Weixiong Zhang (Chair Professor in Bioinformatics and Integrative Genomics)



QUALIFICATIONS

PhD	University of California, Los Angeles	1994	Computer Science
MS	University of California, Los Angeles	1991	Computer Science
MS	Tsinghua University	1986	Computer Engineering
BS	Tsinghua University	1984	Computer Engineering

RIEF OUTLINE OF EXPERIENCE AND POSTS HELD				
Hong Kong Global STEM Scholar				
Chair Professor in Bioinformatics and Integrative Genomics, Dept of Health				
Technology and Informatics, The Hong Kong Polytechnic University, Hong Kong				
Professor, Dept of Computer Science and Engineering, School of Engineering,				
Dept of Genetics, School of Medicine, Washington University in St. Louis, USA				
Associate Professor, Dept of Computer Science and Engineering, School of				
Engineering, Dept of Genetics, School of Medicine, Washington University in St.				
Louis, USA				
Senior Scientist, Information Sciences Institute, University of Southern California,				
Los Angeles, USA				

RESEARCH INTERESTS

Genetics/Genomics: Genetic architecture and transcriptome of complex trait and disease

Noncoding RNA: Biogenesis and function of (small) noncoding transcript

Medical imaging: Segmentation of tumor and organs at risk

Disease study: Etiology and biomarker (e.g., cancer, neuronal and psychiatric disorders)

Big data analytics: Novel algorithm for massive (biological) data analysis

Artificial intelligence: Heuristic search, constraint satisfaction, and combinatorial optimization

SERVICE TO PROFESSIONAL & SCIENTIFIC BODIES, CONSULTANCY, MEMBERSHIP OF PROFESSIONAL & LEARNED SOCIETIES

Editorial Service (since 2000)

2011 – present	Deputy Editor, PLoS Computational Biology
2004 – present	Associate Editor, Artificial Intelligence Communication
2013 – present	Editorial Board Member, Biology Direct
2015 – 2016	Editorial Board Member, Nature Scientific Reports (Resigned)
2009 – 2015	Associate Editor, Artificial Intelligence
2007 – 2015	Editorial Board Member, Artificial Intelligence
2009 – 2012	Associate Editor, Journal of Alzheimer's Disease
2008 – 2011	Associate Editor, PLoS Computational Biology

Professional Service (since 2000)

Most years since 2000	Area Chair, SPC or PC, National Conf on Artificial Intelligence (AAAI)
Various years since 2003	Area Chair, SPC or PC, Intern. Joint Conf on Artificial Intelligence (IJCAI)
2004, 2008 – 11	PC, Intern. Conf. on Automated Planning and Scheduling (ICAPS)
2009, 2017 – 19	PC, Intern. Conf. on Intelligent Systems for Molecular Biology (ISMB)
2014 – 18	PC, RECOMB/ISCB Conf on Regulatory and Systems Genomics with
	DREAM Challenges
2011, 12, 14 – 18	PC, ISMB/Bioinformatics for Regulatory Genomics Special Interest
	Group Meeting (BioRegSIG)

Grant Review (since 2010)

2013, 15 – 21	External Reviewer, Hong Kong Health and Medical Research Fund (HMRF)
2010, 12 – 22	External Reviewer, Hong Kong Research Grants Council (RGC)
US NIH	e.g., NIH Director's New Innovator Award, RNA Biomarkers, Alzheimer's
	Center for Discovery of New Medicines, Neural Basis of Psychopathology,
	Lewy Body Dementia Center Without Walls, GTEx Stored Biospecimens,
	BioData Management and Analysis, and Molecular Neurogenetics
US NSF	e.g., BIGDATA and IIS

RESEARCH FUNDING:

More than US\$12 million in total and more than \$10 million as PI or co-PI since 2000, funding agents included US National Institutes of Health (NIH), US National Science Foundation (NSF), US Defense Advanced Research Project Agency (DARPA), US Department of Agriculture (USDA), International Alzheimer's Association, and Monsanto and Varian Corporations.

STUDENT TRAINING AND SUPERVISION:

- Trained 12 PhDs in the areas of computer science and computational biology, who landed academic jobs for teaching and research in universities in the US (e.g., UT San Antonio and the University of Missouri), started careers in research labs (e.g., Facebook AI Lab and Google Research) and leading pharmaceutical and agriculture and financial companies (e.g., Roche Pharmaceuticals, Monsanto, and Bank of America).
- Trained three postdocs, two are now professors (Fudan University in China and University Halle in Germany).
- Supervised about a dozen visiting scholars, most were from universities in China (e.g., Tsinghua University, Tianjin University, and Northeast University)

REPRESENTATIVE PUBLICATIONS (JOURNAL ARTICLES, BOOK CHAPTERS, MONOGRAPHS AND CONF PAPERS; TOTAL> 200):

Publications are grouped into research areas: <u>Genomics</u> and <u>transcriptomics</u>, <u>Noncoding RNA</u>, <u>Medical imaging</u>, <u>Big data analytics</u>, and <u>Artificial intelligence</u> (heuristic search, constraint satisfaction, and combinatorial optimization)

Research Monograph

• **W. Zhang**, *State-Space Search: Algorithms, Complexity, Extensions, and Applications*, Springer-Verlag, New York, NY, 1999.

Genetics, Genomics, and Transcriptomics

M. Chang, F. Womer, X. Gong, X. Chen, L. Tang, R. Feng, S. Dong, J. Duan, Y. Chen, R. Zhang, Y. Wang, S. Ren, Y. Wang, J. Kang, Z. Yin, Y. Wei, S. Wei, X. Jian, K. Xu, B. Cao, Y. Zhang, W. Zhang, Y. Tang, X. Zhang, F. Wang*, Identifying and validating subtypes within major psychiatric disorders based on frontal-posterior functional imbalance via deep learning, <u>Molecular Psychiatry</u>, 2021, accepted and published online on Nature website in October 2020. (Impact factor=15.992)

- L. Chen, J. Zhou, T. Li, Z. Fang, L. Li, G. Huang, L. Gao, X. Zhu, X. Zhou, H. Xiao, J. Zhang, Q. Xiong, J. Zhang, A. Ma, W. Zhai, W. Zhang*, and H. Peng*, GmoDetector: An accurate and efficient GMO identification approach and its application, <u>Food Research Intern.</u>, 149:110662, 2021. (Impact factor = 4.97)
- 3. L. Li, H. Peng, S. Tan, J. Zhou, Z. Fang, Z. Hu, L. Gao, T. Li, **W. Zhang***, and L. Chen*, Effects of early cold stress on gene expression in Chlamydomonas reinhardtii, *Genomics*, 112(2):1128-38, 2020. (Impact factor=6.205)
- 4. L. Li, G. Tian, H. Peng, D. Meng, L. Wang, X. Hu, C. Tian, M. He, J. Zhou, L. Chen, C. Fu, **W. Zhang*** and Z. Hu*, New class of transcription factors controls flagellar assembly by recruiting RNA polymerase II in *Chlamydomonas*, *Proc of National Academy of Sciences of the USA* (*PNAS*), 115(17):4435-4440, 2018. (Impact factor=11.205)
- L. Li, Z. Fang, J. Zhou, H. Chen, Z. Hu, L. Gao, L. Chen, S. Ren, H. Ma, L. Lu, W. Zhang* and H. Peng*, An accurate and efficient method for large-scale SSR genotyping and applications, <u>Nucleic Acids</u> <u>Research</u>, 45(10):e88, 2017. (Impact factor=16.971)
- T.P. Michael, D. Bryant, R. Gutierrez, N. Borisjuk, P. Chu, H. Zhang, J. Xia, J. Zhou, H. Peng, M.E. Baidouri, B. ten Hallers, AR. Hastie, T. Liang, K. Acosta, S. Gilbert, C. McEntee, SA. Jackson, TC. Mockler, W. Zhang and E. Lam*, Comprehensive definition of genome features in *Spirodela polyrhiza* by high-depth physical mapping and short-read DNA sequencing strategies, *The Plant Journal*, 89(3):617-35, 2017. (Impact factor=6.141)
- D. Tiosano, L. Audi, S. Climer, W. Zhang, A.R. Templeton*, M. Fernandez-Cancio, R. Gershoni-Baruch, J.M. Sanchez-Muro, M.E. Kholy, Z. Hochberg, Latitudinal Clines of the human Vitamin D receptor and skin color-genes, <u>Genes, Genomes, Genetics</u>, 6(5):1251-66, 2016. (Based on the work that <u>received Henning Anderson Price</u> at the European Society for Paediatric Endocrinology 51st Annual Meeting) (Impact factor=2.781)
- 8. S. Climer*, A. Templeton and **W. Zhang***, Human *gephyrin* is encompassed within giant functional noncoding yin-yang sequences, *Nature Communications*, 6:6534, 2015. (Impact factor=14.919)
- 9. W. Wang, B. Feng, J. Xiao, Z. Xia, X. Zhou, P. Li, **W. Zhang**, et al., Cassava genome from a wild ancestor to cultivated varieties, *Nature Communications*, 5:5110, 2014. (Impact factor=14.919)
- S. Climer, A. Templeton and W. Zhang*, Allele-specific network reveals combinatorial interactions that transcends small effects in psoriasis GWAS, <u>PLOS Computational Biology</u>, 10(9):e1003766, 2014. (Impact factor=4.475)
- Z. Chen and W. Zhang*, Integrative analysis using module-guided Random Forests reveals correlated genetic factors related to mouse weight, <u>PLOS Computational Biology</u>, 9(3):e1002956, 2013. (Impact factor=4.475)
- J.A. Webster, J.R. Cibbs, J. Clarke, M. Ray, W. Zhang, P. Holmans, K. Rohrer, A. Zhao, L. Marlowe, M. Kaleem, D.S. McCorquodale III, C. Cuello, D. Leung, L. Bryden, P. Nath, V.L. Zisman, K. Joshipura, M.J. Huentelman, D. H Lince, K.D. Coon, D.W. Craig, J.V. Pearson, C.B. Heward, E.M. Reiman, D. Stephan, J. Hardy, A.J. Myers*, Genetic control of human brain transcript expression in Alzheimer's disease, *American J. of Human Genetics*, 84:445-58, 2009. (Impact factor=11.025)
- 13. S. Climer, G. Jaegerg, A. Templeton and **W. Zhang***, How frugal is mother nature with haplotypes? *Bioinformatics*, 25(1):68-74, 2009. (Impact factor=6.937)
- 14. M. Ray J. Ruan and **W. Zhang***, Variations in the transcriptome of Alzheimer's disease reveal molecular networks involved in cardiovascular diseases, *Genome Biology*, 9(10):R148, 2008. (Impact factor=13.583)
- 15. M. Ray, S. Dharmarajan, J. Freudenberg, **W. Zhang*** and G.A. Patterson*, Use of gene expression profiling and machine learning to understand primary graft dysfunction, *American J. of Transplantation*, 7:2396-405, 2007. (Impact factor=8.086)

- 16. X. Zhou, J. Ruan, G. Wang and **W. Zhang***, Characterization and identification of microRNA core promoters in four model species, <u>PLoS Computational Biology</u>, 3(3):e37, 2007. (Impact factor=4.475)
- 17. H. Zeng, L. Luo, **W. Zhang**, J. Zhou, Z. Li, H. Liu, T. Zhu, X. Feng and Y. Zhong*, PlantQTL-GE: A database for searching candidate genes by gene expression and QTL information, *Nucleic Acids Research*, 35:D879-D882, 2007. (Impact factor=16.971)
- 18. G. Wang and W. **Zhang***, A steganalysis-based approach to comprehensive identification and characterization of functional regulatory elements, *Genome Biology*, 7(6):R49, 2006. (Impact factor=13.583)
- 19. J.Ruan and **W. Zhang***, A two-dimensional regression tree approach to the modeling of gene expression regulations, *Bioinformatics*, 22(3):332-40, 2006. (Impact factor=6.937)
- 20. **W. Zhang***, J.Ruan, T-h. D.Ho, Y. You, T. Yu and R.S. Quatrano, Cis-regulatory element based targeted gene finding: Genome-wide identification of ABA and abiotic stress responsive genes in Arabidopsis thaliana, *Bioinformatics*, 21(14):3074-81, 2005. (Impact factor=6.937)
- 21. G. Wang, T. Yu and W. **Zhang***, WordSpy: Identify transcription factor biding motifsby building a dictionary and learning a grammar, <u>Nucleic Acids Research</u>, 33:W4126, 2005. (Impact factor=16.971)
- 22. J. Ruan, G. Stormo and **W. Zhang***, ILM: A web server for predicting RNA secondary structures with pseudoknots, *Nucleic Acids Research*, 32:W146-9, 2004. (Impact factor=16.971)
- 23. J. Ruan, G. Stormo and **W. Zhang***, An iterated loop matching approach to the prediction of RNA secondary structures with pseudoknots, *Bioinformatics*, 20(1):58-66, 2004. (Impact factor=6.937)

Noncoding RNA (microRNA, siRNA, circular RNA)

- X. Liu, J. Frost, A. Bowcock, W. Zhang*, Canonical and interior circular RNAs function as competing endogenous RNAs in psoriatic skin, <u>Intern. J. Molecular Sciences</u>, 22(10), 5182, 2021. (Impact factor=5.923)
- 2. X. Liu, Z. Hu, J. Zhou, C. Tian, G. Tian, M. He, L. Gao, L. Chen, T. Li, P. Peng, **W. Zhang***, Interior circular RNA, *RNA Biology*, 17(1):87-97, 2020. (Impact factor=5.350)
- 3. Y. Zhong, P. Xuan*, X. Wang, T. Zhang, J. Li, Y. Liu and **W. Zhang**, A non-negative matrix factorization based method for predicting disease-associated miRNAs in miRNA-disease bilayer network, *Bioinformatics*, 34(2):267-77, 2018. (Impact factor=6.937)
- 4. J. Xia, L. Li, T. Li, Z. Fang, K. Zhang, J. Zhou, H. Peng, and **W. Zhang***, Detecting and characterizing microRNAs of diverse genomic origins via miRvial, *Nucleic Acids Research*, 45(21):e176, 2017. (Impact factor=16.971)
- 5. D. Nie, J. Xia, C. Jiang, B. Qi, X. Ling, S. Lin, **W. Zhang**, J. Guo, H. Jin and H. Zhao, Bacillus cereus AR156 primes induced systemic resistance by suppressing miR825/825* and activating defense related genes in Arabidopsis, *J. Integrative Plant Biology*, 58(4):426-39, 2015. (Impact factor=5.86)
- 6. J. Xia and **W. Zhang***, MicroRNAs in normal and psoriatic skin, *Physiological Genomics*, 46(4):113-22, 2014, <u>invited review</u>. (Impact factor=3.107)
- J. Xia and W. Zhang*, A meta-analysis revealed insights into the sources, conservation and impact
 of microRNA 5'-isoforms in four model species, <u>Nucleic Acids Research</u>, 42(3):1427-41, 2014.
 (Impact factor=16.971)
- 8. J. Xia, C.E. Joyce, A.M. Bowcock* and **W. Zhang***, Noncanonical microRNAs and endogenous siRNAs in normal and psoriatic human skin, <u>Human Molecular Genetics</u>, 22(4):737-48, 2013. (Impact factor=6.150)
- 9. X. Zhang, X. Jin, Y. Lii, B.E. Barrera-Figueroa, X. Zhou, S. Gao, L. Lu, D. Nie, Z. Chen, C. Leung, T. Wong, H. Zhang, J. Guo, Y. Li, R. Liu, W. Liang, J-K. Zhu, **W. Zhang***, H. Jin*, Genome-wide analysis of plant nat-siRNAs reveals insights into their distribution, biogenesis and function, *Genome*

- Biology, 13:R20, 2012. (Impact factor=13.583)
- 10. Y. Zheng*, Y-F. Li, R. Sunkar and **W. Zhang**, SeqTar: An effective method for identifying microRNA guided cleavage sites from degradome of polyadenylated transcripts in plants, *Nucleic Acids Research*, 40(4):e28, 2012. (Impact factor=16.971)
- 11. C.E. Joyce, X. Zhou, J. Xia, C. Ryan, B. Thrash, A. Menter, **W. Zhang*** and A.M. Bowcock*, Deep sequencing of small RNAs from human skin reveals major alterations in the psoriasis miRNAome, *Human Molecular Genetics*, 20(20):4025-40, 2011. (Impact factor=6.150)
- 12. **W. Zhang***, S. Guo, J. Xia, X. Zhou, P. Chellappan, X. Zhou, X. Zhang and H. Jin*, Multiple distinct small RNAs originated from the same microRNA precursors, *Genome Biology*, 11:R81, 2010. (Impact factor=13.583)
- 13. P. Chellappan, J. Xia, X. Zhou, S. Gao, X. Zhang, G. Coutino, F. Vazquez, **W. Zhang*** and H. Jin*, siRNAs from miRNA sites mediate DNA methylation of target genes, *Nucleic Acids Research*, 38(20):6883-94, 2010. (Impact factor=16.971)
- 14. C. Zeng, W. Wang, Y. Zheng, X. Chen, X. Bo, S. Song, **W. Zhang***, M. Peng*, Conservation and divergence of microRNAs and their functions in Euphorbiaceous plants, *Nucleic Acids Research*, 38(3):981-95, 2010. (Impact factor=16.971)
- T.A. Reese, J. Xia, L.S. Johnson, X. Zhou, W. Zhang* and H.W. Virgin*, Identification of novel microRNA-like molecules generated from herpesvirus and host tRNA transcripts, <u>J. Virology</u>, 84(19):10344-53, 2010. (Impact factor=4.501)
- 16. Y-F. Li, Y. Zheng, C. Addo-Quaye, L. Zhang, A. Saini, G. Jagadeeswaran, M. Axtell, **W. Zhang**, R. Sunkar*, Transcriptome-wide identification of microRNA targets in rice, *The Plant Journal*, 62(5):742-59, 2010. (Impact factor=6.141)
- X. Zhou, R. Sunkar, H. Jin, J-K. Zhu and W. Zhang*, Genome-wide identification and analysis of small RNAs originated from natural antisense transcripts in *Oryza sativa*, *Genome Research*, 19:70-8, 2009. (Impact factor=11.093)
- G. Jagadeeswaran, Y. Zheng, Y-f. Li, L.I. Shukla, J. Matts, P. Hoyt, S.L. Macmil, G.B. Wiley, B.A. Roe, W. Zhang, R. Sunkar*, Cloning and characterization of small RNAs from Medicago truncatula reveals novel legume-specific and candidate microRNAs, <u>New Phytologist</u>, 184(1):85-98, 2009. (Impact factor=8.512)
- 19. Y. Xu, X. Zhou and **W. Zhang***, MicroRNA prediction with a novel ranking algorithm based on random walks, *Bioinformatics*, 24:i50-8, 2008. (Impact factor=6.937)
- 20. X. Zhou, G. Wang and **W. Zhang***, UV-B light responsive microRNA genes in Arabidopsis thaliana, *Molecular Systems Biology*, 3:103, 2007. (Impact factor=11.429)

Medical imaging

- 1. Z. Zhang, T. Zhao, H. Gay, **W. Zhang***, B. Sun*, Weaving attention U-net: A novel hybrid CNN and attention-based method for organs-at-risk segmentation in head and neck CT images, <u>Medical Physics</u>, 48:7052-62, 2021. (Impact factor=4.071)
- 2. Z. Zhang, T. Zhao, H. Gay, **W. Zhang***, B. Sun*, ARPM-net: A novel CNN-based adversarial method with Markov Random Field enhancement for prostate and organs at risk segmentation in pelvic CT images, *Medical Physics*, 48(1):227-37, 2021. (Impact factor=4.071)
- 3. D. Lam, X. Zhang, H. Li, Y. Deshan, B. Schott, T. Zhao, **W. Zhang**, S. Mutic, and B. Sun*, Predicting gamma passing rates for portal dosimetry-based IMRT QA using machine learning, *Medical Physics*, 46(10):4666-75, 2019. (Impact factor=4.071)

Big data analytics – Journal

1. D. He, C. Liang, C. Huo, Z. Feng, D. Jin, L. Yang, and **W. Zhang**, Analyzing heterogeneous networks with missing attributes by unsupervised contrastive learning, <u>IEEE Trans. On Neural Networks and Learning Systems</u>, in press. (Impact factor=8.793)

- 2. D. Jin, Z. Yu, P. Jiao, S. Pan, D. He, J. Wu, P. Yu, and **W. Zhang**, A survey of community detection approaches: From statistical modeling to deep learning, *IEEE Trans. on Knowledge and Data Engineering*, in print, available online. (Impact factor=6.977)
- 3. M. Li, D. Jin, D. He, and **W. Zhang**, Modeling with node popularities for autonomous overlapping community detection, <u>ACM Transactions on Information Systems</u>, 11(3):27, 2020. (Impact factor=2.889)
- 4. X. Wang, D. Jin, D. He, and **W. Zhang**, Robust detection of link communities with summary description in social networks, *IEEE Transactions on Knowledge and Data Engineering*, 2019, doi: 10.1109/TKDE.2019.2958806. (Impact factor=6.977)
- L. Yang, Y. Wang, J. Gu, X. Cao, X. Wang, D. Jin, G. Ding, J. Han, and W. Zhang, Autonomous semantic community detection via adaptively weighted low-rank approximation, <u>ACM Transactions on Multimedia Computing, Communications, and Applications</u> (TOMM), 15(3s), 2019. (Impact factor=3.275)
- 6. X. Zhang*, J. Han and W. **Zhang**, An efficient algorithm for finding all possible input nodes for controlling complex networks, *Scientific Reports*, 7(1):10677, 2017. (Impact factor=4.379)
- 7. D. He, D. Jin, Z. Chen and **W. Zhang***, Identification of hybrid node and link communities in complex networks, *Scientific Reports*, 5:8638, 2015. (Impact factor=4.379)
- 8. J. Fu, **W. Zhang** and J. Wu*, Identification of leader and self-organizing communities in complex networks, *Scientific Reports*, 7(1):704, 2017. (Impact factor=4.379)
- 9. S. Climer and **W. Zhang**, Rearrangement clustering: Pitfalls, remedies and applications, <u>J. Machine</u> <u>Learning Research</u>, 7:919-43, 2006. (Impact factor=4.091)

Big data analytics – Peer-reviewed Conferences

Note: IJCAI and AAAI are two leading International AI Confs that adopt double-blind reviews and whose acceptance rates are typically around 20%

- 1. D. He, Y. Song, D. Jin, Z. Feng, B. Zhang, Z. Yu and **W. Zhang**, Community-centric graph Convolutional Network for unsupervised community detection, *Proc 29-th Intern. Joint Conf. on AI* (IJCAI-20).
- 2. D. Jin, B. Li, P. Jiao, D. He and **W. Zhang**, Network-specific variational Auto-Encoder for embedding of attribute networks, *Proc 28-th Intern. Joint Conf. on AI* (IJCAI-19).
- 3. D. Jin, Z. Liu, W. Li, D. He and **W. Zhang**, Graph convolutional networks meet Markov Random Fields: Semi-supervised community detection in attribute networks, *Proc 33-th AAAI Conf on AI* (AAAI-19).
- 4. G. Meng, D. Jin and **W. Zhang**, Integrative network embedding via deep joint reconstruction, *Proc* 27-th Intern. Joint Conf. on AI (IJCAI-18).
- 5. D. He, X. You, Z. Feng, D. Jin, X. Yang and **W. Zhang**, A network-specific Markov Random Field approach to community detection, *Proc 32-nd AAAI Conf on AI* (AAAI-18).
- 6. D. Jin, X. Wang, R. He, D. He and **W. Zhang**, Robust detection of link communities in large social networks by exploiting link semantics, *Proc 32-nd AAAI Conf on AI* (AAAI-18).
- 7. D. He, D. Jin and **W. Zhang**, Joint identification of network communities and semantics via integrative modeling of network topologies and node contents, *Proc 31-st AAAI Conf on AI* (AAAI-17).
- 8. L. Yang, X. Cao, D. He, **W. Zhang**, Modularity based community detection with deep learning, *Proc 25-th Intern. Joint Conf. on AI* (IJCAI-16), Buenos Aires, July 25-31, 2016
- 9. D. Jin, H. Wang, J. Dang, D. He and **W. Zhang**, Detect overlapping communities via ranking node popularities, *Proc 30-th AAAI Conf on AI* (AAAI-16)

- 10. X. Wang, D. Jin, X. Cao, L. Yang and **W. Zhang**, Semantic community identification in large attribute networks, *Proc 30-th AAAI Conf on AI* (AAAI-16)
- 11. Z. Chen, M. Chen, K. Weinberger and **W. Zhang**, Marginalized denoising for link prediction and multi-label learning, *Proc. 29th AAAI Conf on Artificial Intelligence* (AAAI-15)
- 12. D. Jin, Z. Chen, D. He and **W. Zhang**, Modeling with node degree preservation can accurately find communities, *Proc. 29th AAAI Conf on Artificial Intelligence* (AAAI-15)
- 13. D. He, D. Liu, D. Jin and **W. Zhang**, A stochastic model for the detection of heterogeneous link communities in complex networks, *Proc. 29th AAAI Conf on Artificial Intelligence* (AAAI-15)
- 14. Z. Chen and **W. Zhang** (2014) A marginalized denoising method for link prediction in relational data, *Proc. SIAM Intern. Conf. on Data Mining* (SDM-14)
- 15. Z. Chen and **W. Zhang** (2013) Domain adaptation with topical correspondence learning, *Proc. 23rd Intern. Joint Conf. on Artificial Intelligence* (IJCAI-13)
- 16. X. Zhou, J. Ruan and **W. Zhang** (2010) Promoter prediction based on a multiple instance learning scheme, *ACM Intern. Conf. on Bioinformatics and Computational Biology*, Aug. 2-4, 2010
- 17. S. Climer, A. Templeton and **W. Zhang** (2010) SplittingHeirs: Inferring haplotypes by optimizing resultant dense graphs, *ACM Intern. Conf. on Bioinformatics and Computational Biology*, 2010
- J. Ruan and W. Zhang (2007) An efficient spectral algorithm for network community discovery and its applications to biological and social networks, *Proc. IEEE Intern. Conf. on Data Mining* (ICDM-2007), 2007.
- 19. J. Ruan and **W. Zhang** (2006) Identification and evaluation of weak community structures in networks, *Proc. 21st National Conf. on Artificial Intelligence*, (AAAI-2006)
- 20. G. Wang and **W. Zhang*** (2005) Build a dictionary, learn a grammar, decipher stegoscripts, and discover genomic regulatory elements, *Proc. of 1st Annual RECOMB Satellite Workshop on Systems Biology and the Second Annual RECOMB Satellite Workshop on Regulatory Genomics*, 2005.
- 21. X. Zhou, J. Ruan, G. Wang and **W. Zhang*** (2005) Computational characterization and identification of core promoters of microRNA genes in C. elegans, H. sapiens and A. thaliana, *Proc. of 1st Annual RECOMB Satellite Workshop on Systems Biology and the Second Annual RECOMB Satellite Workshop on Regulatory Genomics*, 2005.
- 22. S. Climer and **W. Zhang** (2004) Take a walk and cluster genes: A TSP-based approach to optimal rearrangement clustering, *Proc. Intern. Conf. on Machine Learning* (ICML-2004)
- 23. J. Buhler, R. Souvenir, **W. Zhang** and R. Mitra (2004) Design of a high-throughput assay for alternative splicing using polymerase colonies, *Proc. Pacific Symposium on Biocomputing*, (PSB-2004), 2004
- 24. R. Souvenir, J. Buhler, G. Stormo and **W. Zhang*** (2003) Selecting degenerate multiplex PCR primers, *Proc. Workshop on Algorithms in Bioinformatics* (WABI-2003), 2003.
- 25. **W. Zhang** (2000) Association-based multiple imputation in multivariate datasets: A summary, *Proc of 16th Intern. Conf on Data Engineering* (ICDE-2000), 2000

Artificial intelligence (Heuristic search, constraint satisfaction, optimization) – Journal

Note: Artificial Intelligence and J. of Artificial Intelligence Research (JAIR) are two leading Intern. journals for the field of AI.

- 1. Q. Lu, R. Huang, Y. Chen, Y. Xu, **W. Zhang**, G. Sun and G. Chen, A SAT-based approach to cost sensitive temporally expressive planning, <u>ACM Transactions on Intelligent Systems and Technology</u>, 5(1):18, 2013. (2018 Impact factor=2.861)
- 2. R. Huang, Y. Chen and **W. Zhang** (2012) SAS+ planning as Satisfiability, <u>J. Artificial Intelligence</u> <u>Research</u>, 43:293-328, 2012 (the AAAI-2010 <u>Outstanding Paper Award</u>). (Impact factor=2.441)

- 3. G. Jaeger and **W. Zhang** (2010) An efficient algorithm for and phase transitions of the directed Hamiltonian cycle problem, *J. Artificial Intelligence Research*, 39:663-87, 2010. (Impact factor=2.441)
- 4. Y. Chen, R. Huang, Z. Xing and **W. Zhang** (2009) Long-distance mutual exclusion for planning, *Artificial Intelligence*, 173:365-91, 2009. (Impact factor=6.628)
- 5. S. Climer and **W. Zhang** (2006) Cut-and-solve: A linear search strategy for combinatorial optimization problems, *Artificial Intelligence*, 170(8-9):714-38, 2006. (Impact factor=6.628)
- 6. R. Korf, **W. Zhang**, I. Thayer and H. Hohwald (2005) Frontier search, *J. ACM*, 52(5):71548, 2005. (2018 Impact factor=4.55; this is a leading journal in theoretical computer science)
- 7. Z. Xing and **W. Zhang** (2005) MaxSolver: An efficient exact algorithm for maximum satisfiability, Artificial Intelligence, 164(1-2):47-80, 2005. (Impact factor=6.628)
- 8. **W. Zhang**, G. Wang, Z. Xing and L. Wittenberg (2005) Distributed stochastic search and distributed breakout: Properties, comparison and applications to constraint optimization problems in sensor networks, *Artificial Intelligence*, 161(1-2):55-87, 2005. (Impact factor=6.628)
- 9. **W. Zhang** (2004) Configuration landscape analysis and backbone guided local search: Part I: satisfiability and maximum satisfiability, <u>Artificial Intelligence</u>, 158(1):1-26, 2004. (Impact factor=6.628)
- 10. A. K. Sen, A. Bagchi and **W. Zhang** (2004) Average-case analysis of best-first search in directed acyclic graphs, *Artificial Intelligence*, 155(1-2):183-206, 2004. (Impact factor=6.628)
- 11. **W. Zhang** (2004) Phase transitions and backbones of the asymmetric Traveling Salesman Problem, *J. Artificial Intelligence Research*, 20:471-97, 2004. (Impact factor=2.441)
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