

# Curriculum Vitae

## Marinka Zitnik

Department of Computer Science  
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<b>Research Interests</b>	Machine learning and large-scale data science for biomedicine, focusing on new methods for the analysis, modeling, and learning on large graphs with applications to biology, genomics, and medicine.	
<b>Current Position</b>	<b>Stanford University, USA</b> Postdoctoral Research Scholar <b>Biohub Postdoctoral Research Fellow</b> Department of Computer Science	2016-
<b>Education</b>	<b>University of Ljubljana, Slovenia</b> Ph.D. in Computer Science Department of Computer and Information Science Advisor: Blaz Zupan Committee: Peter Semrl, Igor Kononenko, Saso Dzeroski, Florian Markowetz <i>summa cum laude</i> (GPA 10.00/10) <b>Jozef Stefan Golden Emblem</b>	2012-2015
	<b>Stanford University, Department of Computer Science, USA</b> Research Fellow with Jure Leskovec	2014
	<b>Baylor College of Medicine, Department of Molecular and Human Genetics, USA</b> Predoctoral Fellow with Gad Shaulsky and Adam Kuspa	2013-2014
	<b>Imperial College London, Department of Computing, UK</b> Research Student with Natasa Przulj	2012
	<b>University of Toronto, Donnelly Centre for Cellular and Biomolecular Research, Canada</b> Research Student with Charles Boone	2012
	<b>University of Ljubljana, Slovenia</b> B.Sc. in Computer Science and Mathematics Department of Computer and Information Science Department of Mathematics and Physics <i>summa cum laude</i> (GPA 10.00/10) <b>University of Ljubljana Prešeren Award</b>	2008-2012
<b>Academic Honors</b>	<ul style="list-style-type: none"><li>◇ ♣<sup>1</sup> <b>Next Generation in Biomedicine</b>, 20 awardees worldwide, Broad Institute of MIT and Harvard 2018</li><li>◇ ♣ <b>Rising Star in Electrical Engineering and Computer Science</b>, 60 awardees in North America, MIT 2018</li><li>◇ <b>National Guest Scholar</b> at Stanford Clinical Excellence Research Center (CERC), invited to teach the CERC fellows about data science 2018</li><li>◇ ♣ <b>Jozef Stefan Golden Emblem</b>, 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</li><li>◇ <b>Nominated for the Best European Doctoral Dissertation in Artificial Intelligence</b> by the European Association for Artificial Intelligence 2016</li><li>◇ ♣ <b>National award for Early Graduation from PhD</b>, 2 years and 10 months after my B.Sc. degree 2015</li><li>◇ <b>DREAM Olfaction Prediction Challenge</b>, Competition on predicting how a molecule smells from its physical and chemical features; rank: 3/19 and invited as a co-author on a <i>Science</i> paper 2015</li></ul>	

<sup>1</sup>The symbol ♣ is used to highlight some of the key achievements and results.

- ◇ ♣ *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<sup>2</sup>'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

- [55] ♣ **M. Zitnik**, R. Susic, M.W. Feldman, J. Leskovec. Evolution of Resilience in Protein Interactomes Across the Tree of Life. In Review in *Proceedings of the National Academy of Sciences (PNAS)*, 2018. [bioRxiv: 10.1101/454033]
- [54] ♣ **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. [in press; arXiv:1807.00123]
- [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*, 2018. [in press; arXiv:1801.09851]
- [52] ♣ 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)
- [51] ♣ **M. Zitnik**, R. Susic, J. Leskovec. Prioritizing Network Communities. *Nature Communications*, 9, 2544, 2018.
- [50] ♣ **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.**  
**Highlighted in Stanford News and covered by 30 other news outlets in the US and Europe.**  
**6th most read paper ever in Bioinformatics.**
- [49] A. Copar, **M. Zitnik**, B. Zupan. Scalable Non-Negative Matrix Tri-Factorization. *BioData Mining*, 10, 41, 2017.
- [48] ♣ 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 the computational analyses in this project.**

- [47] ♣ **M. Zitnik**, J. Leskovec. Predicting Multicellular Function Through Multi-Layer Tissue Networks. *Bioinformatics*, 33, 14:190-198, 2017.  
**Oral presentation at ISMB 2017.**
- [46] 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.
- [45] ♣ **M. Zitnik**, B. Zupan. Jumping Across Biomedical Contexts Using Compressive Data Fusion. *Bioinformatics*, 32, 12:90-100, 2016.  
**Oral presentation at ISMB 2016.**
- [44] 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.
- [43] 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.
- [42] ♣ **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.**
- [41] ♣ **M. Zitnik**, B. Zupan. Gene Network Inference by Fusing Data from Diverse Distributions. *Bioinformatics*, 31, 12:230-239, 2015.  
**Oral presentation at ISMB 2015.**
- [40] M. M. Usaj\*, M. Brloznic\*, 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)
- [39] **M. Zitnik**, B. Zupan. Survival Regression by Data Fusion. *Systems Biomedicine*, 2, 3:47-53, 2015.
- [38] ♣ **M. Zitnik**, B. Zupan. Data Imputation in Epistatic MAPs by Network-Guided Matrix Completion. *Journal of Computational Biology*, 22, 6:595-608, 2015.
- [37] ♣ **M. Zitnik**, B. Zupan. Data Fusion by Matrix Factorization. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 37, 1:41-53, 2015.
- [36] ♣ **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.**
- [35] **M. Zitnik**, B. Zupan. Matrix Factorization-Based Data Fusion for Drug-Induced Liver Injury Prediction. *Systems Biomedicine*, 2, 1:16-22, 2014.
- [34] ♣ **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.**
- [33] J. Demsar, ... **M. Zitnik**, et al. Orange: Data Mining Toolbox in Python. *Journal of Machine Learning Research*, 14:2349-2353, 2013.
- [32] ♣ **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**
- [31] ♣ W. Hamilton, P. Bajaj, **M. Zitnik**, D. Jurafsky, J. Leskovec. Embedding Logical Queries on Knowledge Graphs. In Proceedings of Neural Information Processing Systems, NIPS, 32, 2018. [in press; arXiv:1806.01445]
- [30] ♣ 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.
- [29] ♣ 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)
- [28] ♣ **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.
- [27] **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.

- [26] ♣ **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.**
- [25] ♣ **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.
- [24] ♣ **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.
- [23] ♣ **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.**
- [22] ♣ 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.**
- [21] 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**

- [20] **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.
- [19] 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*)
- [18] **M. Zitnik**, J. Leskovec. Predicting Multicellular Function Through Multi-Layer Tissue Networks. 25th International Conference on Intelligent Systems for Molecular Biology, ISMB/ECCB, 2017.
- [17] **M. Zitnik**, B. Zupan. Jumping Across Gene-Disease Contexts Using Compressive Data Fusion. 24th International Conference on Intelligent Systems for Molecular Biology, ISMB, 2016.
- [16] **M. Zitnik**, B. Zupan. Jumping Across Biomedical Contexts Using Compressive Data Fusion. Pacific Symposium on Biocomputing, 2016.
- [15] **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.
- [14] ♣ **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<sup>2</sup>, 2015.  
**Best poster award.**
- [13] 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.
- [12] **M. Zitnik**. Learning by Fusing Heterogeneous Data. Heidelberg Laureate Forum, 2014.
- [11] **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.
- [10] ♣ **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.**
- [9] **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.
- [8] 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**

- [7] **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.**

- [6] **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.**

◇ **In Submission to Journals and Conferences**

- [5] With W. Nelson, A. Goldenberg, R. Sharan, and J. Leskovec. Network Embedding as a Paradigm in Computational Biology.  
 [4] With S. Eyuboglu, and J. Leskovec. Uncovering Disease Pathways in the Incomplete Interactome.  
 [3] With K. Grimes, R.B. Altman, and J. Leskovec. Interpretable Deep Learning for Drug Discovery and Repositioning.  
 [2] With C. Ruiz, and J. Leskovec. Network-Based Discovery of Drug Mechanisms.  
 [1] With R. Ying, and J. Leskovec. Interpretable Explanations of Graph Neural Networks by Meaningful Perturbation.

**Tutorial & Workshop Organizer**

- ◇ **M. Zitnik**, J. Leskovec. Deep Learning for Network Biology. 26th International Conference on Intelligent Systems for Molecular Biology, ISMB, 2018.  
 ◇ **M. Zitnik**, B. Zupan. Large-Scale Data Fusion by Collective Matrix Factorization. Basel Computational Biology Conference, BC<sup>2</sup>, 2015.  
 ◇ **M. Zitnik**, B. Zupan. Data Fusion of Everything. 37th Annual International Conference of the IEEE Engineering in Medicine and Biology Society, EMBC, 2015.

**Data Collections**

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

**Scientific Community Activities**

- ◇ **Invited Talks**
- at *NIPS 2018 Workshop on Relational Representation Learning (R2L)* on Graph Neural Networks for Biomedicine
  - at **Broad Institute Next Generation Symposium in Biomedicine** on New Machine Learning for Biomedical Sciences
  - at **National Academies of Sciences, Engineering, and Medicine** on Next-Generation Algorithms for Drug Discovery and Development
  - at **European Bioinformatics Institute (EMBL-EBI) Meeting on Machine Learning in Drug Discovery and Precision Medicine** on Modeling Polypharmacy with Graph Neural Networks
  - at *Stanford Clinical Excellence Research Center, Stanford* on Network Biology and Deep Learning Concepts for Modeling Polypharmacy
  - at **AI in Medicine: Inclusion & Equity (AiMIE 2018) Stanford Symposium** on Frameworks for an Inclusive Future of AI in Healthcare
  - **AMS-MAA Joint Mathematics Meetings 2018**, Clustering of Graphs: Theory, Practice, and Applications on Prioritizing Network Communities
  - at **NetSci 2017 Network Medicine** on Uncovering Cellular Functions Through Multi-Layer Tissue Networks
  - at *Jozef Stefan Institute* on Learning by Fusing Heterogeneous Data
  - at **DARPA Cancer Analytics Workshop, White House Cancer Moonshot** on Structure, Organization and Dynamics of Complex Networks for Cancer Analytics
  - at *15th Conference on Artificial Intelligence in Medicine (AIME)* on Learning Latent Factor Models by Data Fusion
  - at *Baylor College of Medicine, Department of Molecular and Human Genetics* on Data Fusion by Matrix Factorization
  - at *University of Toronto* on Matrix Factorization Approaches for Inference of Prediction Models from Heterogeneous Data Sources
- ◇ **ACM Ubiquity Next Gen Advisory Panel**, Association for Computing Machinery 2016–2018  
 ◇ **ECML/PKDD Demo Co-chair**, 27th Joint European Conference on Machine Learning 2017 and Knowledge Discovery in Databases  
 ◇ **ACM XRDS Crossroads**, Department Leader and Editor, ACM flagship magazine for students 2012–2016  
 ◇ **Editorial Board Member**. ACM XRDS Crossroads 2013–2016, ECML PKDD 2017, ECML PKDD 2018, Frontiers in Genetics

- ◇ **Program Committee Member or Journal Reviewer.** 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, ACM Conference on Knowledge Discovery and Data Mining (SIGKDD) 2016, BMC Bioinformatics, Swiss National Science Foundation (SNFS), ECML PKDD 2017 PC member, Machine Learning Journal, BioData Mining, Data Mining and Knowledge Discovery Journal, AI in Medicine (AIME) 2017, IEEE Transactions on Knowledge and Data Engineering, Nature Neuroscience, ACM SIGKDD 2018 PC member, Intelligent Systems for Molecular Biology (ISMB) 2018 PC member, ECML PKDD 2018 PC member, European Research Council (ERC) 2018, ECML PKDD 2019 PC member, SDM 2019, ICML 2019, ICLR 2019

### Teaching, Advising & Mentoring

- ◇ **Stanford University**, CS191: Senior Thesis Project (mentor) 2016-
- ◇ **Stanford University**, CS199: Independent Project (mentor) 2016-
- ◇ **Stanford University**, CS341: Project in Mining Massive Data Sets (mentor) 2016-
- ◇ **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<sup>2</sup> 2015, and EMBC 2015 2015-2018
- ◇ **Stanford University**, CURIS: Undergraduate Research in CS (mentor) 2016, 2017, 2018
- ◇ **Stanford University**, CS341: Project in Mining Massive Data Sets (instructor) 2016
- ◇ **Stanford University**, CS399: Independent Project (mentor) 2016, 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

### Fellowships & Funding

- ◇ Helped in successful project proposals: 2014-2018
  - *CZ Biohub Investigator Program* proposal on Computational Tools for Biology
  - *DARPA project* proposal on Simplifying Complexity in Scientific Discovery
  - *Stanford Big Ideas Grant* on Neuro-omics
  - *NIH K-award* with Harvard University on Data Science Tools for Patient Transfers between Hospitals
- ◇ *Travel Fellowships* for ISMB'14, ISMB'15, ISMB'16, ISMB'17, and ISMB'18 from International Society for Computational Biology 2014-2018
- ◇ *Travel Fellowships* for PSB'14 and PSB'15 from International Society for Computational Biology 2014-2015
- ◇ Obtained \$15,000 donation from Google to design programs and workshops that promote inclusion and diversity in computer science 2014
- ◇ *Predocctoral Research Scholarship*, ASEF & Stanford Computer Science Department, \$5,000 2014
- ◇ *Grace Hopper Fellowship*, Google, \$5,000 2014
- ◇ *Research Fellowship*, Slovenian National Research Institute, \$20,000 2013
- ◇ *Google Anita Borg Scholarship*, Google, \$11,000 2011
- ◇ *Zois Scholarship for Gifted Students*, top 0.1% students nationwide 2004-2012

### 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. We provided students with material that stimulate, inform, and educate of computing, along with helpful information about calls for papers, fellowships, grants, and other opportunities
- ◇ 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 the computer science field

- ◇ 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
- ◇ Active in Stanford initiatives on diversity, 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.

## References

### Jure Leskovec

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### Natasa Przulj

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