# Weixiong Zhang

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## **Professional Experience**

- *Professor* (6/2007 present) Department of Computer Science and Engineering, Washington University in St. Louis, St. Louis, MO, USA
- Professor (1/2008 present) Department of Genetics, Washington University School of Medicine, St. Louis, MO, USA
- Associate Professor (8/2000 5/2007) Department of Computer Science and Engineering, Washington University in St. Louis, St. Louis, MO, USA
- Associate Professor (7/2001 12/2007) Department of Genetics, Washington University School of Medicine, St. Louis, MO, USA
- Research Assistant Professor (5/1995 8/2000) Computer Science Department, University of Southern California, Los Angeles, CA, USA
- Senior Research Scientist (10/1994 8/2000) Information Sciences Institute, University of Southern California, Los Angeles, CA, USA

### Education

٠	Ph.D. in Computer Science, University of California, Los Angeles (UCLA)	(6/1994)
•	M.S. in Computer Science, University of California, Los Angeles (UCLA)	(11/1991)
•	M.S. in Computer Engineering, Tsinghua University, Beijing, China	(3/1986)

• *B.S.* in Computer Engineering, Tsinghua University, Beijing, China (6/1984)

# Honors / Awards

- *Henning Anderson Price* for the highest rated basic abstract at the European Society for Paediatric Endocrinology 51<sup>st</sup> Annual Meeting. (from 1,012 abstracts by a double-blind review)
- *Outstanding Paper Award*, The AAAI National Conference on Artificial Intelligence, Atlanta, GA, July, 11-15, 2010. (from 984 submissions by a double-blind review)
- *First Place Award*, Optimal Planning Track of the Fifth International Planning Competition, hosted at *The 16th International Conference on Automated Planning and Scheduling (ICAPS 2006)*, June 6-10, English Lake District, Cumbria, UK. (2006)
- Best Paper Award, A multi-agent operator interface for unmanned aerial vehicles, The 18th AIAA Digital Avionics Systems Conference, St. Louis, MO, October 24-29 (1999)
- Paper at International Conference on Multi-Agent Systems (ICMAS-98) selected to Autonomous Agents and Multi-Agent Systems special issue of Best of ICMAS-98 (1998)
- UCLA Chancellor's Dissertation Fellowship, UCLA (1993–1994)
- *GTE Graduate Fellowship*, GTE Corporation (1992–1993)
- Student Author Scholarships, National Association on AI (1992, 1993, 1994)
- *Graduate Fellowship*, UCLA (1990–1992)

## **Professional Service – Editorial Duties**

- PLoS Computational Biology, Deputy Editor, 2011 present; Associate Editor, 2008 2011.
- Biology Direct, Editorial Board Member, 2013 present.
- Artificial Intelligence, Associate Editor, 2009 2015; Editorial Board Member, 2007 2015
- *Artificial Intelligence Communication The European Journal on Artificial Intelligence*, <u>Associate Editor</u>, 2004 present.
- *Scientific Reports* (by Nature Publishing Group), <u>Editorial Board Member</u> in the area of molecular biology, 2015 2016. (resigned in January, 2016, due to different opinions on publication policies)
- Journal of Alzheimer's Disease, Associate Editor, 2009 2012.
- Journal of Artificial Intelligence Research, Editorial Board Member, 2005 2009.
- The Open Systems Biology Journal, Advisory Board Member, 2008 2010.3; resigned in 2010.3.
- Guest Editor, Artificial Intelligence special issue on Heuristic Search, vol.129, no.1-2, 2001.
- <u>Book Editor</u>, *Distributed Constraint Problem Solving and Reasoning in Multi-agent Systems*, editors, Weixiong Zhang and Volker Sorge, IOS Press, 2004.
- <u>Lecture Notes Editor</u>, *Search Techniques for Problem Solving under Uncertainty and Incomplete Information*, editors, Weixiong Zhang and Sven Koenig, AAAI Press, 1999.

## Keynote Speech, Invited Talks and Seminars, Tutorials and Presentations

- Plenary talk, Computational ncRNAomics: Accomplishments and challenges, *Symposium on Development and Applications of New Technologies and Methods for RNA Research*, Shanghai, China, Sept. 10-11, 2013, organized by Chinese Academy of Sciences.
- Invited talk, Sources, causes and consequences of microRNA isoforms, *The 4<sup>th</sup> Conf. on Technologies and Applications of small RNAs (RNAi China)*, June 20-23, Kunshan, Jiangsu, China.
- Keynote speech, Systems-biology approach to Alzheimer's disease, *IEEE Intern. Conf. on Systems Biology*, Zhuhai, China, Sept. 2-4, 2011
- Invited talk, Transcriptome analysis to identify plant microRNAs responding environmental stress. *International Bioinformatics Workshop* (IBW-2011), Xi'an, China, July 7-10,
- Keynote speech, Where microRNAs originate, *The Annual National Conference of Chinese RNA Society*, Guangzhou, China, Oct. 19-20, 2010.
- Invited talk, A steganographic approach to genome-wide motif finding and its applications, *ISMB-2010/Bioinformatics for Regulatory Genomics Special Interest Group Meeting*, Boston, MA, July 10, 2010.
- Invited talk, Identification of cis-element modules and characterization of their roles in tissue- and stressspecific gene expression regulation, *The 9<sup>th</sup> International Plant Molecular Biology Congress Symposium on Transcription Factors*, St. Louis, MO, Oct. 30, 2009.
- Invited talk, Transcriptional and posttranscriptional regulatory networks underlying plant abiotic stress response, *Gordon Research Conferences: Salt and Water Stress in Plants*, Big Sky, MT, Sept. 7-12, 2008.
- Invited talk, MicroRNAs in Cassava: their conservation and possible functions for abiotic stress response, *Global Cassava Partnership First Scientific Meeting*, Ghent University, Belgium, July 21-25, 2008. (cancelled due to family reason)
- Invited talk, Integrated computational analysis of microRNA transcriptional regulation *NSF/IPAM Workshop* on Search and Knowledge Building for Biological Datasets, Los Angeles, CA, Nov. 26-30, 2007.
- Invited talk, Identification of communities in large networks and applications, IBM Watson Research Center, Nov. 1, 2007
- Invited seminar talk, Identification of stress-inducible microRNA genes in plants: A computational approach, Program in Molecular and Computational Biology, University of Southern California, Oct. 4, 2007.

- Invited seminar talk, Genome-wide motif identification and applications, Department of Computer Science, University of California at Los Angeles, Oct. 2, 2007.
- Invited talk, How robust is pure parsimony haplotype inference? *The 3rd RECOMB Satellite Workshop on Computational Methods for SNPs and Haplotypes*, Los Angeles, CA, Jan. 27-28, 2007.
- Invited talk, Data mining methods for modeling gene expression regulation and their applications, *IEEE International Conference on Data Mining* (ICDM-2006), Hong Kong, Dec. 18-22, 2006.
- Invited seminar talk, Finding stress inducible microRNA genes in plants, Fall 2006 Seminar Series, Department of Genetics, Washington University School of Medicine, St. Louis, MO, Oct. 12, 2006.
- Invited talk, Phase transitions and backbones in combinatorial optimization problems and heuristic search methods, *Symp. on Hybrid Methods and Branching Rules in Combinatorial Optimization*, Montreal, Canada, Sept. 18-22, 2006.
- Keynote speech, Phase transitions and backbones in combinatorial optimization problems and heuristic search methods, *The 9th Pacific Rim International Conference on Artificial Intelligence* (PRICAI-2006), Guiling, China, August 7-11, 2006.
- Invited talk, Phase transitions and backbones in combinatorial optimization problems, *Workshop on Hybrid Methods and Branching Rules in Combinatorial Optimization*, Sept. 18-22, 2006.
- Invited talk, Discovering temporal gene regulatory networks, NSF/IPAM (Proteomics: Sequence, Structure, Function) *Workshop on High Throughput Technologies and Methods of Analysis*, University of California at Los Angeles, California, March 22-26, 2004.
- Invited talk, Genome-wide identification and analysis of regulatory elements of ABA-and stree-inducible genes in Arabidopsis and rice, *International Symposium on Plant Functional Genomics*, Taipei, Taiwan, November 17-19, 2003.
- Keynote speech, Exploiting phase transitions and backbones for efficient problem solving, *The 15th International Conference on Tools for Artificial Intelligence* (ICTAI-2003), Sacramento, CA, USA, November 3-5, 2003.
- Invited talk, Phase Transitions and Backbones of Combinatorial Optimization Problems and Heuristic Search, *The 18th International Joint Conference on Artificial Intelligence Workshop on Stochastic Search Algorithms*, Acapulco, Mexico, Aug. 9, 2003.
- Invited Lecture, Phase transitions, backbones, measurement precision, and phase-inspired approximation, NSF/UCLA Institute for Pure and Applied Mathematics Workshop on Phase Transitions and Algorithmic Complexity, University of California at Los Angeles, California, June 3 -5, 2002.
- Tutorial, Phase Transitions and Structures in Combinatorial Problems, *The 18th National Conference on Artificial Intelligence* (AAAI-2002), Edmonton, Alberta, Canada, July 28August 1, 2002.
- Tutorial, Phase Transitions and Structures in Combinatorial Problems, *The 17th International Joint Conference on Artificial Intelligence* (IJCAI-2001), Seattle, Washington, August 4-10, 2001.
- Invited seminar, Combinatorial optimization: Complexity, phase transitions, backbones and flexible computation, U.S. Air Force Research Labs, Rome, NY, June 18, 2001.
- Invited seminar, Best-first search vs. dynamic programming for multiple sequence alignment, U.S. Air Force Research Labs, Rome, NY, June 18, 2001; also invited to give the same talk at Cornell University on June 19, 2001.
- Invited seminar, Datamining and search techniques, School of Computing, Georgia Tech, May, 1999.
- Invited plenary presentation, *SPIE Symposium on Data Mining and Knowledge Discovery: Theory, Tools, and Technology*, Orlando, Florida, April 5-6, 1999.
- Invited plenary presentation, AAAI Fall Symposium on Flexible Computation in Intelligent Systems: Results, Issues, and Opportunities, November 9-11, 1996, Cambridge, MA.

Professional Service – Grant Review (list only since 2010)

• National Institutes of Health - NIH, Proposal Review Panelist

- o Alzheimer's Center for Discovery of New Medicines, 2019
- o Special Emphasis Review Panel, 2019, 2018, 2017, 2016.
- Neural Basis of Psychopathology, Addictions and Sleep Disorder Study Section, 2016.
- o RNA Biomarkers Review Panel, 2013, 2014.
- o GTEx Stored Biospecimens Study Section Review Panel, 2013.
- o BioData Management and Analysis (BDMA) Study Section Review Panel, 2011.
- o Molecular Neurogenetics (MNG) Study Section Review Panel, 2010.
- National Science Foundation NSF, Proposal Review Panelist
  - BIGDATA Program, 2016; 2015; 2012
  - o IIS Panel on Graph Data Analytics, 2016
- The Government of Hong Kong, Proposal Review Panelist
  - o Health and Medical Research Fund, 2019, 2018, 2017, 2016, 2015, 2014, 2013
  - o Research Grants Council (RGC), 2019, 2018, 2017, 2016, 2015, 2014, 2013, 2012, 2010
- The European Union, Large-scale European Research Initiative, Panelist,
  - Human Brain Project (HBP), 2014.

## Professional Service – Major AI Conferences (list only since 2000)

- The AAAI National Conference on Artificial Intelligence AAAI
  - o Area Chair: 2019; 2018
  - o Senior program committee member: 2017; 2016; 2015; 2005; 2003; 2002
  - o Program committee member: 2008; 2007; 2006; 2000; 1996
- The International Joint Conference on Artificial Intelligence IJCAI
  - Area Chair: 2015.
  - Senior program committee member: 2018; 2013.
  - o Program committee member: 2009; 2005 (post session); 2003
- The International Conference on Automated Planning and Scheduling ICAPS
  - o Program committee member: 2011; 2010; 2009; 2008; 2004
- The International Symposium on Combinatorial Search SoCS
  - Program committee member: 2011; 2010; 2009

# Professional Service – Major Computational Biology Conferences (affiliated since 2010)

- The International Conference on Intelligent Systems for Molecular Biology ISMB
  - Program committee member: 2019; 2018; 2017; 2009.
- International Conference on Algorithms for Computational Biology AICoB
  - Program committee member: 2017; 2016.
- RECOMB/ISCB Conference on Regulatory and Systems Genomics with DREAM Challenges
  - Program committee member: 2018; 2017; 2016; 2015; 2014.
- ISMB/Bioinformatics for Regulatory Genomics Special Interest Group Meeting BioRegSIG
  - Program committee member: 2018; 2017; 2016; 2015; 2014; 2012; 2011.

# **Research Funding** (> <u>\$12 million total</u>, > <u>\$10 million as PI and co-PI</u>)

• Accurate semantic image segmentation by integrating deep learning and Markov random fields modeling and its application to Varian image system (\$174,000, 5/1/2019 – 4/30/2021) Weixiong Zhang (PI), Baozhou Sun (co-PI). Funding source: Varian Corp.

- *Mendelian randomization for unbias biomarker discovery for AD and other complex diseases* (\$1,850,000, 9/15/2018 5/31/2023), **Weixiong Zhang** (investigator), Oscar Harari (PI). Funding agency: National Institute on Aging (NIH), USA
- Understanding the role of APP, PSEN1, PSEN2, TREM2, and PLD3 in AD (\$450,000, 2/2016 1/2019), Weixiong Zhang (co-PI). Carlos Cruchaga (PI), Funding agency: International Alzheimer's Association
- A novel co-expression network approach that is robust to genetic heterogeneity and its applications (R01 grant, \$1,185,600, 8/2012–7/2017), Weixiong Zhang (PI). Funding agency: National Institute of General Medical Sciences (NIH), USA
- Computational approaches to transcriptome modeling and applications to plant stress regulation (\$419,267, 8/2008–10/2013) Weixiong Zhang (PI) and Ralph Quatrano (co-PI). Funding agency: National Science Foundation (NSF), USA
- *Genes and genetic interactions underlying pharmacological variation in yeast* (R01, Challenge grant, \$842,688, 9/2009–8/2012) Weixiong Zhang (joint PI) and Justin Fay (joint PI). Funding agency: National Institute of General Medical Sciences (NIH), USA
- Supplemental Grant to MRCE Biodefense & Emerging Infectious Disease Center Grant (Program Director: Samuel Stanley), Project 5: Novel IFN-dependent innate antiviral mechanisms (\$1,540,000, 3/2009–2/2012), Weixiong Zhang (co-PI) and Herbert Virgin (PI), Funding agency: National Institute of Allergy and Infectious Diseases (NIH), USA
- *MRCE Biodefense & Emerging Infectious Disease Center Grant* (Program Director: Samuel Stanley), Project 5: *Novel IFN-dependent innate antiviral mechanisms* (\$780,000, 3/2009–2/2012), Herbert Virgin (PI), Weixiong Zhang (investigator, 6% support), Funding agency: National Institute of Health (NIH), USA
- *Systems biology of psoriasis* (Challenge grant, \$1,536,005, 9/2009–8/2011) Weixiong Zhang (joint PI) and Anne Bowcock (joint PI). Funding agency: National Institute of Arthritis and Musculoskeletal and Skin Diseases (NIH), USA.
- *Small RNA gene regulation in soybean seed development* (\$20,000, 9/2010–8/2011) Weixiong Zhang (PI), Funding agency: US Department of Agriculture, USA.
- Variable selection in genetic epidemiological studies of cardiovascular diseases (R01, \$450,000, 8/2008–7/2011) Charles Gu (PI), Weixiong Zhang (investigator, 5% support), Funding agency: National Institute of Health (NIH), USA
- The plasticity of the systemic inflammatory response in ventilator-associated pneumonia (R01, \$750,000, 1/2009–1/2011) Perren Cobb (PI), Weixiong Zhang (investigator, 5% support), Funding agency: National Institute of Health (NIH), USA
- Mechanistic heuristic problem solving and heuristic search algorithms that exploit phase transitions and backbones (\$315,126, 11/2005–10/2009) Weixiong Zhang (PI). Funding agency: National Science Foundation (NSF), USA
- NSF/ITR: Best-first search algorithms for sequence alignment problems in computational biology (\$448,039, 9/2001–9/2006) Weixiong Zhang (PI), Richard E. Korf (co-PI) and Gary Stormo (co-PI) Funding agency: National Science Foundation (NSF), USA
- *Flexible and approximate computation through state-space reduction* (\$228,000, 6/1997–5/2003) Weixiong Zhang (PI) Funding agency: National Science Foundation (NSF), USA
- Flexible and scalable methods for multi-agent distributed resource allocations by exploiting phase transitions (\$934,591, 5/2000–12/2003) Weixiong Zhang (PI) Funding agency: Department of Advanced Research Program Agency (DARPA), USA
- *CATScan:* Constraint-based approaches to time-bounded synthesis customization and adaptation in networked embedded systems (\$1,030,102, 6/2001–9/2003) Weixiong Zhang (PI) and Ron Cytron (co-PI) Funding agency: Department of Advanced Research Program Agency (DARPA), USA
- Discovery of causal regulatory networks and elucidation of complex traits (\$97,500, 1/2008–12/2008) Weixiong Zhang (PI) Funding source: Monsanto Corp, USA

- A network integrated functional genomics approach and its applications to abiotic stress regulation and tolerance in Arabidopsis (\$95,000, 1/2007–12/2007) Weixiong Zhang (PI) Funding source: Monsanto Corp, USA
- Identification and characterization of Arabidopsis microRNAs responsive to cold and drought (\$75,000, 5/2006–12/2006) Weixiong Zhang (PI) Funding source: Monsanto Corp, USA
- *Regulatory networks for abiotic stress and ABA regulation in Arabidopsis* (\$300,000, 1/2005–12/2006) **Weixiong Zhang (PI)** Funding source: Monsanto Corp, USA.
- Computational methods for genome-wide identification of stress-induced genes in plants (\$214,000, 1/2003–12/2004) Weixiong Zhang (PI) Funding source: Monsanto Corp, USA

### **Student Training** (postdoc fellows and graduated Ph.D. students only)

- Xiaoxin Liu, passed Ph.D. thesis proposal, October, 2018.
- Zhuangzhuang Zhang, first year Ph.D. student, 2018.
- Zheng Chen, received Ph.D. in Computer Science, April, 2015; Placement: research scientist, Facebook, USA.
- Jing Xia, received Ph.D. in Computer Science, December, 2014; Placement: postdoc at Department of Cell Biology, Yale University, USA.
- Xuefeng Zhou, received Ph.D. in Computer Science, August, 2012; Placement: Senior research scientist at Monsanto Company, USA.
- Ruoyun Huang, received Ph.D. in Computer Science, July, 2011 (supervised jointly with Yixin Chen); Placement: Senior scientist at Google, USA
- Monika Ray, received Ph.D. in Computer Science, December, 2008; placement: Senior research scientist at Roche Pharmaceuticals, USA.
- Zhao Xin, received Ph.D. in Computer Science, November, 2008; Placement: Project leader at Bank of America
- Jianhua Ruan, received Ph.D. in Computer Science, July, 2007; Placement: Associate professor, UT San Antonio, TX
- Sharlee Climer, received Ph.D. in December, 2006; Placement: Assistant professor, University of Missouri in St. Louis, MO
- Yun Zheng, Postdoctorial research associate, 8/2006 1/2009; Placement: Associate professor at Fudan University, Shanghai, China
- Gerold Jaeger, Postdoctorial research associate, 9/2006 9/2007; Placement: Professor at University Halle, Germany
- Weihong Zhang, Postdoctorial research associate, 5/2003 5/2005; Placement: Staff researcher at HP Lab

### **Publications**

- One research monograph and 183 peer reviewed journal and conference papers. h-index 54.
- In AI, 12 papers in *Artificial Intelligence* and more than 30 papers in IJCAI and AAAI Conf.
- In Biology and Biomedicine, papers in such journals as <u>Nature Communications</u>, <u>PNAS</u>, <u>Genome Biology</u>, <u>Genome Research</u>, <u>Nucleic Acids Research</u>, <u>American J. of Human Genetics</u>, <u>Molecular Human Genetics</u>.
- \*: corresponding author)

### **Research Monograph**

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

#### Journal – Machine Learning and Computational & Molecular Biology (selected from 76 total)

- 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, <u>*RNA Biology*</u>, 2019, DOI: 10.1080/154762862.2019.1669391.
- 3. 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*, *Proceedings of National Academy of Sciences of the USA* (PNAS), 115(17):4435-4440, 2018.
- 4. 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.
- 5. P. Xuan, T. Shen, X. Wang, T. Zhang and W. Zhang, Inferring disease-associated microRNAs in heterogeneous networks with node attributes, *IEEE/ACM Trans. Comput Biol Bioinform.*, 2018, in press.
- 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.
- 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, *Nucleic Acids Research*, 45(10):e88, 2017.
- 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.
- 9. S. Climer\*, A. Templeton and **W. Zhang**\*, Human *gephyrin* is encompassed within giant functional noncoding yin-yang sequences, *Nature Communications*, 6:6534, 2015.
- 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.
- 11. S. Climer, A. Templeton and **W. Zhang**\*, Allele-specific network reveals combinatorial interactions that transcends small effects in psoriasis GWAS, *PLOS Computational Biology*, 10(9):e1003766, 2014.
- 12. J. Xia and W. Zhang\* (2014) MicroRNAs in normal and psoriatic skin, *Physiological Genomics*, 46(4):113-22, 2014, <u>invited review</u>.
- 13. J. Xia and **W. Zhang\*** (2014) A meta-analysis revealed insights into the sources, conservation and impact of microRNA 5'-isoforms in four model species, *Nucleic Acids Research*, 42(3):1427-41, 2014.
- 14. J. Xia, C.E. Joyce, A.M. Bowcock\* and **W. Zhang\*** (2013) Noncanonical microRNAs and endogenous siRNAs in normal and psoriatic human skin, *Human Molecular Genetics*, 22(4):737-48, 2013.
- 15. Z. Chen and W. Zhang\* (2013) Integrative analysis using module-guided Random Forests reveals correlated genetic factors related to mouse weight, *PLOS Computational Biology*, 9(3):e1002956, 2013.
- 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\* (2012) Genome-wide analysis of plant nat-siRNAs reveals insights into their distribution, biogenesis and function, <u>Genome Biology</u>, 13:R20, 2012.
- W. Zhang\*, S. Guo, X. Zhou, P. Chellappan, Z. Chen, X. Zhou, X. Zhang, N. Fromuth, G. Coutino, M. Coffey and H. Jin\* (2011) MicroRNAs regulate plant innate immunity by modulating plant hormone networks, *Plant Molecular Biology*, 75(1-2):93-105, 2011.
- C.E. Joyce, X. Zhou, J. Xia, C. Ryan, B. Thrash, A. Menter, W. Zhang\* and A.M. Bowcock\* (2011) Deep sequencing of small RNAs from human skin reveals major alterations in the psoriasis miRNAome, <u>Human</u> <u>Molecular Genetics</u>, 20(20):4025-40, 2011
- 19. W. Zhang\*, S. Guo, J. Xia, X. Zhou, P. Chellappan, X. Zhou, X. Zhang and H. Jin\* (2010) Multiple distinct small RNAs originated from the same microRNA precursors, *Genome Biology*, 11:R81, 2010.

- P. Chellappan, J. Xia, X. Zhou, S. Gao, X. Zhang, G. Coutino, F. Vazquez, W. Zhang\* and H. Jin\* (2010) siRNAs from miRNA sites mediate DNA methylation of target genes, <u>Nucleic Acids Research</u>, 38(20):6883-94, 2010.
- C. Zeng, W. Wang, Y. Zheng, X. Chen, X. Bo, S. Song, W. Zhang\*, M. Peng\* (2010) Conservation and divergence of microRNAs and their functions in Euphorbiaceous plants, <u>Nucleic Acids Research</u>, 38(3):981-95, 2010.
- T.A. Reese, J. Xia, L.S. Johnson, X. Zhou, W. Zhang\* and H.W. Virgin\* (2010) Identification of novel microRNA-like molecules generated from herpesvirus and host tRNA transcripts, <u>J. Virology</u>, 84(19):10344-53, 2010.
- 23. J. Ruan, A.K. Dean and W. Zhang\* (2010) A general co-expression network-based approach to gene expression analysis: Comparison and applications, *BMC Systems Biology*, 4:8, 2010.
- 24. X. Zhou, R. Sunkar, H. Jin, J-K. Zhu and W. Zhang\* (2009) Genome-wide identification and analysis of small RNAs originated from natural antisense transcripts in *Oryza sativa*, *Genome Research*, 19:70-8, 2009.
- 25. 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\* (2009) Genetic control of human brain transcript expression in Alzheimer's disease, <u>American J. of Human Genetics</u>, 84:445-58, 2009.
- 26. M. Ray and W. Zhang\* (2009) Integrating genetic and phenotypic information to analyze Alzheimer's disease, *J. of Alzheimer's Disease*, 16(1):73-84, 2009.
- 27. M. Ray J. Ruan and W. Zhang\* (2008) Variations in the transcriptome of Alzheimer's disease reveal molecular networks involved in cardiovascular diseases, *Genome Biology*, 9(10):R148, 2008.
- 28. Y. Xu, X. Zhou and **W. Zhang\*** (2008) MicroRNA prediction with a novel ranking algorithm based on random walks, *Bioinformatics*, 24:i50-8, 2008.
- 29. J. Ruan and **W. Zhang** (2008) Identifying network communities with high resolution, *Physical Review E*, 77:016104, 2008.
- 30. X. Zhou, G. Wang and **W. Zhang\*** (2007) UV-B light responsive microRNA genes in Arabidopsis thaliana, *Nature Molecular Systems Biology*, 3:103, 2007.
- X. Zhou, J. Ruan, G. Wang and W. Zhang\* (2007) Characterization and identification of microRNA core promoters in four model species, <u>*PLoS Computational Biology*</u>, 3(3):e37, 2007.
- 32. G. Wang and W. **Zhang**\* (2006) A steganalysis-based approach to comprehensive identification and characterization of functional regulatory elements, *Genome Biology*, 7(6):R49, 2006.
- 33. S. Climer and **W. Zhang** (2006) Rearrangement clustering: Pitfalls, remedies and applications, *J. Machine Learning Research*, 7:919-43, 2006.
- W. Zhang\*, J.Ruan, T-h. D.Ho, Y. You, T. Yu and R.S. Quatrano (2005) 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.
- G. Wang, T. Yu and W. Zhang\* (2005) WordSpy: Identify transcription factor biding motifsby building a dictionary and learning a grammar, *Nucleic Acids Research*, 33:W4126, 2005.
- J. Ruan, G. Stormo and W. Zhang\* (2004) ILM: A web server for predicting RNA secondary structures with pseudoknots, *Nucleic Acids Research*, 32:W146-9, 2004.
- 37. J. Ruan, G. Stormo and **W. Zhang**\* (2004) An iterated loop matching approach to the prediction of RNA secondary structures with pseudoknots, *Bioinformatics*, 20(1):58-66, 2004.

#### Journal – Artificial Intelligence and Heuristic Search (selected from 28 total)

 G. Jager, S. Climer and W. Zhang. Complete Parsimony Haplotype Inference Problem and Algorithms Based on Integer Programming, Branch-and-Bound and Boolean Satisfiability, <u>J. Discrete Algorithms</u>, 37:68-83, 2016.

- 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.
- 40. R. Huang, Y. Chen and W. Zhang (2012) SAS+ planning as Satisfiability, *J. Artificial Intelligence* <u>Research</u>, 43:293-328, 2012 (Winner of the AAAI-2010 Outstanding Paper Award).
- 41. 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.
- 42. Y. Chen, R. Huang, Z. Xing and **W. Zhang** (2009) Long-distance mutual exclusion for planning, <u>Artificial</u> <u>Intelligence</u>, 173:365-91, 2009.
- 43. S. Climer and **W. Zhang** (2006) Cut-and-solve: A linear search strategy for combinatorial optimization problems, *<u>Artificial Intelligence</u>*, 170(8-9):714-38, 2006.
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