

Biographical Sketch

Hairong Wei

Professor in Plant Bioinformatics and Molecular Biology
School of Forest Resources and Environmental Science (home)
Department of Computer Science (Adjunct)
Michigan Technological University
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A. Current Research Interests:

- Bioinformatics tool and software development
- Large-scale biological data analysis
- Algorithms for gene network construction
- Tree functional genomics
- Genome assembly and annotation
- R-loop and gene regulation

B. Education and Training:

University of Alabama at Birmingham	Biostatistics	Post-doc	2004-2005
University of Minnesota	Bioinformatics	Post-doc	2003-2004
University of Chicago	Computer Science	MS	2003
University of Hawaii at Manoa	Plant Molecular Biology	Ph.D.	2001
Beijing Forestry University, P.R. China	Forest Genetics	MS	1989
Beijing Forestry University, P.R. China	Agricultural Science	BS	1986

C. Appointments:

2018 ~ now	Full Professor, Michigan Technological University, Houghton, MI
2014 ~ 2018	Associate Professor, Michigan Technological University, Houghton, MI
2008~2014	Assistant Professor, Michigan Technological University, Houghton, MI
2006~2008	Microarray Data Analyst, WiCell Research Institute, Inc., Madison, WI
2005~2006	Microarray Design Scientist, Operon Biotechnologies, Inc., Huntsville, AL
2004~2005	Postdoc, Biostatistics, University of Alabama, Birmingham, AL
2003~2004	Postdoc, Bioinformatics, University of Minnesota, Minneapolis, MN
1996~2001	Res. Assistant, Plant Mol. Biology, University of Hawaii, Honolulu, HI
1995~1996	Res. Assistant, Plant Genetics, University of Hawaii, Honolulu, HI
1989~1995	Assistant Professor, and Lecturer, Forest Genetics, Beijing Forestry University

D. Publications & Patents (Total citations = 3856. * Correspondence author)

- 1) Deng, W., K. Zhang, Z. Wei, L. Wang, C. He, S. Liu* and **H. Wei***. 2020. HB-PLS: An algorithm for identifying biological process or pathway regulators by integrating Huber loss and Berhu penalty with partial least squares regression. **bioRxiv**, doi: <https://doi.org/10.1101/2020.05.16.089623>
- 2) He, C., G. Lin, **H. Wei**, H. Tang, F. F. White, B. Valent, and S. Liu. 2020. Estimating assembly base errors using k-mer abundance difference (kad) between short reads and genome assembled sequences. **bioRxiv**, doi: <https://doi.org/10.1101/2020.03.17.994566>
- 3) Lv, K., J. Li, K. Zhao, S. Chen, J. Nie, W. Zhang, G. Liu* and **H. Wei***. 2019. Overexpression of an AP2/ERF family gene, BpERF13, in birch enhances cold tolerance through upregulating CBF genes and mitigating reactive oxygen species. **Plant Science** 292:110375. (**IF =3.8**)
- 4) Zhang, P., Y. Feng, **H. Wei*** and W. Zhang*. 2019, R-loop identification and profiling in plants. **Trends in Plant Science** 24(10):971-972. (**IF =14.0**)
- 5) Fang, Y, L. Chen, K. Lin, Y. Feng, P. Zhang, J. Sanders, X. Pan, Y. Wu, X. Wang, Z. Su, C. Chen, **H. Wei***, W. Zhang*. 2019. Characterization of functional relationships of R-loops with gene transcription and epigenetic modifications in rice. **Genome Research** 29(8):1287-1297. (**IF =10.1**)
- 6) **Wei. H***. 2019. Construction of a hierarchical gene regulatory network centred around a transcription factor (Review). **Briefings in Bioinformatics** 20(3):1021-1031. (**IF =9.3**).
- 7) Wang, L, Z. Luo, Z. Liu, J. Zhao, W. Deng, **H. Wei**, P. Liu, M. Liu. 2019. Genome size variation within species of Chinese jujube (*Ziziphus jujuba* Mill.) and its wild ancestor sour jujube. **Forests** 10(5):460 (**IF =2.0**)
- 8) Li, M, S. Wang, L. Liu, T. Lu, Y. Liu, Y. Zhang, M. Ren, **H. Wei**, Z. Wei. 2019. Overexpression of PsnSuSy1, 2 genes enhances secondary cell wall thickening, vegetative growth, and mechanical strength in transgenic tobacco. **Plant Molecular Biology**, 100(3):215-230. (**IF =3.6**)
- 9) Wang, L, Z. Luo, L. Wang, W. Deng, **H. Wei**, P. Liu, M. Liu. 2019. Morphological, cytological and nutritional changes of autotetraploid compared to its diploid counterpart in Chinese jujube (*Ziziphus jujuba* Mill.). *Scientia Horticulture* 249: 263-270. (**IF =1.8**)
- 10) Gunasekara, C, K. Zhang, W. Deng, L. Brown and **H. Wei***. 2018. TGMI: an efficient algorithm for identifying pathway regulators through evaluation of triple-gene mutual interaction. **Nucleic Acids Res.** 46(11):e67. (**IF = 11.53**)
- 11) Deng, W., K. Zhang, S. Liu, P. Zhao and S. Xu and **H. Wei***. 2018. JRmGRN: Joint reconstruction of multiple gene regulatory networks with common hub genes using data from multiple tissues or conditions. **Bioinformatics** 34(20):3470-3478. (**IF =7.3**).

- 12) Zheng, J., C. He, Y. Qin, G. Lin, D. Park, M. Sun, J. Li, X. Lu, C. Zhang, C. Zhang, D. D Bade, CT “Eddy” Yeh, E. Zeng, **H. Wei**, P. S. Schnable, G. Wang, S. Liu. 2018. Co-expression analysis aids in the identification of new genes in the epicuticular wax pathway. *Plant Journal* 97: 530-542 (IF =5.8)
- 13) Peng, T., M. Qiao, H. Liu, S. Teotia, Y. Zhao, D. Zhao, L. Shi, B. Le, K. Rogers, C. Gunasekara, H. Duan, Y. Gu, L. Tian, Z. Zhang, F. Meng, L. Huang, Q. Chen, Z. Wang, J. Tang, X. Tang, **H. Wei***, X. Chen*, Q. Zhao* and G. Tang*. 2018. A resource for inactivation of microRNAs using short tandem target mimic technology in model and crop plants. *Molecular Plant* 11(11):1400-1417. doi:1 (IF =9.3).
- 14) Liu, Z., J. Zhu, X. Yang, H. Wu, Q. Wei, **H. Wei**, H. Zhang*. 2018. Growth performance, ion organ-level relations and osmotic regulation of *Elaeagnus angustifolia* in response to salt stress. *PLoS ONE* 13(1): e0191552. (IF =3.0).
- 15) Lu, T., L. Liu, M. Wei, Y. Liu, Z. Qu, C. Yang, **H. Wei*** and Z. Wei*. 2018. The effect of poplar PsnGS1 overexpression on growth and secondary cell wall and fibre characteristics in tobacco. *Frontier of Plant Science* 9:9. doi: 10.3389/fpls.2018.00009. (IF=4.2)
- 16) Dash, M, Y. Yordan, T. Georgieva, **H. Wei** and V. Busov*. 2018. Gene network analysis of poplar root transcriptome in response to drought stress identifies a PtaJAZ3 and PtaRAP2.6 centered hierarchical network. *PLoS ONE* 13(12): e0208560. <https://doi.org/10.1371/journal.pone.0208560>
- 17) Ji, X. S. Chen, J. Li, W. Deng, Z. Wei and **H. Wei***. 2017. SSGA and MSGA: two seed-growing algorithms for constructing collaborative subnetworks. *Scientific Reports*. 7:1446, DOI:10.1038/s41598-017-01556-z (IF=5.3).
- 18) Liu, Y., M. Wei, C. Hou, T. Lu, L. Liu, **H. Wei**, Y. Cheng and Z. Wei. 2017. Functional characterization of Populus PsnSHN2 in coordinate regulation secondary wall components in tobacco. *Scientific Reports* 7(1):42. doi: 10.1038/s41598-017-00093-z. (IF=5.3).
- 19) Mitchell, C.L., C.E. Latuszek, K. R. Vogel, I. M. Greenlund, R. E. Hobmeier, O. K. Ingram, S. R. Dufek, J. L. Pecore, F. R. Nip, Z. J. Johnson, X. Ji, **H. Wei**, O. Gailing, and T. Werner. 2017. α -amanitin resistance in *Drosophila melanogaster*: a genome-wide association approach. *PLoS ONE*. 12(2): e0173162. doi:10.1371/journal.pone.0173162. (IF=3.23). (Cited 1 time)
- 20) Deng, W., K. Zhang, V. Busov and **H. Wei***. 2017. Recursive random forest algorithm for constructing multilayered hierarchical gene regulatory networks that govern biological pathways. *PLoS ONE* 12(2):e0171532. DOI:10.1371/journal.pone.0171532. (Correspondence author) (IF=3.23).
- 21) Ma, H., G.M. Weber, H. Wei, and J. Yao. 2016. Identification of mitochondrial genome-encoded small RNAs related to egg deterioration caused by post-ovulatory aging in rainbow trout. *Marine Biotechnology* 18(5): 584-597 (IF=3.27).

- 22) Dash, M, Y. Yordan, S. Kumari, T. Georgieva, H. Wei and V. Busov. 2016. A network of genes associated with poplar root development in response to low nitrogen. *Plant Signaling & Behavior* 11(8):e1214792.
- 23) Tang, F. **H. Wei**, S. Zhao, L. Wang, H. Zheng, M. Lu. 2016. Identification of microRNAs involved in regeneration of the secondary vascular system in *Populus tomentosa* Carr. *Frontiers in Plant Science*. 2016, 7(Article 724):1-17 (IF=4.0).
- 24) Gunasekara, C. A. Subramanian, Avvari, R. K., B. Li, Chen, S. and **H. Wei***. 2016. ExactSearch: A web-based plant motif search tool (<http://sys.bio.mtu.edu/motif/index.php>). *Plant Methods* 12:26 (IF =3.1).
- 25) Kumari, S., W. Deng, C. Gunasekara, V. Chiang, H.S. Chen, H. Ma, X. Davis, and **H. Wei***. 2016. Bottom-up GGM algorithm for constructing multilayered hierarchical gene regulatory networks that govern biological pathways or processes. *BMC Bioinformatics* 17: 132 (IF=2.58). (Cited 1 time)
- 26) Dash, M, Y. Yordan, S. Kumari, T. Georgieva, **H. Wei** and V. Busov. 2015. A system biology approach identifies new regulators of poplar root development under low nitrogen. *Plant Journal* 84(2): 335-46 (Cited 4 times) (IF = 5.97).
- 27) Li, J. **H. Wei**, T. Liu, X. Dai, P.X. Zhao. 2015. Legume: An integrative platform for comparative genomics and transcriptomics of model legumes. Frans J. de Bruijn (eds). Biological Nitrogen Fixation. Vol2. Wiley-Black.
- 28) Wei, Z, Z. Qu, L. Zhang, S. Zhao, Z. Bi, X. Ji, X. Wang and **H. Wei***. 2015. Overexpression of poplar xylem sucrose synthase in tobacco leads to a thickened cell wall and increased height. *PLoS ONE*. 10(3):e0120669. (Cited 2 time) (IF = 3.5).
- 29) Ma, H., M. Weber, M. Hostuttler, **H. Wei**, L. Wang and J. Yao. 2015. MicroRNA expression profiles from eggs of different qualities associated with post-ovulatory ageing in rainbow trout. *BMC Genomics*. 16:201. doi:10.1186/s12864-015-1400-0. (IF = 4.05).
- 30) Wei, Z., Z. Qu, C. Hou, Y. Liu, L. Zhang, C. Yang and **H. Wei***. 2015. Genetic diversity and paternal analysis of open-pollinated progenies of *Larix olgensis* seed orchard. *Journal of Nature and Science*. Vol.1 No.1 E19.
- 31) Yang, C and **H. Wei***. 2014. Designing microarray and RNA-seq experiments for greater systems biology discovery in modern plant genomics (Review). *Molecular Plant* 8, 196–206. (IF=8.8).
- 32) Zhang, W., R. Wei, S. Chen, J. Jiang, H. Li, H. Huang, G. Yang, S. Wang, H. Wei and G. Liu. 2014. Functional Characterization of Cinnamoyl-CoA Reductase (CCR) in Birch (*Betula platyphylla* × *Betula pendula*) through overexpression and suppression analysis. *Physiologia Plantarum* 154(2):283-96. (Cited 4 time) (IF=3.2).

- 33) Li, X, C. Gunasekara, Y. Guo, H. Zhang, L. Lei, S. Tunlaya-Anukit, V. Busov, V. Chiang, and **H. Wei***. 2014. Pop's Pipes: poplar gene expression data analysis pipelines (<http://sys.bio.mtu.edu/index.php>). **Tree Genetics & Genome**. **10:1093-1101**. (IF =2.45).
- 34) Mitchell, C. M. Saul, L. Lei, **H. Wei**, and T. Werner. 2014. The mechanisms underlying α -amanitin resistance in *Drosophila melanogaster*: a microarray analysis. **PLoS ONE** 9(4): e93489. doi:10.1371/journal.pone.0093489. (IF=3.5).
- 35) Wang, S., W. Yao, **H. Wei**, T. Jiang, and B. Zhou. 2014. Expression patterns of ERF genes underlying abiotic stresses in dihaploid *Populus simonii* X *P. nigra*. **The Scientific World Journal**. Vol. 2014, Article ID 745091. (Cited 7 time) (IF=1.7).
- 36) **Wei, H.** Y. Yordan, S. Kumari, T. Georgieva, V. Busov. 2013. Genetic networks involved in poplar root response to low nitrogen. **Plant Signal and Behavior**. 8(11). pii: e27211
- 37) Lin, Y.C.*, Li, W., Sun, Y.H., Kumari, S., **Wei, H.**, Li, Q.Z., Tunlaya-Anukit, S., Sederoff, R.R., and Chiang, V.L. 2013. SND1 transcription factor-directed quantitative functional hierarchical genetic regulatory network in wood formation in *Populus trichocarpa*. **Plant Cell** 25(11) 4324-4341. (**IF=10.22**).
- 38) Li, J. **H. Wei**, T. Liu and P. Zhao. 2013. GPLEXUS: Enable genome-scale gene regulatory network analysis for plants through ultrafast mutual information computing and filtering. **Nucleic Acids Research** 42(5): e32 doi:10.1093/nar/gkt983. (**IF = 8.3**).
- 39) **Wei, H.** Y. Yordan, T. Georgieva, X. Li, V. Busov. 2013. Nitrogen deprivation promotes *Populus* root growth via global transcriptomic reprogramming and activation of hierarchical genetic networks. **New Phytologist**. 200 (2):483-497. (**IF =6.5**).
- 40) Li, J., **H. Wei** and P. X. Zhao. 2013. DeGNServer: Deciphering genome-scale gene networks through high performance reverse engineering analysis. **Biomed Research International** Vol. 2013 (856325):1-10. (IF =2.13) (Cited 9 time).
- 41) Lu, S., Q. Li, **H. Wei**, M.J. Chang, S.T. Anukit, H. Kim, Liu, J., J. Song, Y.H. Sun, L. Yuan, T.F. Yeh, I. Peszlen, J. Ralph. R. R. Sederoff, V. L. Chiang. 2013. Ptr-miR397a is a negative regulator of laccase genes affecting lignin content in *Populus trichocarpa*. **Proc Natl Acad Sci USA** 110 (26) 10848-10853. (**IF =9.9**).
- 42) Liu, Z., H. Zhang, X. Yang, and H. Wei. 2013. Effect of Soil Salinity on growth, ion relations and compatible solute accumulation of two sumac species: *Rhus glabra* and *Rhus trilobata*. **Communications in Soil Science and Plant Analysis**. 44(21): 3187-3204. (IF=0.51).
- 43) Wei, H*. J. Gou, Y. Yordanov, H. Zhang, R. Thakur, W. Jones, A. Burton. 2013. Global transcriptome profiling of aspen trees under elevated [CO₂] for identifying potential molecular mechanisms responsible for enhanced growth. **Journal of Plant Research**. V126, No 2: 305-320. (IF=2.0).

- 44) Kumari, S., J. Nie., H.S. Chen, R. Stewart, H. Ma, X. Li, M. Lu, W.M. Taylor, and **H. Wei***. 2012. Evaluation of gene association methods for coexpression network construction and biological knowledge discovery. **PLoS ONE** 7(11): e50411. (IF=4.1).
- 45) Ma. H. Houttler, C., H. Wei, M. Recroad III, J. Yao. 2012. Characterization of the rainbow trout oocyte microRNA transcriptome (*Oncorhynchus mykiss*). **PLoS ONE** 7(6): e39649. doi:10.1371/journal.pone.0039649. (IF=4.1).
- 46) Nie, J., R. Stewart, F. Ruan, J. Thomson, H. Zhang, X. Cui and **H. Wei***. 2011. TF-Cluster: a pipeline for identifying functionally coordinated transcription factors via network decomposition of the shared coexpression connectivity matrix (SCCM). **BMC Systems Biology**, 5:53. (IF=4.05).
- 47) Cui, X, T. Wang, H.S. Chen, V. Busov and **H. Wei***. 2010. TF-Finder: A software package for identifying transcription factors involved in biological processes using microarray data and existing knowledge base. **BMC Bioinformatics**, 11:425. (Cited 12 times) (IF=3.56).
- 48) **Wei, H.**, P. F. Kuan, S. Tian, C. Yang, J. Nie, S. Sengupta, V. Ruotti, G. Jonsdottir, S. Keles, J. Thomson and R. Stewart. 2008. A study of the relationships between oligonucleotide properties and hybridization intensities in NimbleGen platform. **Nucleic Acids Res**, Vol. 36, No. 9:2926-2938. (IF=7.2).
- 49) Ming, R., S. Hou, Y. Feng, Q. Yu, A. Dionne-Laporte, J. Saw, P. Senin, W. Wang, S. Salzberg, X. Wang, E. Lyons, D. Rice, M. Riley, R. Skelton, J. Murray, C. Chen, M. Eustice, E. Tong, H. Albert, R. E. Paull, M.-L. Wang, Y. Zhu, M. Schatz, N. Nagarajan, R. Agbayani, P. Guan, A. Blas, J. Wang, J.-K. Na, T. Michael, E. V. Shakirov, B. Haas, J. Thimmapuram, D. Nelson, H. Tang, J. E. Bowers, J. Suzuki, S. Tripathi, K. Neupane, **H. Wei**, R. Singh, B. Irikura, N. Jiang, W. Zhang, K. Wall, G. Presting, A. Gschwend, Y. Li, A. Windsor, R. N. Pérez, M. J. Torres, F. A. Feltus, B. Porter, M. Paidi, M.-C. Luo, L. Liu, D. Christopher, P. H. Moore, T. Sugimura, C. dePamphilis, J. Jiang, M. Schuler, T. Mitchell-Olds, D. Shippen, J. Palmer, M. R. Freeling, A. H. Paterson, D. Gonsalves, L. Wang and M. Alam. 2008. The draft genome of the transgenic tropical fruit tree papaya (*Carica papaya* Linnaeus). **Nature**, Vol. 452, No. 7190:991-996. (IF=31).
- 50) Pan, P., S. Tian, J. Nie, C. Yang, V. Ruotti, **H. Wei**, G. Jonsdottir, R. Stewart, and J. Thomson. 2007. Whole genome analysis of Histone H3 lysine 4 and lysine 27 methylation in human embryonic stem cells. **Cell Stem Cell**, Vol. 1, No 3:299~312. (IF=25)
- 51) **Wei, H**, S. Persson, T. Mehta, V. Srinivasasainagendra, L. Chen, G. Page, C. Somerville, A. Loraine. 2006. Transcriptional coordination of the metabolic network in *Arabidopsis thaliana*. **Plant Physiology**. 142(2):762-74. (IF=7.08).
- 52) Persson, S., **H. Wei**, J. Milne, G. Page, C. Somerville. 2005. Identification of genes required for cellulose synthesis by regression analysis of public microarray data sets. **Proc Natl Acad Sci USA**, 102: 8633-8638. (Faculty 1000 evaluation) (IF=9.9).

- 53) **Wei, H.**, Y. Kaznessis. 2005. Inferring gene regulatory relationships by combining target-target pattern recognition and regulator-specific motif examination. *Biotechnology and Bioengineering*. Vol. 89, No1: 53-77. (IF =4.12).
- 54) **Wei, H.** & Yiannis Kaznessis. 2004. Inferring gene regulatory networks using microarray data and SQL SERVER. Minnesota Supercomputing Institute Research Bulletin. Vol. 20, NO 2: 1-3.
- 55) Albert, H and **H. Wei**. Sugarcane Ubi9 gene promoter and methods of use thereof. 2004, U.S. Patent No. 6706948 (<http://www.uspto.gov>).
- 56) Albert, H and **H. Wei**. Promoter of the sugarcane Ubi9 gene. 2004. U.S. Patent No. 6686513 B1 (<http://www.uspto.gov>).
- 57) Albert, H and **H. Wei**. Promoter of the sugarcane Ubi4 Gene. 2003. U.S. Patent No. 6638766 (<http://www.uspto.gov>).
- 58) Lee, K.M., S. Bhawan, T. Majima, **H. Wei**, V. Kumar. 2003. Cutting Edge: The NK cell receptor 2B4 augments Ag-specific CTL activity through CD48 ligation on neighboring T cells. *Journal of Immunology*. Vol.170, No 10: 4881. (IF=6.31).
- 59) **Wei, H.**, H. Albert and P. Moore. 2003. Comparative expression analysis of two sugarcane polyubiquitin promoters and flanking sequences in transgenic plants. *Journal of Plant Physiology* 160, 1241-1251. (Cited 85 times) (IF=2.96).
- 60) **Wei, H.**, H. Albert and P. Moore. 1999. Differential expression of sugarcane polyubiquitin gene and isolation of promoters from two highly expressed members of the gene family. *Journal of Plant Physiology*, Vol. 155, p513-519. (IF=2.96).
- 61) **Wei, H.** F. Li., Y. Zhu, T. Dong. 1995. Some correlations between leaf structures of elms and resistance to leaf beetles. *Journal of Beijing Forestry University* (English edition). Vol.4, No. 1, pp.17-26.
- 62) **Wei, H.** 1994. Heterosis and cross breeding of forest trees (review). *Journal of Heibei Forestry College*. Vol.9, No.1, pp. 92-96.
- 63) **Wei, H.** and Y., Zhu. 1991. Breeding strategies of *Ulmus pumila*. Genetic Improvement on Broadleaf Trees. Huang, M and Tu, Z (eds). Scientific and Technical Document Publisher, pp. 263-270.
- 64) **Wei, H.**1990. Comparison of genetics gain between two breeding strategies: clonal selection and seed orchard. *Forestry Science and Technology*. Vol. 236. No.1, pp 13-14.
- 65) **Wei, H.** 1989. Studies on juvenile-mature correlation between quantitative traits and early selection ages of *Ulmus pumila*. *Journal of Inner Mongolia Forestry College*. Vol.11.

E. SOFTWARE AND COMPUTING TOOLS

1. **TF-Finder** (<http://sys.bio.mtu.edu/software.php>). *BMC Bioinformatics*, 2010.
2. **TF-Cluster** (<http://sys.bio.mtu.edu/software.php>). *BMC System Biology*, 2011.
3. **DeGNServer** (<http://plantgrn.noble.org/DeGNServer/>). *Biomed Research International*, 2013.
4. **GPLUXUS** (<http://plantgrn.noble.org/GPLEXUS/>). *Nucleic Acid Research*, 2013
5. **8GAM**: Eight gene association methods for constructing co-expression network
(R script: <http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0050411>)
6. **Pop's Pipes** (<http://sys.bio.mtu.edu/index.php>). *Tree Genetics & Genome*, 2014
7. **Blossom Plasmid Vector** (<https://blossom.ffr.mtu.edu/index.php>). A tool for designing plasmid vectors that target microRNAs for degradation (NSF project, unpublished). *Molecular Plant*. 2018
8. **ExactSearch**: A web-based plant motif search tool. <http://sys.bio.mtu.edu/motif/index.php>. *Plant Method* 2016. (Corresponding author)
9. **BWERF**: Backward elimination random forests for constructing multilayered gene regulatory networks. *PLoS ONE* 2017: 12(2): e0171532. R package is available at:
(<http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0171532>)
10. **SSGA** and **MSGa**: two seed-growing algorithms for constructing collaborative subnetworks. *Scientific Reports*. 2017.
11. **TF-Miner**: <http://sys.bio.mtu.edu/cluster/> . Submitted to *BMC Genomics*
12. **Top-down and Bottom-up GGM**. *BMC Bioinformatics* 2016: 17:132.
<http://sys.bio.mtu.edu/topdown/>
13. **TGMI**: An algorithm for identifying pathway regulators. Mar 2018.
(R package is available on NAR Web page). *Nucleic Acids Research*. 46(11):e67
<https://doi.org/10.1093/nar/gky210>
14. **JRmGRN**: Joint reconstruction of multiple gene regulatory networks with common hub genes
(R package is available on Bioinformatics Web page). 2018. *Bioinformatics* 5;34(20):3470-3478.
<https://academic.oup.com/bioinformatics/article/34/20/3470/4990490>
15. **HB-PLS**: Huber loss and Berhu penalty with Partial Least Square (PLS) for identifying pathway regulators. 2019.

E. TEACHING

FW5510	Experimental Design, Spring 2018
FW4099	Programming Skills for Bioinformatics, Fall 2009, 2011, 2013, 2015, 2017 and 2019
FW5082	Gene Expression Data Analysis, Fall 2010, 2012 and 2018

CS2321	Data Structure in Java, Spring 2011
FW5510	Informative graphics with R, Spring 2012
BMB6030	Advanced Molecular Biology Lab, Spring 2013, 2014 and 2015
FW3320	Fundamental of Genetics, Spring 2013
FW3200	Forest Biometrics and Data Analysis, Spring 2014, 2015 and 2016

F. GRADUATE STUDENTS

Current:

Ph.D. Ling Zhang, Computer Science & Engineering. 2019

Past: Ph.D. Wenping Deng, 2018, Forest Molecular Genetics (Bioinformatics), Huawei, Inc. China
 Ph.D. Chathura Gunasekare, 2017, Computer Science & Engineering, Baylor College, USA
 Ph.D. Sapna Kumari, 2013, Mathematics, FDA. Maryland. USA.
 MS Avinash Subramanian, 2017, Computer Science, Midwest Veterinary Inc. MN, USA.
 MS Jialin Lei, 2017, Computer Science, Apple Inc, CA. USA
 MS Saeed Binsabaan, 2014, Molecular Biology. Tobacco Industry, Saudi Arabia
 MS Xiang Li, 2012, Computer Science, Senior Developer, Anthem, Inc. Virginia. USA.
 MS Hang Zhang, 2011, Computer Science, Web Developer at US Biotek Laboratories. USA.
 MS Yang Li, 2011, Molecular Biology. Beijing Pharmaceutical Company, China.

G. Editorial Board Members of Scientific Journals

- 1) The Frontier of Plant Physiology 2011 ~ present
- 2) aBiotech (Springer -Nature) 2017 ~ present
- 3) Scientific Reports, 2018 ~ present

H. EXTRAMURAL FUNDING: \$6.91 million from ABI/NSF, Plant Genome/NSF, DOE and USDA as PI and Co-PI. \$2.95 million to Michigan Tech.