

PATRICK XUECHUN ZHAO, Ph.D.

November 2016

Associate Professor

Zhao Bioinformatics Lab

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SUMMARY

Dr. Patrick X. Zhao is an Associate Professor of Bioinformatics and Computational Biology at the Samuel Roberts Noble Foundation (The Noble Foundation). He also holds an appointment as Adjunct Professor in the Department of Computer Science at Oklahoma State University. Dr. Zhao received his Ph.D. in Communication and Information Systems from Shanghai Jiao Tong University, Shanghai, China in 2000. After graduation, he joined Dr. Eugenia Wang's Lab in the School of Medicine, University of Louisville, Kentucky, USA, first as a Postdoctoral Fellow and then as a Bioinformatics Research Associate, to develop bioinformatics methods and tools for the discovery of genes and biological networks essential to the determination of the normal aging process and in particular those related to successful aging in centenarians. In July 2004, Dr. Zhao joined The Noble Foundation as a Faculty Principal Investigator and Assistant Professor of Bioinformatics in the Plant Biology Division of The Noble Foundation. He was promoted to Associate Professor of Bioinformatics and Computational Biology in August, 2010. Dr. Zhao's current research centers on bioinformatics and computational biology, and their applications in plant and soil microbe functional genomics and comparative 'omics'. His lab develops innovative computational methods that tackle large-scale plant 'omics' data, with a specific focus on: 1) gene function, regulation, and networks; 2) comparative 'omics' and genome annotation; 3) functional genomics and metagenomics to understand plant-microbe interactions; and 4) statistics and machine learning for big bio-data integration, data analysis and biological knowledge discovery. The publications, bioinformatics tools, and web services produced by Dr. Zhao's research are publicly available and used by life scientists around the world.

CURRENT POSITION

Associate Professor of Bioinformatics & Computational Biology, Samuel Roberts Noble Foundation, 2510 Sam Noble Parkway, Ardmore, OK 73401, USA

CURRENT RESEARCH INTERESTS

- Development of innovative bioinformatics and functional genomics approaches for understanding plant gene function, regulation, and interactive networks
- Development of innovative methods and tools for discovery and annotation of function-specific genes, proteins, and metabolites in plants, fungi, and bacteria
- Advancing and applying bioinformatics and metagenomics for understanding plant-microbe interactions
- Development of statistics and machine learning methods and tools for integration, analysis and mining of big bio-data, facilitating biological knowledge discovery, such as understanding plant genotype-phenotype (G2P) associations

PROFESSIONAL EXPERIENCE

- Associate Professor, Samuel Roberts Noble Foundation, Ardmore, Oklahoma, 2010-present
- Assistant Professor, Samuel Roberts Noble Foundation, Ardmore, Oklahoma, 2004-2010
- Research Associate, University of Louisville, School of Medicine, Louisville, Kentucky, 2000-2004
- Systems Engineer, Guoxin Lucent Technologies, Shanghai, China, 1999-2000
- Application Engineer and Project Manager, CASCO Signal Co. Ltd., Shanghai, China, 1995-1997
- Lecturer, then Assistant Professor in Electrical Engineering, Tong Ji University, Shanghai, China, 1993-1996

EDUCATION & TRAINING

- Tong Ji University, Shanghai, China, Electrical Engineering specializing in Telecommunication Engineering, B.S. 1990
- Tong Ji University, Shanghai, China, Electrical Engineering specializing in Automation Control, M.S., 1993
- Shanghai Jiao Tong University, Shanghai, China, Communication & Information Systems, Ph.D., 2000
- University of Louisville, Louisville, Kentucky, USA, Postdoctoral Fellow in Bioinformatics, 2000

SCIENTIFIC SERVICES

A) Scientific Review Panels

- National Science Foundation (NSF)-Advances in Biological Informatics (ABI), Division of Molecular and Cellular Biosciences (MCB)
- National Institutes of Health (NIH)-Technology Development for Metabolomics
- BARD-ISUS - The United States Israel Binational Agricultural Research and Development Fund
- French National Research Agency (ANR)-“Blue Sky” (Blanc) Program
- ANR-PLANT-KBBE, jointly launched by the Spanish Ministry of Science and Innovation (MICINN), the German Ministry of Education and Research (BMBF), the French Ministry of Research (MdR), and the French National Agency for Research (ANR)
- GABI (Genome Analysis of the Plant Biological System)-FUTURE Program, by the German Federal Ministry of Education and Research (BMBF)
- CPBR (The Consortium for Plant Biotechnology Research) Competitions "Bioenergy and Environment"
- Ohio Plant Biotechnology Consortium (OPBC)

B) Editorial Boards

- Editorial Board Member of the *International Journal of Data Mining Modeling and Management (IJDMMM)*
- Associate Editor of *Frontiers in Technical Advances in Plant Science*

C) Reviewing (Served as a Peer Reviewer)

- *Briefings in bioinformatics, Bioinformatics, Nucleic Acids Research, BMC Bioinformatics, BMC Plant Biology, BMC Genomics, Evolutionary Bioinformatics, Critical Reviews in Biotechnology, Database: The Journal of Biological Databases and Curation, Journal of Bioinformatics and Computational Biology, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Plant Molecular Biology, PLOS One, Journal of Computer*

Science and Technology, OMICS - A Journal of Integrative Biology, Frontiers in Bioengineering and Biotechnology, Functional Plant Biology, Plant Cell Report, BBA-biomembranes, Genome Biology, Molecular Plant, Plant Physiology, Planta, Molecular Plant-Microbe Interactions, RNA Biology, Scientific Reports

D) Organized International Conferences

- Organized and hosted the 2016 NSF Project/Bioinformatics Workshop entitled "*Collaborative Research: Plant Genotype Phenotype (G2P) Association Discovery via Integrative Genome scale Biological Network & Genome wide Association Analysis*", April 28-30, 2016, Ardmore, OK, USA
- Program Committee Member of the *IEEE International Conference on Bioinformatics & Biomedicine (BIBM)*, December 15-18, 2016, Shenzhen, P.R. China
- Session Chair, *International Conference on Transcriptomics*, July 27-29, 2015, Orlando, FL, USA
- Workshop Chair, *BIT's 5th Annual World Congress of Molecular & Cell Biology (CMCB)*, April 25-28, 2015, Nanjing, P. R. China
- Workshop Chair, *BIT's 6th World DNA and Genome Day (WDD)*, April 25-28, 2015, Nanjing, P. R. China
- Program Committee Member of the *IEEE International Conference on Bioinformatics & Biomedicine (BIBM 2015)*, November 9-12, 2015, Washington, D.C., USA
- Session Chair, *International Conference on Intelligent Biology and Medicine (ICIBM 2014)*, December 4-6, 2014, San Antonio, TX, USA
- Program Committee Member of the *IEEE International Conference on Bioinformatics & Biomedicine (BIBM 2014)*, November 2-5, 2014, Belfast, UK
- Program Committee Member of the *IEEE International Conference on Bioinformatics & Biomedicine (BIBM 2013)*, December 18-21, 2013, Shanghai, China
- Hosted the 2012 *NSF Project/Bioinformatics Workshop*, April 18-20, 2012, Samuel Roberts Noble Foundation, Ardmore, Oklahoma, USA
- Program Committee Member of the *IEEE International Conference on Bioinformatics & Biomedicine (BIBM 2012)*, October 4-7, 2012, Philadelphia, USA
- Program Committee Member of the *IEEE International Conference on Bioinformatics & Biomedicine (BIBM 2011)*, November 12-15, 2011, Atlanta, USA
- Program Committee Member of the *IEEE International Conference on Bioinformatics & Biomedicine (BIBM 2010)*, December 19-22, 2010, Hong Kong
- Program Committee Member of the *IEEE International Conference on Bioinformatics & Biomedicine (BIBM 2009)*, November 1-4, 2009, Washington, D.C., USA
- Co-Chair of the special session on bioinformatics and computational biology, the *IEEE Symposium on Signal Processing and Information Technology (ISSPIT 2008)*, December 16-19, 2008, Sarajevo, Bosnia and Herzegovina

E) Postdoctoral/Research Associates Supervised (with current or recent employer information)

- Jun Li University of Texas MD Anderson Cancer Center, TX
- Nitish K. Mishra University of Nebraska Medical Center, NE
- Firoz Ahmed New York University, NY
- Tingsong Liu Delaware State University, DE
- Junil Chang Samuel Roberts Noble Foundation, OK
- Michael Parker Yale University, CT
- Ruixin Li Carnegie Mellon University, PA
- Yingying Lei Southern California University, CA
- Ji He OmniSeq Precision Medicine Technology, NY

- Rakesh Kaundal University of California, Riverside, CA
- James Susaimuthu Washington State University, WA
- Haiquan Li University of Arizona, AZ
- Indira Reddy Mayo Clinic, MN
- Yuanji Zhang Monsanto Company, MO

F) Visiting Scientists

- Dr. Ji Huang, Nanjing Agricultural University, Nanjing 210095, P. R. China, Visiting Professor, 2013-2014
- Dr. Yuan Harmonie Zhong, Biology Department, Millersville University of Pennsylvania, Sabbatical 2008.

G) Current Membership in Scientific Societies

- American Association for the Advancement of Science (AAAS)
- Intelligent Systems for Molecular Biology (ISMB)
- Institute of Electrical and Electronics Engineers (IEEE)
- American Society of Plant Biologists (ASPB)
- American Chemical Society (ACS)
- Full Member of Sigma Xi, The Scientific Research Society

RECENT INVITED SEMINARS/TALKS

- HRGRN: enabling graph search and integrative analysis of Arabidopsis signaling transduction, metabolism and gene regulation networks, *Plant and Animal Genome XXIII Conference*, January 9-13, 2016, San Diego, California, USA.
- Large-scale Gene Association Network Inference and Functional Module Discovery in Plants, *Plant and Animal Genome XXIII Conference*, January 9-13, 2016, San Diego, California, USA.
- Getting Connected: Advancing Bioinformatics to Modeling and Deciphering Biological Networks in Plants, *Plant Genomics Congress USA*, September 13-16, 2015, St. Louis, MO, USA
- LegumeIP (2015 Release): a Web-Based Comparative Genomics and Gene Expression Atlas Platform to Study Gen Function and Genome Evolution in Legumes, *International Conference on Transcriptomics*, July 27-29, 2015, Orlando, FL, USA
- *Modeling and Mining Functional Modules in Heterogeneous Biological Networks in Plants*, April 28, 2015, Nanjing Agricultural University, Nanjing, P. R. China
- Large-scale Gene Association Network Inference and Functional Module Discovery in Plants, *BIT's 5th Annual World Congress of Molecular & Cell Biology*, April 25-28, 2015, Nanjing, P. R. China
- Development of an Integrative Platform to Study Gene Function and Genome Evolution in Legumes, *BIT's 6th World DNA and Genome Day*, April 25-28, 2015, Nanjing, P. R. China
- LegumeIP: An Integrative Platform to Study Gene Function and Genome Evolution in Legumes (Year 2015 Update), *Plant and Animal Genome XXIII Conference*, January 10-14, 2015, San Diego, CA, USA.
- HRGRN: A Graph Search-Empowered Integrative Database of Arabidopsis Signaling Transduction, Metabolism and Gene Regulation Networks, *Plant and Animal Genome XXIII Conference*, January 10-14, 2015, San Diego, CA, USA.

- Mining Functional Modules in Heterogeneous Biological Networks Using Multiplex PageRank Method, *2014 International Conference on Intelligent Biology and Medicine (ICIBM)*, December 4-6, 2014, San Antonio, TX, USA
- GSEAserver: Gene Set Enrichment Analysis for de novo Transcriptome Assemblies, *2014 Annual Mid-south Computational Biology & Bioinformatics Society (MCBIOS) Conference*, March 6-8, 2014, Stillwater, OK, USA
- Quality evaluation of extracted ion chromatograms and chromatographic peaks in liquid chromatography/mass spectrometry-based metabolomics data, *2014 Annual Mid-south Computational Biology & Bioinformatics Society (MCBIOS) Conference*, March 6-8, 2014, Stillwater, OK, USA
- Inferring Genome-Scale Transcriptional Networks from Large-Scale Gene Expression Data, *Plant and Animal Genome XXII Conference*, January 10-15, 2014, San Diego, CA, USA.
- HRGRN: A Graph Search-Empowered Integrative Database of Arabidopsis Hormone Signaling and Regulatory Networks, *Plant and Animal Genome XXII Conference*, January 10-15, 2014, San Diego, CA, USA.
- Genome-scale Gene Association Network Reconstruction and Analysis for Very Large-scale Expression Data and ‘Omics’ Data Integration and Analysis, *Plant Genomics Congress USA*, September 23-24, 2013, St. Louis, MO, USA
- Modeling and Deciphering Genome-scale Biological Networks in Plants - Enabling Discoveries from Genes to Structures, August 26, 2013, *University of Tennessee*, Knoxville, TN, USA
- Advancing Systems Bioinformatics to Modeling and Deciphering Plant Gene Regulatory Networks, March 22-23, 2013, *South Dakota State University*, Brookings, SD, USA
- Advancing Bioinformatics for Plant Genomics and Metabolomics, November 9, 2012, *University of North Texas*, Denton, TX, USA
- Medicago Genome Annotation & Database Development: LegumeIP-An Integrative Platform to Study Gene Function and Genome Evolution in Legumes, July 25-27, 2012, *J. Craig Venter Institute*, Rockville, MD, USA
- System Bioinformatics Approaches to Model and Decipher Plant Hormonal Regulatory Networks, *BIT's 2nd Annual World Congress of Molecular & Cell Biology (CMCB)*, May 18-20, 2012, Beijing, P. R. China
- LegumeIP: An Integrative Platform for Comparative Genomics and Transcriptomics of Model Legumes, *2011 Alliance of Independent Plant Institutes (AIPI) Meeting*, September 12, 2011, Donald Danforth Plant Sciences Center, St. Louis, MO, USA
- Advancing Bioinformatics for Studying Gene Function and Genome Evolution in Plants, October 20-21, 2011, *Department of Biochemistry & Molecular Biology, Oklahoma State University*, Stillwater, OK, USA
- Talk and Computer demonstration on psRNATarget: A Plant Small RNA Regulator Target Analysis Server. *Plant & Animal Genomes (PAG) XIX Conference*, January 15-19, 2011, San Diego, CA, USA
- An Introduction on the www.grassendophyte.org - An Integrated Database for Studying Grass and Endophyte Genomics, *7th International Symposium on Fungal Endophyte of Grasses*, June 27-July 1, 2010, Lexington, KY, USA
- CiPort: Combining Comparative Genomics and Machine Learning Approaches for Accurate Membrane Transporter Prediction, *Cold Spring Harbor Asia conference on Membrane Proteins: Structure & Function*, May 10-14, 2010, Suzhou, Jiangsu Province, P. R. China
- Systematic Bioinformatics Approaches to Deciphering Plant Transcriptional Regulatory Networks, November 15-16, 2010, *Botany Department, Oklahoma State University*, Stillwater, OK, USA

CURRENT AND PAST EXTERNAL GRANT SUPPORT

- **Project title:** Collaborative Research: ABI Innovation: Plant Genotype-Phenotype (G2P) Association Discovery via Integrative Genome-scale Biological Network & Genome-wide Association Analysis
Source of support: National Science Foundation Advances in Biological Informatics (ABI)
Investigators: **Patrick X. Zhao (Lead PI)**, The Samuel Roberts Noble Foundation, Ardmore, OK; Hairong Wei (Co-PI), Michigan Technological University (MTU); Shizhong Xu (Co-PI), University of California, Riverside (UCR)
Unfunded collaborators: Nevin Young (University of Minnesota, St. Paul, MN, USA), Kui Zhang (University of Alabama at Birmingham, Birmingham, AL, USA), Dong Xu (University of Missouri - Columbia, Columbia, MO, USA), Christopher Town (J. Craig Venter Institute, Rockville, MD, USA), Stephen Goff, (iPlant Collaborative, Tucson, AZ, USA)
Total Noble Foundation award (NSF Award [#1458597](#)): \$815,306
Total Michigan Technological University award (NSF Award [#1458130](#)): \$384,351
Total University of California at Riverside award (NSF Award [#1458515](#)): \$246,123
Duration of award: July 1, 2015 – June 30, 2018 (Estimated)
- **Project title:** Genome-wide Analysis of Small Signaling Peptides in *Medicago truncatula* with an Emphasis on Macro-nutrient Regulation of Root and Nodule Development
Source of support: National Science Foundation Plant Genome Research Project
Investigator: Wolf Scheible (PI); Michael Udvardi (Co-PI) and **Patrick X. Zhao** (Co-PI) and Hideki Takahashi (Co-PI) (Michigan State University)
Key Collaborators: Michael Sussman (University of Wisconsin-Madison), Hiroo Fukuda (University of Tokyo, Japan), and Fiona McAlister (Southern Oklahoma Technology Center, Ardmore, OK, USA)
Total award (NSF Award [#1444549](#)): \$3,319,729
Duration of award: August 1, 2015 – July 31, 2019 (Estimated)
- **Project title:** The Association of Independent Plant Research Institutes (AIPI) Plant Genome Annotation Group
Source of support: AIPI Collaborative Grant Award
Investigators: Seung Yon (Sue) Rhee (Carnegie Institution for Science), **Patrick X. Zhao** (Co-PI) and Zhangjun Fei (Boyce Thompson Institute)
Total Noble Foundation award: \$16,650
Duration of award: January 1, 2014 – December 31, 2014
- **Project title:** ABI: Systems bioinformatics approaches to modeling and deciphering plant transcriptional regulatory networks
Source of support: National Science Foundation Advances in Biological Informatics (ABI)
Investigators: **Patrick X. Zhao** (PI)
Total Noble Foundation award (NSF Award [#0960897](#)): \$1,183,305
Duration of award: July 1, 2010 – September 30, 2014 (Estimated)
- **Project title:** MRI: Acquisition of a UPLC/MS/SPE/NMR for plant metabolomics
Source of support: National Science Foundation
Investigators: Lloyd Sumner (PI), Co-PIs: Randy Allen, Richard Dixon, Kiran Mysore, and Joel Smith
Senior Personnel: Rujin Chen, Xiaoqiang Wang, Carolyn Young, **Patrick X. Zhao**
Total Noble Foundation award (NSF Award [#1126719](#)): \$1,057,587

Duration of award: September 1, 2011 – August 31, 2015

- **Project title:** Advancing bioinformatics to understand mechanisms of plant non-coding small RNA-target interactions
Source of support: Oklahoma Center for the Advancement of Science & Technology (OCAST)
Investigators: **Patrick X. Zhao** (PI)
Total Noble Foundation award: \$100,000
Duration of award: March 1, 2011 – February 28, 2013
- **Project title:** Development of graph-based models to stimulate and decipher plant gene regulatory networks
Source of Support: Oklahoma Center for the Advancement of Science & Technology (OCAST)
Investigators: **Patrick X. Zhao** (PI)
Total Noble Foundation award: \$89,550
Duration of award: August 1, 2009 – July 31, 2011
- **Project title:** Development of genetic resources to dissect the regulatory networks governing nodule development and differentiation in *Medicago truncatula*
Source of support: National Science Foundation Plant Genome
Investigators: **Patrick X. Zhao** (Collaborator - Bioinformatics), PI: Michael Udvardi, Other Co-PIs: Kiran Mysore and Rujin Chen
Total Noble Foundation award (NSF Award [#0703285](#)): \$3,831,732 (\$~200,000 for Zhao lab)
Duration of award: September 15, 2007 – August 31, 2011
- **Project title:** Development and application of genomic tools for drought tolerance enhancement in alfalfa (*Medicago sativa* L.)
Source of support: Oklahoma Bioenergy Center
Investigator: **Patrick X. Zhao** (Co-PI), PI: Maria Monteros, Other Co-PIs: Michael Udvardi, Yuhong Tang, Patrick X. Zhao and Zeng-yu Wang
Total Noble Foundation award: \$146,480
Duration of award: December 15, 2010 – December 14, 2011
- **Project title:** Development and application of genomic tools for drought tolerance enhancement in Alfalfa (*Medicago sativa* L.)
Source of support: Oklahoma Department of Energy – Oklahoma Bioenergy Center
Investigators: **Patrick X. Zhao** (Co-PI), PI: Dr. Michael Udvardi, Other Co-PIs: Drs. Yuhong Tang, Maria Monteros, Patrick X. Zhao and Zeng-Yu Wang
Total Noble Foundation award: \$199,850
Duration of award: January 1, 2008 – December 31, 2010
- **Project title:** Comparative genomics of secretory trichomes-Biofactories for production of plant secondary metabolites
Source of support: National Science Foundation Plant Genome
Investigators: PI: Dr. Richard A. Dixon, **Patrick X. Zhao** (Faculty Associate/Co-PI), other Co-PI: Dr. David. Marks, U. of Minnesota
Total award (NSF Award [#0605033](#)): \$1,406,741 (Noble Foundation: \$1,133,074; U. of Minnesota: \$273,667)
Duration of award: September 27, 2006 – September 30, 2010

PUBLICATIONS

Please visit my Google Scholar citation profile at <http://scholar.google.com/citations?hl=en&user=zW-jGvcAAAAJ>; * as corresponding author.

PUBLISHED JOURNAL PAPERS

1. Wenchao Zhang, Xinbin Dai, Qishan Wang, Shizhong Xu and **Patrick X. Zhao*** (2016). PEPIS: A Pipeline for Estimating Epistatic Effects in Quantitative Trait Locus Mapping and Genome-Wide Association Studies. *PLOS Computational Biology* **12**(5), p. e1004925.
2. Yi Zheng, Chen Jiao, Honghe Sun, Hernan G. Rosli, Marina A. Pombo, Peifen Zhang, Michael Banf, Xinbin Dai, Gregory B. Martin, James J. Giovannoni, **Patrick X. Zhao**, Seung Y. Rhee and Zhangjun Fei (2016). iTAK: a program for genome-wide prediction and classification of plant transcription factors, transcriptional regulators, and protein kinases. *Molecular Plant*, doi: 10.1016/j.molp.2016.09.014.
3. Jun Li and **Patrick X. Zhao*** (2016). Mining Functional Modules in Heterogeneous Biological Networks Using Multiplex PageRank Approach. *Frontiers in Plant Science*, **7**: 903.
4. Jiading Yang, Eric Worley, Qin Ma, Jun Li, Ivone Torres-Jerez, Gaoyang Li, **Patrick X. Zhao**, Ying Xu, Yuhong Tang and Michael Udvardi (2016). Nitrogen remobilization and conservation, and underlying senescence-associated gene expression in the perennial switchgrass *Panicum virgatum*. *New Phytologist* **211**(1), 75-89.
5. Xinbin Dai, Jun Li, Tingsong Liu and **Patrick X. Zhao*** (2016). HRGRN: A Graph Search-Empowered Integrative Database of Arabidopsis Signaling Transduction, Metabolism, and Gene Regulation Networks. *Plant and Cell Physiology* (2016 Database Issue), **57**(1): p. e12.
6. Jun Li, Xinbin Dai, Zhaohong Zhuang and **Patrick X. Zhao*** (2015). LegumeIP 2.0 - A Platform for the Study of Gene Function and Genome Evolution in Legumes. *Nucleic Acids Research* (2016 Database Issue), **44**(D1):D1189-94.
7. Wenchao Zhang, Zhentian Lei, David Huhman, Lloyd W. Sumner and **Patrick X. Zhao*** (2015). MET-XAlign: A Metabolite Cross-Alignment Tool for LC/MS-Based Comparative Metabolomics. *Analytical Chemistry* **87**(18), 9114-9.
8. Jamie A. O'Rourke, Fengli Fu, Bruna Bucciarelli, S. Yang, Deborah Samac, JoAnn Lamb, Maria Monteros, Michelle Graham, John Gronwald, Nick Krom, Jun Li, Xinbin Dai, **Patrick Zhao** and Carroll Vance (2015). The *Medicago sativa* gene index 1.2: a web-accessible gene expression atlas for investigating expression differences between *Medicago sativa* subspecies. *BMC Genomics* **16**(1), 502.
9. Wenchao Zhang and **Patrick X. Zhao*** (2014). Quality evaluation of extracted ion chromatograms and chromatographic peaks in liquid chromatography/mass spectrometry-based metabolomics data. *BMC Bioinformatics* **15**(Suppl 11), S5.
10. Wenchao Zhang, Junli Chang, Zhentian Lei, David Huhman, Lloyd W. Sumner and **Patrick X. Zhao*** (2014). MET-COFEA: A Liquid Chromatography/Mass Spectrometry Data Processing Platform for Metabolite Compound Feature Extraction and Annotation. *Analytical Chemistry* **86**(13), 6245-6253.
11. Michael T. Parker, Yuan Zhong, Xinbin Dai, Shiliang Wang and **Patrick Zhao** (2014). Comparative genomic and transcriptomic analysis of terpene synthases in Arabidopsis and Medicago. *IET Syst Biol* **8**(4), 146-53.

12. Jamie A. O'Rourke, Luis Iniguez, Fengli Fu, Bruna Bucciarelli, Susan Miller, Scott Jackson, Philip McClean, Jun Li, Xinbin Dai, **Patrick Zhao**, Georgina Hernandez and Carroll Vance (2014). An RNA-Seq based gene expression atlas of the common bean. *BMC Genomics* **15**(1), 866.
13. Nitish K. Mishra, Junil Chang and **Patrick X. Zhao*** (2014). Prediction of Membrane Transport Proteins and Their Substrate Specificities Using Primary Sequence Information. *PLOS ONE* **9**(6), e100278.
14. Jun Li, Hairong Wei, Tingsong Liu and **Patrick X. Zhao*** (2014). GPLEXUS: enabling genome-scale gene association network reconstruction and analysis for very large-scale expression data. *Nucleic Acids Research* **42**(5), e32.
15. Wolfgang Goettel, Zongrang Liu, Jing Xia, Weixiong Zhang, **Patrick X. Zhao** and Yong-Qiang An (2014). Systems and Evolutionary Characterization of MicroRNAs and Their Underlying Regulatory Networks in Soybean Cotyledons. *PLOS ONE* **9**(1), e86153.
16. Firoz Ahmed, Muthappa Senthil-Kumar, Seonghee Lee, Xinbin Dai, Kirankumar S. Mysore and **Patrick X. Zhao*** (2014). Comprehensive analysis of small RNA-seq data reveals that combination of miRNA with its isomiRs increase the accuracy of target prediction in *Arabidopsis thaliana*. *RNA Biology* **11**(11), 1414-1429.
17. Zhipeng Liu, Tianlong Chen, Lichao Ma, Zhiguang Zhao, **Patrick X. Zhao**, Zhibiao Nan and Yanrong Wang (2013). Global Transcriptome Sequencing Using the Illumina Platform and the Development of EST-SSR Markers in Autotetraploid Alfalfa. *PLOS ONE* **8**(12), e83549.
18. Jun Li, Hairong Wei and **Patrick X. Zhao*** (2013). DeGNServer: Deciphering Genome-Scale Gene Networks through High Performance Reverse Engineering Analysis. *BioMed Research International* **2013**, 10.
19. Dong-Man Khu, Rafael Reyno, Yuanhong Han, **Patrick X. Zhao**, Joseph H. Bouton, E. Charles Brummer and Maria J. Monteros (2013). Identification of Aluminum Tolerance Quantitative Trait Loci in Tetraploid Alfalfa. *Crop Science* **53**(1), 148-163.
20. Xinbin Dai, Senjuti Sinharoy, Michael Udvardi and **Patrick X. Zhao*** (2013). PlantTFcat: an online plant transcription factor and transcriptional regulator categorization and analysis tool. *BMC Bioinformatics* **14**(1), 321.
21. Michael Puckette, Niranjani J. Iyer, Yuhong Tang, Xin-Bin Dai, **Patrick Zhao** and Ramamurthy Mahalingam (2012). Differential mRNA Translation in *Medicago truncatula* Accessions with Contrasting Responses to Ozone-Induced Oxidative Stress. *Molecular Plant* **5**(1), 187-204.
22. Jun Li, Xinbin Dai, Tingsong Liu and **Patrick X. Zhao*** (2012). LegumeIP: an integrative database for comparative genomics and transcriptomics of model legumes. *Nucleic Acids Research* **40**(D1), D1221-D1229.
23. Zhentian Lei, Haiquan Li, Junil Chang, **Patrick X. Zhao** and LloydW Sumner (2012). MET-IDEA version 2.06; improved efficiency and additional functions for mass spectrometry-based metabolomics data processing. *Metabolomics* **8**(1), 105-110.
24. Jagdeep Kaur, Mercy Thokala, Alexandre Robert-Seilaniantz, **Patrick Zhao**, Hadrien Peyret, Howard Berg, Sona Pandey, Jonathan Jones and Dilip Shah (2012). Subcellular targeting of an evolutionarily conserved plant defensin MtDef4.2 determines the outcome of plant-pathogen interaction in transgenic Arabidopsis. *Molecular Plant Pathology* **13**(9), 1032-1046.
25. Nevin D. Young, Frederic Debelle, Giles E. D. Oldroyd, Rene Geurts, Steven B. Cannon, Michael K. Udvardi, Vagner A. Benedito, Klaus F. X. Mayer, Jerome Gouzy, Heiko Schoof, Yves Van de Peer, Sebastian Proost, Douglas R. Cook, Blake C. Meyers, Manuel Spannagl, Foo Cheung, Stephane De Mita, Vivek Krishnakumar, Heidrun Gundlach, Shiguo Zhou, Joann Mudge, Arvind K. Bharti,

- Jeremy D. Murray, Marina A. Naoumkina, Benjamin Rosen, Kevin A. T. Silverstein, Haibao Tang, Stephane Rombauts, **Patrick X. Zhao**, Peng Zhou, Valerie Barbe, Philippe Bardou, Michael Bechner, Arnaud Bellec, Anne Berger, Helene Berges, Shelby Bidwell, Ton Bisseling, Nathalie Choisne, Arnaud Couloux, Roxanne Denny, Shweta Deshpande, Xinbin Dai, Jeff J. Doyle, Anne-Marie Dudez, Andrew D. Farmer, Stephanie Fouteau, Carolien Franken, Chrystel Gibelin, John Gish, Steven Goldstein, Alvaro J. Gonzalez, Pamela J. Green, Asis Hallab, Marijke Hartog, Axin Hua, Sean J. Humphray, Dong-Hoon Jeong, Yi Jing, Anika Jocker, Steve M. Kenton, Dong-Jin Kim, Kathrin Klee, Hongshing Lai, Chunting Lang, Shaoping Lin, Simone L. Macmil, Ghislaine Magdelenat, Lucy Matthews, Jamison McCorrison, Erin L. Monaghan, Jeong-Hwan Mun, Fares Z. Najar, Christine Nicholson, Celine Noirot, Majesta O'Bleness, Charles R. Paule, Julie Poulain, Florent Prion, Baifang Qin, Chunmei Qu, Ernest F. Retzel, Claire Riddle, Erika Sallet, Sylvie Samain, Nicolas Samson, Iryna Sanders, Olivier Saurat, Claude Scarpelli, Thomas Schiex, Beatrice Segurens, Andrew J. Severin, D. Janine Sherrier, Ruihua Shi, Sarah Sims, Susan R. Singer, Senjuti Sinharoy, Lieven Sterck, Agnes Viollet, Bing-Bing Wang, Keqin Wang, Mingyi Wang, Xiaohong Wang, Jens Warfsmann, Jean Weissenbach, Doug D. White, Jim D. White, Graham B. Wiley, Patrick Wincker, Yanbo Xing, Limei Yang, Ziyun Yao, Fu Ying, Jixian Zhai, Liping Zhou, Antoine Zuber, Jean Denarie, Richard A. Dixon, Gregory D. May, David C. Schwartz, Jane Rogers, Francis Quetier, Christopher D. Town and Bruce A. Roe (2011). The Medicago genome provides insight into the evolution of rhizobial symbioses. *Nature* **480**(7378), 520-524.
26. Zhentian Lei, Xinbin Dai, Bonnie S. Watson, **Patrick X. Zhao** and Lloyd W. Sumner (2011). A legume specific protein database (LegProt) improves the number of identified peptides, confidence scores and overall protein identification success rates for legume proteomics. *Phytochemistry* **72**(10), 1020-1027.
 27. Yuanhong Han, Yun Kang, Ivone Torres-Jerez, Foo Cheung, Christopher Town, **Patrick X. Zhao**, Michael Udvardi and Maria Monteros (2011). Genome-wide SNP discovery in tetraploid alfalfa using 454 sequencing and high resolution melting analysis. *BMC Genomics* **12**(1), 350.
 28. Xinbin Dai, Zhaohong Zhuang and **Patrick X. Zhao*** (2011). Computational analysis of miRNA targets in plants: current status and challenges. *Briefings in Bioinformatics* **12**(2), 115-121.
 29. Xinbin Dai and **Patrick X. Zhao*** (2011). psRNATarget: a plant small RNA target analysis server. *Nucleic Acids Research* **39**(suppl 2), W155-W159.
 30. Firoz Ahmed, Vagner A. Benedito and **Patrick X. Zhao*** (2011). Mining functional elements in messenger RNAs: overview, challenges, and perspectives. *Frontiers in Plant Science* **2**(84).
 31. Mingyi Wang, Vagner Augusto Benedito, **Patrick X. Zhao** and Michael Udvardi (2010). Inferring large-scale gene regulatory networks using a low-order constraint-based algorithm. *Molecular BioSystems* **6**(6), 988-998.
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POSTER PRESENTATIONS AT SCIENTIFIC MEETINGS

- Presented over sixty posters in various scientific meetings (details are not listed).

PUBLISHED STANDALONE SOFTWARE

- **MPageRank**: Mining Functional Modules in Heterogeneous Biological Networks Using Multiplex PageRank Approach
URL: <http://plantgrn.noble.org/MPageRank/>
Publication: Li *et al.*, 2016, *Frontiers in Plant Science*.

- **MET-XAlign**: A Novel Extracted and Annotated Metabolite Alignment Tool for LC-MS based Comparative Metabolomics
URL: <http://bioinfo.noble.org/manuscript-support/met-xalign/>
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URL: <http://bioinfo.noble.org/manuscript-support/met-cofea/>
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- **MET-IDEA**: Data Extraction Tool for Mass Spectrometry-based Metabolomics
URL: http://bioinfo.noble.org/gateway/index.php?option=com_wrapper&Itemid=57
Publications: Lei *et al.*, 2012, *Metabolomics*; Broeckling *et al.*, 2006, *Analytical Chemistry*.

PUBLISHED BIOINFORMATICS WEB SERVERS

- **PEPIS**: A Pipeline for Estimating EPIStatic effect in Linkage Mapping and Genome-Wide Association Studies
URL: http://bioinfo.noble.org/PolyGenic_QTL/
Publication: Zhang *et al.*, 2016, *PLOS Computational Biology*.
- **GPLEXUS**: The High-performance Gene Association Network Analysis Server
URL: <http://plantgrn.noble.org/GPLEXUS/>
Publication: Li *et al.*, 2014, *Nucleic Acids Research*.
- **TrSSP**: the Transporter Substrate Specificity Prediction Server
URL: <http://bioinfo.noble.org/TrSSP/>
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URL: <http://plantgrn.noble.org/DeGNServer/>
Publication: Li *et al.*, 2013, *BioMed Research International*.
- **PlantTFcat**: An Online Plant Transcription Factor and Transcriptional Regulator Categorization and Analysis Tool
URL: <http://plantgrn.noble.org/PlantTFcat/>
Publication: Dai *et al.*, 2013, *BMC Bioinformatics*.
- **DOBLAST**: Blast Server For Genome Scale Sequence Analysis and Sequence Retrieval
URL: <http://bioinfo3.noble.org/doblast/>
Publication: Unpublished.
- **psRNATarget**: A Plant Small RNA Regulator Target Analysis Server
URL: <http://plantgrn.noble.org/psRNATarget/>
Publication: Dai *et al.*, 2011, *Nucleic Acids Research*.
- **AtSubP**: Arabidopsis Subcellular Localization predictor
URL: <http://bioinfo3.noble.org/AtSubP/>
Publication: Kaundal *et al.*, 2010, *Plant Physiology*.
- **TransportTP**: A Two-phase Membrane Transport Protein Prediction and Characterization Server System
URL: <http://bioinfo3.noble.org/transporter/>
Publications: Li *et al.*, 2009, *BMC Bioinformatics*; Li *et al.*, 2008, *Bioinformatics*.

- **pssRNAMiner**: A Plant Short Small RNA Regulatory Cascade Analysis Server
URL: <http://bioinfo3.noble.org/pssRNAMiner/>
Publication: Dai *et al.*, 2008, *Nucleic Acids Research*.
- **PLAN**: Personal BLAST Navigator
URL: <http://bioinfo.noble.org/plan/>
Related Publication: He *et al.*, 2007, *BMC Bioinformatics*.

PUBLISHED SCIENTIFIC DATABASES

- **AtlasCADL**: An Alfalfa Gene Expression Atlas Database developed using the reference CADL (Alfalfa Cultivated Alfalfa at the Diploid Level) Genome
URL: <http://www.alfalfatoolbox.org/atlasCADL/>
Publications: unpublished (2016/2017); the AtlasCADL database is currently password protected.
- **LegumeIP**: An Integrative Platform to Study Gene Function and Genome Evolution in Legumes
URL: <http://plantgrn.noble.org/LegumeIP/>
Publications: Li *et al.*, 2016, *Nucleic Acids Research*; Li *et al.*, 2012, *Nucleic Acids Research*.
- **HRGRN**: Hormone Related Signaling and Gene Expression Regulatory Networks
URL: <http://plantgrn.noble.org/hrgrn/>
Publication: Dai *et al.*, 2016, *Plant and Cell Physiology (2016 Database Issue)*.
- **AGED**: The Alfalfa Gene Index and Expression Atlas Database
URL: <http://plantgrn.noble.org/AGED/>
Publication: O'Rourke *et al.*, 2015, *BMC Genomics*.
- **PvGEA**: A Common Bean Gene Expression Atlas
URL: <http://plantgrn.noble.org/PvGEA/>
Publication: O'Rourke *et al.*, 2014, *BMC Genomics*.
- **MtGEA**: The *Medicago truncatula* Gene Expression Atlas
URL: <http://mtgea.noble.org/v3/>
Publications: He *et al.*, 2010, *BMC Bioinformatics*; Benedito *et al.*, 2008, *Plant Journal*.
- **TrichOME**: A Comparative Omics Database for Plant Trichomes
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