Curriculum Vitae
Marinka Zitnik

Department of Biomedical Informatics
Harvard University
10 Shattuck Street
Boston, MA 02115, USA

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http://zitniklab.hms.harvard.edu

Research Interests	Machine learning and large-scale data science, focusing on new methods for the analysis, fusion, and learning on large graphs with applications to biology, genomics, and medicine.

Current Position

Harvard University, USA — December 2019-
Assistant Professor, Department of Biomedical Informatics
Associate Member, Broad Institute of MIT and Harvard
Faculty Affiliate, Harvard Data Science Initiative

Education

Stanford University, USA — 2016-2019
Postdoctoral Research Scholar
Department of Computer Science
Advisor: Prof. Jure Leskovec
Biohub Postdoctoral Research Fellow

University of Ljubljana, Slovenia — 2012-2015
Ph.D. in Computer Science
Department of Computer and Information Science
Advisor: Prof. Blaz Zupan
Committee: Peter Semrl, Igor Kononenko, Saso Dzeroski, Florian Markowetz
summa cum laude (GPA 10.00/10)
Jozef Stefan Golden Emblem
Nominated for the Best European Doctoral Dissertation in Artificial Intelligence

Stanford University, Department of Computer Science, USA — 2014
Research Fellow with Prof. Jure Leskovec

Baylor College of Medicine, Department of Molecular and Human Genetics, USA — 2013-2014
Predoctoral Fellow with Prof. Gad Shaulsky and Prof. Adam Kuspa

Imperial College London, Department of Computing, UK — 2012
Research Student with Prof. Natasa Przulj

University of Toronto, Donnelly Centre for Cellular and Biomolecular Research, Canada — 2012
Research Student with Prof. Charles Boone

University of Ljubljana, Slovenia — 2008-2012
B.Sc. in Computer Science and Mathematics
Department of Computer and Information Science
Department of Mathematics and Physics
summa cum laude (GPA 10.00/10)
University of Ljubljana Prešeren Award

Academic Honors

- ⬦ **Next Generation in Biomedicine**, 20 awardees worldwide, Broad Institute of MIT and Harvard — 2018
- ⬦ **Rising Star in Electrical Engineering and Computer Science**, 60 awardees in North America, MIT — 2018
- ⬦ **National Guest Scholar** at Stanford Clinical Excellence Research Center (CERC), invited to teach the CERC fellows about data science — 2018
- ⬦ **Jozef Stefan Golden Emblem**, Highest national award for Ph.D. dissertation in natural sciences, medicine, and biotechnology, a maximum of 3 prizes are awarded for theses in the last 3 years — 2017

◇ **Nominated for the Best European Doctoral Dissertation in Artificial Intelligence** by the European Association for Artificial Intelligence   2016

◇ **National Award for Early Graduation from PhD**, 2 years and 10 months after my B.Sc. degree   2015

◇ **DREAM Olfaction Prediction Challenge**, Competition on predicting how a molecule smells from its physical and chemical features; rank: 3/19 and invited as a co-author on a *Science* paper   2015

◇ *University of Ljubljana Outstanding Research Award*, Highest research award given to 10 out of 40,000 researchers   2015

◇ **Best Poster Award** at the 11th Basel Computational Biology Conference (BC^2'15), awarded to 2 posters out of several hundred at the conference   2015

◇ *Google Anita Borg & Grace Hopper Fellowship*, 1 out of 20 winners worldwide   2014

◇ **Best Paper Award for Outstanding Research** in Critical Assessment of Massive Data Analysis at the 23rd International Conference on Intelligent Systems for Molecular Biology (ISMB)   2014

◇ **Heidelberg Laureate Forum**, Young researcher at the forum of Turing, Fields, Nevanlinna, and Abel Prize laureates; 1 out of 100 computer science graduate students worldwide   2014

◇ **Best Poster Award** at the 18th Annual International Conference on Research in Computational Molecular Biology (RECOMB'14), awarded to 2 posters out of several hundred at the conference   2014

◇ **Winner of the BioNLP Gene Regulation Network Challenge**, Competition on gene regulatory network inference; rank: 1/30 and invited to give a talk at the 51st Annual Meeting of the Association for Computational Linguistics (ACL'13)   2013

◇ **Best Paper Award for Outstanding Research** in Critical Assessment of Massive Data Analysis at the 22nd International Conference on Intelligent Systems for Molecular Biology (ISMB)   2013

◇ **Winner of the Biomedical Literature Search Competition**, Competition on classifying biomedical research literature; rank: 1/126 and invited to give a talk at the 7th Joint Rough Set Symposium (JRS'12)   2012

◇ *EMC Israel Data Science Challenge*, Competition on classifying programming code from open-source projects; rank: 2/91 and awarded a prize of $10,000   2012

◇ *University of Ljubljana Prešeren Award*, Highest university award for students given to 10 out of 40,000 students   2012

◇ *University of Ljubljana Best Student Award*, Highest research award given to 10 students nationwide   2011

◇ **Google Anita Borg Scholarship**, 1 out of 20 winners in Europe, Google   2011

◇ *Outstanding Student Award*, 4 times awarded as the best student in the class of 300 (based on average grade) at the University of Ljubljana   2009-2012

◇ *Swiss Talent Forum*, Young researcher at the Meeting of Nobel Laureates; 1 out of 60 students in Europe   2009

◇ *19th European Union Contest for Young Scientists*, Prize for a chemical Strunz classification of the largest national collection of minerals and rocks   2007

◇ *First-prize Winner of the Year* for research on the impact of EU accession on technology, Hewlett-Packard   2007

Publications   ◇ **Articles in Peer-Reviewed Journals**

[67] K. Huang, C. Xiao, L. Glass, **M. Zitnik**, J. Sun. SkipGNN: Predicting Molecular Interactions with Skip-Graph Networks. *In Review*. [arXiv: 2004.14949]

[66] D. M. Gysi*, I. Do Valle*, **M. Zitnik***, A. Ameli*, X. Gan*, O. Varol, H. Sanchez, R.M. Baron, D. Ghiassian, J. Loscalzo, A.-L. Barabasi. Network Medicine Framework for Identifying Drug Repurposing Opportunities for COVID-19. *In Review*. [arXiv: 2004.07229]

[65] K. Huang, T. Fu, L. Glass, **M. Zitnik**, C. Xiao, J. Sun. DeepPurpose: A Deep Learning Library for Drug-Target Interaction Prediction. *In Review*. [arXiv: 2004.08919]

[64] C. Ruiz, **M. Zitnik**, J. Leskovec. Discovery of Disease Treatment Mechanisms through the Multiscale Interactome. *In Review*. [bioRxiv: 2020.04.30.069690]

[63] M. Brbic, **M. Zitnik**, S. Wang, A.O. Pisco, R.B. Altman, S. Darmanis, J. Leskovec. Discovering Novel Cell Types Across Heterogeneous Single-Cell Experiments. *In Review*. [bioRxiv: 2020.02.25.960302]

[62] G. Stiglic, P. Kocbek, N. Fijacko, **M. Zitnik**, K. Verbert, L. Cilar. Interpretability of Machine Learning based Prediction Models in Healthcare. *In Review*. [arXiv: 2002.08596]

[61] S. Wang, A.O. Pisco, A. McGeever, M. Brbic, **M. Zitnik**, S. Darmanis, J. Leskovec, J. Karkanias, R.B. Altman. Unifying Single-Cell Annotations Based on the Cell Ontology. *In Review*. [bioRxiv: 810234]

[60] **M. Zitnik**, R. Sosic, M.W. Feldman, J. Leskovec. Evolution of Resilience in Protein Interactomes Across the Tree of Life. *Proceedings of the National Academy of Sciences (PNAS)*, 116, 10:4426-4433, 2019.

[59] W. Nelson, **M. Zitnik**, B. Wang, J. Leskovec, A. Goldenberg, R. Sharan. To Embed or Not: Network

Embedding as a Paradigm in Computational Biology. *Frontiers in Genetics*, 10, 381, 2019.

[58] **M. Zitnik**, F. Nguyen, B. Wang, J. Leskovec, A. Goldenberg, M.M. Hoffman. Machine Learning for Integrating Data in Biology and Medicine: Principles, Practice, and Opportunities. *Information Fusion*, 50, 71-91, 2019.

[57] A. Copar, B. Zupan, **M. Zitnik**. Fast Optimization of Non-negative Matrix Tri-factorization. *PLoS One*, 14, 6, e0217994, 2019.

[56] **M. Zitnik**, R. Sosic, J. Leskovec. Prioritizing Network Communities. *Nature Communications*, 9, 2544, 2018.

[55] B. Wang*, A. Pourshafeie*, **M. Zitnik***, J. Zhu, C.D. Bustamante, S. Batzoglou, J. Leskovec. Network Enhancement as a General Method to Denoise Weighted Biological Networks. *Nature Communications*, 9, 3108, 2018. *(* first co-authors)*

[54] **M. Zitnik**, M. Agrawal, J. Leskovec. Modeling Polypharmacy Side Effects with Graph Convolutional Networks. *Bioinformatics*, 34, 13:457-466, 2018.
Oral presentation at ISMB 2018.
Covered by 30 news outlets in the US and Europe.
6th most-read paper in *Bioinformatics* (source: Altmetric by Oxford University Press).

[53] X. Wang, Y. Zhang, X. Ren, Y. Zhang, **M. Zitnik**, J. Shang, C. Langlotz, J. Han. Cross-type Biomedical Named Entity Recognition with Deep Multi-Task Learning. *Bioinformatics*, 35, 10:1745-1752, 2018.

[52] A. Copar, **M. Zitnik**, B. Zupan. Scalable Non-Negative Matrix Tri-Factorization. *BioData Mining*, 10, 41, 2017.

[51] J.C. Puigvert, **M. Zitnik**, A.-S. Jemth, M. Carter, J. Unterlass, B. Hallstrom, O. Loseva, Z. Karem, J.M. Calderon-Montano, C. Lindskog, P.H. Edqvist, D. Matuszewski, H.A. Blal, R. Berntsson, M. Haggblad, U. Martens, M. Studham, M. Uhlen, B. Lundgren, C. Wahlby, E. Sonnhammer, E. Lundberg, P. Stenmark, B. Zupan, T. Helleday. A Comprehensive Structural, Biochemical and Biological Profiling of the Human NUDIX Hydrolase Family. *Nature Communications*, 8, 1541, 2017.
I led all computational analyses in this project.

[50] **M. Zitnik**, J. Leskovec. Predicting Multicellular Function Through Multi-Layer Tissue Networks. *Bioinformatics*, 33, 14:190-198, 2017.
Oral presentation at ISMB 2017.

[49] A. Keller, R.C. Gerkin, Y. Guan, A. Dhurandhar, G. Turu, B. Szalai, J.D. Mainland, Y. Ihara, C.W. Yu, R. Wolfinger, C. Vens, L. Schietgat, K. De Grave, R. Norel, **DREAM Olfaction Consortium**, G. Stolovitzky, G. Cecchi, L.B. Vosshall, P. Meyer. Predicting Human Olfactory Perception from Chemical Features of Odor Molecules. *Science*, 355, 6327:820-826, 2017.

[48] **M. Zitnik**, B. Zupan. Jumping Across Biomedical Contexts Using Compressive Data Fusion. *Bioinformatics*, 32, 12:90-100, 2016.
Oral presentation at ISMB 2016.

[47] M. Strazar, **M. Zitnik**, B. Zupan, J. Ule, T. Curk. Orthogonal Matrix Factorization Enables Integrative Analysis of Multiple RNA Binding Proteins. *Bioinformatics*, 32, 10:1527-1535, 2016.

[46] S. Zitnik, **M. Zitnik**, B. Zupan, M. Bajec. Sieve-Based Relation Extraction of Gene Regulatory Networks from Biological Literature. *BMC Bioinformatics*, 16, Suppl 16:S1, 2015.

[45] **M. Zitnik**, E. A. Nam, C. Dinh, A. Kuspa, G. Shaulsky, B. Zupan. Gene Prioritization by Compressive Data Fusion and Chaining. *PLoS Computational Biology*, 11, 10:e1004552, 2015.
The computer science department award for outstanding research.

[44] **M. Zitnik**, B. Zupan. Gene Network Inference by Fusing Data from Diverse Distributions. *Bioinformatics*, 31, 12:230-239, 2015.
Oral presentation at ISMB 2015.

[43] M. M. Usaj*, M. Brloznik*, P. Kaferle*, **M. Zitnik**, H. Wolinski, F. Leitner, S. D. Kohlwein, B. Zupan, U. Petrovic. Genome-Wide Localization Study of Yeast Pex11 Identifies Peroxisome-Mitochondria Interactions through the ERMES Complex. *Journal of Molecular Biology*, 427, 11:2072–2087, 2015. *(* first co-authors)*

[42] **M. Zitnik**, B. Zupan. Survival Regression by Data Fusion. *Systems Biomedicine*, 2, 3:47-53, 2015.

[41] **M. Zitnik**, B. Zupan. Data Imputation in Epistatic MAPs by Network-Guided Matrix Completion. *Journal of Computational Biology*, 22, 6:595-608, 2015.

[40] **M. Zitnik**, B. Zupan. Data Fusion by Matrix Factorization. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 37, 1:41-53, 2015.

[39] **M. Zitnik**, B. Zupan. Gene Network Inference by Probabilistic Scoring of Relationships from a Factorized

Model of Interactions. *Bioinformatics*, 30, 12:246-254, 2014.
Oral presentation at ISMB 2014.
The computer science department award for outstanding research.

[38] **M. Zitnik**, B. Zupan. Matrix Factorization-Based Data Fusion for Drug-Induced Liver Injury Prediction. *Systems Biomedicine*, 2, 1:16-22, 2014.

[37] **M. Zitnik**, V. Janjic, C. Larminie, B. Zupan, N. Przulj. Discovering Disease-Disease Associations by Fusing Systems-Level Molecular Data. *Scientific Reports*, 3, e3202, 2013.
The computer science department award for outstanding research.

[36] J. Demsar, ... **M. Zitnik**, *et al.* Orange: Data Mining Toolbox in Python. *Journal of Machine Learning Research*, 14:2349-2353, 2013.

[35] **M. Zitnik**, B. Zupan. Nimfa: A Python Library for Nonnegative Matrix Factorization. *Journal of Machine Learning Research*, 13:849-853, 2012.

◇ **Articles in Peer-Reviewed Conference Proceedings**

[34] E. Alsentzer, S.G. Finlayson, M.M. Li, **M. Zitnik**. Subgraph Neural Networks. Proceedings of Neural Information Processing Systems, NeurIPS, 34, 2020.

[33] K. Huang, **M. Zitnik**. Graph Meta Learning via Local Subgraphs. In Proceedings of Neural Information Processing Systems, NeurIPS, 34, 2020.

[32] X. Zhang, **M. Zitnik**. GNNGuard: Defending Graph Neural Networks against Adversarial Attacks. In Proceedings of Neural Information Processing Systems, NeurIPS, 34, 2020.

[31] W. Hu, M. Fey, **M. Zitnik**, Y. Dong, H. Ren, B. Liu, M. Catasta, J. Leskovec. Open Graph Benchmark: Datasets for Machine Learning on Graphs. In Proceedings of Neural Information Processing Systems, NeurIPS, 34, 2020.

[30] K. Huang, T. Fu, D. Khan, A. Abid, A. Abdalla, A.Abid, L.M. Glass, **M. Zitnik**, C. Xiao, J. Sun. MolDesigner: Interactive Design of Efficacious Drugs with Deep Learning. In Proceedings of Neural Information Processing Systems, Demo, NeurIPS, 34, 2020.

[29] W. Hu, B. Liu, J. Gomes, **M. Zitnik**, P. Liang, V. Pande, J. Leskovec. Pre-training Graph Neural Networks. In Proceedings of the International Conference on Learning Representations, ICLR, 8, 2020.

[28] R. Ying, D. Bourgeois, J. You, **M. Zitnik**, J. Leskovec. GNN Explainer: Generating Explanations for Graph Neural Networks. In Proceedings of Neural Information Processing Systems, NeurIPS, 33, 2019.

[27] W. Hamilton, P. Bajaj, **M. Zitnik**, D. Jurafsky, J. Leskovec. Embedding Logical Queries on Knowledge Graphs. In Proceedings of Neural Information Processing Systems, NeurIPS, 32, 2018.

[26] C. Donnat, **M. Zitnik**, D. Hallac, J. Leskovec. Learning Structural Node Embeddings via Diffusion Wavelets. In ACM SIGKDD Conference on Knowledge Discovery and Data Mining, KDD, 2018.

[25] M. Agrawal*, **M. Zitnik***, J. Leskovec. Large-Scale Analysis of Disease Pathways in the Human Interactome. In Pacific Symposium on Biocomputing, 23:111-122, 2018. *(* first co-authors)*

[24] **M. Zitnik**, B. Zupan. Collective Pairwise Classification for Multi-Way Data Analysis of Diseases and Drugs. In Pacific Symposium on Biocomputing, 21:81-92, 2016.

[23] **M. Zitnik**, B. Zupan. Large-Scale Data Fusion. In Minisymposia at 37th Annual International Conference of the IEEE Engineering in Medicine and Biology, EMBC, 2015.

[22] **M. Zitnik**, B. Zupan. Survival Regression by Data Fusion. In International Conference on Intelligent Systems for Molecular Biology, ISMB, CAMDA, 2014.
Best paper award for outstanding research at ISMB/CAMDA 2014.

[21] **M. Zitnik**, B. Zupan. Imputation of Quantitative Genetic Interactions in Epistatic MAPs by Interaction Propagation Matrix Completion. In Proceedings of 18th Annual International Conference on Research in Computational Molecular Biology, RECOMB, 8394:448-462, 2014.

[20] **M. Zitnik**, B. Zupan. Matrix Factorization-Based Data Fusion For Gene Function Prediction in Baker's Yeast and Slime Mold. In Pacific Symposium on Biocomputing, 19:400-411, 2014.

[19] **M. Zitnik**, B. Zupan. Matrix Factorization-Based Data Fusion for Drug-Induced Liver Injury Prediction. In International Conference on Intelligent Systems for Molecular Biology, ISMB, CAMDA, 2013.
best paper award for outstanding research at ISMB/CAMDA 2013.

[18] S. Zitnik, **M. Zitnik**, B. Zupan, M. Bajec. Extracting Gene Regulation Networks Using Linear-Chain Conditional Random Fields and Rules. In Association for Computational Linguistics, ACL, BioNLP, 2013.
First-prize winner in gene regulatory network extraction at ACL BioNLP 2013.

[17] J. Zbontar, **M. Zitnik**, M. Zidar, G. Majcen, M. Potocnik, B. Zupan. Team ULjubljana's Solution to the JRS 2012 Data Mining Competition. In Rough Sets and Current Trends in Computing, 7413/2012, 471-478, 2012.

◇ **Abstracts in Peer-Reviewed Conference Proceedings**

[16] S. Kunz, **M. Zitnik**, J. Zupancic, J. Leskovec, J. Rigdon, J. Profit. Variation in Neonatal Referral Networks across Patient Groups. Pediatric Academic Societies Meeting, PAS, 2019.

[15] **M. Zitnik**, M. Agrawal, J. Leskovec. Modeling Polypharmacy Side Effects with Graph Convolutional Networks. 26th International Conference on Intelligent Systems for Molecular Biology, ISMB/ECCB, 2018.

[14] M. Agrawal*, **M. Zitnik***, J. Leskovec. Large-Scale Analysis of Disease Pathways in the Human Interactome. Pacific Symposium on Biocomputing, PSB, 2018. *(* first co-authors)*

[13] **M. Zitnik**, J. Leskovec. Predicting Multicellular Function Through Multi-Layer Tissue Networks. 25th International Conference on Intelligent Systems for Molecular Biology, ISMB/ECCB, 2017.

[12] **M. Zitnik**, B. Zupan. Jumping Across Gene-Disease Contexts Using Compressive Data Fusion. 24th International Conference on Intelligent Systems for Molecular Biology, ISMB, 2016.

[11] **M. Zitnik**, B. Zupan. Jumping Across Biomedical Contexts Using Compressive Data Fusion. Pacific Symposium on Biocomputing, 2016.

[10] **M. Zitnik**, B. Zupan. Integrate Everything but the Kitchen Sink: Data Set Selection and Sensitivity Estimation in Collective Factor Models. 23rd International Conference on Intelligent Systems for Molecular Biology, ISMB, 2015.

[9] **M. Zitnik**, E. A. Nam, C. Dinh, A. Kuspa, G. Shaulsky, B. Zupan. Gene Prioritization by Compressive Data Fusion and Chaining. Basel Computational Biology Conference, BC^2, 2015.
Best poster award.

[8] M. M. Usaj, M. Usaj, **M. Zitnik**, D. Kablawi, B. Zupan, B. J. Andrews, C. Boone. Exploring the Yeast Endocytic Pathway by Combining High-Throughput Genetics and High-Content Microscopy. International Specialised Symposium on Yeast, 2014.

[7] **M. Zitnik**. Learning by Fusing Heterogeneous Data. Heidelberg Laureate Forum, 2014.

[6] **M. Zitnik**, E. A. Nam, C. Dinh, A. Kuspa, G. Shaulsky, B. Zupan. Data Fusion for Gene Prioritization. 22nd International Conference on Intelligent Systems for Molecular Biology, ISMB, 2014.

[5] **M. Zitnik**, B. Zupan. Biomedical Data Fusion by Simultaneous Matrix Tri-factorization. 18th Annual International Conference on Research in Computational Molecular Biology, RECOMB, 2014.
Best poster award.

[4] **M. Zitnik**, B. Zupan. Matrix Factorization-Based Data Fusion For Gene Function Prediction in Baker's Yeast and Slime Mold. Pacific Symposium on Biocomputing, 2014.

[3] M. M. Usaj, M. Usaj, **M. Zitnik**, B. Zupan, D. G. Drubin, B. J. Andrews, C. Boone. Studying Yeast Endocytosis with High-throughput Multi-channel Fluorescence Microscopy: a Tale of Cortical Actin Patches, Endosomes and Vacuoles. 13th International Conference on Systems Biology, ICSB, 2012.

◇ **Theses**

[2] **M. Zitnik**. A Matrix Factorization Approach for Inference from Heterogeneous Data. B.Sc. Thesis, University of Ljubljana, 2012.
Summa cum laude.
University of Ljubljana Prešeren Award.

[1] **M. Zitnik**. Learning by Fusing Heterogeneous Data, Ph.D. Thesis, University of Ljubljana, 2015.
Summa cum laude.
Jozef Stefan Golden Emblem.
Nominated for the Best European Doctoral Dissertation in Artificial Intelligence by the European Association for Artificial Intelligence.

Tutorial & Symposium Organizer

◇ National Symposium on Drug Repurposing for Future Pandemics, 2020.
◇ Trustworthy AI for Healthcare. Workshop at the 35th AAAI Conference on Artificial Intelligence, AAAI, 2021.
◇ PhD Forum, European Conference on Machine Learning and Principles and Practice of Knowledge Discovery in Databases , ECML-PKDD, 2020.

◇ Graph Representation Learning and Beyond. Workshop at the 37th International Conference on Machine Learning, ICML, 2020.
◇ Representation Learning on Graphs and Manifolds. Workshop at the 7th International Conference on Learning Representations, ICLR, 2019.
◇ Machine Learning for Drug Development. Tutorial at the 29th International Joint Conference on Artificial Intelligence, IJCAI, 2020.
◇ Deep Learning for Network Biology. Tutorial at the 26th International Conference on Intelligent Systems for Molecular Biology, ISMB, 2018.
◇ Large-Scale Data Fusion by Collective Matrix Factorization. Tutorial at the 11th Basel Computational Biology Conference, BC^2, 2015.
◇ Data Fusion of Everything. Tutorial at the 37th Annual International Conference of the IEEE Engineering in Medicine and Biology Society, EMBC, 2015.

Data Collections

◇ **M. Zitnik**, R. Sosic, S. Maheshwari, J. Leskovec. BioSNAP Datasets: Stanford Biomedical Network Dataset Collection. http://snap.stanford.edu/biodata, 2018.

Scientific Community Activities

◇ **Selected Invited Talks and Seminars**
· MLCB, Machine Learning in Computational Biology (11/2020) -- *Keynote Talk*
· University of Cambridge, Department of Computer Science and Technology (11/2020)
· Harvard Center of Mathematical Sciences and Applications, New Technologies in Mathematics (10/2020)
· KDD, Workshop on Knowledge Graphs: Mining Knowledge Graphs for Deep Insights (07/2020)
· ISMB BioVis (07/2020) -- *Keynote Talk*
· NSF Workshop on Future Directions in Network Biology (06/2020)
· Graph Exploitation Symposium, MIT Lincoln Laboratory (04/2020)
· Dagstuhl Seminar, Visualization of Biological Data -- From Analysis to Communication (04/2020)
· B3D Seminar, Harvard Biomedical Informatics and Biostatistics (04/2020)
· MIT Bioinformatics Seminar, MIT Math & MIT CSAIL (03/2020)
· Swiss Applied Machine Learning Days (01/2020)
· Beth Israel Deaconess Medical Center, Harvard Newborn Health Services and Epidemiology (01/2020)
· NeurIPS Workshop on Graph Representation Learning (GRL) (12/2019)
· DS, 22nd International Conference on Discovery Science (10/2019) -- *Keynote Talk*
· US Food and Drug Administration (FDA) Science Forum (09/2019)
· ISMB/ECCB Machine Learning in Computational & Systems Biology (07/2019) -- *Keynote Talk*
· ICGEB-TRAIN High Content Imaging and Data Science for Virtual Screening and Drug Discovery (05/2019)
· NetSci Meeting on Network Medicine (05/2019)
· Harvard University (04/2019)
· University of Pennsylvania (04/2019)
· Georgia Institute of Technology (04/2019)
· University of California, San Diego (04/2019)
· University of California, Santa Barbara (04/2019)
· University of Illinois at Urbana-Champaign (04/2019)
· University of California, Irvine (04/2019)
· Emory University (04/2019)
· EPFL Ecole Polytechnique Federale de Lausanne (03/2019)
· University of California, San Francisco (03/2019)
· Johns Hopkins University (03/2019)
· Northeastern University (03/2019)
· University of Washington (03/2019)
· Stanford Symposium of Computational, Evolutionary and Human Genomics (CEHG) (02/2019)
· Boston University (02/2019)
· Yale University (02/2019)
· Carnegie Mellon University (02/2019)
· Cornell University (02/2019)
· University of Notre Dame (02/2019)
· University of California, Berkeley (01/2019)
· University of California, Los Angeles (01/2019)

- NeurIPS Workshop on Relational Representation Learning (12/2018)
- The Broad Institute of Harvard and Medicine, Next Generation Symposium (11/2018)
- The US National Academies of Sciences, Engineering, and Medicine (10/2018)
- European Bioinformatics Institute (EMBL-EBI) (09/2018)
- Stanford Clinical Excellence Research Center (CERC) (09/2018)
- AI in Medicine: Inclusion & Equity (AiMIE) (08/2018)
- AMS-MAA Joint Mathematics Meetings, Clustering of Graphs: Theory, Practice, and Applications (01/2018)
- NetSci Meeting on Network Medicine (06/2017)
- International Conference for Big Data and AI in Medicine (04/2017)
- Jozef Stefan Institute (01/2017)
- DARPA Cancer Analytics Workshop, White House Cancer Moonshot (10/2016)
- AIME Workshop on Matrix Computations in Biomedical Informatics (06/2015)
- TEDx University of Ljubljana (10/2014)
- Baylor College of Medicine, Department of Molecular and Human Genetics (01/2014)
- University of Toronto, Donnelly Centre for Cellular and Biomolecular Research (09/2012)

◇ **Conference Chair.** Demo Co-Chair for ECML/PKDD 2017, PhD Forum Co-Chair for ECML/PKDD 2020, National Science Foundation (NSF) Workshop on Future Directions in Network Biology (2020), Co-Chair for Network Biology Track at ISMB 2020

◇ **Advisory Board Member.** Association for Computing Machinery (ACM) Ubiquity Next Generation Advisory Board (2016-2018)

◇ **Editorial Board Member.** ACM XRDS Crossroads (Department Leader and Editor, 2012-2016), ECML PKDD (Editorial Board Member, 2017-2018, 2020), Frontiers in Genetics (Guest Editor, 2018), Artificial Intelligence in Medicine (2019-), Data Mining and Knowledge Discovery (2020-), IEEE/ACM Transactions on Computational Biology and Bioinformatics (Guest Editor for Special Issue on Deep Learning and Graph Embeddings for Network Biology, 2020)

◇ **Panels and Proposal Reviewing.** Swiss National Science Foundation (SNFS), European Research Council (ERC), National Science Foundation (NSF) IIS Division, Swiss Data Science Center (ETH Zurich & EPFL)

◇ **Program Committee Membership.** KDD 2016-2019, ECML PKDD 2017-2019, AIME 2017, ISMB 2018-2019, PSB 2016-2020, SDM 2019-2020, ICML 2019, ICLR 2019, WWW 2019-2020, IJCAI 2019-2020, UAI 2019, NeurIPS 2018-2019, MLCB 2019, AAAI 2020, RECOMB 2020, ISMB 2020

◇ **Journal Reviewing.** Nature Communications, Nature Neuroscience, Proceedings of the National Academy of Sciences of the United States of America (PNAS), Bioinformatics, Journal of Machine Learning Research, IEEE Transactions on Neural Networks and Learning Systems, IEEE Journal of Biomedical and Health Informatics, Computers in Biology and Medicine, IEEE Signal Processing Letters, Journal of Cheminformatics, IEEE Transactions on Computational Biology and Bioinformatics, Nucleic Acids Research, Journal of Biomedical Informatics, Knowledge and Information Systems, BMC Bioinformatics, Machine Learning Journal, BioData Mining, Data Mining and Knowledge Discovery Journal, IEEE Transactions on Knowledge and Data Engineering, PLoS One, PLoS Computational Biology, Nature Scientific Reports, Nature Machine Intelligence

Teaching, Advising & Mentoring		
◇ **Stanford University**, CS191: Senior Thesis Project (mentor)	2016-2019
◇ **Stanford University**, CS199: Independent Project (mentor)	2016-2019
◇ **Stanford University**, CS341: Project in Mining Massive Data Sets (mentor)	2016-2019
◇ **Stanford Clinical Excellence Research Center (CERC)**, I taught the CERC fellows about the potential of data science to reduce healthcare costs in the US	2018
◇ **Tutorials** on deep learning for biomedicine, integrative machine learning, and data fusion at ISMB 2018, BC^2 2015, and EMBC 2015	2015-2018
◇ **Stanford University**, CURIS: Undergraduate Research in CS (mentor)	2016, 2017, 2018
◇ **Stanford University**, CS399: Independent Project (mentor)	2016, 2018
◇ **Stanford University**, Co-designed course CS224W: Analysis of Networks	2018
◇ **Stanford University**, CS224W Guest Lecture: Graph Convolutional Networks	2018
◇ **Stanford University**, CS224W Guest Lecture: Biological network analysis	2017, 2018
◇ **University of Graz**, Co-advising a Ph.D. student in bioinformatics (with Prof. Gregor Gorkiewicz)	2018
◇ **University of Pavia**, Machine Learning (instructor hosted by Prof. Riccardo Bellazzi)	2015
◇ **University of Ljubljana**, Machine Learning (head teaching assistant with Prof. Blaz Zupan)	2015
◇ **Baylor College of Medicine**, Introduction to Data Mining (head teaching assistant with Prof. Blaz Zupan, Prof. Janez Demsar, and Prof. Gad Shaulsky)	2014-2015

◇ **Teaching Assistant of the Year Award**, Computer Science Department, University of Ljubljana	2015
◇ **University of Ljubljana**, Network Analysis (teaching assistant with Prof. Jure Leskovec)	2013-2015
◇ **Cisco Computer Networking Academy,** Computer Networks and Systems (instructor)	2009-2011

Contributions to Diversity, Equity, and Inclusion

◇ Wrote 14 research columns for *XRDS Crossroads*, published by the Association for Computing Machinery (ACM), which is the world's largest scientific and educational computing society. XRDS Crossroads is the ACM's flagship magazine for students that is distributed to over 40,000 students worldwide

◇ Mentored 3 undergraduate students in *Stanford Summer Research in Computer Science* (CURIS) program. The program encourages undergraduate students to get involved in computer science research early in their careers

◇ Founding member of the *Google Anita Borg Scholars Community*. Together with other Google Anita Borg Scholars and Google we launched the global alumni community whose goal is to provide alumni with a platform to connect with each other and inspire more women to enter and stay in computer science

◇ Member of the Executive Board (34 members worldwide) of the *Google Global Planning Committee for Women in Computer Science*. In the pilot year of 2014, we held 160 events all around the world and reached 23,500 people through community events and partnership with Google on numerous innovative projects

◇ Helped in a successful project proposal for *Google's Computer Science for High School* (CS4HS) program

◇ Organized *Computer Science Summer School* program (over 50 students) at University of Ljubljana

◇ Organized *Rails Girls* workshops (over 100 women of age 20-60) in Ljubljana

◇ Organized *Django Girls* workshops (over 150 women of age 20-60) in Ljubljana

◇ Member of Stanford initiatives, including *Women in AI*, *Stanford Gates Women Club*, and *Inclusion in AI*

Science Outreach

◇ The Infinite Mixtures of Food Products. *XRDS Crossroads*, 23, 1:66-67, 2016.
◇ The Brownian Wanderlust of Things. *XRDS Crossroads*, 22, 3:81-83, 2016.
◇ According to Sensor 22 Benny is Preparing Dinner. *XRDS Crossroads*, 22, 2:72-74, 2015.
◇ Sorry Kids, Iron Man's Superpowers aren't Unique. *XRDS Crossroads*, 22, 1:66-67, 2015.
◇ Understanding Cancer Data with Matrix Factorization. *XRDS Crossroads*, 21, 4:72-74, 2015.
◇ The Anatomy of Human Disease Network. *XRDS Crossroads*, 21, 2:58-60, 2014.
◇ Dynamics of News from The New York Times. *XRDS Crossroads*, 21, 1:64-66, 2014.
◇ Exploring Data with Topological Tools. *XRDS Crossroads*, 20, 4:65-66, 2014.
◇ Efficient Sensor Placement for Environmental Monitoring. *XRDS Crossroads*, 20, 3:73-75, 2014.
◇ On Constructing the Tree of Life. *XRDS Crossroads*, 20, 2:65-67, 2013.
◇ Zero-Knowledge Proofs. *XRDS Crossroads*, 20, 1:65-67, 2013.
◇ Matrix Function: VIP in Linear Algebra and its Applications. *XRDS Crossroads*, 19, 3:66-67, 2013.
◇ Iterative Numerical Methods for Nonlinear Systems. *XRDS Crossroads*, 19, 2:64-66, 2012.
◇ Using Sentiment Analysis to Improve Business Operations. *XRDS Crossroads*, 18, 4:42-43, 2012.