Hairong Wei

Curriculum Vitae

Professor in Genomics and Computational Biology
College of Forest Resources and Environmental Science
Department of Computer Science (Adjunct)
Department of Mathematics (Adjunct)
Center of Applied Statistics & Mathematics
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A. Education and Training

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

B. Professional Appointments

2018 ~ now Full Professor, Michigan Technological University, Houghton, MI 49931
2009 ~ present, Professor in Computer Science, Michigan Technological University, Houghton, MI 49931
2009 ~ present, Professor in Mathematics, Michigan Technological University, Houghton, MI 49931
2014 ~ 2018 Associate Professor, Michigan Technological University, Houghton, MI 49931
2008 ~ 2014 Assistant Professor, Michigan Technological University, Houghton, MI 49931
2006 ~ 2008 Human Omics Data Analyst, Morgridge Institute, Madison, WI 53706
2005 ~ 2006 Bioinformatics Scientist, Operon Biotechnologies, Inc. Huntsville, AL 76504
2004 ~ 2005 Postdoc, Biostatistics, University of Alabama, Birmingham, AL 35249
2003 ~ 2004 Postdoc, Bioinformatics, Supercomputing Institute, University of Minnesota, MN 55455
2001 ~ 2003 Technical supporter in human immunology, University of Chicago, IL 60637
1996 ~ 2001 Research Assistant, Plant Molecular Biology, University of Hawaii at Manoa, HI 96822
1995 ~ 1996 Research Assistant, Plant Genetics, University of Hawaii at Manoa, HI 95822
1989 ~ 1995 Assistant Professor, and Lecturer, Forest Genetics, Beijing Forestry University

C. Publications (**Google Scholar Citations = 7419, h-index=38, * Correspondence/co-correspondence author**)

Machine Learning, Deep Learning and AI

1) **[Method]** Mummadi, S. T., Islam, M. K., Busov, V., and **Wei, H***. 2025. Gene regulatory network prediction using machine learning, deep learning, and hybrid approaches, ***Forestry Research***. 5: e014.

2) **[Method]** Islam, Md Khairul, H. Wagh, H. Wei*. 2025. Dynamic Gene Attention Focus (DyGAF): Enhancing biomarker identification through dual-model attention networks. ***Bioinformatics and Biology Insights*** 19:1-15. https://journals.sagepub.com/doi/10.1177/11779322251325390.

3) **[Method]** Cao, X., L. Zhang, M. Zhao, C. He, K. Zhang, S. Liu, Q. Sha* and **H. Wei***. 2023. TGPred: Efficient methods for predicting target genes of a transcription factor by integrating statistics, machine learning, and optimization. ***NAR Genomics and Bioinformatics*** 5(3):1-13 https://doi.org/10.1093/nargab/lqad083

4) **[Method]** Deng, W., K, Zhang, V. Busov an **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.

5) **[Method]** Deng, W., K. Zhang, C. He, S. Liu and **H. Wei** *. 2021. HB-PLS: A statistical method for identifying biological process or pathway regulators by integrating Huber loss and Berhu penalty with partial least squares regression. ***Forestry Research***. 1: 6 doi: https://doi.org/10.48130/FR-2021-0006.

6) **[Method]** Hong,J., C. Gunasekara, C. He, C., S. Liu, J. Huang and **H. Wei** *. 2021. Identification of biological pathway and process regulators using sparse partial least squares and triple-gene mutual interaction. ***Scientific Reports*** **11**, Article number: 13174. https://doi.org/10.1038/s41598-021-92610-4

7) **[Method]** Gao, C., **H. Wei** and K. Zhang. 2021. LORSEN: fast and efficient eQTL mapping with low rank penalized regression. ***Frontier of Genetics***. 12:690926. https://doi.org/10.3389/fgene.2021.690926

8) **Wei. H***. 2019. Construction of a hierarchical gene regulatory network centered around a transcription factor (Review). ***Briefings in Bioinformatics*** 20(3):1021-1031. http://www.genome.org/cgi/doi/10.1101/gr.246009.118

9) **[Method]** 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

10) **[Method]** 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. https://doi.org/10.1093/bioinformatics/bty354

11) **[Method]** 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. https://doi.org/10.1186/1471-2105-11-425

Bioinformatics and Statistical Methods:

12) Islam, M.K., S. T. Mummadi, S, Liu, and H. **Wei** *. 2023. Regulation of regeneration in Arabidopsis thaliana. ***aBiotech*** 4:332-351 https://link.springer.com/article/10.1007/s42994-023-00121-9

13) **[Method]** 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. https://doi.org/10.1093/nar/gky210

14) **[Method]** 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

15) **[Method]** Gunasekara, C., A. Subramanian, Avvari, R. K., B. Li, Chen, S. and **H. Wei*.** 2016. ExactSearch: A web-based plant motif search tool. ***Plant Methods*** 12:26 http://sys.bio.mtu.edu/motif/index.php

16) 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.***

17) **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. https://doi.org/10.1093%2Fnar%2Fgkn133

18) **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. https://doi.org/10.1104/pp.106.080358

19) 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. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3511551/

20) Yang, C. and **H. Wei*.** 2014. Designing microarray and RNA-seq experiments for greater systems biology discovery in modern plant genomics (Review Article). ***Molecular Plant*** 8, 196–206. https://doi.org/10.1093/mp/ssu136

Identification of Significant Genes That Regulate Biological Pathway and Complex Traits

(21) Zhang, Q., G. Fang, Z. Zheng, C. Gu, **H. Wei**, G. Liu, Y. Feng, Q. Yu, Y. Li, C. Yang, J. Jiang* 2024. ASYMMETRIC LEAVES2 repression confers lobed leaves by downregulating lignin biosynthesis of leaf veins in *Betatula pendula*. ***Industrial Crops and Products*** 222(Part 3), 119708. https://doi.org/10.1016/j.indcrop.2024.119708

(22) Gu, C., R. Han, C. Liu, G. Fang, Q. Yuan, Z. Zheng, Q. Yu, J. Jiang, S. Liu, **H. Wei***, Q. Zhang* and G. Liu *. 2023. Heritable epigenetic modification of BpPIN1 is associated with leaf shapes in *Betula pendula*. ***Tree Physiology.*** tpad085, https://doi.org/10.1093/treephys/tpad085

(23) Wang, H., S. Pak, J. Yang, Y. Wu, W. Li, H. Feng, J. Yang, **H. Wei** * and C. Li *. 2022. Two high hierarchical regulators, PuMYB40 and PuWRKY75, control the low phosphorus driven adventitious root formation in *Populus ussuriensis*. ***Plant Biotechnology Journal***, pp. 1-17 https://doi.org/10.1111/pbi.13833

(24) Wei, M., M. Zhang, J. Sun, Y. Zhao, S. Pak, M. Ma, Y. Chen, H. Lu, J. Yang, **H. Wei**, Y. Li, C. Li. 2022. PuHox52 promoted coordinated uptake of nitrate, phosphate and iron under nitrogen deficiency in *Populus ussuriensis.* ***Journal of Integrative Plant Biology.*** https://doi.org/10.1111/jipb.13389

(25) Ren, M., Y. Zhang, R. Wang, Y. Liu, M. Li, X. Wang, X. Chen, X. Luan, H. Zhang, **H. Wei**, C. Yang, Z. Wei. 2022. PtrHAT22, as a higher hierarchy regulator, coordinately regulates secondary cell wall component biosynthesis in *Populus trichocarpa*. ***Plant Science*** 316 (2022) 111170. https://doi.org/10.1016/j.plantsci.2021.111170

(26) Wang, Q., X. Dai, H. Pang, Y. Cheng, X. Huang, H. Li, X. Yan, F. Lu, **H. Wei**, R. R. Sederoff, Q. Li. 2021. BEL1-like homeodomain protein BLH6a is a negative regulator of CAld5H2 in syringyl monolignol biosynthesis in poplar. ***Frontiers in Plant Science*** 12:695223 https://doi.org/10.3389/fpls.2021.695223

(27) Lv, K., W. Wu, **H. Wei**, G. Liu*. 2021. A systems biology approach identifies *BplERF1* as a regulator of cold tolerance in *Betula platyphylla*. ***Forestry Research*** 1: 13 doi: https://doi.org/10.48130/FR-2021-0013

(28) Ren, M., Y. Zhang, C. Liu, Y. Liu, S. Tian, H. Cheng, H. Zhang, **H. Wei**, and Z. Wei*. 2021. Characterization of a high hierarchical regulator, PtrGATA12, functioning in differentially regulating secondary wall component biosynthesis in *Populus trichocarpa*. ***Frontier of Plant Science*** 12 Article 657787. https://doi.org/10.3389/fpls.2021.657787

(29) Lv, Kaiwen, **H. Wei**, and Guifeng Liu. 2021. A R2R3-MYB transcription factor gene, BpMYB123 regulates BpLEA14 to improve drought tolerance in *Betula platyphyll*. ***Frontier of Plant Science*** 12:791390. doi: 10.3389/fpls.2021.791390.

(30) Wu, W., J. Li, Q. Wang, K. Lv, K. Du, W. Zhang, Q. Li, X. Kang and **H. Wei*.** 2021. Growth-regulating factor 5 (GRF5)-mediated gene regulatory network promotes leaf growth and expansion in triploid poplar. ***New Phytologist*** 230: 612–628. https://doi.org/10.1111/nph.17179

(31) Lv, K., **H. Wei** and G. Liu. 2021. A R2R3-MYB transcription factor gene, *BpMYB123*, regulates *BpLEA14* to improve drought tolerance in *Betula platyphylla*. ***Frontier of Plant Science*** 12:791390. doi: 10.3389/fpls.2021.791390 https://doi.org/10.3389/fpls.2021.791390

(32) Wei, M., Q. Liu, Z. Wang, J. Yang, W. Li, Y. Chen, H. Lu, J. Nie, B. Liu, K. Lv, X. Mao, S. Chen, J. Sanders, **H. Wei*** and Chenghao Li *. 2020. PuHox52-mediated hierarchical multilayered gene regulatory

network promotes adventitious root formation in *Populus ussuriensis*. ***New Phytologist***. 228(4): 1369-1385. https://nph.onlinelibrary.wiley.com/doi/full/10.1111/nph.16778

(33) Lv, K., **H. Wei**, J. Jiang, 2020. Overexpression of *BplERD15* enhances drought tolerance in *Betula platyphylla.* ***Forests*** 11(9): 978.

(34) 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.

(35) 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.

(36) 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

(37) 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.

(38) **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. https://doi.org/10.1111/nph.12375

(39) 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.

(40) 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: 86338638. (Faculty 1000 evaluation). https://doi.org/10.1073/pnas.0503392102

Genome Methylation and R-loops

(41) Li, J., C. Li., Y. Deng, **H. Wei** and S. Lu, 2023. Characteristics of Salvia miltiorrhiza methylome and the regulatory mechanism of DNA methylation in tanshinone biosynthesis. ***Horticulture Research,*** https://doi.org/10.1093/hr/uhad114

(42) Li, J., F. Han, T. Yuan, W. Li, Y. Li, H. X. Wu, **H. Wei** and S. Niu. 2023. The methylation landscape of giga-genome and the epigenetic timer of age in Chinese pine. ***Nature Communication*** **14**, 1947. https://doi.org/10.1038/s41467-023-37684-6

(43) Gao, J., P. Zhang, W. Wu, **H. Wei*** and W. Zhang*. 2021. Toward an understanding of the detection, and function of R-loops in plants (Review paper). ***Journal of Experimental Botany*** 72(18):6110-6122. https://doi.org/10.1093/jxb/erab280. (Review)

(44) Zhang, Y., C. Liu, H. Cheng, S. Tian, Y. Liu, S. Wang, H. Zhang, M. Saqib, **H. Wei**, Z. Wei*. 2020. The DNA methylation and its effects on gene expression during primary to secondary growth in poplar stems. ***BMC Genomics***. 21:489. https://doi.org/10.1186/s12864-020-06902-6

(45) 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.

(46) 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. https://doi.org/10.1101/gr.246009.118

(47) 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***, (1):3:299~312. https://doi.org/10.1016/j.stem.2007.08.003.

Genome Sequencing, Assembly and Evolution

(48)Liu, W., C. Liu, S. Chen, M. Wang, X. Wang, Y. Yu, R. Sederoff, **H. Wei**, X. You, G. Qu, S. Chen. 2024. A nearly gapless, highly contiguous reference genome for a doubled haploid line of *Populus ussuriensis*, enabling advanced genomic studies. ***Forestry Research*** 4: e019. https://www.maxapress.com/article/doi/10.48130/forres-0024-0016

(49)Niu, S*., J. Li, W. Bo, W. Yang, A. Zuccolo, S. Giacomello, J. Ma, F. Han, X. Chen, J. Yang, Y. Song, Y. Nie, B. Zhou, P. Wang, Q. Zuo, H. Zhang, J. Wang, L. Wang, Z. Liu, X. Zhang, T. Liu, S. Pei, Z. Li, Y. Hu, Y. Yang, W. Li, J. Lin, Y. Zan, L. Zhou, T. Yuan, W. Li, Y. Li, **H. Wei *** and H. X. Wu*. 2022. The Chinese pine genome and methylome unveil key features of conifer evolution. ***Cell*** 185(1):204-217. https://doi.org/10.1016/j.cell.2021.12.006

(50)Huang, X., W. Wang, T. Gong, D. A. Wickell, L.Y. Kuo, X. Zhang, J. Wen, H. Kim, F. Lu, H. Li, W. Wu, W. Fan, S. Chen, X. Bao, L. Li, D. Zhang, L. Jiang, X. Peng, X. Dai, X. Yan, Z. Liao, J. Ralph, R. R. Sederoff, **H. Wei** *, P. Zhu *, F. Li*, R. Ming * and Q. Li *. 2022. The flying spider-monkey tree fern genome provides insights into fern evolution and arborescence. ***Nature Plants*** 8, 500-512. https://doi.org/10.1038/s41477-022-01146-6

(51)Lin, G, C. He, J. Zheng, D.H. Koo, H. Le, H. Zheng, T. M. Tamang, J. Lin, Y. Liu, M. Zhao, Y. Hao, F. McFraland, B. Wang, Y. Qin, H. Tang, D.R. McCarty, **H. Wei**, M.J. Cho, S. Park, H. Kaeppler, S. Kaeppler, N. Springer, Y/ Liu, P.S. Schnable, G. Wang, F. F. White, S. Liu. 2021. Chromosome-level genome assembly of a regenerable maize Inbred line A188. ***Genome Biology* 22,** 175 (2021).

https://doi.org/10.1186/s13059-021-02396-x

(52) Chen, S., G., Y. Wang, L. Yu, T. Zheng, S. Wang, Z. Yue, J. Jiang, S. Kumari, C. Zheng, H. Tang, J. Li, Y. Li, J. Chen, W. Zhang, H. Kuang, J. Robertson, P. Zhao, H. Li, S. Shu, Y. Yordanov, H. Huang, D. Goodstein, Y. Gai, Q. Qi, J. Min, C. Xu, S. Wang, G. Qu, A. Paterson, D. Sankoff, **H. Wei**, G. Liu and C. Yang. 2021. Genome sequence and evolution of *Betula platyphylla*. ***Horticulture Research*** 8: 37(2021). https://doi.org/10.1038/s41438-021-00481-7

(53) **[Method]** He, C., G. Lin, **H. Wei**, H. Tang, F. F. White, B. Valent, and S. Liu. 2020. Factorial estimating assembly base errors using *k*-mer abundance difference (KAD) between short reads and genome assembled sequences. ***NAR Genomics and Bioinformatics*** Vol. 2, No. 3: 1-14. https://doi.org/10.1093/nargab/lqaa075

(54) Li, Y., **H. Wei**, J. Yang, L. K. Du, J.Li, Y. Zhang, T. Qiu,Z. Liu, Y. Ren, L. Song, X. Kang. 2020. High quality de novo assembly of the *Eucommia ulmoides* haploid genome provides new insights into the evolution and rubber biosynthesis. ***Horticulture Research***. 7:183. https://doi.org/10.1038/s41438-020-00406-w

(55) 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***

(56) Ming, R., S. Hou, Y. Feng, Q. Yu, A. Dionne-Laporte, J. Saw, P. Senin, W. Wang, S. Salzberg, X. Wang, 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. 7190:991996. https://doi.org/10.1038/nature06856

Small RNAs and Their Functions

(57) Wang, R., M. Ren, S. Tian, C. Liu, H. Cheng, Y. Liu, H. Zhang, S. Muhammad, **H. Wei**, Z. Wei. 2021. Transcriptome-wide identification and characterization of microRNAs in diverse phases of wood formation in *Populus trichocarpa*. ***G3: Genes, Genomes, Genetics*** https://doi.org/10.1093/g3journal/jkab195.

(58) Cheng,Y, L. Wang, M. Abbas, X. Huang, Q. Wang, A. Wu, **H. Wei**, S. Peng, X. Dai, and Q. Li. 2021. MicroRNA319-mediated gene regulatory network impacts leaf development and morphogenesis in poplar. ***Forestry Research 1: 4,*** doi: 10.48130/FR-2021-0004

(59) 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, X. Chen*, **H. Wei*,** 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. https://doi.org/10.1016/j.molp.2018.09.003

(60) 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

(61) 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

(62) 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.

(63) 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. https://doi.org/10.1073/pnas.1308936110

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Gene Network Construction

(65) (Review article) Wei, Z. and **H. Wei** *. 2024. Deciphering the intricate hierarchical gene regulatory network: unraveling multi-level regulation and modifications driving secondary cell wall formation. ***Horticulture Research*** 11(2) https://doi.org/10.1093/hr/uhad281.

(66) 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.

(67) 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. 2019. Co-expression analysis aids in the identification of new genes in the epicuticular wax pathway. ***Plant Journal*** 97: 530-542.

(68) 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 https://doi.org/10.1111/tpj.13002

(69) Li, J., **H. Wei,** T. Liu and P. Zhao. 2013. GPLEXUS: Enabling genome-scale gene association network reconstruction and analysis for very large-scale expression data. ***Nucleic Acids Research*** 42(5): e32. https://doi.org/10.1093/nar/gkt983.

(70) 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. https://doi.org/10.1186/1752-0509-5-53.

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Other Articles

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D. Bioinformatics Software and Tools

I have published 20 software tools and online platforms. Among them, tools such as **CollaborativeNET**, **TF-Cluster**, **Top-down GGM algorithm**, **Bottom-up GGM algorithm**, **BWERF**, **TGMI**, **JRmGRN**, and **HB-PLS** are capable of identifying key genes that govern complex traits and diverse biological processes.

(Note that sys.bio.mtu.edu server is currently under re-construction)

1. **DyGAF:** Dynamic Gene Attention Focus (DyGAF). A deep learning method that employs a dual-model attention-based mechanism to enhance biomarker detection, track disease progression, and improve diagnostics using transcriptomic data. ***Bioinformatics and Biology Insights*** 2025（Python package http://prosper.ffr.mtu.edu/ ）

2. **ML_DL_4GRNs:** Machine and deep learning as well as hybrid methods for constructing gene network construction (GRNs). 2025. ***Forestry Research*** (Correspondence author) (Python package: ML_DL_4GRNs: http://prosper.ffr.mtu.edu/)

3. **Web Portal:** Genomic Surveillance and Epidemiology in the Upper Peninsula **(Team leader). 2023. (**https://mtu.bxngs.com/web/index.php**)**

4. **LORSEN** (low rank penalized regression method): a fast and efficient eQTL mapping method. 2021. ***Frontier Genetics***. (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8636089/)

5. **TGPred:** A highly effective package that comprises six methods for target gene prediction (TGPred) of a transcription factor of interest using OMICS data. The six methods include **Huber-ENET, Huber-Lasso**, **Huber-Net, MSE-ENET, MSE-Lasso, and MSE-Net**. ***NAR Genomics and Bioinformatic 2023*** (Correspondence author)
   R code: (https://zenodo.org/record/8297854) Python: (https://zenodo.org/record/)

6. **HB-PLS:** Huber loss and Berhu penalty with Partial Least Square (PLS) for identifying pathway regulators. ***Forestry Research*** 2021. (Correspondence author) (https://github.com/hwei0805/)

7. **JRmGRN:** Joint reconstruction of multiple gene regulatory networks with common hub genes using OMICS data from multiple tissues or conditions (R package is available on Bioinformatics Web page). 2018. ***Bioinformatics*** 5;34(20):3470-3478. (Correspondence author)
   R Package: (http://prosper.ffr.mtu.edu/)

8. **TGMI:** An algorithm for identifying pathway regulators. Mar 2018. (R package is available on NAR Web page). ***Nucleic Acids Research.*** 2018 (Correspondence author) (http://prosper.ffr.mtu.edu/)

9. **Blossom Plasmid Vector**. A tool for designing plasmid vectors that target microRNAs for degradation. ***Molecular Plant***. 2018. (Correspondence author) (https://blossom.ffr.mtu.edu/index.php)

10. **BWERF**: Backward elimination random forests for constructing multilayered gene regulatory networks. ***PLoS ONE*** 2017: 12(2): e0171532. (Correspondence author).
    R package is available at: (https://doi.org/10.1371/journal.pone.0171532.s004)

11. **SSGA** and **MSGA**: two seed-growing algorithms for constructing collaborative subnetworks. ***Scientific Reports***. 2017. (Correspondence author) (https://www.nature.com/articles/s41598-017-01556-z)

12. **ExactSearch**: A web-based plant motif search tool. ***Plant Method*** 2016. (Corresponding author) (http://sys.bio.mtu.edu/motif/index.php).

13. **Bottom-up GGM algorithm:** An algorithm that uses Gaussian Graphical Model (GGM) to construct hierarchical gene regulatory networks governing biological processes/pathways. ***BMC Bioinformatics*** 2016 (Correspondence author). (http://sys.bio.mtu.edu/topdown/)

14. **TF-Miner**: A tool for identifying critical TFs that regulate a biological process or pathway. 2016 (http://sys.bio.mtu.edu/cluster/).

15. **Pop's Pipes.** Automated gene expression pipeline for poplar species. ***Tree Genetics & Genome***, 2014. (Correspondence author) (http://sys.bio.mtu.edu/index.php).
16. **DeGNServer**: Analysis of genome-scale gene networks (GNs) using large-scale gene expression data ***Biomed Research International***, 2013. (http://plantgrn.noble.org/DeGNServer/).

17. **GPLUXUS**. A tool for reconstructing genome-wide gene association study using very large expression data. ***Nucleic Acid Research***, 2013.

(http://plantgrn.noble.org/GPLEXUS/)

18. **Gene association methods**: Eight gene association methods for constructing co-expression network. PloS One 2012. (Correspondence author)
(**R** script: http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0050411)

19. **TF-Cluster:** A tool for identifying genes that govern biological process and complex trait. ***BMC System Biology***, 2011. (Correspondence author) (https://github.com/hwei0805/TF_CollaborativeNet).

20. **TF-Finder:** A tool for identifying genes involved in a biological process. ***BMC Bioinformatics***, 2010. (Correspondence author) (http://sys.bio.mtu.edu/software.php).

E. Data analyses

1). Bulk RNA sequencing (RNA-seq),
2). Chromatin immunoprecipitation sequencing (ChIP-seq)
3). Single-cell RNA sequencing (scRNA-seq).
4). Histone modification ChIP-seq,
5). Chromatin accessibility profiling via ATAC-seq
6. Whole-genome bisulfite sequencing (WGBS)

E. USA Patents

1) Albert, H and **H. Wei.** Sugarcane Ubi9 gene promoter and methods of use thereof. 2004, U.S. Patent No. 6706948 (http://www.uspto.gov).

2) Albert, H and **H. Wei**. Promoter of the sugarcane Ubi9 gene. 2004. U.S. Patent No. 6686513 B1 (http://www.uspto.gov).

3) Albert, H and **H. Wei**. Promoter of the sugarcane Ubi4 Gene. 2003. U.S. Patent No. 6638766 (http://www.uspto.gov).

F. Courses instructed

FW2995	Introduction to R Programming, Fall 2025 (R)
FW5092	Experimental Design, Spring 2018, 2022, and 2024 (R).
FW4099	Programming Skills for Bioinformatics, Fall 2009-2019, and 2023 (Perl & Python).
FW5082	Gene Expression Data Analysis, Fall 2010, 2012, 2018, and 2020 (R)
CS2321	Data Structure in Java, Spring 2011 (Java)
FW5084	Data Representation with R, Spring 2012, 2021 and 2023 (R).
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 (Excel & R)

G. Graduate Students

Current:

Ph.D.	Md Khairul Islam, Computational Science & Engineering, Fall 2022 – now

Past:

Ph.D.	Wenping Deng, 2018, Bioinformatics, Huawei, Inc. China
Ph.D.	Chathura Gunasekara, 2017, Computational Science, Baylor College, USA
Ph.D.	Sapna Kumari, 2013, Mathematics, FDA, Maryland
Ph.D.	Wenbo Zhang, 2014, Northeast Forestry University
MS	Sai Teja Mummadi, 2023, Computer Science.
MS	Joshua Marshall, 2019, Computer Science, The Jackson Laboratory. CT, USA
MS	Avinash Subramanian, 2017, Computer Science, Midwest Veterinary Inc. MN, USA.
MS	Jialin Lei, 2017, Computer Science, Amazon, 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.

Postdocs: Jiqing Gou, 2011-2012. Meibo Group, California, USA.
Jiang Li, 2018-2021. Assistant Professor at Peking Union Medical College, China
Wenqi Wu, 2018-2021. Institute of Crop Sciences, Chinese Academy of Agricultural Science

Graduate Committees:

Biology:

Christine Zawaski, Ph.D. 2009; Fuyu Xu, Ph.D., 2009; Zijun Xu, Ph.D., 2009; Yiru, Chen, Ph.D. 2012; Surendar Dhadi, Ph.D., Biology, 2012; Yiru Chen, Ph.D. 2012, Kefeng Li, Ph.D., 2012, Rafi Shaik, Ph.D., 2013; Sermsawat Tunlaya-Anukit, Ph.D. NCSU (external) 2014, Weilue He, Ph.D. 2015; Lukai Zhai, Ph.D. 2018; Mujeeb Shittu, Ph.D., 2021; Deepak Kumar, MS, 2010; Mengmeng Qiao, MS. 2015, Priyanka Dipak Kadav, MS, 2015, Chelsea Elizabeth Mundell, MS, 2016, James Rauschendorfer, MS, 2017; Ryan Williams, MS, 2019, Will Dion, MS, 2020, and Emma Burke, MS, 2023.

Mathematics and statistics:

Xiaoqi Cui, Ph.D., 2010; Beini Jiang, Ph.D., 2012; Erin Thomas, Ph.D. 2012, Xiaoyu Liang, Ph.D. 2018, Cheng Gao, Ph.D., 2021; Xiaoqing Gao, Ph.D. 2023, Tessa Kriz, MS, 2021; Sunyoung Ahn, Ph.D. 2024; Meiling Zhou, 2025, Megh Raj Subedi, Ph.D. 2025, Md Mutasim Billah, Ph.D. 2025.

Bioinformatics and Data Science:

William Roland, MS, 2021; Zayne Knuth, 2022, Ling Zhang, 2021

H. Editorial Board Members of Scientific Journals

1) Editor-in-Chief, ***Forestry Research***, 2020 ~ present (JIF 2024: 5.0)
   http://www.maxapress.com/journal/forres
2) Associate Editor for ***Horticulture Research***, 2022 ~ Present

https://academic.oup.com/hr/pages/editorial-board

3) Associate Editor for ***Frontier of Plant Science: Plant Biotechnology***, 2011 ~ present.
https://www.frontiersin.org/journals/plant-science/sections/plant-biotechnology#editorial-board
4) Advisory Editor of ***Smart Forestry***, 2025-present
https://www.maxapress.com/smartfor/editorial_board
5) Guest Co-editor. Forestry Biosafety (6 articles published). 2022. **Frontiers in Bioengineering and Biotechnology**.
6) Guest Co-editor. Molecular mechanisms of Fruit Quality Formation in Fruit Trees (8 articles published). 2023. ***Frontier in Plant Science.***

J. Service

1) Member of the American Association for the Advancement of Science (AAAS), 2021-now)
Member of American Association of Plant Biology (ASPB), USA
2) Tenure, Promotion, and Reappointment (TPR) Committee, 2018-2024. College of Forest Resources and Environmental Science, Michigan Technological University.
3) International Society for Computational Biology
4) BIOINFORMATICS 2025-2026 - Program Committee. INSTICC, Portugal.
5) Member of the American Association for the Advancement of Science (AAAS).
6) Member of American Association of Plant Biology (ASPB).
7) Tenure, Promotion, and Reappointment (TPR) Committee, 2018-Present.

H. Extramural Funding: A total of $14.52 million from ABI/NSF, Plant Genome/NSF, DOE, MDHHS, MI and USDA as PI, and Co-PI. $8.09 million to Michigan Tech.

Proposals that are pending or under preparation