# Tijana Milenković: Curriculum Vitæ (as of 02/02/2017)

**Associate Professor, Department of Computer Science and Engineering**
Head of the Complex Networks Lab (`http://nd.edu/∼cone/`)
Interdisciplinary Center for Network Science and Applications
ECK Institute for Global Health
**University of Notre Dame**
Office: 381 Fitzpatrick Hall, Notre Dame, IN 46556, USA
Contact: `tmilenko@nd.edu`; +1-574-631-8975; `http://cse.nd.edu/∼tmilenko/`

## Research Interests

**Complex networks, network science, network mining, big data:** developing computational and mathematical (graph theoretic) algorithms for efficient extraction of function from topology of complex (large, noisy, dynamic, heterogeneous, etc.) real-world networks, such as biological, physiological, social, and technological networks.

**Computational (systems) biology:** studying interplay between network topology and biological function, disease, and evolution in molecular (protein-protein interaction) networks.

**Computational chemistry:** protein folding; computational drug discovery and design.

**Theoretic computer science:** computational graph theory; algorithms; network models.

## Higher Education

**Ph.D., Computer Science, University of California, Irvine (UCI), 2006–2010.**
Dissertation Title: *From topological network analyses and alignments to biological function, disease, and evolution.*
Advisor: Prof. Nataša Pržulj.

**M.Sc., Computer Science, University of California, Irvine (UCI), 2006–2008.**
Thesis Title: *Interplay of topology and biology in protein-protein interaction networks.*
Advisor: Prof. Nataša Pržulj.

**B.Sc., Electrical Engineering, Information and Computer Science, 2000–2005.**
**University of Sarajevo, Bosnia and Herzegovina.**
Thesis Title: *M-Commerce.*
Advisor: Prof. Dženana Djonko.

## Academic and Professional Positions

2016–present: Associate Professor, Department of Computer Science and Engineering, University of Notre Dame.
2010–2016: Assistant Professor, Department of Computer Science and Engineering, University of Notre Dame.
2010: Research Assistant, Department of Computing, Imperial College London.
2007–2010: Research Assistant and Graduate Student Researcher, Department of Computer

Science, University of California, Irvine.
2007–2009: Substitute Instructor, Teaching Assistant, and Reader, Department of Computer Science, University of California, Irvine.
2006: Expert System Developer, JP Elektroprivreda, Sarajevo, Bosnia and Herzegovina.
2005: Conference Assistant, United Nations Development Programme (UNDP), Sarajevo, Bosnia and Herzegovina.

## Distinctions, Honors, Awards, Scholarships, and Fellowships

The Air Force Young Invertigator Award (AFOSR YIP), $360K, 2016–2019, sole Principal Investigator (sole-PI) award.
The National Science Foundation (NSF) CAREER CCF-1452795, $540K, 2015–2020, sole-PI award; CAREERs are "the highest honor given by the U.S. government to young faculty in engineering and science."
The National Science Foundation (NSF) CCF-1319469, $453K, 2013–2016, sole-PI award.
Google Faculty Research Award, $33K, 2013-2014, collaboration with Dr. A. Striegel.
The National Science Foundation (NSF) EAGER CCF-1243295 grant, $208K, 2012–2014, sole-PI award; EAGERs are special awards intended for "potentially transformative research."
Four collaborative awards by the National Institutes for Health (NIH) (see under "Grants and Funding" below).
Chair's Fellowship, Donald Bren School of Information and Computer Sciences, University of California, Irvine, 2006–2010.
Travel Fellowships for the International Conference on Intelligent Systems for Molecular Biology (ISMB) and European Conference on Computational Biology (ECCB), 2008–2009.
Winner of McGaugh Hall Display Case Design Challenge, Center for Complex Biological Systems, University of California, Irvine, 2008.
Semifinals (world's top 30) of Microsoft Imagine Cup, Business Plan Competition, 2005.
$2^{nd}$ Place at the Balkan Case Challenge Finals, Information and Communication Technology Case, 2004/2005.
$1^{st}$ Place at the Balkan Case Challenge, Bosnia and Herzegovina Sub-competition, Information and Communication Technology Case, 2004/2005.
Scholarship from JP Elektroprivreda, Sarajevo, Bosnia and Herzegovina, 2001–2005.
Scholarship from the Ministry of Education and Science, Sarajevo, Bosnia and Herzegovina, 1999–2001.
Scholarship from HKD Napredak, Sarajevo, Bosnia and Herzegovina, 1996–1999.

## Refereed Journal Publications

(Milenković's students are indicted in **bold**, and undergraduates are also **<u>underlined</u>**.)

### Submitted

J-35 **V. Vijayan**, **<u>D. Critchlow</u>**, and T. Milenković, " Alignment of dynamic networks," under review, 2017. Also, arXiv:1701.08842 [cs.SI].

J-34 **V. Vijayan** and T. Milenković, "Multiple network alignment via multiMAGNA++," under review, 2017. Also, arXiv:1604.01740 [q-bio.MN].

J-33 **F.E. Faisal**, J.L. Chaney, **K. Newaz**, J. Li, S. Emrich, P. Clark, and T. Milenković, "Network approach integrates 3D structural and sequence data to improve protein structural comparison," under review, 2017. Also, arXiv:1605.07247 [q-bio.MN].

## Published

J-32 P.H. Guzzi and T. Milenković, "Survey of local and global biological network alignment: the need to reconcile the two sides of the same coin," *Briefings in Bioinformatics*, DOI: 10.1093/bib/bbw132, 2017. (Journal impact factor: 8.399.)

J-31 O. Yaveroglu, N. Malod-Dognin, T. Milenković, and N. Pržulj, "Rebuttal to the Letter to the Editor in response to the paper: Proper evaluation of alignment-free network comparison methods," *Bioinformatics*, DOI: 10.1093/bioinformatics/btw388, 2017. (Journal impact factor: 5.766. Journal 5-year impact factor: 7.685.)

J-30 **Y. Hulovatyy** and T. Milenković, "SCOUT: simultaneous time segmentation and community detection in dynamic networks," *Nature Scientific Reports*, 6, article number: 37557, 2016. (Cited: 1 times. Journal impact factor: 5.228.)

J-29 S.S.C. Rund†, **B. Yoo**†, C.D.C. Alamb, **T. Green**, M.T. Stephens, E. Zeng, A.D. Sheppard, G.E. Duffield, T. Milenković, and M.E. Pfrender, "Genome-wide profiling of 24 hr diel rhythmicity in the water flea, *Daphnia pulex*: Network analysis reveals rhythmic gene expression and enhances functional gene annotation," *BMC Genomics*, 17:653, 2016. This paper was **featured** on the BMC Genomics homepage for over three months. (Journal impact factor: 3.867.) †These authors contributed equally to this work.

J-28 **L. Meng**, A. Striegel, and T. Milenković, "Local versus global biological network alignment," *Bioinformatics*, DOI: 10.1093/bioinformatics/btw348, 2016. (Cited: 8 times. Journal impact factor: 5.766. Journal 5-year impact factor: 7.685.)

J-27 **L. Meng**, **Y. Hulovatyy**, A. Striegel, and T. Milenković, "On the Interplay Between Individuals' Evolving Interaction Patterns and Traits in Dynamic Multiplex Social Networks," *IEEE Transactions on Network Science and Engineering*, 3(1): 32-43, 2016. (Cited 4 times. Journal impact factor: unknown.)

J-26 **B. Yoo**, **F.E. Faisal**, **H. Chen**, and T. Milenković, "Improving identification of key players in aging via network de-noising and core inference," *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, PP(99): 1, 2015. (Cited 5 times. Journal impact factor: 1.536.)

J-25 **Y. Hulovatyy**, **H. Chen**, and T. Milenković, "Exploring the structure and function of temporal networks with dynamic graphlets," *Bioinformatics*, 31(12): i171-i180, 2015. (Cited 12 times. Journal impact factor: 5.766. Journal 5-year impact factor: 7.685.) Also, in *Proceedings of the International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB)*, Dublin, Ireland, July 10-14, 2015. (Acceptance rate: 18%.)

J-24 **F.E. Faisal**, **L. Meng**, **J. Crawford**, and T. Milenković, "The post-genomic era of biological network alignment," *EURASIP Journal on Bioinformatics and Systems Biology*, 2015: 3, 2015. (Invited submission. Cited 14 times. Journal impact factor: unknown.)

J-23 **J. Crawford**, **Y. Sun**, and T. Milenković, "Fair Evaluation of Global Network Aligners," *Algorithms for Molecular Biology*, 10: 19, 2015. (Cited 12 times. Journal impact factor: 1.86.)

J-22 **V. Vijayan**, **V. Saraph**, and T. Milenković, "MAGNA++: Maximizing Accuracy in Global Network Alignment via both node and edge conservation," *Bioinformatics*, 31(14): 2409-2411, 2015. (Cited 23 times. Journal impact factor: 5.766. Journal 5-year impact factor: 7.685.)

J-21 O. Yaveroglu, T. Milenković, and N. Pržulj, "Proper Evaluation of Alignment-Free Network Comparison Methods," *Bioinformatics*, 31(16): 2697-2704, 2015. (Cited 12 times. Journal impact factor: 5.766. Journal 5-year impact factor: 7.685.)

J-20 **Y. Hulovatyy**, S. D'Mello, R.A. Calvo, and T. Milenković, "Network Analysis Improves Interpretation of Affective Physiological Data," *Journal of Complex Networks*, 2(4): 614-636, 2014. (Cited 8 times. Journal impact factor: unknown.)

J-19 **V. Saraph** and T. Milenković, "MAGNA: Maximizing Accuracy in Global Network Alignment," *Bioinformatics*, 30(20): 2931-2940, 2014. (Cited 46 times. Journal impact factor: 5.766. Journal 5-year impact factor: 7.685.)

J-18 A. Rider, T. Milenković, G. Siwo, R. Pinapati, S.J. Emrich, M.T. Ferdig, and N.V. Chawla, "Networks' characteristics are important for systems biology," *Network Science*, 2(02): 139-161, 2014. (Cited 2 times. Journal impact factor: unknown.)

J-17 **F.E. Faisal**, **H. Zhao**, and T. Milenković, "Global Network Alignment In The Context Of Aging," *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 12(1), 40 - 52, 2014. (Cited 27 times. Journal impact factor: 1.536.)

J-16 **Y. Hulovatyy**, **R.W. Solava** and T. Milenković, "Revealing missing parts of the interactome via link prediction," *PLOS ONE*, 9(3): e90073, 2014. (Cited 17 times. Journal impact factor: 3.53.)

J-15 **F.E. Faisal** and T. Milenković, "Dynamic networks reveal key players in aging," *Bioinformatics*, 30(12): 1721-1729, 2014. (Cited 28 times. Journal impact factor: 5.766. Journal 5-year impact factor: 7.685.)

J-14 **R.W. Solava**, **R.P. Michaels**, and T. Milenković, "Graphlet-based edge clustering reveals pathogen-interacting proteins," *Bioinformatics*, 28(18): i480-i486, 2012. (Cited 42 times. Journal impact factor: 5.766. Journal 5-year impact factor: 7.685.)

J-13 Arabidopsis Interactome Mapping Consortium, "Evidence for Network Evolution in an Arabidopsis Interactome Map," *Science*, 333(6042): 601-607, 2011. (Cited 439 times. Journal impact factor: 31.48. Journal 5-year impact factor: 34.4.)

J-12 T. Milenković, V. Memišević, A. Bonato, and N. Pržulj, "Dominating biological networks," *PLOS ONE*, 6(8): e23016, 2011. (Cited 69 times. Journal impact factor: 4.092.)

J-11 T. Milenković, W.L. Ng, W. Hayes, and N. Pržulj, "Optimal network alignment with graphlet degree vectors," *Cancer Informatics*, 9: 121-137, 2010. This paper has been reported as **highly visible** by the Cancer Informatics website. (Cited 121 times. Journal impact factor: 1.6406.)

J-10 H. Ho[†], T. Milenković[†], V. Memišević, 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, 2010. This paper has been reported as **highly accessed** by the BMC Systems Biology website. (Cited 38 times. Journal impact factor: 2.85.) [†]These authors contributed equally to this work.

J-9 R. Kaake, T. Milenković, N. Pržulj, P. Kaiser, and L. Huang, "Characterization of Cell Cycle Specific Protein Interaction Networks of the Yeast 26S Proteasome Complex by the QTAX Strategy," *Journal of Proteome Research*, 9(4): 2016-2029, 2010. (Cited 46 times. Journal impact factor: 5.001.)

J-8 V. Memišević, T. Milenković, and N. Pržulj, "Complementarity of network and sequence structure in homologous proteins," *Journal of Integrative Bioinformatics*, 7(3): 135, 2010. (Cited 32 times. Journal impact factor: unknown.)

J-7 V. Memišević, T. Milenković, and N. Pržulj, "An integrative approach to modeling biological networks," *Journal of Integrative Bioinformatics*, 7(3): 120, 2010. (Cited 24 times. Journal impact factor: unknown.)

J-6 O. Kuchaiev[†], T. Milenković[†], V. Memišević, W. Hayes, N. Pržulj, "Topological network alignment uncovers biological function and phylogeny," *Journal of the Royal Society Interface*, 7: 1341-1354, 2010. (Cited 203 times. Journal impact factor: 3.856.)

J-5 T. Milenković, V. Memišević, 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, 2010. (Cited 79 times. Journal impact factor: 3.856.)

J-4 T. Milenković†, I. Filippis†, M. Lappe, and N. Pržulj, "Optimized Null Model of Protein Structure Networks," *PLOS ONE*, 4(6): e5967, 2009. (Cited 35 times. Journal impact factor: 4.351.) †These authors contributed equally to this work.

J-3 C. Guerrero, T. Milenković, 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 109 times. Journal impact factor: 9.809.)

J-2 T. Milenković and N. Pržulj, "Uncovering Biological Network Function via Graphlet Degree Signatures," *Cancer Informatics*, 2008: 6, 257-273, 2008. This paper has been reported as **highly visible** by the Cancer Informatics website. (Cited 203 times. Journal impact factor: 1.6406.)

J-1 T. Milenković, J. Lai, and N. Pržulj, "GraphCrunch: A Tool for Large Network Analyses," *BMC Bioinformatics*, 9: 70, January 30, 2008. This paper has been reported as **highly accessed** by the BMC Bioinformatics website. (Cited 97 times. Journal impact factor: 2.67.)

## Refereed Full Conference Publications

(Milenković's students are indicted in **bold**, and undergraduates are also **underlined**.)

### Published

C-12 **V. Vijayan** and T. Milenković, "Multiple network alignment via multiMAGNA++," in *Proceedings of the 15th International Workshop on Data Mining in Bioinformatics (BIOKDD) at the 22nd ACM SIGKDD 2016 Conference on Knowledge Discovery and Data Mining (KDD)*, San Francisco, CA, USA, August 13-17, 2016. Also, arXiv:1604.01740 [q-bio.MN]. (Acceptance rate: unknown.)

C-11 **L. Meng**, **J. Crawford**, A. Striegel, and T. Milenković, "IGLOO: Integrating global and local biological network alignment," in *Proceedings of the 12th International Workshop on Mining and Learning with Graphs (MLG) at the 22nd ACM SIGKDD 2016 Conference on Knowledge Discovery and Data Mining (KDD)*, San Francisco, CA, USA, August 13-17, 2016. Also, arXiv:1604.06111 [q-bio.MN]. (Cited 2 times. Acceptance rate: unknown.)

C-10 **J. Crawford** and T. Milenković, "GREAT: GRaphlet Edge-based network AlignmenT," in *Proceedings of IEEE International Conference on Bioinformatics and Biomedicine (IEEE BIBM)*, Washington D.C., USA, November 9-12, 2015. (Cited 10 times. Acceptance rate: 19%.)

C-9 **Y. Sun**, **J. Crawford**, J. Tang, and T. Milenković, "Simultaneous Optimization of Both Node and Edge Conservation in Network Alignment via WAVE," in *Proceedings of the 15th International Workshop on Algorithms in Bioinformatics (WABI)*, Atlanta, GA, USA, September 10-12, 2015, pages 16-39. (Cited 12 times. Acceptance rate: 40%.)

C-8 **Y. Hulovatyy**, **H. Chen**, and T. Milenković, "Exploring the structure and function of temporal networks with dynamic graphlets," in *Proceedings of the International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB)*, Dublin, Ireland, July 10-14, 2015. (Cited 12 times. Acceptance rate: 18%.). Also, in *Bioinformatics*, 31(12): i171-i180, 2015. (Journal impact factor: 5.766. Journal 5-year impact factor: 7.685.)

C-7 **B. Yoo**, **H. Chen**, **F.E. Faisal**, and T. Milenković, "Improving identification of key players in aging via network de-noising," in *Proceedings of the ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM BCB)*, Newport

Beach, CA, USA, September 20-23, 2014, pages 164-173. (Cited 5 times. Acceptance rate: 22%.)

C-6 **L. Meng**, T. Milenković, and A. Striegel, "Systematic Dynamic and Heterogeneous Analysis of Rich Social Network Data," in Springer-Verlag *Proceedings of Complex Networks (CompleNet) V*, Bologna, Italy, March 12-14, 2014. (Cited 12 times. Acceptance rate: 25%.)

C-5 **Y. Hulovatyy**, S. D'Mello, R.A. Calvo, and T. Milenković, "Network Analysis Improves Interpretation of Affective Physiological Data," in *IEEE Proceedings* of the *International Workshop on Complex Networks and their Applications* at the *International Conference on Signal-Image Technology and Internet-Based Systems (SITIS)*, Kyoto, Japan, December 2-5, 2013, pages: 470-477. (Cited 8 times. Acceptance rate: 42%.)

C-4 T. Milenković, **H. Zhao**, and **F.E. Faisal**, "Global Network Alignment In The Context Of Aging," in *Proceedings of the ACM Conference on Bioinformatics, Computational Biology, Biomedical Informatics (ACM BCB)*, Washington DC, USA, September 22-25, 2013, pages 23-32. (Cited 27 times. Acceptance rate: 28%.)

C-3 **R.W. Solava**, **R.P. Michaels**, and T. Milenković, "Graphlet-based edge clustering reveals pathogen-interacting proteins," in *Proceedings of the European Conference on Computational Biology (ECCB)*, Basel, Switzerland, September 9-12, 2012. (Cited 42 times. Acceptance rate: 14%.) Also, in *Bioinformatics*, 28(18): i480-i486, 2012. (Journal impact factor: 5.766. Journal 5-year impact factor: 7.685.)

C-2 V. Memišević, T. Milenković, and N. Pržulj, "Complementarity of network and sequence structure in homologous proteins," in *Proceedings of the International Symposium on Integrative Bioinformatics*, 22-24 March 2010, Cambridge, United Kingdom. (Cited 32 times. Acceptance rate: unknown.)

C-1 V. Memišević, T. Milenković, and N. Pržulj, "An integrative approach to modeling biological networks," in *Proceedings of the International Symposium on Integrative Bioinformatics*, 22-24 March 2010, Cambridge, United Kingdom. (Cited 24 times. Acceptance rate: unknown.)

## Refereed Book Chapters

BC-2 T. Milenković 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.

BC-1 N. Pržulj and T. Milenković, "Computational Methods for Analyzing and Modeling Biological Networks," a chapter in *Biological Data Mining*, edited by J. Chen and S. Lonardi, Chapman & Hall/CRC, 2009.

## Refereed Conference Tutorials

T-2 T. Milenković and F.E. Faisal, "Network approaches in aging research with focus on biological network alignment," *ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM BCB)*, Newport Beach, CA, USA, September 22-23, 2014.

T-1 N. Pržulj and T. Milenković, "Biological Networks: Analyses, Models, Functions, and Disease," *International Conference on Systems Biology (ICSB)*, Gothenburg, Sweden, August 22-28, 2008. (According to ICSB organizers, this tutorial was the most visited of all tutorials held at the conference.)

## Refereed Conference Workshops

W-4 T. Milenković, N. Pržulj, and I. Jurisica, "Challenges and approaches in comprehensive and informative complex network analysis for precision medicine," *European Conference on Computational Biology (ECCB)*, Hague, Netherlands, September 3-7, 2016.

W-3 I. Jurisica, N. Pržulj, and T. Milenković, "Challenges and approaches in comprehensive and informative complex network analysis for precision medicine," *Basel Computational Biology Conference ([BC$^2$])*, Basel, Switzerland, June 7-10, 2015. (According to [BC$^2$] organizers, this workshop was the most visited of all workshops held at the conference.)

W-2 N. Pržulj and T. Milenković, "Integrative Dynamic Analyses of Large Biomedical Network Data," *European Conference on Computational Biology (ECCB)*, Strasbourg, France, September 7-10, 2014.

W-1 T. Milenković, "Networks are everywhere!," *Expanding Your Horizons in Science and Mathematics* career conference for middle school girls, the University of Notre Dame, yearly since 2012.

## Refereed Conference Posters

*70+ posters* at the following conferences:

11 International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB) 2016, 2015, 2014, 2013, 2012, 2011, 2010, 2009, 2008, and 2007.

10 ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM BCB) 2015, 2014, and 2013.

9 Great Lakes Bioinformatics Conference (GLBIO) 2016 and 2015.

8 ACM SIGKDD Conference on Knowledge Discovery and Data Mining, 2016.

7 ACM Richard Tapia Celebration of Diversity in Computing, 2016.

6 "Systems Biology - Networks" Meeting at Cold Spring Harbor Laboratory, 2015 and 2011.

5 International Conference on Research in Computational Molecular Biology (RECOMB) 2010.

4 RECOMB Computational Cancer Biology 2010.

3 RECOMB Satellite Conference on Systems Biology 2007.

2 International Conference on Systems Biology (ICSB) 2009, 2008, and 2007.

1 American Society for Mass Spectrometry Conference 2009 and 2008.

## Invited Conference Talks

IT-13 T. Milenković, "Integrative, dynamic, and comparative biological network research of aging," *Workshop W7: Challenges and approaches in comprehensive and informative complex network analysis for precision medicine*, *European Conference on Computational Biology (ECCB)*, Hague, Netherlands, September 3-7, 2016.

IT-12 T. Milenković, "Redefining homology by transferring function between conserved network regions," *Great Lakes Bioinformatics Conference (GLBIO)*, Purdue University, West Lafayette, May 18-20, 2015.

IT-11 T. Milenković, "Comparative and Dynamic Biological Network Research of Human Aging," *BioPhysics VII - From Basic to Life Sciences*, Dubrovnik, Croatia, June 7-14, 2014.

IT-10 T. Milenković, "What can complex networks tell us about human aging?," *International Conference on Information Technologies and Information Society (ITIS)*, Dolenjske Toplice, Slovenia, November 7-9, 2013.

IT-9 T. Milenković, "Sensitive Graph-theoretic Approaches for Extracting Function from Biological Networks," *Biological Networks Minisymposium* at *SIAM Conference on Discrete Mathematics*, Halifax, Nova Scotia, Canada, June 18-21, 2012.

IT-8 T. Milenković, "Biology through network lenses," *Network Links: Connecting Social, Communication and Biological Network Analysis* Workshop, University of Minnesota, February 27-March 2, 2012.

IT-7 T. Milenković, "Novel algorithmic directions for network analysis in computational biology: implications for aging and disease," Department of Electrical and Computer Engineering, University of Texas at Austin, March 2015.

IT-6 T. Milenković, "Biological network research of aging," the Buck Institute for Research on Aging, March 2015.

IT-5 T. Milenković, "Novel directions for biological network comparison: implications for aging," Toyota Technological Institute at Chicago, November 2014.

IT-4 T. Milenković, "Novel strategies for efficient network mining: implications for aging and disease," Department of Computer Science, Purdue University, October 2014.

IT-3 T. Milenković, "Network Mining: Computational Approaches for Inferring Function in Biological and Social Networks," Mälardalen Real-Time Research Centre, Mälardalen University Sweden, June 2011.

IT-2 T. Milenković, "Mining Biological Networks: Computational Approaches for Inferring Function from Network Topology," Max Planck Institute for Intelligent Systems, Tübungen, Germany, June 2011.

IT-1 T. Milenković, "Network Data Mining: Computational Approaches for Inferring Function in Biological and Social Networks," School of Computing, Union University, Belgrade, Serbia, May 2011.

## Contributed Conference Talks

CT-28 V. Vijayan and T. Milenković, "Multiple network alignment via multiMAGNA++," *Workshop on Data Mining in Bioinformatics 2016 (BIOKDD 2016)*, in conjunction with *ACM International Conference on Knowledge Discovery and Data Mining (SIGKDD 2016)*, San Francisco, CA, USA, August 13-17, 2016.

CT-27 L. Meng, V. Vijayan, and Tijana Milenković, "The Post-Genomic Era of Biological Network Alignment: Latest Insights," *International Conference on Intelligent Systems for Molecular Biology (ISMB 2016)*, Orlando, FL, USA, July 8-12, 2016.

CT-26 F. Faisal, Y. Hulovatyy, H. Chen, and T. Milenković, "Dynamic and integrative biological network research of aging," *Great Lakes Bioinformatics and the Canadian Computational Biology Conference (GLBIO/CCBC)*, Toronto, Canada, May 16-19, 2016.

CT-25 F. Faisal, Y. Hulovatyy, H. Chen, and T. Milenković, "Dynamic and integrative biological network research of aging," *Workshop on Network Biology*, Simons Institute for the Theory of Computing, University of California Berkley, April 11-15, 2016.

CT-24 L. Meng, Y. Hulovatty, A. Striegel, and T. Milenković, "On the Interplay Between Individuals' Evolving Interaction Patterns and Traits in Dynamic Multiplex Social Networks," *Network Frontier Workshop*, Northwestern University, December 6-7, 2015.

CT-23 J. Crawford and T. Milenković, "GREAT: GRaphlet Edge-based network AlignmenT," *IEEE International Conference on Bioinformatics and Biomedicine (IEEE BIBM)*, Washington D.C., USA, November 9-12, 2015.

CT-22 Y. Sun, J. Crawford, J. Tang, and T. Milenković, "Simultaneous Optimization of Both Node and Edge Conservation in Network Alignment via WAVE," *Workshop on Algorithms in Bioinformatics (WABI)*, Atlanta, GA, USA, September 10-12, 2015.

CT-21 F. Faisal, H. Zhao, and T. Milenković, "Dynamic networks reveal key players in aging," **Highlights Track** at the *International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB)*, Dublin, Ireland, July 10-14, 2015.

CT-20 Y. Hulovatyy, H. Chen, and T. Milenković, "Exploring the structure and function of temporal networks with dynamic graphlets," *International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB)*, Dublin, Ireland, July 10-14, 2015.

CT-19 Y. Hulovatyy, F. Faisal, H. Chen, and T. Milenković, "Exploring the structure and function of temporal networks with dynamic graphlets: implications for aging," *Network Biology (NetBio) Special Interest Group (SIG)* at the *International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB)*, Dublin, Ireland, July 10-14, 2015.

CT-18 Y. Hulovatyy, B. Yoo, H. Chen, F. Faisal, and T. Milenković, "Revealing Missing Parts of the Interactome via Link Prediction: Implications for Aging," *Great Lakes Bioinformatics Conference (GLBIO)*, Purdue University, West Lafayette, May 18-20, 2015.

CT-17 B. Yoo, H. Chen, F.E. Faisal, and T. Milenković, "Improving identification of key players in aging via network de-noising," *ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM BCB)*, Newport Beach, CA, USA, September 20-23, 2014.

CT-16 F.E. Faisal, Y. Hulovatyy, H. Zhao, V. Saraph, and T. Milenković, "Integrative, dynamic, and comparative biological network research of aging," *Integrative Dynamic Analyses of Large Biomedical Network Data (IDANET) Workshop* at the *European Conference on Computational Biology (ECCB)*, Strasbourg, France, September 6-10, 2014.

CT-15 F.E. Faisal, H. Zhao, and T. Milenković, "Network-based prediction of protein function: implications for aging," *Automated Function Prediction (AFP) Special Interest Group (SIG)* at the *International Conference on Intelligent Systems for Molecular Biology (ISMB)*, Boston, MA, July 11-15, 2014.

CT-14 V. Saraph, F.E. Faisal, H. Zhao, and T. Milenković, "Novel Directions for Biological Network Alignment: MAGNA (Maximizing Accuracy in Global Network Alignment)," *Network Biology (NetBio) Special Interest Group (SIG)* at the *International Conference on Intelligent Systems for Molecular Biology (ISMB)*, Boston, MA, July 11-15, 2014.

CT-13 Y. Hulovatyy, S. D'Mello, R.A. Calvo, and T. Milenković, "Network Analysis Improves Interpretation of Affective Physiological Data," the $2^{nd}$ *International Workshop on Complex Networks and their Applications at the 9th International Conference on Signal-Image Technology and Internet-Based Systems (SITIS)*, Kyoto, Japan, December 2-5, 2013.

CT-12 T. Milenković, H. Zhao, and F.E. Faisal, "Global Network Alignment In The Context Of Aging," *ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM BCB)*, Washington DC, USA, September 22-25, 2013.

CT-11 F.E. Faisal, H. Zhao, and T. Milenković, "What can biological networks tell us about aging?," *Network Biology (NetBio) Special Interest Group (SIG)* at the *International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB)*, Berlin, Germany, July 19-23, 2013.

CT-10 T. Milenković, "Graphlet-based edge clustering reveals pathogen-interacting proteins," *European Conference on Computational Biology (ECCB)*, Basel, Switzerland, September 9-12, 2012.

CT-9 T. Milenković, "Biological networks reveal pathogen-interacting proteins," *Network Biology (NetBio) Special Interest Group (SIG)* at *International Conference on Intelligent Systems for Molecular Biology (ISMB)*, Long Beach, California, July 13, 2012.

CT-8 N. Pržulj and T. Milenković, "Topological network alignment uncovers biological function and phylogeny," **Highlights Track** at *International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB)*, Vienna, Austria, July 15-19, 2011.

CT-7 N. Pržulj, T. Milenković, O. Kuchaiev, H. Ho, V. Memišević, A. Stevanović, A. K. Ganesan, J. Aruri, "Uncovering melanogenesis regulatory pathways from protein-protein interaction networks: the computational method and software tool," *International Conference on Research in Computational Molecular Biology (RECOMB) Computational Cancer Biology*, Oslo, Norway, June 24-25, 2010.

CT-6 V. Memišević, T. Milenković, and N. Pržulj, "An integrative approach to modelling biological networks," *International Symposium on Integrative Bioinformatics*, Cambridge, UK, March 22-24, 2010.

CT-5 V. Memišević, T. Milenković, and N. Pržulj, "Complementarity of network and sequence information in homologous proteins," *International Symposium on Integrative Bioinformatics*, Cambridge, UK, March 22-24, 2010.

CT-4 O. Kuchaiev[†], T. Milenković[†], V. Memišević, W. Hayes, N. and Pržulj, "Topological network alignment uncovers biological function and phylogeny," *BioPathways Special Interest Group (SIG)* at the *International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB)*, Stockholm, Sweden, June 2009.

[†]These authors contributed equally to this work.

CT-3 T. Milenković and N. Pržulj, "Uncovering Biological Network Function via Graphlet Degree Signatures," *12th Serbian Mathematical Congress*, Novi Sad, Serbia, August 28 - September 2, 2008.

CT-2 T. Milenković and N. Pržulj, "From network structure to biological function in protein-protein interaction networks," *BioPathways Special Interest Group (SIG)* at the *International Conference on Intelligent Systems for Molecular Biology*, Toronto, Canada, July 18-19, 2008.

CT-1 T. Milenković and N. Pržulj, "Uncovering Biological Network Function via Graphlet Degree Signatures," *BioPathways Special Interest Group (SIG)* at the *International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB)*, Vienna, Austria, July 19-20, 2007.

## Grants and Funding

### As Principal Investigator (PI):

11. Title: Integrative computational framework for pattern mining in big -omics data: linking synonymous codon usage to protein biogenesis
    Source of Support: NIH
    Grant Type/Number: 1R01GM120733-01A1
    Award Period: July 2016–April 2020
    Personnel: T. Milenković (Contact PI/Project Leader), P. Clark (PI), S. Emrich (PI), J. Li (PI)

Award Amount: $1,112,400
Amount Awarded to Milenković Lab: $254,217

10. Title: Efficient Comparison of Multiple Complex Networks
Source of Support: The Department of Air Force
Grant Type/Number: AFOSR YIP FA9550-16-1-0147
Award Period: July 2016– June 2019
Personnel: T. Milenković (PI)
Award Amount: $358,879
Amount Awarded to Milenković Lab: $358,879

9. Title: CAREER: Novel Algorithms for Dynamic Network Analysis in Computational Biology
Source of Support: NSF
Grant Type/Number: CAREER CCF-1452795
Award Period: March 2015–February 2020
Personnel: T. Milenković (PI)
Award Amount: $540,000
Amount Awarded to Milenković Lab: $540,000

8. Title: AF: Small: Novel Directions for Biological Network Alignment
Source of Support: NSF
Grant Type/Number: CCF-1319469
Award Period: July 2013–June 2016
Personnel: T. Milenković (PI), M. Ferdig (key personnel)
Award Amount: $452,863
Amount Awarded to Milenković Lab: $421,713

7. Title: What can Networks Tell us About Aging?
Source of Support: NSF
Grant Type/Number: EAGER CCF-1243295
Award Period: August 2012–July 2014
Personnel: T. Milenković (PI)
Award Amount: $207,935
Amount Awarded to Milenković Lab: $207,935

## As Co-Principal Investigator (Co-PI) or Co-Investigator (Co-I):

6. Title: NetHealth: Modeling the Co-Evolution of Social Networks and Health Behaviors
Source of Support: NIH
Grant Type/Number: 1R01HL117757-01A1
Award Period: September 2014–May 2018
Personnel: O. Lizardo (Contact PI/Project Leader), N. Chawla (PI), D. Hachen (PI), T. Milenković (Co-I), Jessica Payne (Co-I), C. Poellabauer (PI), A. Striegel (PI)
Total Award Amount: $2,913,061
Amount Awarded to Milenković Lab: ∼$60,000

5. Title: Visualization/Analytics of the Evolution of Heterogeneous Smartphone Data
Source of Support: Google
Grant Type/Number: Faculty Research Award
Award Period: May 2013–April 2014
Personnel: A. Striegel (PI), T. Milenković (co-PI)
Award Amount: $33,000
Amount Awarded to Milenković Lab: $16,500

### As Key Personnel:

4. Title: II New: Infrastructure for Supporting Biomedical Application Algorithms, Runtime Development and Resource Management
   Source of Support: NSF
   Grant Type/Number: CISE Research Infrastructure (CRI) CNS-1629914
   Award Period: August 2016–July 2019
   Personnel: 5 PIs/Co-PIs (lead PI: S. Hu), 9 senior personnel (including T. Milenković)
   Total Award Amount: $500,000
   Amount Awarded to Milenković Lab: N/A
3. Title: REU Site: Data Intensive Scientific Computing (DISC)
   Source of Support: NSF
   Grant Type/Number: IIS-1560363
   Award Period: February 2016–January 2019
   Personnel: 4 core faculty (lead PI: D. Thain), 7 additional faculty (including T. Milenković)
   Total Award Amount: $359,757
   Amount Awarded to Milenković Lab: N/A
2. Title: A Network-based Method for Predicting Gene Interactions in Artemisinin Resistance
   Source of Support: NIH
   Grant Type/Number: R21 No. 1R21AI111286-01A1
   Award Period: October 2014–September 2016
   Personnel: M. Ferdig (PI), T. Milenković (key personnel)
   Total Award Amount: $418,000
   Amount Awarded to Milenković Lab: ∼$25,000
1. Title: Influence of Translation on Protein Folding
   Source of Support: NIH
   Grant Type/Number: R01 Supplement No. 3R01GM074807-07S1
   Award Period: April 2012–March 2014
   Personnel: P. Clark (PI), S.J. Emrich (co-PI), T. Milenković (key personnel)
   Total Award Amount: $248,625
   Amount Awarded to Milenković Lab: ∼$45,000

## Research Supervision

### Current Notre Dame Ph.D. Students:

6. **Joseph Crawford** (June 2013–current; recipient of a Deans' Fellowship; IEEE BIBM 2015, ACM BCB 2015, and ISMB 2014 travel fellowship).
5. **Shawn Gu** (June 2016–current).
4. **Cameron Lamir** (May 2016–current).
3. **Shikang (Andy) Liu** (August 2016–current).
2. **Khalique Newaz** (August 2015–current).
1. **Vipin Vijayan** (August 2014–current; Best poster winner, the 10th Annual Poster Contest, Department of Computer Science and Engineering, University of Notre Dame, November 2015; advanced to Ph.D. candidacy in August 2015).

### Graduated Ph.D. Students:

3. **Fazle Faisal** (Continued to work at Microsoft starting August 2016; defended his Ph.D. dissertation in June 2016; selected among total of 100 students from the US to participate with travel fellowship in the NSF-sponsored Graduate Data Science Workshop,

University of Washington, Seattle, WA, August 5-7, 2015; outstanding research assistant award, Department of Computer Science and Engineering, University of Notre Dame, 2015; advanced to Ph.D. candidacy in May 2014; IBM research internship in summer 2014; ACM BCB 2013, ISMB 2014, ACM BCB 2014, and NetBio SIG at ISMB/ECCB 2015 travel fellowships).

2. **Yuriy Hulovatty** (Continued to work at Facebook starting July 2016; defended his Ph.D. dissertation in May 2016; outstanding research asistant award, Department of Computer Science and Engineering, University of Notre Dame, 2016; Facebook internship in summer 2015; advanced to Ph.D. candidacy and gained M.Sc. degree under Milenković's supervision in December 2014; ISMB 2014 travel fellowship).

1. **Lei Meng** (Co-supervised with Prof. Aaron Striegel; continued to work at Google starting April 2016; defended her Ph.D. dissertation in March 2016; advanced to Ph.D. candidacy in May 2014, Notre Dame's Graduate Student Union travel fellowship for ISMB/ECCB 2015).

Current Notre Dame Undergraduate Students:

5. **Natalie Alvarez** (January 2017–current).
4. **John Johnson** (January 2016–current).
3. **Ryan Loizzo** (January 2017–current).
2. **Ryan Mackey** (January 2016–May 2016; January 2017–current).
1. **Jonathan Xu** (January 2017–current).

Former Notre Dame Undergraduate Students:

(Undergraduates who co-authored Milenković's publications are <u>underlined</u>.)

11. **Erin Bradford** (January 2016–May 2016).
10. **<u>Huili Chen</u>** (January 2013–December 2014; continued onto graduate studies at MIT; recipient of the 2016 Steiner Award – the only winner in the department; Tau Beta Pi Scholarship for 2015-2016; Reilly Scholar 2016 honoree; recipient of a Reilly Center Dual Degree Summer Research Scholarship, 2015, 2014, and 2013).
9. **<u>Taryn Green</u>** (January 2012–May 2013; continued onto working at Palantir, Palo Alto, CA; recipient of the 2014 Steiner Award – the only winner in the Department of Computer Science and Engineering, University of Notre Dame; recipient of a Grace Hopper Conference 2013 Scholarship).
8. **Casey Hanley** (January 2014–May 2014).
7. **Eric Krebs** (January 2016–December 2016; recipient of NSF REU supplemental funding, 2016).
6. **Jennifer Long** (January 2014 – December 2015; continued to work at Palantir, Palo Alto, CA starting summer 2016).
5. **Antwane Mason** (August 2011–May 2012; continued onto Ph.D. at Rensselaer Polytechnic Institute).
4. **<u>Vikram Saraph</u>** (August 2011–May 2013; continued onto Ph.D. at Brown University; honors senior thesis under Milenković's supervision, May 2013; recipient of a UPE Scholarship; ISMB 2014 travel fellowship).
3. **<u>Ryan Solava</u>** (January 2011–May 2012; continued onto Ph.D. at Vanderbilt University; recipient of a Notebaert Premier Fellowship at the University of Notre Dame).
2. **Nicholas Taylor** (January 2012–December 2012).

1. **Boyoung Yoo** (January 2013–May 2015; continued onto Ph.D. at Stanford University; faculty choice award, Department of Computer Science and Engineering, University of Notre Dame; recipient of NSF REU supplemental funding, 2014 and 2013; ACM BCB 2014 travel fellowship).

### External Summer Undergraduate Students

(Undergraduates who co-authored Milenković's publications are underlined. )

3. **Dominic Critchlow** (May 2016–July 2016; NSF's DISC REU program, summer 2016).
2. **Yihan Sun** (Continued onto Ph.D. at Carnegie Mellon University; iSure Program between University of Notre Dame and Tsinghua University, summer 2013).
1. **Han Zhao** (Continued onto Ph.D. at Carnegie Mellon University; iSure Program between University of Notre Dame and Tsinghua University, summer 2012).

## Teaching

### Graduate Courses:

7. CSE 60884: Network Science, University of Notre Dame, Spring 2017.
   Enrollment: 29 students.
6. CSE 60884: Complex Networks, University of Notre Dame, Spring 2015.
   Enrollment: 11 students.
5. CSE 60884: Complex Networks, University of Notre Dame, Spring 2014.
   Enrollment: 11 students.
4. CSE 60884: Complex Networks, University of Notre Dame, Spring 2013.
   Enrollment: 12 students.
3. CSE 60884: Complex Networks, University of Notre Dame, Spring 2012.
   Enrollment: 9 students.
2. CSE 60884: Complex Networks, University of Notre Dame, Spring 2011.
   Enrollment: 6 students.
1. CSE 60543: Algorithms for Biological Networks, University of Notre Dame, Fall 2010.
   Enrollment: 10 students.

### Undergraduate Courses:

13. CSE 40884: Network Science, University of Notre Dame, Spring 2017.
    Enrollment: 29 students.
12. CSE 20110-01: Discrete Mathematics (Section 01), University of Notre Dame, Fall 2016.
    Enrollment: 73 students.
11. CSE 20110: Discrete Mathematics, University of Notre Dame, Fall 2015.
    Enrollment: 148 students.
10. CSE 40884: Complex Networks, University of Notre Dame, Spring 2015.
    Enrollment: 11 students.
9. CSE 20110: Discrete Mathematics, University of Notre Dame, Fall 2014.
   Enrollment: 98 students.
8. CSE 40884: Complex Networks, University of Notre Dame, Spring 2014.
   Enrollment: 11 students.

7. CSE 20110: Discrete Mathematics, University of Notre Dame, Fall 2013.
   Enrollment: 90 students.
6. CSE 40884: Complex Networks, University of Notre Dame, Spring 2013.
   Enrollment: 12 students.
5. CSE 20110: Discrete Mathematics, University of Notre Dame, Fall 2012.
   Enrollment: 83 students.
4. CSE 40884: Complex Networks, University of Notre Dame, Spring 2012.
   Enrollment: 9 students.
3. CSE 20110: Discrete Mathematics, University of Notre Dame, Fall 2011.
   Enrollment: 60 students.
2. CSE 40884: Complex Networks, University of Notre Dame, Spring 2011.
   Enrollment: 6 students.
1. CSE 40543: Algorithms for Biological Networks, University of Notre Dame, Fall 2010.
   Enrollment: 10 students.

Course description:

- CSE 40884/60884 Complex Networks/Network Science: Elective advanced undergraduate- and graduate-level course, offering introduction to different types of real-world networks (including biological, social, technological, and information networks), plus computational and application questions related to network inference, network characterization, network modeling and evolution, community structure (i.e., cluster) identification, network comparison and alignment, network integration, dynamic network analysis, and network visualization.
- CSE 40543/60543 Algorithms for Biological Networks: Similar to CSE 40884/60884, but focusing exclusively on biological network research.
- CSE 20110 Discrete Mathematics: Required sophomore undergraduate-level course, offering introduction to mathematical techniques fundamental to computer engineering and computer science. Topics: mathematical logic, induction, set theory, relations, functions, recursion, recurrence relations, introduction to asymptotic analysis, algebraic structures, graphs, and machine computation.

## Professional Service

**Associate Editor** for:
IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014–current. (This appointment is by invitation only.)

**Government grant proposal reviewing**:
The National Science Foundation (NSF) panelist for Computer & Information Science & Engineering (CISE) Computing and Communication Foundations (CCF) program, 2017.
The National Institutes for Health (NIH) panelist, 2016.
The National Science Foundation (NSF) panelist for Computer & Information Science & Engineering (CISE) Computing and Communication Foundations (CCF) program, 2016.
The National Science Foundation (NSF) panelist for Computer & Information Science & Engineering (CISE) Computing and Communication Foundations (CCF) program, 2015.
The Natural Sciences and Engineering Research Council of Canada (NSERC), 2015.
The National Institutes for Health (NIH) panelist for Biodata Management and Analysis (BDMA) study section, 2014.
The National Science Foundation (NSF) panelist for Computer & Information Science & Engineering (CISE) Computing and Communication Foundations (CCF) program, 2014.

**Conference organization**:
Co-organizer of Network Biology (NetBio) Community of Special Interest (COSI) at Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB) 2017.
Co-organizer of Network Medicine Satellite Meeting at International School and Conference on Network Science (NetSci) 2017.
Publications Co-Chair for Great Lakes Bioinformatics Conference (GLBIO) 2017.
Workshop Co-Organizer at European Conference on Computational Biology (ECCB) 2016, Hague, Netherlands, September 3-7, 2016.
Publications Co-Chair for the Great Lakes Bioinformatics Conference (GLBIO) 2016.
Tutorial Co-Chair for IEEE International Conference on Bioinformatics and Biomedicine (IEEE BIBM) 2015.
Workshop Co-Organizer at Basel Computational Biology Conference ([BC2]) 2015, Basel, Switzerland, June 7-10, 2015. (According to [BC2] organizers, our "Challenges and approaches in comprehensive and informative complex network analysis for precision medicine" workshop was the most visited of all workshops held at the conference.)
Publications Co-Chair for the Great Lakes Bioinformatics Conference (GLBIO) 2015.
"Network approaches in aging research with focus on biological network alignment" tutorial at ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM BCB) 2014.
"Integrative Dynamic Analyses of Large Biomedical Network Data" workshop at European Conference on Computational Biology (ECCB) 2014.
"Biological Networks: Analyses, Models, Functions, and Disease" tutorial at International Conference on Systems Biology (ICSB) 2008.

**Conference program committee member** for:
International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB) 2017.
ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM BCB) 2016.
International Conference on Intelligent Systems for Molecular Biology (ISMB) 2016.
International Joint Conference on Artificial Intelligence (IJCAI) 2016.
International Workshop on Complex Networks and their Applications (COMPLEX NETWORKS) 2016.
International Conference on Research in Computational Molecular Biology (RECOMB) 2016.
ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM BCB) 2015.
International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB) 2015.
International Conference on Research in Computational Molecular Biology (RECOMB) 2015.
Automated Function Prediction (AFP) Special Interest Group (SIG) at International Conference on Intelligent Systems for Molecular Biology (ISMB) 2014.
International Conference on Research in Computational Molecular Biology (RECOMB) 2014.
ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM BCB) 2013.
International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB) 2013.
International Conference on Intelligent Systems for Molecular Biology (ISMB) 2012.

**Reviewer** for the following journals (in alphabetical order):
Algorithms for Molecular Biology
Bioinformatics
BMC Bioinformatics

BMC Systems Biology
Computational Biology and Chemistry
Computer Networks Journal
Data Mining and Knowledge Discovery
IEEE/ACM Transactions on Computational Biology and Bioinformatics
IEEE Transactions on Knowledge and Data Engineering
Integrative Biology
Internet Mathematics
Journal of the Royal Society Interface
Molecular Genetics and Genomics
Nature Communications
Pattern Recognition Letters
PLOS Computational Biology
PLOS ONE
PLOS Pathogens

**Outreach**:
Panelist for a meeting organized by Graduate Society of Women Engineers (Grad-SWE) at University of Notre Dame, September 2016.
Educational collaboration with John Adams high school in South Bend, IN, yearly since 2014.
Workshop organizer and presenter at the "Expanding Your Horizons in Science and Mathematics" career conference for middle school girls, yearly since 2012.
Panelist for the documentary "Code: Debugging the Gender Gap," University of Notre Dame, November 2015.
Member of the "Women in Bioinformatics" panel, ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM BCB), Newport Beach, CA, USA, September 20-23, 2014.

**Faculty search committee member**, the Data Analytics AOV, Department of Computer Science and Engineering (CSE), University of Notre Dame, 2016/2017 and 2015/2016.

**Faculty search committee member**, position in Network Science, Department of Physics and Interdisciplinary Center for Network Science and Applications (iCeNSA), University of Notre Dame, 2010/2011.

**Graduate studies committee member**, Department of CSE, University of Notre Dame, 2016/2017 and 2015/2016.

**Graduate student admission committee member**, Department of CSE, University of Notre Dame, 2014/2015, 2013/2014, 2012/2013, 2011/2012, and 2010/2011.

**Ph.D. dissertation defense committee member** for the following students:
Fazle Faisal, Department of CSE, University of Notre Dame, 2016.
Yuriy Hulovatyy, Department of CSE, University of Notre Dame, 2016.
Lei Meng, Department of CSE, University of Notre Dame, 2016.
Jian Mu, Department of CSE, University of Notre Dame, 2014.
James E. Gentile, Department of CSE, University of Notre Dame, 2013.
Ryan Kennedy, Department of CSE, University of Notre Dame, 2010.

**Ph.D. candidacy exam committee member** for the following students:
Jian Xu, Department of CSE, University of Notre Dame, 2016.
Sage Davis, Department of Biological Sciences, University of Notre Dame, 2016.
Tomer Levinboim, Department of CSE, University of Notre Dame, 2015.
Vipin Vijayan, Department of CSE, University of Notre Dame, 2015.

Yuriy Hulovatyy, Department of CSE, University of Notre Dame, 2014.
Lei Meng, Department of CSE, University of Notre Dame, 2014.
Fazle E. Faisal, Department of CSE, University of Notre Dame, 2014.
Yang Yang, Department of CSE, University of Notre Dame, 2014.
Wei Zhang, Department of CSE, University of Notre Dame, 2012.
Jian Mu, Department of CSE, University of Notre Dame, 2012.
James E. Gentile, Department of CSE, University of Notre Dame, 2011.
Ryan Lichtenwalter, Department of CSE, University of Notre Dame, 2011.

**Undergraduate honors thesis committee** for the following students:
Vikram Saraph, Department of CSE, University of Notre Dame, 2013.

## Affiliations

Association for Computing Machinery (ACM)
International Society for Computational Biology (ISCB)
American Society for Engineering Education (ASEE)