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<b>Research Areas</b>	Data science, machine learning, network science, data fusion, and their 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	<b>2016–</b>
<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 Prize</b>	<b>2012–2015</b>
	<b>Stanford University, Department of Computer Science, USA</b> ASEF Research Fellow with Jure Leskovec	<b>2014</b>
	<b>Baylor College of Medicine, Department of Molecular and Human Genetics, USA</b> Predoctoral Fellow with Gad Shaulsky and Adam Kuspa	<b>2013–2014</b>
	<b>Imperial College London, Department of Computing, United Kingdom</b> Research Student with Natasa Przulj	<b>2012</b>
	<b>University of Toronto, Donnelly Centre for Cellular and Biomolecular Research, Canada</b> Research Student with Charles Boone	<b>2012</b>
	<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>2008–2012</b>
<b>Awards and Fellowships</b>	<b>Rising Stars in EECS, MIT, MA, USA</b>	<b>2018</b>
	<b>Travel Fellowship</b> , International Society for Computational Biology ( <i>ISCB</i> ), Intelligent Systems for Molecular Biology ( <i>ISMB'18</i> ), Chicago, IL, USA	<b>2018</b>
	<b>Travel Fellowship</b> , <i>ISCB</i> , <i>ISMB/ECCB'17</i> , Prague, Czech Republic	<b>2017</b>
	<b>Jozef Stefan Golden Emblem Prize</b> , Award for the best PhD dissertation in the fields of natural sciences, medicine and biotechnology; 1 out of 3 awardees nationwide	<b>2017</b>
	<b>Travel Fellowship</b> , <i>ISCB</i> , <i>ISMB'16</i> , Orlando, FL, USA	<b>2016</b>

	<b>DREAM Olfaction Prediction Challenge</b> , Rank: 3/19, Co-author of a <i>Science</i> paper	<b>2015</b>
	<b>The 2015 Outstanding Research Award</b> , 1 out of 10 awardees nationwide, Slovenia	<b>2015</b>
	<b>Best Teaching Assistant of the Year</b> , Computer Science Department, University of Ljubljana	<b>2015</b>
	<b>Award for the Early Completion of PhD Study</b> , 2 years and 10 months, Slovenia	<b>2015</b>
	<b>Travel Fellowship</b> , ISCB, Pacific Symposium on Biocomputing ( <i>PSB'16</i> ), Hawaii, HI, USA	<b>2015</b>
	<b>Travel Fellowship</b> , ISCB, ISMB'15, Dublin, Ireland	<b>2015</b>
	<b>Best Poster Award</b> , Basel Computational Biology Conference ([BC] <sup>2</sup> '15), Switzerland	<b>2015</b>
	<b>Google Anita Borg Committee &amp; G. Hopper Grant</b> , 1 out of 20 winners worldwide, Google	<b>2014</b>
	<b>First Prize Winner for Outstanding Research</b> , Critical Assessment of Massive Data Analysis ( <i>CAMDA</i> ), ISMB'14, Boston, MA, USA	<b>2014</b>
	<b>Travel Fellowship</b> , ISCB, ISMB'14, Boston, MA, USA	<b>2014</b>
	<b>Heidelberg Laureate Forum</b> , 100 CS graduate students selected worldwide. Forum of Turing, Fields, Nevanlinna and Abel Prize laureates, Heidelberg, Germany	<b>2014</b>
	<b>Predoctoral Research Scholarship</b> , ASEF & Stanford Computer Science Department	<b>2014</b>
	<b>Best Poster Award</b> , Research in Comp. Mol. Bio. ( <i>RECOMB'14</i> ), Pittsburgh, PA, USA	<b>2014</b>
	<b>Travel Fellowship</b> , ISCB, PSB'14, Hawaii, HI, USA	<b>2014</b>
	<b>BioNLP Shared Task 2013: Gene Regulation Network</b> , Rank: 1/30, Invited talk at ACL	<b>2013</b>
	<b>Fellowship for Research Visit to USA</b> , Slovenian National Research Institute	<b>2013</b>
	<b>Award for Outstanding Research Work</b> , University of Ljubljana	<b>2013, 2014, 2015</b>
	<b>First Prize Winner for Excellent Research</b> , <i>CAMDA</i> , ISMB'13, Berlin, Germany	<b>2013</b>
	<b>JRS 2012 Data Mining Competition</b> , Rank: 1/126, Invited talk at Joint Rough Set (JRS)	<b>2012</b>
	<b>EMC Israel Data Science Challenge</b> , Rank: 2/91, Prize: \$10,000	<b>2012</b>
	<b>University of Ljubljana Preseren Award</b> , Rank: 1/8,500, Award for the best thesis work	<b>2012</b>
	<b>University of Ljubljana Best Student Award</b> , 1 out of 10 awardees nationwide, Slovenia	<b>2011</b>
	<b>Google Anita Borg Scholarship</b> , 1 out of 20 winners in Europe, Google	<b>2011</b>
	<b>Zois Scholarship Fund for Gifted Students</b> , top 0.1% students nationwide, Slovenia	<b>2004–2012</b>
	<b>Outstanding Student Award</b> , GPA: 10.0/10, Rank: 1/350, University of Ljubljana	<b>2009–2012</b>
<b>Teaching, Advising &amp; Mentoring Experience</b>	<b>Stanford University</b> , CS191: Senior Project (mentor)	<b>2016–</b>
	<b>Stanford University</b> , CS199: Independent Project (mentor)	<b>2016–</b>
	<b>Stanford University</b> , CS341: Project in Mining Massive Data Sets (mentor)	<b>2016–</b>
	<b>Stanford University</b> , CURIS: Undergraduate Research in CS (mentor)	<b>2016, 2017</b>
	<b>Stanford University</b> , CS341: Project in Mining Massive Data Sets (instructor)	<b>2016</b>
	<b>Stanford University</b> , CS399: Independent Project (mentor)	<b>2016, 2018</b>
	<b>Stanford University</b> , CS224W Guest Lecture: Biological network analysis	<b>2017, 2018</b>
	<b>University of Pavia</b> , Italy, Machine Learning in Python (instructor)	<b>2015</b>
	<b>University of Ljubljana</b> , Machine Learning (head teaching assistant)	<b>2015</b>
	<b>Baylor College of Medicine</b> , TX, USA, Introduction to Data Mining (head teaching assistant)	<b>2015</b>
	<b>University of Ljubljana</b> , Social and Information Network Analysis (teaching assistant)	<b>2013–2015</b>
	<b>University of Ljubljana</b> , Programming, Algorithms & Data Structures, Business Intelligence, Data Mining (tutor)	<b>2010–2012</b>
	<b>Cisco Computer Networking Academy</b> , CCNA Courses (instructor)	<b>2009–2011</b>

<b>Academic Community Service</b>	<p><b>Google Global Planning Committee for Women in Computer Science</b>, Europe &amp; USA    <b>2014–</b></p> <p><b>ACM Ubiquity Next Gen Advisory Panel</b>, Association for Computing Machinery, USA    <b>2016–</b></p> <p><b>ECML/PKDD Demo Co-chair</b>    <b>2017</b></p> <p><b>ACM XRDS Crossroads</b>, Department lead, Association for Computing Machinery    <b>2012–2016</b></p> <p><b>Outreach to High School and Undergraduate Students</b>. CS Summer School at    <b>2011–</b> University of Ljubljana, Rails Girls Ljubljana, Django Girls Ljubljana, Stanford Summer Research in Computer Science (CURIS)</p> <p><b>(Guest) Editorial Board Member</b>. ECML PKDD 2017, ECML PKDD 2018, Frontiers in Genetics</p> <p><b>Program Committee Member or Journal Reviewer</b>. Bioinformatics, Journal of Machine Learning Research, IEEE Transactions on Neural Networks and Learning Systems, IEEE Journal of Biomed- ical 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 Bioinformat- ics, Swiss National Science Foundation (SNFS), ECML PKDD 2017 PC member, Machine Learn- ing 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</p>
<b>Invited Talks</b>	<p>Modeling Polypharmacy with Graph Neural Networks. Sept 19 2018. EMBL-EBI Workshop on Machine Learning in Drug Discovery and Precision Medicine, Hinxton, UK. (to appear)</p> <p>Network Biology and Deep Learning Concepts for Modeling Polypharmacy. Sept 4 2018. Stan- ford Clinical Excellence Research Center, Stanford, CA, USA. (to appear)</p> <p>Panel on Frameworks for an Inclusive Future of AI in Healthcare. Aug 22 2018. AI in Medicine: Inclusion &amp; Equity (AiMIE) Symposium, Stanford, CA, USA. (to appear)</p> <p>Prioritizing Network Communities. Jan 10-13 2018. AMS-MAA Joint Mathematics Meetings, Clustering of Graphs: Theory, Practice, and Applications, San Diego, CA, USA.</p> <p>Uncovering Cellular Functions Through Multi-Layer Tissue Networks. Jun 19 2017. NetSci 2017, Network Medicine, Indianapolis, IN, USA.</p> <p>Boosting Biomedical Discovery Through Network Data Analytics. Apr 13 2017. International Conference for Big Data and AI in Medical &amp; FinTech, Taiwan.</p> <p>Predictive Network Medicine. Apr 12 2017. Asia University, Taiwan.</p> <p>Learning by Fusing Heterogeneous Data. Jan 5 2017. Jozef Stefan Institute, Ljubljana, Slovenia.</p> <p>Structure, Organization and Dynamics of Complex Networks for Cancer Analytics. Oct 19 2016, DARPA Cancer Analytics Workshop, White House Cancer Moonshot, D.C., USA.</p> <p>Learning Latent Factor Models by Data Fusion. Jun 20 2015, 15th Conference on Artificial Intel- ligence in Medicine, AIME, Pavia, Italy.</p> <p>Compressive Data Fusion and Persistent Homology. Jun 24 2015, Summer School on Computa- tional Topology and Topological Data Analysis, University of Ljubljana, Slovenia.</p> <p>If Computer Science is a Science about Computers then Biology is a Science about Microscopes. Oct 15 2014, TEDx, University of Ljubljana, Slovenia.</p> <p>Data Fusion by Matrix Factorization. Jan 30 2014, Department of Molecular and Human Genet- ics, Baylor College of Medicine, Houston, TX, USA.</p> <p>Topological Methods in Machine Learning. Jul 2 2013, Summer School on Computational Topol- ogy and Topological Data Analysis, University of Ljubljana, Slovenia.</p>

Data Fusion for Dictyostelium Bacterial Response Gene Prioritization. Jun 12 2013, 8th CFGBC Symposium, Faculty of Medicine, University of Ljubljana, Slovenia.

Biomedical Data Fusion: The Whole can be More than the Sum of its Components. May 24 2013, BioDay: Trends in Bioinformatics, Ljubljana, Slovenia.

A Matrix Factorization Approach for Inference of Prediction Models from Heterogeneous Data Sources. Sept 8 2012, University of Toronto, Toronto, Canada.

## **Publications**    **Articles in peer-reviewed journals**

[50] **M. Zitnik**, M. Agrawal, J. Leskovec. Network-Based Discovery of Drug Indications. *In Review*, 2018.

[49] **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. *In Review*, arXiv:1807.00123, 2018.

[48] 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. *In Review*, arXiv:1801.09851, 2018.

[47] 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)

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

[45] **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 several other news outlets.**

**The most read paper in *Bioinformatics*.**

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

[43] 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. Sonnhhammer, 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.

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

**Oral presentation at ISMB/ECCB 2017.**

[41] 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.

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

**Oral presentation at ISMB 2016.**

[39] 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.

[38] 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.

- [37] **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.  
**CS department award for excellent research work.**
- [36] **M. Zitnik**, B. Zupan. Gene Network Inference by Fusing Data from Diverse Distributions. *Bioinformatics*, 31, 12:230-239, 2015.  
**Oral presentation at ISMB 2015.**
- [35] 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)
- [34] **M. Zitnik**, B. Zupan. Survival Regression by Data Fusion. *Systems Biomedicine*, 2, 3:47-53, 2015.
- [33] **M. Zitnik**, B. Zupan. Data Imputation in Epistatic MAPs by Network-Guided Matrix Completion. *Journal of Computational Biology*, 22, 6:595-608, 2015.
- [32] **M. Zitnik**, B. Zupan. Data Fusion by Matrix Factorization. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 37, 1:41-53, 2015.
- [31] **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.**  
**CS department award for excellent research work.**
- [30] **M. Zitnik**, B. Zupan. Matrix Factorization-Based Data Fusion for Drug-Induced Liver Injury Prediction. *Systems Biomedicine*, 2, 1:16-22, 2014.
- [29] **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.  
**CS department award for excellent research work.**
- [28] J. Demsar, ... **M. Zitnik**, et al. Orange: Data Mining Toolbox in Python. *Journal of Machine Learning Research*, 14:2349-2353, 2013.
- [27] **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**
- [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, Hawaii, HI, USA, 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, Hawaii, HI, USA, 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, Milan, Italy, 2015.
- [22] **M. Zitnik**, B. Zupan. Survival Regression by Data Fusion. In International Conference on Intelligent Systems for Molecular Biology, ISMB, CAMDA, Boston, MA, USA, 2014.  
**First prize winner for excellent 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, Pittsburgh, PA, USA, 2014.
- [20] **M. Zitnik**, B. Zupan. Matrix Factorization-Based Data Fusion For Gene Function Predic-

- tion in Baker's Yeast and Slime Mold. In Pacific Symposium on Biocomputing, 19:400-411, Hawaii, HI, USA, 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, Berlin, Germany, 2013.  
**First prize winner for excellent 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 Shared Task Workshop, Sofia, Bulgaria, 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, Chengdu, China, 2012.

#### **Abstracts in peer-reviewed conference proceedings**

- [16] **M. Zitnik**, M. Agrawal, J. Leskovec. Modeling Polypharmacy Side Effects with Graph Convolutional Networks. Poster session presented at International Conference on Intelligent Systems for Molecular Biology, ISMB/ECCB, Jul 6-10 2018, Chicago, IL, USA.
- [15] M. Agrawal\*, **M. Zitnik\***, J. Leskovec. Large-Scale Analysis of Disease Pathways in the Human Interactome. Poster session presented at Pacific Symposium on Biocomputing, PSB, Jan 3-7 2018, Hawaii, HI, USA. (\* first co-authors)
- [14] **M. Zitnik**, J. Leskovec. Predicting Multicellular Function Through Multi-Layer Tissue Networks. Poster session presented at International Conference on Intelligent Systems for Molecular Biology, ISMB/ECCB, Jul 21-25 2017, Prague, Czech Republic.
- [13] **M. Zitnik**, B. Zupan. Jumping Across Gene-Disease Contexts Using Compressive Data Fusion. Poster session presented at International Conference on Intelligent Systems for Molecular Biology, ISMB, Jul 8-12 2016, Orlando, FL, USA.
- [12] **M. Zitnik**, B. Zupan. Jumping Across Biomedical Contexts Using Compressive Data Fusion. Poster session presented at Pacific Symposium on Biocomputing, Jan 4-8 2016, Hawaii, HI, USA.
- [11] **M. Zitnik**, B. Zupan. Integrate Everything but the Kitchen Sink: Data Set Selection and Sensitivity Estimation in Collective Factor Models. Poster session presented at International Conference on Intelligent Systems for Molecular Biology, ISMB, Jul 10-14 2015, Dublin, Ireland.
- [10] **M. Zitnik**, E. A. Nam, C. Dinh, A. Kuspa, G. Shaulsky, B. Zupan. Gene Prioritization by Compressive Data Fusion and Chaining. Poster session presented at Basel Computational Biology Conference, [BC]<sup>2</sup>, Jun 7-10 2015, Basel, Switzerland.  
**Best poster award.**
- [9] 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. Poster session presented at International Specialised Symposium on Yeast, Oct 9-12 2014, Vipava, Slovenia.
- [8] **M. Zitnik**. Learning by Fusing Heterogeneous Data. Poster session presented at Heidelberg Laureate Forum, Sept 21-26 2014, Heidelberg, Germany.
- [7] **M. Zitnik**, E. A. Nam, C. Dinh, A. Kuspa, G. Shaulsky, B. Zupan. Data Fusion for Gene Prioritization. Poster session presented at International Conference on Intelligent Systems for Molecular Biology, ISMB, Jul 11-15 2014, Boston, MA, USA.
- [6] **M. Zitnik**, B. Zupan. Biomedical Data Fusion by Simultaneous Matrix Tri-factorization. Poster session presented at RECOMB, Apr 2-5 2014, Pittsburgh, PA, USA.  
**Best poster award.**

- [5] **M. Zitnik**, B. Zupan. Matrix Factorization-Based Data Fusion For Gene Function Prediction in Baker's Yeast and Slime Mold. Poster session presented at Pacific Symposium on Biocomputing, Jan 3-7 2014, Hawaii, HI, USA.
- [4] **M. Zitnik**, B. Zupan. Data Fusion by Matrix Factorization. Poster session presented at Machine Learning Summer School, Sept 25 2013, Max Planck Institute for Intelligent Systems, Tuebingen, Germany.
- [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. Poster session presented at 13th International Conference on Systems Biology, Aug 19-23 2012, Toronto, Canada.

### Theses

- [2] **M. Zitnik**. A Matrix Factorization Approach for Inference from Heterogeneous Data. B.Sc. Thesis, University of Ljubljana, 2012.  
**Summa cum laude.**  
**University Preseren's award for the best thesis work.**
- [1] **M. Zitnik**. Learning by Fusing Heterogeneous Data, Ph.D. Thesis, University of Ljubljana, 2015.  
**Summa cum laude.**  
**Jozef Stefan Golden Emblem Prize.**

### Tutorial & Workshop Co-Organizer

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

### Data Resources

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

### Science Outreach

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