:
 PI: Athina Markopoulou; co-PIs: Carter Butts and Natasa Przulj
 Funding Organization: National Science Foundation
 Funding period: 10/01/2010 – 09/30/2014
 Funds received: \$1,999,503.00

7. GlaxoSmithKline Ph.D. studentships
Imperial College London, Dept. of Computing
Funding period: 2010–2013
Funds received: £80,000
6. Imperial College London, Dept. of Computing, Start-up:
One Ph.D. studentship
Research and travel support
Funding period: 2009–present
5. NSF CAREER: Tools for Analyzing, Modeling, and Comparing Protein-Protein Interaction Networks
PI: Natasa Przulj
Funding Organization: National Science Foundation
Funding period: 2007–2011
Funds received: \$569,905
4. UCI Set-up:
PI: Natasa Przulj
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: Natasa Przulj, 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: Natasa Przulj
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: Natasa Przulj
co-PI: Anand Ganesan, Dermatology, UCI
Funding Organization: Center for Complex Biological Systems (CCBS), UCI
Funding period: 2008
Funds received: \$10,000

EXPERIENCE DETAILS

Lecturer (Assistant Professor), Dept. of Computing, Imperial College London, UK.
October 2009 – present.

Visiting Research Scientist, California Institute for Telecommunications and Information Technology.
October 2010–present.

Associate Professor (0% appointment), School of Computing (RAF), Union University, Belgrade.
October 2008–present.

Assistant Professor, Department of Computer Science, UC Irvine, Irvine, CA, USA.
July 2005 – July 2010.

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

- I analyzed and modeled protein-protein interaction networks. My models were used to guide biological experiments for identifying protein-protein interactions.

Research Assistant, Banting and Best Institute, University of Toronto, ON, Canada.
Sept 2002 - May 2003.

- I 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

- I 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.
Jan 2000 - Dec 2000.

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

- I 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. I 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. I also performed System Administration GIS tasks such as image building and maintenance.

Research Assistant, Simon Fraser University, Burnaby, BC, Canada.
Sept 1996 - Dec 1996 and Sept 1997 - Dec 1997.

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

Teaching Assistant, Simon Fraser University, Burnaby, BC, Canada.
Jan 1996 - Apr 1996.

- MAT 154, 155, 157, 158 Applied Calculus Courses. I 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.

- I 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 my 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

International Society for Computational Biology (ISCB),
Society for Industrial and Applied Mathematics (SIAM),
American Physical Society (APS).

REFERENCES

Available upon request.