# Tijana Milenković: Curriculum Vitæ (as of 07/14/2025)

**Professor (with tenure)**
**Department of Computer Science and Engineering (CSE)**
Head, Complex Networks (CoNe) Lab
Member, Eck Institute for Global Health
Member, Harper Cancer Research Institute
Member, Bioengineering Graduate Program
**University of Notre Dame**
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## RESEARCH INTERESTS

**Computational (systems) biology and bioinformatics, network biomedicine:** studying interplay between network topology and biological function, disease, aging, and evolution in molecular (e.g., protein-protein interaction) networks; -omics data integration.

**Health and well-being:** personalized recommendations for improving health and preventing disease by integrating molecular, electronic health record, behavioral, environmental, physiological, physical activity tracking, social interaction, and other data.

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

**Complex networks, network science, data mining, big data:** developing computational approaches for efficient extraction of function from topology of complex (large, noisy, dynamic, heterogeneous, etc.) real-world networks.

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

**Social networks:** studying the relationship between people's social interactions and their behaviors.

## HIGHER EDUCATION

**Ph.D., Computer Science, University of California, Irvine (UCI), 2006–2010.**
Official graduation date: March 12, 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.**
Official graduation date: September 10, 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.**
Official graduation date: November 22, 2005.
THESIS TITLE: *M-Commerce.*
ADVISOR: Prof. Dženana Djonko.

ACADEMIC AND PROFESSIONAL POSITIONS

2022–2025: Director of Inclusive Excellence and Engagement, Department of Computer Science and Engineering, University of Notre Dame.

2022–2025: Director of Diversity, Equity, and Inclusion, Department of Computer Science and Engineering, University of Notre Dame.

2021–2025: Frank M. Freimann Collegiate Professor of Engineering, Department of Computer Science and Engineering, University of Notre Dame.

2021–current: Professor (with tenure), Department of Computer Science and Engineering, University of Notre Dame.

2020–2021: Frank M. Freimann Collegiate Associate Professor of Engineering, Department of Computer Science and Engineering, University of Notre Dame.

2016–2021: Associate Professor (with tenure), 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

- **CSE Outstanding Teacher and Faculty Speaker at CSE Graduation**, Department of Computer Science and Engineering (CSE), University of Notre Dame, 2025. Note: this is a student-voted honor.

- **Winner of the Catherine F. Pieronek Women in Engineering Impact Award**, University of Notre Dame, 2023. The annual award honors a faculty or staff member in the Notre Dame College of Engineering who has made a dramatic positive impact on women's engineering experience through teaching and mentoring; service and support; and advocacy for women in engineering. Award recipients are selected based on feedback from women graduate and undergraduate students in engineering.

- **Re-elected to the Board of Directors of the International Society for Computational Biology (ISCB)** to represent the Society's Communities of Special Interest (COSIs), 2023-2026.

- **Named a Distinguished Member of the Association for Computing Machinery (ACM)**, 2022. Honorees are longstanding ACM members and are selected by their peers for work that has spurred innovation, enhanced computer science education, and moved the field forward. The ACM Distinguished Member program recognizes up to 10 percent of ACM worldwide membership based on professional experience and significant achievements in the computing field.

- **Winner of the CRA-E Undergraduate Research Faculty Mentoring Award**, 2021. One of two winners in the US in 2021. This award recognizes faculty members who have provided exceptional mentorship, undergraduate research experiences, and, in parallel, guidance on admission and matriculation of these students to research-focused graduate programs in computing.

- **Appointed as a Frank M. Freimann Collegiate Professor of Engineering, University of Notre Dame**, 2021-2025.

- **Appointed as a Frank M. Freimann Collegiate Associate Professor of Engineering, University of Notre Dame**, 2020-2021.

- **Elected to the Board of Directors of the International Society for Computational Biology (ISCB)** to represent the Society's Communities of Special Interest (COSIs), 2020-2023.

- Named a Senior Member of the International Society for Computational Biology (ISCB), 2020.

- Named a Senior Member of the Association for Computing Machinery (ACM), 2020.

- National Science Foundation (NSF) award (CCF-1941447) as the sole Principal Investigator (PI), 2019–2022; this is a grant to organize a workshop on future directions in the field of network biology.

- National Science Foundation (NSF) award (CCF-1917325) as the sole PI, 2019–2020; this is a travel fellowship grant intended to support participation of students at the Great Lakes Bioinformatics Conference (GLBIO) 2019.

- National Institutes for Health (NIH) award (1R01GM120733) as the lead PI, 2016-2021.

- **National Science Foundation (NSF) Faculty Early Career Development Program (CAREER) award** (CCF-1452795) as the sole PI, 2015–2022; CAREERs are "the highest honor given by the U.S. government to young faculty in engineering and science".

- **Air Force Office of Scientific Research (AFOSR) Young Investigator Program (YIP) award** (FA9550-16-1-0147) as the sole PI, 2016–2019; this is AFOSR's equivalent of the NSF CAREER program.

- National Science Foundation (NSF) award (CCF-1319469) as the sole PI, 2013–2017.

- National Science Foundation (NSF) EAGER award (CCF-1243295) as the sole PI, 2012–2014; EAGERs are special awards intended for **"highly risky, potentially transformative research."**

- Google Faculty Research Award, 2013-2014.

- Multiple additional 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.

## CONTRIBUTIONS TO RESEARCH AND DEVELOPMENT: SUMMARY

| **Citation indices** (Google Scholar) | All | Since 2020 |
|---|---|---|
| Number of citations | 5615 | 2260 |
| h-index | 35 | 25 |
| i10-index | 58 | 50 |

| **Funding:** | Total award amount | Milenković lab's award amount |
|---|---|---|
| As PI | $2.77M | $1.94M |
| As co-PI | $2.95M | $142K |
| As key personnel | $13.49M | $103K |
| Total (in any role) | $19.21M | $2.19M |

## REFEREED JOURNAL PUBLICATIONS

**Summary:** One submitted paper, and 61 papers published in the following journals (sorted by their impact factors): 1 (consortium) paper in **Science (impact factor: 41.84)**, 1 paper in **Briefings in Bioinformatics (impact factor: 11.62)**, 2 papers in Proceedings of the National Academy of Sciences **(PNAS) (impact factor: 11.2)**, 15 papers in **Bioinformatics (impact factor: 6.937)**, 1 paper in **Protein Science (impact factor: 6.725)**, 1 paper in IEEE Transactions on Network Science and Engineering **(IEEE TNSE) (impact factor: 5.213)**, 4 papers in **Scientific Reports (impact factor: 5.133)**, 2 papers in **Journal of the Royal Society Interface (impact factor: 4.118)**, 1 paper in **Journal of Proteome Research (impact factor: 4.074)**, 1 paper in **BMC Genomics (impact factor: 3.969)**, 1 paper in **PROTEINS: Structure, Function, and Bioinformatics (impact factor: 3.756)**, 1 paper in **IEEE Access (impact factor: 3.367)**, 2 papers in **Journal of Integrative Bioinformatics (impact factor: 3.321)**, 6 papers in **PLOS ONE (impact factor: 3.24)**, 3 papers in BMC Bioinformatics **(impact factor: 3.169)**, 6 papers in IEEE/ACM Transactions on Computational Biology and Bioinformatics **(IEEE/ACM TCBB) (impact factor: 3.015)**, 1 paper in **Royal Society Open Science (impact factor: 2.963)**, 1 paper in **ACM Transactions on Knowledge Discovery from Data (ACM TKDD) (impact factor: 2.713)**, 2 papers in **Bioinformatics Advances (impact factor: 2.4)**, 1 paper in **Applied Network Science (impact factor: 2.33)**, 2 papers

in **Cancer Informatics (impact factor: 2.06)**, 1 paper in **BMC Systems Biology (impact factor: 2.048)**, 1 paper in **Journal of Complex Networks (impact factor: 2.011)**, 1 paper in **EURASIP Journal on Bioinformatics and Systems Biology (impact factor: 1.61)**, 1 paper in **Algorithms for Molecular Biology (impact factor: 1.405)**, 1 paper in **Network Science (impact factor: 1.31)**.

(In the journal publication list below, Milenković's postdocs and students are indicated in **bold**, postdocs are also indicated with *, and undergraduate students are also <u>underlined</u>.)

J-62 **A. Wells**, K. Newaz, <u>**J. Morones**</u>, J. Cheng, and T. Milenković, "Unavailability of experimental 3D structural data on protein folding dynamics and necessity for a new generation of structure prediction methods in this context," *under review*, 2025. Also, arXiv:2507.08188 [q-bio.BM], `https://doi.org/10.48550/arXiv.2507.08188`, 2025.

J-61 K. Borgwardt and T. Milenković, "ISMB/ECCB 2025 Proceedings," *Bioinformatics*, in press, 2025. Note: invited submission.

J-60 A. Rodriguez, J.D. Diehl, **G. Wright**†, C.D. Bonar, T. Lundgren, M.J. Moss, J. Li, T. Milenković, P. Huber, M.M. Champion, S.J. Emrich, and P.L. Clark, "Synonymous codon substitutions regulate transcription and translation of an upstream gene," *Proceedings of the National Academy of Sciences (PNAS)*, 121(36): e2405510121, 2024. †Co-advised by S.J. Emrich.

J-59 Marinka Zitnik†, Michelle M. Li†, **Aydin Wells**†, Kimberly Glass#, Deisy Morselli Gysi#, Arjun Krishnan#, T. M. Murali#, Predrag Radivojac#, Sushmita Roy#, Anaïs Baudot, Serdar Bozdag, Danny Z. Chen, Lenore Cowen, Kapil Devkota, Anthony Gitter, Sara Gosline, Pengfei Gu, Pietro H. Guzzi, Heng Huang, Meng Jiang, Ziynet Nesibe Kesimoglu, Mehmet Koyuturk, Jian Ma, Alexander R. Pico, Nataša Pržulj, Teresa M. Przytycka, Benjamin J. Raphael, Anna Ritz, Roded Sharan, Yang Shen, Mona Singh, Donna K. Slonim, Hanghang Tong, Xinan Holly Yang, Byung-Jun Yoon, Haiyuan Yu, and Tijana Milenković◇, "Current and future directions in network biology, *Bioinformatics Advances*, 4(1): vbae099, 2024.

J-58 **Q. Li**, K.A. Button-Simons, M.A.C. Sievert, <u>**E. Chahoud**</u>, G.F. Foster, K. Meis, M.T. Ferdig, and T. Milenković, "Enhancing gene co-expression network inference for the malaria parasite *Plasmodium falciparum*," *Genes*, 15(6): 685, 2024.

J-57 T. Milenković and Y. Ponty, "ISMB 2024 Proceedings," *Bioinformatics*, 40(Supplement_1): i1–i2, 2024. Note: invited submission.

J-56 **Q. Li**, **K. Newaz**, and T. Milenković, "Towards future directions in data-integrative supervised prediction of human aging-related genes," *Bioinformatics Advances*, 2(1): vbac081, 2022.

J-55 **K. Newaz**, **J. Piland**, P.L. Clark, S.J. Emrich, J. Li, and T. Milenković, "Multi-layer sequential network analysis improves protein 3D structural classification," *PROTEINS: Structure, Function, and Bioinformatics*, 90(9): 1721-1731, 2022.

J-54 **S. Gu**, M. Jiang, P.H. Guzzi, and T. Milenković, "Modeling multi-scale data via a network of networks," *Bioinformatics*, 38(9): 2544–2553, 2022.

J-53 **G. Wright**†, A. Rodriguez, J. Li, T. Milenković, S.J. Emrich, and P.L. Clark, "CHARMING: Harmonizing synonymous codon usage to replicate a desired codon usage pattern," *Protein Science*, 31: 221-231, 2021. †Co-advised by S.J. Emrich.

J-52 **Q. Li**[†], **K. Newaz**[†], and T. Milenković, "Improved supervised prediction of aging-related genes via weighted dynamic network analysis," ***BMC Bioinformatics***, 22: 520, 2021. [†]These authors contributed equally to this work.

J-51 **Q. Li** and T. Milenković, "Supervised prediction of aging-related genes from a context-specific protein interaction subnetwork," ***IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)***, 19(4): 2484-2498, 2021.

J-50 **S. Gu** and T. Milenković, "Data-driven biological network alignment that uses topological, sequence, and functional information," ***BMC Bioinformatics***, 22: 34, 2021.

J-49 **S. Liu**, **F. Vahedian**[*], D. Hachen, O. Lizardo, C. Poellabauer, A. Striegel, and T. Milenković, "Heterogeneous network approach to predict individuals' mental health," ***ACM Transactions on Knowledge Discovery from Data (TKDD)***, 15(2), article number: 25, 2021.

J-48 **K. Newaz** and T. Milenković, "Improving inference of the dynamic biological network underlying aging via network propagation," ***IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)***, 19(2): 974-988, 2020.

J-47 **K. Newaz**, **G. Wright**[†], **J. Piland**, J. Li, P.L. Clark, S.J. Emrich, and T. Milenković, "Network analysis of synonymous codon usage," ***Bioinformatics***, 36(19): 4876–4884, 2020. [†]Co-advised by S.J. Emrich.

J-46 **S. Gu** and T. Milenković, "Data-driven network alignment," ***PLOS ONE***, 15(7): e0234978, 2020.

J-45 **K. Newaz**, **M. Ghalehnovi**[†], A. Rahnama[†], P.J. Antsaklis, and T. Milenković, "Network-based protein structural classification," ***Royal Society Open Science***, 7: 191461, 2020. [†]These authors contributed equally to this work.

J-44 **G. Wright**[†], A. Rodriguez, J. Li, P.L. Clark, T. Milenković, and S.J. Emrich, "Analysis of computational codon usage models and their association with translationally slow codons," ***PLOS ONE***, 15(4): e0232003, 2020. [†]Co-advised by S.J. Emrich.

J-43 **V. Vijayan**, **S. Gu**, **E. Krebs**, and T. Milenković, "Pairwise versus multiple global network alignment," ***IEEE Access***, 8: 41961-41974, 2020.

J-42 M. Milano, M. Cannataro, T. Milenković, and P.H. Guzzi, "L-HetNetAligner: A novel algorithm for local alignment of heterogeneous biological networks," ***Scientific Reports***, 10, article number: 3901, 2020.

J-41 D. Aparicio, P. Ribeiro, T. Milenković, and F. Silva, "Temporal network alignment via GoT-WAVE," ***Bioinformatics***, 35(18): 3527-3529, 2019.

J-40 **S. Liu**, D. Hachen, O. Lizardo, C. Poellabauer, A. Striegel, and T. Milenković, "Network analysis of the NetHealth data: Exploring co-evolution of individuals' social networks and physical activities," ***Applied Network Science***, 3: 45, 2018.

J-39 **S. Gu**, **J. Johnson**, **F.E. Faisal**, and T. Milenković, "From homogeneous to heterogeneous network alignment via colored graphlets," ***Scientific Reports***, 8, article number: 12524, 2018.

J-38 T. Milenković and S.C. Janga, "Great Lakes Bioinformatics Conference (GLBIO) 2015 Special Section Editorial," ***IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)***, 15(4): 1229-1230, 2018. Note: invited submission.

J-37 **J. Crawford** and T. Milenković, "ClueNet: Clustering a temporal network based on topological similarity rather than denseness," ***PLOS ONE***, 13(5): e0195993, 2018.

J-36 **V. Vijayan** and T. Milenković, "Aligning dynamic networks with DynaWAVE," ***Bioinformatics***, 34(10): 1795-1798, 2018.

J-35 **V. Vijayan** and T. Milenković, "Multiple network alignment via multiMAGNA++," ***IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)***, 15(5): 1669-1682, 2018.

J-34 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***, 19(3): 472-481, 2018.

J-33 **F.E. Faisal**, **K. Newaz**, J.L. Chaney, J. Li, S.J. Emrich, P.L. Clark, and T. Milenković, "GRAFENE: Graphlet-based alignment-free network approach integrates 3D structural and sequence (residue order) data to improve protein structural comparison," ***Scientific Reports***, 7, article number: 14890, 2017.

J-32 **V. Vijayan**, **D. Critchlow**, and T. Milenković, "Alignment of dynamic networks," ***Bioinformatics***, 33(14): i180-i189, 2017. Also, in *Proceedings of the International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB)*, Prague, Czech Republic, July 21-25, 2017 (conference acceptance rate: 16.5%.)

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***, 33(7): 1107-1109, 2017.

J-30 **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 (TCBB)***, 14(5): 1056-1069, 2017.

J-29 **Y. Hulovatyy** and T. Milenković, "SCOUT: simultaneous time segmentation and community detection in dynamic networks," ***Scientific Reports***, 6, article number: 37557, 2016.

J-28 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.
[†]These authors contributed equally to this work.

J-27 **L. Meng**, A. Striegel, and T. Milenković, "Local versus global biological network alignment," ***Bioinformatics***, 32(20): 3155-3164, 2016.

J-26 **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 (TNSE)***, 3(1): 32-43, 2016.

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. 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.

J-23 **J. Crawford**, <u>**Y. Sun**</u>, and T. Milenković, "Fair Evaluation of Global Network Aligners," ***Algorithms for Molecular Biology***, 10: 19, 2015.

J-22 **V. Vijayan**, <u>**V. Saraph**</u>, and T. Milenković, "MAGNA++: Maximizing Accuracy in Global Network Alignment via both node and edge conservation," ***Bioinformatics***, 31(14): 2409-2411, 2015.

J-21 O. Yaveroglu, T. Milenković, and N. Pržulj, "Proper Evaluation of Alignment-Free Network Comparison Methods," ***Bioinformatics***, 31(16): 2697-2704, 2015.

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.

J-19 **V. Saraph** and T. Milenković, "MAGNA: Maximizing Accuracy in Global Network Alignment," ***Bioinformatics***, 30(20): 2931-2940, 2014.

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.

J-17 **F.E. Faisal**, <u>**H. Zhao**</u>, and T. Milenković, "Global Network Alignment In The Context Of Aging," ***IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)***, 12(1), 40 - 52, 2014.

J-16 **Y. Hulovatyy**, <u>**R.W. Solava**</u> and T. Milenković, "Revealing missing parts of the interactome via link prediction," ***PLOS ONE***, 9(3): e90073, 2014.

J-15 **F.E. Faisal** and T. Milenković, "Dynamic networks reveal key players in aging," ***Bioinformatics***, 30(12): 1721-1729, 2014.

J-14 <u>**R.W. Solava**</u>, **R.P. Michaels**, and T. Milenković, "Graphlet-based edge clustering reveals pathogen-interacting proteins," ***Bioinformatics***, 28(18): i480-i486, 2012. Also, in *Proceedings of the European Conference on Computational Biology (ECCB)*, Basel, Switzerland, September 9-12, 2012 (acceptance rate: 14%).

J-13 Arabidopsis Interactome Mapping Consortium, "Evidence for Network Evolution in an Arabidopsis Interactome Map," ***Science***, 333(6042): 601-607, 2011.

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

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.

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.
[†]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.

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.

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

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. [†]These authors contributed equally to this work.

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.

J-4 T. Milenković[†], I. Filippis[†], M. Lappe, and N. Pržulj, "Optimized Null Model of Protein Structure Networks," *PLOS ONE*, 4(6): e5967, 2009. [†]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," *Proceedings of the National Academy of Sciences (PNAS)*, 105(36), 13333-13338, 2008.

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.

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.

## REFEREED FULL CONFERENCE PUBLICATIONS

(In the conference publication list below, Milenković's postdocs and students are indicated in **bold**, postdocs are also indicated with [*], and undergraduate students are also **underlined**.)

C-16 **S. Liu**, D. Hachen, O. Lizardo, C. Poellabauer, A. Striegel, and T. Milenković, "The power of dynamic social networks to predict individuals' mental health," in *Proceedings of the Pacific Symposium on Biocomputing (PSB)*, the Big Island of Hawaii, HI, USA, January 3-7, 2020 (**acceptance rate** for papers with oral presentations like ours: **30%**).

C-15 **Q. Li** and T. Milenković, "Supervised prediction of aging-related genes from a context-specific protein interaction subnetwork," in *Proceedings of the IEEE International Conference on Bioinformatics and Biomedicine (IEEE BIBM)*, San Diego, CA, USA, November 18-21, 2019, pages 130-137 (**acceptance rate: 18%**).

C-14 **S. Gu** and T. Milenković, "Graphlets versus node2vec and struc2vec in the task of network alignment," in *Proceedings of the International Workshop on Mining and Learning with Graphs (MLG) at the ACM SIGKIDD 2018 Conference on Knowledge Discovery and Data Mining (KDD)*, London, UK, August 19-23, 2018 (**acceptance rate: unknown**).

C-13 **V. Vijayan**, **D. Critchlow**, and T. Milenković, "Alignment of dynamic networks," in *Proceedings of the International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB)*, Prague, Czech Republic, July 21-25, 2017 (**acceptance rate: 16.5%**). Also, *Bioinformatics*, 33(14): i180-i189, 2017.

C-12 **V. Vijayan** and T. Milenković, "Multiple network alignment via multiMAGNA++," in *Proceedings of the 15th International Workshop on Data Mining in Bioinformatics (*<span style="color:red">**BIOKDD**</span>*) at the 22nd ACM SIGKDD 2016 Conference on Knowledge Discovery and Data Mining (*<span style="color:red">**KDD**</span>*)*, San Francisco, CA, USA, August 13-17, 2016 (<span style="color:red">**acceptance rate: unknown**</span>).

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 (*<span style="color:red">**MLG**</span>*) at the 22nd ACM SIGKDD 2016 Conference on Knowledge Discovery and Data Mining (*<span style="color:red">**KDD**</span>*)*, San Francisco, CA, USA, August 13-17, 2016 (<span style="color:red">**acceptance rate: unknown**</span>).

C-10 **J. Crawford** and T. Milenković, "GREAT: GRaphlet Edge-based network AlignmenT," in *Proceedings of IEEE International Conference on Bioinformatics and Biomedicine (*<span style="color:red">**IEEE BIBM**</span>*)*, Washington D.C., USA, November 9-12, 2015 (<span style="color:red">**acceptance rate: 19%**</span>).

C-9 <u>**Y. Sun**</u>, **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 (*<span style="color:red">**WABI**</span>*)*, Atlanta, GA, USA, September 10-12, 2015, pages 16-39 (<span style="color:red">**acceptance rate: 40%**</span>).

C-8 **Y. Hulovatyy**, <u>**H. Chen**</u>, 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 (*<span style="color:red">**ISMB/ECCB**</span>*)*, Dublin, Ireland, July 10-14, 2015 (<span style="color:red">**acceptance rate: 18%**</span>). Also, in *Bioinformatics*, 31(12): i171-i180, 2015.

C-7 <u>**B. Yoo**</u>, <u>**H. Chen**</u>, **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 (*<span style="color:red">**ACM BCB**</span>*)*, Newport Beach, CA, USA, September 20-23, 2014, pages 164-173 (<span style="color:red">**acceptance rate: 22%**</span>).

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 (*<span style="color:red">**CompleNet**</span>*) V*, Bologna, Italy, March 12-14, 2014 (<span style="color:red">**acceptance rate: 25%**</span>).

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 (*<span style="color:red">**SITIS**</span>*)*, Kyoto, Japan, December 2-5, 2013, pages: 470-477 (<span style="color:red">**acceptance rate: 42%**</span>).

C-4 T. Milenković, <u>**H. Zhao**</u>, and **F.E. Faisal**, "Global Network Alignment In The Context Of Aging," in *Proceedings of the ACM Conference on Bioinformatics, Computational Biology, Biomedical Informatics (*<span style="color:red">**ACM BCB**</span>*)*, Washington DC, USA, September 22-25, 2013, pages 23-32 (<span style="color:red">**acceptance rate: 28%**</span>).

C-3 <u>**R.W. Solava**</u>, **R.P. Michaels**, and T. Milenković, "Graphlet-based edge clustering reveals pathogen-interacting proteins," in *Proceedings of the European Conference on Computational Biology (*<span style="color:red">**ECCB**</span>*)*, Basel, Switzerland, September 9-12, 2012 (<span style="color:red">**acceptance rate: 14%**</span>). Also, in *Bioinformatics*, 28(18): i480-i486, 2012.

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*, Cambridge, United Kingdom, March 22-24, 2010 (<span style="color:red">**acceptance rate: unknown**</span>).

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*, Cambridge, United Kingdom, March 22-24, 2010 (**acceptance rate: unknown**).

## Refereed Book Chapters

BC-3 K. Newaz and T. Milenković, "Graphlets in network science and computational biology," a chapter in *Analyzing Network Data in Biology and Medicine: A textbook for training biological, medical and computational inter-disciplinary scientists*, edited by N. Pržulj, Cambridge University Press, 2019.

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.

## 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.)

## Conference and Other Workshops

W-6 T. Milenković and M. Žitnik, "Workshop on Future Directions in Network Biology," University of Notre Dame, IN, USA, June 13-14, 2022. Note: Funded by the NSF CCF1941447 award.

W-5 A. Sharma, M. Calderwood, and T. Milenković, "Network Medicine: Quantitative interactome and multilayer networks taking medicine beyond the genome," *International School and Conference on Network Science (NetSci)*, Indianapolis, IN, USA, June 19-23, 2017.

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.

Keynote or Invited Talks

KIT-22 T. Milenković, "Future directions in network biology," *Belgrade Bioinformatics Conference (BelBi)*, Belgrade, Serbia, June 17-20, 2024.

KIT-21 T. Milenković, "Network science reveals a protein's role in aging and a person's risk of mental health problems," *International School and Conference on Network Science (NetSciX)*, held in hybrid mode, February 8-11, 2022.

KIT-20 T. Milenković, "Dynamic graphlets and other measures of temporal network structure reveal a protein's role in aging and a person's risk of mental health problems," *Dynamics and Motifs (DynaMo) Satellite at Networks 2021 – A Joint Conference of Sunbelt and NetSci*, held virtually, June 28-29, 2021.

KIT-19 T. Milenković, "Network science reveals a protein's role in aging and a person's risk of mental health problems," *Belgrade BioInformatics Conference (BelBi)*, held virtually, June 21-25, 2021.

KIT-18 T. Milenković, "Network science reveals a protein's role in aging and a person's risk of mental health problems," Mississippi State University, May 2021.

KIT-17 T. Milenković, "Improving human health by analyzing biological or social networks," *International Conference on Information, Communication, and Augomation Techologies (ICAT)*, Sarajevo, Bosnia and Herzegovina, October 20-23, 2019.

KIT-16 T. Milenković, "New computational directions for community detection in dynamic networks (aka What can network science tell us about human aging?)," *Great Lakes Workshop on Data Science*, University of Notre Dame, September 20-22, 2019.

KIT-15 T. Milenković, "From static and homogeneous to dynamic and heterogeneous biological network research of aging and disease," the Theodore L. Badger Lecture, Channing Division of Network Medicine, Department of Medicine, Brigham and Women's Hospital, February 2018.

KIT-14 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.

KIT-13 T. Milenković, "Understanding complex (biological, social, technological, ...) systems via network science," the Computing and Humanity Speaker Series, Valparaiso University, October 2016.

KIT-12 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.

KIT-11 T. Milenković, "Redefining homology by transferring function between conserved network regions," *Great Lakes Bioinformatics Conference (GLBIO)*, Purdue University, West Lafayette, May 18-20, 2015.

KIT-10 T. Milenković, "Biological network research of aging," the Buck Institute for Research on Aging, March 2015.

KIT-9 T. Milenković, "Novel directions for biological network comparison: implications for aging," Toyota Technological Institute at Chicago, November 2014.

KIT-8 T. Milenković, "Novel strategies for efficient network mining: implications for aging and disease," Department of Computer Science, Purdue University, October 2014.

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

KIT-6 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.

KIT-5 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.

KIT-4 T. Milenković, "Biology through network lenses," *Network Links: Connecting Social, Communication and Biological Network Analysis* Workshop, University of Minnesota, February 27-March 2, 2012.

KIT-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.

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

KIT-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

CCT-63 S. Yang and T. Milenković, "Dynamic network analysis of multi-scale -omics data for protein function prediction," *International Conference on Intelligent Systems for Molecular Biology (ISMB)*, Montreal, Canada, July 12-16, 2024.

CCT-62 A. Wells, S. Yang, K. Newaz, and T. Milenković, "Dynamic network analysis of protein structural change," *International Conference on Intelligent Systems for Molecular Biology (ISMB)*, Montreal, Canada, July 12-16, 2024.

CCT-61 K. Newaz, A. Wells, J. Piland, P. Clark, S. Emrich, J. Li, T. Milenković, "Multi-layer sequential network analysis improves protein 3D structural classification", **highlights talk** at *ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)*, Houston, TX, USA, September 3-6, 2023.

CCT-60 K. Newaz, A. Wells, J. Piland, P. Clark, S. Emrich, J. Li, T. Milenković, "Multi-layer sequential network analysis improves protein 3D structural classification", **highlights talk** at *Workshop on Computational Network Biology: Modeling, Analysis, and Control (CNB-MAC)*, Houston, TX, USA, September 3, 2023.

CCT-59 S. Gu, M. Jiang, P. Guzzi, and T. Milenković, "Protein functional prediction via multi-scale data integration," *International Conference on Intelligent Systems for Molecular Biology (ISMB)*, Madison, WI, USA, July 10-14, 2022.

CCT-58 K. Newaz, J. Piland, P. Clark, S. Emrich, J. Li, and T. Milenković, "Multi-layer networks improve protein structural classification," *International Conference on Intelligent Systems for Molecular Biology (ISMB)*, Madison, WI, USA, July 10-14, 2022.

CCT-57 K. Newaz, J. Piland, P. Clark, S. Emrich, J. Li, and T. Milenković, "Dynamic networks improve protein structural classification," *International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB)*, held virtually, July 25-30, 2021.

CCT-56 S. Gu, M. Jiang, P.H. Guzzi, and T. Milenković, "Modeling multi-scale -omics data via a network of networks," *International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB)*, held virtually, July 25-30, 2021.

CCT-55 S. Gu and T. Milenković, "Data-driven network alignment that integrates within- and across-network information," *Networks 2021 – A Joint Conference of Sunbelt and NetSci*, held virtually, July 5-10, 2021.

CCT-54 Q. Li, K. Newaz, and T. Milenković, "Supervised prediction of aging-related genes from a weighted dynamic protein-protein interaction network," *Great Lakes Bioinformatics Conference (GLBIO)*, held virtually, May 10-12, 2021.

CCT-53 S. Gu and T. Milenković, "Data-driven biological network alignment that uses topological, sequence, and functional information," *Great Lakes Bioinformatics Conference (GLBIO)*, held virtually, May 10-12, 2021.

CCT-52 V. Vijayan, S. Gu, E. Krebs, L. Meng, and T. Milenković, "Pairwise versus multiple global network alignment," **highlights talk** at *ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)*, held virtually, September 21-24, 2020.

CCT-51 Q. Li, S. Liu, and T. Milenković, "Dynamic network analysis reveals a protein's role in aging and a person's risk of mental health problems," *Centrality in Networks: Structural and Dynamical Aspects (NetCent) Satellite at the Network Science Society Conference (NetSci)*, held virtually, September 17-25, 2020.

CCT-50 K. Newaz, M. Ghalehnovi, A. Rahnama, G. Wright, J. Piland, P.J. Antsaklis, J. Li, P.L. Clark, S.J. Emrich, and T. Milenković, "A network science approach towards studying protein folding," *Network Science Society Conference (NetSci)*, held virtually, September 17-25, 2020.

CCT-49 S. Gu, V. Vijayan, E. Krebs, L. Meng, and T. Milenković, "Pairwise versus multiple global network alignment," *Network Science Society Conference (NetSci)*, held virtually, September 17-25, 2020.

CCT-48 Q. Li and T. Milenković, "Supervised prediction of aging-related genes from a dynamic context-specific protein interaction subnetwork," *International Conference on Intelligent Systems for Molecular Biology (ISMB)*, held virtually, July 13-16, 2020.

CCT-47 K. Newaz, G. Wright, J. Piland, J. Li, P.L. Clark, S.J. Emrich, and T. Milenković, "Network analysis of synonymous codon usage," *International Conference on Intelligent Systems for Molecular Biology (ISMB)*, held virtually, July 13-16, 2020.

CCT-46 S. Liu, D. Hachen, O. Lizardo, C. Poellabauer, A. Striegel, and T. Milenković, "The power of dynamic social networks to predict individuals' mental health," *Pacific Symposium on Biocomputing (PSB)*, the Big Island of Hawaii, HI, USA, January 3-7, 2020.

CCT-45 Q. Li and T. Milenković, "Supervised prediction of aging-related genes from a context-specific protein interaction subnetwork," *IEEE International Conference on Bioinformatics and Biomedicine (IEEE BIBM)*, San Diego, CA, USA, November 18-21, 2019.

CCT-44 S. Gu and T. Milenković, "Data-driven network alignment," *International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB)*, Basel, Switzerland, July 21-25, 2019.

CCT-43 K. Newaz, G. Wright, J. Li, P.L. Clark, S.J. Emrich, and T. Milenković, "Network analysis of synonymous codon usage," *Great Lakes Bioinformatics Conference (GLBIO)*, Madison, WI, May 19-22, 2019.

CCT-42 F.E. Faisal, K. Newaz, J. L. Chaney, J. Li, S.J. Emrich, P.L. Clark, and T. Milenković, "GRAFENE: Graphlet-based alignment-free network approach integrates 3D structural and sequence (residue order) data to improve protein structural comparison," *the International Workshop on Data Mining in Bioinformatics (BIOKDD) at the ACM SIGKDD 2018 Conference on Knowledge Discovery and Data Mining (KDD)*, London, UK, August 19-23, 2018.

CCT-41 S. Gu, J. Johnson, F. Faisal, and T. Milenković, "From homogeneous to heterogeneous network alignment," *International Conference on Intelligent Systems for Molecular Biology (ISMB)*, Chicago, IL, USA, July 6-10, 2018.

CCT-40 K. Newaz, F.E. Faisal, J. L. Chaney, J. Li, S.J. Emrich, P.L. Clark, and T. Milenković, "Network approach integrates 3D structural and sequence data to improve protein structural comparison," *International Conference on Intelligent Systems for Molecular Biology (ISMB)*, Chicago, IL, USA, July 6-10, 2018.

CCT-39 J. Crawford, Y. Hulovatyy, and T. Milenković, "New computational directions for community detection in dynamic networks," *the International School and Conference on Network Science (NetSci)*, Paris, France, June 11-14, 2018.

CCT-38 A. Rahnama, K. Newaz, P. Antsaklis and T. Milenković, "Network-based protein structural classification," *Machine Learning in Network Science (MLNS) Satellite at the International School and Conference on Network Science (NetSci)*, Paris, France, June 11-14, 2018.

CCT-37 S. Gu, J. Johnson, F.Faisal, and T. Milenković, "Integrating topology and metadata in heterogeneous networks," *Machine Learning in Network Science (MLNS) Satellite at the International School and Conference on Network Science (NetSci)*, Paris, France, June 11-14, 2018.

CCT-36 S. Liu, D. Hachen, O. Lizardo, C. Poellabauer, A. Striegel, and T. Milenković, "Exploring co-evolution of individuals' social networks and physical activities," *More Than Complex: Large and Rich Network Structures Workshop at the International School and Conference on Network Science (NetSci)*, Paris, France, June 11-14, 2018.

CCT-35 S. Gu and T. Milenković, "From Homogeneous to Heterogeneous Network Alignment," *International Workshop on Heterogeneous Network Analysis and Mining (HeteroNAM) at the International Conference on Web Search and Data Mining (WSDM)*, Los Angeles, CA, USA, February 5-9, 2018.

CCT-34 V. Vijayan, D. Critchlow, and T. Milenković, "Alignment of dynamic networks," *International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB)*, Prague, Czech Republic, July 21–25, 2017.

CCT-33 V. Vijayan and T. Milenković, "Network alignment: latest insights," *International School and Conference on Network Science (NetSci)*, Indianapolis, IN, USA, June 19–23, 2017.

CCT-32 S. Gu and T. Milenković, "From Homogeneous to Heterogeneous Network Alignment," *Networks of Networks (Netonets) Satellite in conjunction with International School and Conference on Network Science (NetSci)*, Indianapolis, IN, USA, June 19–23, 2017.

CCT-31 V. Vijayan and T. Milenković, "Alignment of dynamic networks," *Network Models in Cellular Regulation (NetSciReg) Satellite in conjunction with International School and Conference on Network Science (NetSci)*, Indianapolis, IN, USA, June 19–23, 2017.

CCT-30 K. Newaz and T. Milenković, "Inference of the dynamic protein-protein interaction network in the context of aging," *Quantitative Interactome and Multilayer Networks Taking Medicine Beyond the Genome (NetMed) Satellite in conjunction with International School and Conference on Network Science (NetSci)*, Indianapolis, IN, USA, June 19-23, 2017.

CCT-29 S. Gu and T. Milenković, "From Homogeneous to Heterogeneous Network Alignment," *Great Lakes Bioinformatics Conference (GLBIO)*, Chicago, IL, USA, May 15-17, 2017.

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

CCT-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)*, Orlando, FL, USA, July 8-12, 2016.

CCT-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.

CCT-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.

CCT-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.

CCT-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.

CCT-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.

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

CCT-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.

CCT-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.

CCT-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.

CCT-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.

CCT-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.

CCT-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.

CCT-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.

CCT-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.

CCT-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.

CCT-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.

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

CCT-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.

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

CCT-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.

CCT-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.

CCT-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.

CCT-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.

CCT-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.

CCT-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.

CCT-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

SOME HIGHLIGHTS:

– Prof. T. Milenković has acted as the sole Principal Investigator (PI) on 5 NSF awards (including CAREER) and an AFOSR (YIP) award, and as the lead PI on a collaborative NIH (R01) award that spans four different disciplines (i.e., research groups) across different colleges and universities. This illustrates (i) the versatility of Prof. T. Milenković's funding portfolio in terms of funding agencies, (ii) that she has a strong independent research program, and (iii) that she has taken on a leadership role in the multidisciplinary NIH-funded project.

– Prof. T. Milenković has also acted as a co-PI or key personnel on 8 other collaborative awards from NSF, NIH, IARPA, or Google, plus a collaborative gift from NTX Bio.

This illustrates that she has actively sought and been involved in interdisciplinary collaborations, both within her Computer Science and Engineering (CSE) Department at the University of Notre Dame and outside of it.

– Of the above 16 grants from **external** funding sources, 12 are research-focused. The remaining 4 are a conference organizational grant, a conference travel grant, an equipment grant, and an REU site grant. The first two illustrate Prof. T. Milenković's service-related leadership in her research community, the third one illustrates her dedication to strengthen the CSE Department's/Notre Dame University's computing infrastructure, and the last one illustrates her commitment to integration of research and education.

– Prof. Milenković has also participated in 2 "Moment to See, Courage to Act" cluster planning grants awarded **internally** by the University of Notre Dame.

As Principal Investigator (PI):

18. Title: Workshop on Future Directions in Network Biology
    Source of Support: NSF
    Grant Type/Number: CCF-1941447
    Award Period: October 2019–September 2022
    Personnel: T. Milenković (PI)
    Award Amount: $56, 821
    Amount Awarded to Milenković Lab: $56, 821

17. Title: NSF Student Travel Grant for 2019 Great Lakes Bioinformatics Conference (GLBIO)
    Source of Support: NSF
    Grant Type/Number: CCF-1917325
    Award Period: April 2019–March 2020
    Personnel: T. Milenković (PI)
    Award Amount: $10, 000
    Amount Awarded to Milenković Lab: $10, 000

16. 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 2021
    Personnel: T. Milenković (lead PI), P.L. Clark (PI), S.J. Emrich (PI), J. Li (PI)
    Award Amount: $1, 139, 130
    Amount Awarded to Milenković Lab: $339, 160

15. Title: Efficient Comparison of Multiple Complex Networks
    Source of Support: Air Force Office of Scientific Research
    Grant Type/Number: Young Investigator Program (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

14. 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 2022
Personnel: T. Milenković (PI)
Award Amount: $540,000
Amount Awarded to Milenković Lab: $540,000

13. Title: AF: Small: Novel Directions for Biological Network Alignment
Source of Support: NSF
Grant Type/Number: CCF-1319469
Award Period: July 2013–June 2017
Personnel: T. Milenković (PI), M. Ferdig (key personnel)
Award Amount: $452,863
Amount Awarded to Milenković Lab: $421,713

12. 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):

11. 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 2020
Personnel: O. Lizardo (lead PI), N. Chawla (co-I), D. Hachen (co-I), T. Milenković (co-I), Jessica Payne (co-I), C. Poellabauer (co-I), A. Striegel (co-I)
Total Award Amount: $2,913,061
Amount Awarded to Milenković Lab: ∼$125,000

10. 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:

9. Title: Notre Dame Inclusive Health Initiative: The role of fundamental sciences in achieving inclusive health outcomes
Source of Support: University of Notre Dame
Grant Type/Number: "Moment to See, Courage to Act" cluster planning
Award Period: 2021/2022
Personnel: A number of faculty across different colleges at the university, including T. Milenković
Total Award Amount: $25,000
Amount Awarded to Milenković Lab: N/A

8. Title: Data+Science+Crossroads
   Source of Support: University of Notre Dame
   Grant Type/Number: "Moment to See, Courage to Act" cluster planning
   Award Period: 2021/2022
   Personnel: A number of faculty across different colleges at the university, including T. Milenković
   Total Award Amount: $25,000
   Amount Awarded to Milenković Lab: N/A

7. Title: N-DISTANCE: Notre Dame Identification and Social Transmission Advice and Navigation for Covid-19 Evasion
   Source of Support: IARPA
   Grant Type/Number: Seedling
   Award Period: April 2021–August 2021
   Personnel: A. Striegel (lead PI), I. Adjerid (PI at Virginia Tech), C. Angst (co-PI), T. Jung (senior personnel), R, Metoyer (senior personnel), T. Milenković (senior personnel)
   Total Award Amount: $411,275
   Amount Awarded to Milenković Lab: ∼$7,000

6. Title: Natural Products go AI
   Source of Support: NTX Bio
   Grant Type/Number: Gift
   Award Period: 1/6/2019 - 1/31/2024
   Personnel: W. Scheirer (PI), T. Milenković (key personnel)
   Award Amount: $372,634
   Amount Awarded to Milenkovic Lab: $99,226

5. Title: Harnessing the power of experimental genetic crosses and systems genetics to probe drug resistance in malaria
   Source of Support: NIH
   Grant Type/Number: 1P01AI127338-01A1
   Award Period: August 2017–July 2024
   Personnel: M. Ferdig (lead PI), T. Milenković (key personnel), and others
   Total Award Amount: $11,488,257
   Amount Awarded to Milenković Lab: ∼$10,000

4. Title: II-New: Infrastructure for Supporting Biomedical Application Algorithms, Run-time 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: ∼$16,000

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.L. 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

### Some Highlights

- Prof. T. Milenković has provided research supervision to 15 graduate students, a post-doc, 28 undergraduate students, and a high school student.
- To date, Prof. T. Milenković graduated 9 Ph.D. students and 5 M.Sc. students.
- 7 of the undergraduates have continued onto Ph.D. programs at e.g., Stanford, MIT, Carnegie Mellon, or Brown University. 5 have already earned their Ph.D. degrees. All 5 have continued to academia, 4 as faculty, and 1 as a research scientist.
- Prof. T. Milenković has published 13 journal and 6 conference papers with the undergraduates. 6 of the papers have been first-authored by the undergraduates.
- During 2014-2018, when Prof. T. Milenković has been the most active in undergraduate student supervision, of all 6 Notre Dame College of Engineering's Steiner Award winners in the Computer Science and Engineering (CSE) Department, 4 (67%) were Prof. T. Milenković's undergraduate researchers.
- Prof. T. Milenković is one of only two winners of the CRA-E Undergraduate Research Faculty Mentoring Award the US in 2021. This award recognizes faculty members who have provided exceptional mentorship, undergraduate research experiences, and, in parallel, guidance on admission and matriculation of these students to research-focused graduate programs in computing.

### Current Ph.D. Students

- **Aydin Wells** (January 2023–current; ISMB 2024 travel fellowship; CNB-MAC @ ACM BCB 2023 travel fellowship; Lucy Graduate Scholar, Lucy Family Institute for Data and Society, University of Notre Dame, 2023-2025; faculty choice best research poster award, Department of Computer Science and Engineering, University of Notre Dame, 2023; outstanding teaching assistant, Department of Computer Science and Engineering, University of Notre Dame, 2023; note: started as M.Sc. student in August 2022 and then transferred to Ph.D. program in January 2023).

CURRENT UNDERGRADUATE STUDENT RESEARCHERS

- **Eve Goodrow** (January 2025–current).

FORMER POSTDOCTORAL RESEARCHERS:

- **Fatemeh Vahedian** (July 2018–June 2019; continued to work as a postdoctoral researcher in the Department of Computational Medicine and Bioinformatics at the University of Michigan, Ann Arbor).

GRADUATED PH.D. STUDENTS:

- **Joseph Crawford** (Continued to work at Lowe's Home Improvement starting September 2019; defended his Ph.D. dissertation titled "Discovering important patterns across and within networks via network alignment and clustering" in May 2019; the Bank of New York Mellon internship in summer 2017; advanced to Ph.D. candidacy in May 2017; best poster award (2nd place) at the 2016 Richard Tapia Celebration of Diversity in Computing Conference in Austin, TX; recipient of a Dean's fellowship; IEEE BIBM 2015, ACM BCB 2015, and ISMB 2014 travel fellowship).

- **Fazle Faisal** (Continued to work at Microsoft starting August 2016; defended his Ph.D. dissertation titled "New network analysis approaches and their computational biology applications, with focus on dynamic network analysis and network comparison" 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).

- **Shawn Gu** (Continued to work at the Nielsen Corporation starting February 2022; defended his Ph.D. dissertation titled "Novel computational approaches for multi-network analysis to improve protein function prediction" in January 2022; recipient of a Dean's fellowship, 2016-2021; NetSci 2020 registration fellowship; ISMB 2020 registration fellowship; advanced to Ph.D. candidacy by defending his Ph.D. proposal titled "Novel computational approaches for multi-network analysis to improve across-species protein function prediction" in April 2020; member of the Graduate Student Board, Department of Computer Science and Engineering, University of Notre Dame, 2018/2019; ISMB 2018 travel fellowship; honorable mention teaching assistant award, Department of Computer Science and Engineering, University of Notre Dame, 2017).

- **Yuriy Hulovatty** (Continued to work at Facebook starting July 2016; defended his Ph.D. dissertation titled "Exploring structure and dynamics of complex networks: novel methods and interdisciplinary applications" in May 2016; outstanding research assistant 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).

- **Qi Li** (Continued to work at Meta (Facebook) Research starting May 2022; defended her PhD disertation titled "New network biology approaches towards advancement of understanding aging and malaria from -omics data" in March 2022; advanced to Ph.D. candidacy in May 2021; Outstanding Graduate Student Teacher Award, University of Notre Dame, 2021; NetSci 2020 registration fellowship; ISMB 2020 registration fellowship; IEEE BIBM 2019 travel fellowship; GLBIO 2019 travel fellowship).

– **Lei Meng** (Co-supervised with Prof. Aaron Striegel; continued to work at Google starting April 2016; defended her Ph.D. dissertation titled "Computational strategies for analyzing dynamic and heterogeneous networks and their interdisciplinary implications" in March 2016; advanced to Ph.D. candidacy in May 2014, Notre Dame's Graduate Student Union travel fellowship for ISMB/ECCB 2015).

– **Khalique Newaz** (August 2015–July 2021; continued to work as a postdoctoral researcher at University of Hamburg starting October 2021; defended his Ph.D. dissertation titled "Novel network science approaches for a better understanding of protein folding and human aging" in July 2021; NetSci 2020 registration fellowship; ISMB 2020 registration fellowship; advanced to Ph.D. candidacy by defending his Ph.D. proposal titled "Novel network science approaches for deepening our understanding of protein folding and human aging" in May 2019).

– **Vipin Vijayan** (Continued to work at Riverside Research starting December 2017; defended his Ph.D. dissertation titled "Novel algorithmic contributions and evaluation frameworks for network alignment with applications in computational biology" in March 2017; 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; ISMB/ECCB 2017 travel fellowship).

– **Gabriel Wright** (Co-supervised with Prof. Scott J. Emrich; continued to work as an Assistant Professor at the Milwaukee School of Engineering starting August 2021; defended his Ph.D. dissertation titled "Computational analyses of codon usage bias and its effects on protein translation, expression, and folding" in March 2021; Instructor of record, Department of Computer Science and Engineering, University of Notre Dame, spring 2021 semester; recipient of a Schmitt Fellowship, 2016-2020; First-Year Engineering Teaching Apprentice, 2019/2020; advanced to Ph.D. candidacy by defending his Ph.D. proposal titled "Computational analyses of codon usage bias and its effects on protein folding, function, and expression" in September 2019; honorable mention teaching assistant award, Department of Computer Science and Engineering, University of Notre Dame, 2017).

GRADUATED M.SC. STUDENTS:

– **Mahboobeh Ghalehnovi** (Defended her M.Sc. thesis titled "Novel computational approaches for network-based protein structural classification" in May 2019).

– **Shikang Liu** (Defended his M.Sc. thesis titled "Heterogeneous network approach for analyzing NetHealth data: Linking individuals' social interaction, personality, physical health, and mental health data" in June 2019; PSB 2020 travel fellowship; Notre Dame's Graduate Student Union travel fellowship for NetSci 2018).

– **Jacob Piland** (Defended his M.Sc. thesis titled "Network-based approaches to understanding protein structure and folding" in August 2021; GLBIO 2019 travel fellowship).

– **Famim Talukder** (Graduated with a M.Sc. project in May 2019).

– **Siyu Yang** (August 2022–December 2024).

FORMER (NOTRE DAME) UNDERGRADUATE STUDENT RESEARCHERS:

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

– **Natalie Alvarez** (January 2017–May 2018).

– **Erin Bradford** (January 2016–May 2016).

- **Elias Chahoud** (January 2020–May 2022; continued onto M.D. at Indiana University; Glynn Family Honors Program thesis under Milenković's supervision, May 2022; recipient of NSF REU funding, 2020).
- **Huili Chen** (January 2013–December 2014; continued onto M.Sc. and then Ph.D. at MIT, followed by serving as a Fellow at the Harvard Berkman Klein Center for Internet and Society at Harvard University; recipient of the 2016 Steiner Award, College of Engineering, University of Notre Dame – the only winner in the Department of Computer Science and Engineering; 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).
- **Frank Gomulka** (January 2020–November 2020; recipient of NSF REU funding, 2020).
- **Taryn Green** (January 2012–May 2013; recipient of the 2014 Steiner Award, College of Engineering, University of Notre Dame – the only winner in the Department of Computer Science and Engineering, University of Notre Dame; recipient of a Grace Hopper Conference 2013 Scholarship).
- **Casey Hanley** (January 2014–May 2014).
- **John Johnson** (January 2016–May 2018; recipient of the 2018 Steiner Award, College of Engineering, University of Notre Dame – one of only two winners in the Department, the other being Eric Krebs below).
- **Eric Krebs** (January 2016–December 2016; recipient of the 2018 Steiner Award, College of Engineering, University of Notre Dame – one of only two winners in the Department, the other being John Johnson above; recipient of NSF REU supplemental funding, 2016).
- **Jennifer Long** (January 2014 – December 2015).
- **Ryan Mackey** (January 2016–May 2016; January 2017–May 2017).
- **Antwane Mason** (August 2011–May 2012; continued onto Ph.D. at Rensselaer Polytechnic Institute).
- **Ronan McCarter** (January 2020–July 2020; recipient of NSF REU funding, 2020).
- **Simran Moolchandaney** (February 2021–December 2021).
- **Jennifer Moronoes** (May 2023–December 2024; recipient of Summer 2023 Enrichment Program funding, Department of Computer Science and Engineering, University of Notre Dame).
- **Vikram Saraph** (August 2011–May 2013; continued onto Ph.D. at Brown University, and then after earning his Ph.D. degree in 2019, onto a Senior Professional Staff position in the Applied Physics Laboratory at the Johns Hopkins University; honors senior thesis under Milenković's supervision, May 2013; recipient of a UPE Scholarship; ISMB 2014 travel fellowship).
- **Ryan Solava** (January 2011–May 2012; continued onto Ph.D. at Vanderbilt University, and then after earning his Ph.D. degree in 2019, onto an Assistant Professor position in the Department of Mathematics and Computer Science at St. Mary's College; recipient of a Notebaert Premier Fellowship at the University of Notre Dame).
- **Nicholas Taylor** (January 2012–December 2012).
- **Jonathan Xu** (January 2017–May 2017).
- **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).

– **Hind Zahour** (May 2020–July 2020; recipient of a Reilly undergraduate research fellowship, University of Notre Dame, 2020; recipient of NSF REU funding, 2020).

Former external (non-Notre Dame) undergraduate student researchers
(Undergraduates who co-authored Milenković's publications are underlined. )

– **Kendrea Beers** (May 2018–July 2018; NSF's DISC REU program, summer 2018).
– **Dominic Critchlow** (May 2016–July 2016; NSF's DISC REU program, summer 2016).
– **Jon Genty** (May 2018–July 2018; NSF REU funding, summer 2018).
– **Kimberly Orr** (May 2017–July 2017; NSF's DISC REU program, summer 2017).
– **Yihan Sun** (Continued onto Ph.D. at Carnegie Mellon University, and then after earning her Ph.D. degree in 2019, onto an Assistant Professor position in the Department of Computer Science and Engineering at the University of California, Riverside; iSure Program between University of Notre Dame and Tsinghua University, summer 2013).
– **Han Zhao** (Continued onto Ph.D. at Carnegie Mellon University, and then after earning his Ph.D. degree in 2020, onto an Assistant Professor position in the Department of Computer Science at the University of Illinois at Urbana-Champaign; iSure Program between University of Notre Dame and Tsinghua University, summer 2012).

Former high school student researchers

– **Hannah Kovac** (June 2019–August 2019).

Teaching

Graduate Courses:

10. CSE 60884: Network Science, University of Notre Dame, Fall 2020.
    Enrollment: 27 students.
 9. CSE 60111: Complexity and Algorithms, University of Notre Dame, Spring 2019.
    Enrollment: 29 students.
 8. CSE 60884: Network Science, University of Notre Dame, Fall 2018.
    Enrollment: 26 students.
 7. CSE 60884: Network Science, University of Notre Dame, Spring 2017.
    Enrollment: 25 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:

22. CSE 20110: Discrete Mathematics, University of Notre Dame, Spring 2025.
    Enrollment: 24 students.
21. CSE 40113: Design/Analysis of Algorithms, University of Notre Dame, Spring 2024.
    Enrollment: 49 students.
20. CSE 20110: Discrete Mathematics, University of Notre Dame, Fall 2022.
    Enrollment: 157 students.
19. CSE 20110: Discrete Mathematics, University of Notre Dame, Fall 2021.
    Enrollment: 148 students.
18. CSE 40113: Design/Analysis of Algorithms, University of Notre Dame, Spring 2021.
    Enrollment: 48 students.
17. CSE 40884: Network Science, University of Notre Dame, Fall 2020.
    Enrollment: 27 students.
16. CSE 20110: Discrete Mathematics (Section 02), University of Notre Dame, Fall 2019.
    Enrollment: 79 students.
15. CSE 20110: Discrete Mathematics (Section 01), University of Notre Dame, Fall 2019.
    Enrollment: 73 students.
14. CSE 40884: Network Science, University of Notre Dame, Fall 2018.
    Enrollment: 26 students.
13. CSE 40884: Network Science, University of Notre Dame, Spring 2017.
    Enrollment: 25 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: 143 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 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.

– CSE 40884/60884 Network Science (formerly called Complex Networks): 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 40113 Design/Analysis of Algorithms: Required senior undergraduate-level course on techniques for designing efficient computer algorithms and for analyzing computational costs of algorithms. Common design strategies such as dynamic programming, divide-and-conquer, and greedy methods. Problem-solving approaches such as sorting, searching, and selection; lower bounds; data structures; algorithms for graph problems; geometric problems; and other selected problems. Computationally intractable problems (NP-completeness).

– CSE 60111 Complexity and Algorithms: Required graduate-level course on studying the theoretical foundations of computer science and a selection of important algorithmic techniques. One of the main goals is to teach graduate students in computer science and engineering the basic theory of computational complexity and the techniques for dealing with computationally intractable problems. Another goal is to introduce the students to a variety of fundamental algorithmic techniques that are useful in solving computational problems arising in research and applications.

– CSE 40543/60543 Algorithms for Biological Networks: Similar to CSE 40884/60884, but focusing exclusively on biological network research.

PROFESSIONAL SERVICE

**Member of the Board of Directors of the International Society for Computational Biology (ISCB)**, 2020-2026. One of three Communities of Special Interest (COSI) representatives to the Board. The only COSI representative to the Board elected in 2019 and re-elected in 2022. One of ∼25 Directors on the Board who, as volunteer leaders, are responsible for the direction and future of the ISCB toward the advancement of the understanding of living systems through computation.

**Associate Editor** for:
Frontiers in Bioinformatics – Network Bioinformatics, 2020–current.
Scientific Reports, 2018–2021.
IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014–2023.

**Conference organization**

<u>Key roles:</u>

***Proceedings Co-Chair for Intelligent Systems for Molecular Biology (ISMB) 2024 and Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB) 2025***. This role is a critical component to the scientific program of the flagship meeting of the International Society for Computational Biology (ISCB). Primary responsibilities: oversee and manage the proceedings submission process and publication of the accepted papers for the flagship meeting of ISCB, by working with Area Chairs covering different scientific areas to secure sufficient reviewers prior to paper submission and supervise the reviewing of the papers in the given area to ensure high-quality reviews; make final decisions on which papers to accept; work with the Bioinformatics journal to publish the accepted papers; serve on the Steering Committee for ISMB 2024 and ISMB/ECCB 2025. For illustration of effort required by this role (estimated at 1.5 months per conference offering): For ISMB 2024, i.e., during 2023/2024, Prof. Milenković and another Proceedings Co-Chair oversaw and managed 23 Area Chairs covering 11 scientific areas, 318 submitted and 58 accepted papers, and 350+ Program Committee members plus 300+ external reviewers (aka subreviewers). For ISMB/ECCB 2025, i.e., during 2024/2025, Prof. Milenković and another Proceedings Co-Chair oversaw and managed 23 Area Chairs covering 11 scientific areas, 395 submitted and 67 accepted papers, and 400+ Program Committee members plus 450+ external reviewers (aka subreviewers).

***Area Co-Chair for the "Systems Biology and Networks" area at Intelligent Systems for Molecular Biology (ISMB) 2022 and Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB) 2023***. Primary responsibilities: to help secure sufficient reviewers prior to paper submission, to coordinate the reviewing of the papers in the given area and help ensure high-quality reviews, and to make recommendations on which papers to accept. In 2023, this role required managing 52 submitted papers and a 53-member Program Committee for the "Systems Biology and Networks" area. In 2022, this role required managing 28 submitted papers and a 56-member Program Committee.

***Co-organizer of Network Biology (NetBio) Community of Special Interest (COSI) at Intelligent Systems for Molecular Biology (ISMB), 2017-2023***. During 2020-2023, Prof. T. Milenković took two key leadership roles: (i) the NetBio COSI Track Chair and (ii) the NetBio COSI Proceedings Liaison. Starting with 2023, Prof. Milenkovic has been a member of the NetBio COSI Steering Committee.

- NetBio COSI at ISMB is *the* flagship international meeting for the network biology community.
- COSI Track Chair(s): This person(s) is responsible for the scientific program development of the ISMB COSI Track. They will be the recipients of all communications regarding the building of the scientific program, responsible for the review of the abstracts submitted to the COSI, and the delivery of the program to ISCB. This may be more than one person. COSI chair(s) will work with the COSI Proceedings Liaison to ensure the inclusion of the proceedings talks within the overall COSI program.
- COSI Proceedings Liaison: This is the lead person responsible for interacting with the Senior Proceedings Committee in regards to the ISMB proceedings submissions, reviews, and selection of papers accepted as proceedings for the COSI Tracks. They will be the main point of contact throughout the selection of the proceedings. During the proceedings submission and review process, they may be asked to volunteer reviewer names.

This person will be responsible for accepting the final list of papers to be presented in the COSI track and communicating any necessary information back to the rest of their ISMB organizing group.

***Co-organizer of the Great Lakes Bioinformatics Conference (GLBIO), 2015-2021***. For all GLBIO offerings, Prof. T. Milenković held a role of the Publications co-Chair. Also, in 2019, she held an additional role of the Travel Fellowship Chair (NSF award CCF-1917325 on which she is the sole Principal Investigator funded GLBIO 2019 participation for 33 students).

***Member of the Steering Committee*** for:
Intelligent Systems for Molecular Biology (ISMB), 2023-current.
Network Biology (NetBio) Community of Special Interest (COSI), 2023-current.
Great Lakes Bioinformatics Conference (GLBIO), 2022-current.

Other conference organizational roles:

Invited co-organizer of the Network Biology Course at the Summer Institute for Network Science and its Applications (SINSA) 2020. Canceled due to COVID-19.
Co-organizer of Network Medicine Satellite Meeting at International School and Conference on Network Science (NetSci) 2017.
Workshop co-organizer at European Conference on Computational Biology (ECCB) 2016, Hague, Netherlands, September 3-7, 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.)
"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:
(Note that starting 2022, rather than serving on conference program committees per se, as listed above, Prof. Milenković has taken on higher-level roles that include managing conference program committees.)
ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM BCB) 2021.
International Conference on Intelligent Systems for Molecular Biology (ISMB) 2020.
ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM BCB) 2019.
International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB) 2019.
International Conference on Intelligent Systems for Molecular Biology (ISMB) 2018.
International Conference on Research in Computational Molecular Biology (RECOMB) 2018.
International Conference on Research in Computational Molecular Biology (RECOMB) 2017.
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
ACM Transactions on Knowledge Discovery from Data
Integrative Biology
Internet Mathematics
Journal of the Royal Society Interface
Molecular Genetics and Genomics
Nature Communications
Nature Partner Journals (npj) Systems Biology and Applications
Pattern Recognition Letters
Patterns (Cell)
PLOS Computational Biology
PLOS ONE
PLOS Pathogens

**Government grant proposal reviewing**:
The National Science Foundation (NSF) panelist for Computer & Information Science & Engineering (CISE) Computing and Communication Foundations (CCF) program, 2019.

The National Science Foundation (NSF) panelist for Computer & Information Science & Engineering (CISE) Information and Intelligent Systems (IIS) program, 2019.

The National Institutes for Health (NIH) panelist for the Transformative Research Award

(TRA) initiative, 2019.

The National Institutes for Health (NIH) panelist for Biodata Management and Analysis (BDMA) study section, 2018.

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, 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.

**Outreach**:

Workshop organizer and presenter at the "Expanding Your Horizons (EYH) in Science and Mathematics" career conference for middle school girls, annually during 2012-2019 and in 2023. To date, Prof. Milenković interacted with over 400 girls to help attract them to future careers in Computer Science and Engineering. Of all girls, about a third were ethnic minorities. While 16% of all girls had already been positive about their future career possibilities, additional 47% of the girls indicated that because of EYH they also became positive.

Mentor for the Building Bridges Program by Multicultural Student Programs and Services at University of Notre Dame, 2016-2019 and 2021-2023.

Panelist for a meeting organized by Society of Women Engineers (SWE) at University of Notre Dame, September 2016, November 2017, November 2020, November 2022.

Organizer of the Computer Science and Engineering ice cream event at the stadium in celebration of the 50th anniversary of co-education at the University of Notre Dame, August 2022.

Participant in two College of Engineering events (college-wide stadium photo and t-shirt event, and graduate student-focused high tea event) in celebration of the 50th anniversary of co-education at the University of Notre Dame, August 2022.

Panelist at the Future Faculty Workshop, Colleges of Engineering and Science, University of Notre Dame, May 2022.

Speaker at a luncheon organized by the Association of Women in Science (AWIS STEM) at University of Notre Dame, March 2022.

Speaker at the "First Lecture", College of Engineering, University of Notre Dame, August 2021.

Panelist for a meeting organized by Graduate Society of Women Junior Faculty Promotion and Tenure Panel, College of Engineering, University of Notre Dame, March 2020.

Women Engineering Faculty Panel organized for graduate students in the College of Engineering, University of Notre Dame, March 2020.

Educational collaboration with John Adams high school in South Bend, IN, 2014-2016.

Mentor for the University of Notre Dame College of Engineering's Freshman Merit Scholar Program, 2018-2019.

Panelist for the "Tenure Track Master Plan" event organized by the Postdoctoral Women's Committee at University of Notre Dame, July 2017.

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.

**Member of the Selection Committee for the CRA-E Undergraduate Research Faculty Mentoring Award**, Computing Research Association – Education, 2023.

**Member of the International Society for Computational Biology (ISCB) Equity, Diversity and Inclusion Committee**, 2020-2025. The committee's mission is to (i) identify the inclusion strengths, issues, and opportunities within all aspects of ISCB, (ii) develop strategies and plans to examine ways in which we include and exclude (however unintentionally) ISCB members, (iii) systematically examine aspects of ISCB to enhance its effectiveness and ability to meet the needs of its diverse membership, and (iv) respectfully document the successes of inclusivity approaches.

**Member of the University Committee on Women Faculty and Students**, University of Notre Dame, 2018-2021. The committee acted on topics such as the level of service for different faculty (e.g., those of different ranks), parental leave policy, faculty experience survey, graduate student grievances, or involving more faculty into University's innovation, entrepreneurship, and commercialization efforts.

**Director of Inclusive Excellence and Engagement, Department of Computer Science and Engineering**, University of Notre Dame, 2025-2025.

**Director of Diversity, Equity, and Inclusion, Department of Computer Science and Engineering**, University of Notre Dame, 2022-2025.

**Diversity and Inclusion Representative, Department of Computer Science and Engineering**, University of Notre Dame, 2019-2021. As a part of this appointment, Prof. T. Milenković has led a task force on improving the departmental climate for graduate students. Further, with the College's Associate Dean of Diversity and Special Initiatives, Prof. T. Milenković has worked with faculty in her Department to identify faculty across the United States who could be good targeted hires, as well as to invite finishing Ph.D. students and postdocs to the College's Future Faculty Workshop, which aims to provide mentorship to attendees on near-future job search and career success. Moreover, in coordination with the College's Director of Women in Engineering, Prof. T. Milenković periodically hosted lunches with College's faculty to discuss how to improve faculty retention at the University.

**Chair of the Computer Science and Engineering (CSE) Committee on Inclusive Excellence and Engagement**, University of Notre Dame, 2025-2025.

**Chair of the Computer Science and Engineering (CSE) Committee on Diversity, Equity and Inclusion**, University of Notre Dame, 2022-2025.

**Member of the College of Engineering Committee on Inclusive Excellence and Engagement**, University of Notre Dame, 2025-2025.

**Member of the College of Engineering Committee on Diversity, Equity and Inclusion**, University of Notre Dame, 2022-2025.

**Member of the Notre Dame College of Engineering Task Force on Diversity, Equity and Inclusion**, 2020-2021. This task force was in charge of examining and suggesting improvements in various areas related to diversity, equity, and inclusion in the College of Engineering, including the College's climate for all of its members, recruitment and retention of students and faculty, and course curricula.

**Member of the Bioengineering and Life Sciences (BELS) Research Strategy Committee**, University of Notre Dame, 2024-current.

**Member of the Research II Building Committee**, University of Notre Dame, 2021-2022.

**Member of the Task Force 1 – "Grand Challenges" – for the Health and Well-being Initiative**, University of Notre Dame, 2018-2019.

**Member of the Bioinformatics Working Group** initiated by the Vice President for Research, University of Notre Dame, 2018-2019.

**Member of the Steering Committee, Lucy Family Institute for Data and Society**, University of Notre Dame, 2021-2023.

**Member of the Steering Committee, Center for Research Computing**, University of Notre Dame, 2022-2025.

**Faculty search committee member** for four positions, Department of Computer Science and Engineering (CSE), University of Notre Dame, 2021/2022.

**Faculty search committee member** for three positions, Department of Computer Science and Engineering (CSE), University of Notre Dame, 2020/2021.

**Faculty search committee member** for two positions, Department of Computer Science and Engineering (CSE), University of Notre Dame, 2019/2020.

**Faculty search committee member**, the Data Analytics "Advancing Our Vision" (AOV) Initiative, 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.

**Awards committee member**, Department of CSE, University of Notre Dame, 2023/2024 and 2024/2025.

**Graduate studies committee member**, Department of CSE, University of Notre Dame, 2022/2023, 2018/2019, 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:
Justus Hibshman, Department of CSE, University of Notre Dame, 2023.
Qi Li, Department of CSE, University of Notre Dame, 2022.
Shawn Gu, Department of CSE, University of Notre Dame, 2022.
Afzal Hossain, Department of CSE, University of Notre Dame, 2021.

Khalique Newaz, Department of CSE, University of Notre Dame, 2021.
Justin DeBenedetto, Department of CSE, University of Notre Dame, 2021.
Gabriel Wright, Department of CSE, University of Notre Dame, 2021.
Gabriel Foster, Department of Biological Sciences, University of Notre Dame, 2020.
Joseph Crawford, Department of CSE, University of Notre Dame, 2019.
Sage Davis, Department of Biological Sciences, University of Notre Dame, 2019.
Jian Xu, Department of CSE, University of Notre Dame, 2017.
Tomer Levinboim, Department of CSE, University of Notre Dame, 2017.
Vipin Vijayan, Department of CSE, University of Notre Dame, 2017.
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:
Justus Hibshman, Department of CSE, University of Notre Dame, 2022.
Qi Li, Department of CSE, University of Notre Dame, 2021.
Shawn Gu, Department of CSE, University of Notre Dame, 2020.
Gabriel Wright, Department of CSE, University of Notre Dame, 2019.
Khalique Newaz, Department of CSE, University of Notre Dame, 2019.
Justin DeBenedetto, Department of CSE, University of Notre Dame, 2019.
Gabriel Foster, Department of Biological Sciences, University of Notre Dame, 2019.
Sage Davis, Department of Biological Sciences, University of Notre Dame, 2017.
Joseph Crawford, Department of CSE, University of Notre Dame, 2017.
Corey Pennycuff, Department of CSE, University of Notre Dame, 2017.
Jian Xu, Department of CSE, 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.

**M.Sc. thesis defense committee member** for the following students:
Jacob Piland, Department of CSE, University of Notre Dame, 2021.
Shikang Liu, Department of CSE, University of Notre Dame, 2019.
Mahboobeh Ghalehnovi, Department of CSE, University of Notre Dame, 2019.

**Undergraduate honors thesis committee** for the following students:
Vikram Saraph, Department of CSE, University of Notre Dame, 2013.
Elias Chahoud, degree programs in Science-Computing and Philosophy, and thesis in Glynn
Family Honors Program, University of Notre Dame, 2022.

Affiliations

Association for Computing Machinery (ACM), Distinguished Member
International Society for Computational Biology (ISCB), Senior Member