

# Peng Liu

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## EMPLOYMENT

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Associate Professor	<b>Department of Statistics</b> , Iowa State University	2013-present
Assistant Professor	<b>Department of Statistics</b> , Iowa State University	2006-2013

## EDUCATION

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Ph.D.     **Biological Statistics and Computational Biology**, Cornell University, 7/2006

M.S.     **Nutritional Sciences**, Cornell University, 8/2001

B. Med.   **Basic Medical Sciences**, Peking University Health Science Center (previously known as Beijing Medical University), Beijing, China, 7/1998

## RESEARCH INTERESTS

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- ◆ Statistical Genomics, Microbiome Data Analysis
- ◆ Statistical Inference for High-dimensional Data
- ◆ Causal Inference
- ◆ Statistical Learning

## REFEREED JOURNAL PUBLICATIONS

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1. A. Sheflin, D. Chiniquy, C. Yuan, E. Goren, I. Kumar, M. Braud, T. Brutnell, A. Eveland, S. Tringe, P. Liu, S. Kresovich, E. Marsh, D. Schachtman, and J. Prenni (2019), Metabolomics of sorghum roots during nitrogen stress reveals compromised metabolic capacity for defense response, *Plant Direct*, <https://doi.org/10.1002/pld3.122>
2. M. He, K. Wimalanathan, **P. Liu**, C.J. Lawrence-Dill (2019), Compare Expression Profiles for Pre-defined Gene Groups with C-REx. *Journal of Open Source Software*, 4(37), 1255, <http://joss.theoj.org/papers/10.21105/joss.01255>
3. L. Dong 1, L. Qin, X. Dai, Z. Ding, **R. Bi**, **P. Liu**, Y. Chen, T. Brutnell, X. Wang, and P. Li (2019) Transcriptomic Analysis of Leaf Sheath Maturation in Maize, *International Journal of Molecular Sciences*, 20(10), 2472, <https://doi.org/10.3390/ijms20102472>
4. R. Srivastava, Z. Li, G. Russo, J. Tang, **R. Bi**, U. Muppirala, A. Severin, M. He, S. Vaitkevicius, C. Lawrence-Dill, **P. Liu**, A.E. Stapleton, D. Bassham, F. Brandizzi, S. Howell (2018), A multi-level analysis of the transition from cell survival to cell death in response to persistent ER stress in maize seedlings, *The Plant Cell*, 30, 1220-1242, <http://www.plantcell.org/content/30/6/1220>
5. **E. Goren**, **P. Liu**, C. Wang, and C. Wang (2018), BinQuasi: a peak detection method for ChIP-sequencing data with biological replicates, *Bioinformatics*, 34(17), 2909–2917, <https://doi.org/10.1093/bioinformatics/bty227>

6. Y. Zhang, R. Giuliani, Y. Zhang, W. L. Araujo, B. Wang, **P. Liu**, Qi Sun, A. Cousins, G. Edwards, A. Fernie, A. Barkan, T. Brutnell, P. Li (2018), Characterization of maize leaf Pyruvate Orthophosphate Dikinase using high throughput sequencing, *Journal of Integrative Plant Biology*, 60(8): 670-690, <https://onlinelibrary.wiley.com/doi/full/10.1111/jipb.12656>
7. M. He, **P. Liu**, C.J. Lawrence-Dill (2017), A hypothesis-driven approach assessing significance of differences in RNA expression levels among specific groups of genes, *Current Plant Biology*, 11-12, 46-51, <https://doi.org/10.1016/j.cpb.2017.12.003>
8. S. Hu, C. Wang, D. Sanchez, A. Lipka, **P. Liu**, Y. Yin, M. Blanco, T. Lubberstedt (2017), Gibberellins promote brassinosteroids action and both increase heterosis for plant height in maize (*Zea mays* L.), *Frontiers in Plant Science*, 8: 1039 [doi: 10.3389/fpls.2017.01039](https://doi.org/10.3389/fpls.2017.01039)
9. L. Laboissonniere, G. M. Martin, J. J Goetz, **R. Bi**, B. Pope, K. Weinand, L. Ellson, D. Fru, M. Lee, A. K Wester, **P. Liu**, and J. M Trimarchi (2017), Single cell transcriptome profiling of developing chick retinal cells, *The Journal of Comparative Neurology*, 2017, 525: 2735-2781 [doi: 10.1002/cne.24241](https://doi.org/10.1002/cne.24241)
10. N. Cray, Y. Zhao, **Y. Fang**, **P. Liu**, L. Pollak, S. Duvick, D. F. Birt, and E. M. Whitley (2017), Effects of dietary resistant starch on the WNT signaling pathway and pre-neoplastic cells in the colons of azoxymethane-treated rats, *Nutrition and Cancer*, 69(4):632-642 [doi:10.1080/01635581.2017.1299875](https://doi.org/10.1080/01635581.2017.1299875)
11. C. Zhang, F. Zhang, **P. Liu**, J. Peng, D. Hannapel (2017). Transcriptome changes in response to cold acclimation in perennial ryegrass as revealed by a cross-species microarray analysis, *Crop Science*, 57:1-13 doi: 10.2135/cropsci2016.04.0252
12. **F. Liu**, C. Wang, Z. Wu, Q. Zhang, and **P. Liu\*** (2016), A Zero-Inflated Poisson Model for Insertion Tolerance Analysis of Genes Based on Tn-seq Data, *Bioinformatics*, 32: 1701-1708, [doi: 10.1093/bioinformatics/btw061](https://doi.org/10.1093/bioinformatics/btw061)
13. **R. Bi** and **P. Liu\*** (2016), Sample size calculation for designing RNA-sequencing experiments, *BMC Bioinformatics*, 17 :146, [doi: 10.1186/s12859-016-0994-9](https://doi.org/10.1186/s12859-016-0994-9)
14. Z. Ding, Y. Zhang, Y. Xiao, **F. Liu**, M. Wang, X. Zhu, **P. Liu**, Qi Sun, W. Wang, M. Peng, T. Brutnell, P. Li (2016), Transcriptome response of cassava leaves under natural shade, *Scientific Reports*, 6:31673, [doi: 10.1038/srep31673](https://doi.org/10.1038/srep31673)
15. H. Sun, **R. Bi**, **P. Liu**, L. Nolan, and S. Lamont (2016), Combined Analysis of Primary Lymphoid Tissues' Transcriptomic Response to Extra-intestinal *Escherichia coli* (ExPEC) Infection, *Developmental & Comparative Immunology*, 57:99-106, [doi:10.1016/j.dci.2015.12.013](https://doi.org/10.1016/j.dci.2015.12.013)
16. B. Nelson, N. Cray, Y. Ai, **Y. Fang**, **P. Liu**, E. M. Whitley, D. Birt (2016), Effect of Dietary Resistant Starch on Inhibition of Colonic Preneoplasia and Wnt Signaling in Azoxymethane-Induced Rodent Models, *Nutrition and Cancer*, 68(6):1052-63, [doi:10.1080/01635581.2016.1192203](https://doi.org/10.1080/01635581.2016.1192203)
17. H. Sun, **P. Liu**, L. Nolan, and S. Lamont (2016), Thymus Transcriptome Reveals Novel Pathways in Response to Avian Pathogenic *Escherichia coli* (APEC) Infection, *Poultry Science*, 95(12): 2803-2814 [doi: 10.3382/ps/pew202](https://doi.org/10.3382/ps/pew202)

18. **F. Liu**, C. Wang, and **P. Liu\*** (2015), A Semi-parametric Bayesian Approach for Differential Expression Analysis of RNA-seq Data, *Journal of Agricultural, Biological, and Environmental Statistics*, 20(4): 555-576, [doi: 10.1007/s13253-015-0227-0](https://doi.org/10.1007/s13253-015-0227-0)
19. H. Sun, **P. Liu**, L. Nolan, and S. Lamont (2015), Novel Pathways Revealed in Bursa of Fabricius Transcriptome in Response to Extraintestinal Pathogenic *Escherichia coli* (ExPEC) Infection, *PLoS ONE*, 10(11): e0142570. [doi:10.1371/journal.pone.0142570](https://doi.org/10.1371/journal.pone.0142570)
20. H. Sun, **P. Liu**, L. Nolan, and S. Lamont (2015), Avian pathogenic *Escherichia coli* (APEC) infection alters the bone marrow transcriptome in chickens, *BMC Genomics*, 16: 690, [doi:10.1186/s12864-015-1850-4](https://doi.org/10.1186/s12864-015-1850-4)
21. J. E. Koltes, ..., **P. Liu**, S. Carpenter, R. Rowland, J. C.M. Dellers, J. M. Reecy (2015), Identification of a putative quantitative trait nucleotide in Guanylate Binding Protein 5 for host response to PRRS virus infection, *BMC Genomics*, 16: 412, [doi:10.1186/s12864-015-1635-9](https://doi.org/10.1186/s12864-015-1635-9)
22. L. Wang, Czedik-Eysenberg, A. Mertz, R. A., **Y. Si**, ..., **P. Liu**, and T. P. Brutnell (2014), Exploring the mechanism of C<sub>4</sub> photosynthetic differentiation through a unified comparative analysis of maize and rice leaf transcriptomes, *Nature Biotechnology*, 32: 1158–1165, [doi:10.1038/nbt.3019](https://doi.org/10.1038/nbt.3019)
23. **M. Orr**, **P. Liu** and D. Nettleton (2014), An Improved Method for Computing Q-values when the Distribution of Effect Sizes is Asymmetric, *Bioinformatics*, 30 (21) 3044-3053 [doi:10.1093/bioinformatics/btu432](https://doi.org/10.1093/bioinformatics/btu432)
24. **T. Ji**, **P. Liu** and D. Nettleton (2014), Estimation and Testing of Gene Expression Heterosis, *Journal of Agricultural, Biological, and Environmental Statistics* 19(3): 319-337 [doi:10.1007/s13253-014-0173-2](https://doi.org/10.1007/s13253-014-0173-2)
25. **Y. Du**, C. Wang and **P. Liu** (2014), A Permutation Test of Genetic Association between Salmonella Isolated On-farm and At-abattoir using Amplified Fragment Length Polymorphism, *Journal of Biometrics and Biostatistics*, 5:204
26. S. L. Taustra, P. Li, **Y. Si**, N. Gandotra, **P. Liu**, Q. Sun, T. P. Brutnell, and T. Nelson (2014) Developmental dynamics of Kranz cell transcriptional specificity in maize leaf reveals early onset of C<sub>4</sub>-related processes, *Journal of Experimental Botany*, 65(13):3543-55 [doi:10.1093/jxb/eru152](https://doi.org/10.1093/jxb/eru152)
27. **Y. Si**, **P. Liu\***, P. Li and T. Brutnell (2014), Model-based clustering of RNA-seq data, *Bioinformatics*, 30(2): 197-205 [doi: 10.1093/bioinformatics/btt632](https://doi.org/10.1093/bioinformatics/btt632)
28. **Y. Si** and **P. Liu\*** (2013), An Optimal Test with Maximum Average Power While Controlling FDR with Application to RNA-seq Data, *Biometrics*, 69, 594-605. [DOI: 10.1111/biom.12036](https://doi.org/10.1111/biom.12036)
29. **W. Landau** and **P. Liu** (2013), Dispersion Estimation and Its Effect on Test Performance in RNA-seq Data Analysis: A Simulation-Based Comparison of Methods, *PLoS ONE*, 8(12): e81415. [doi:10.1371/journal.pone.0081415](https://doi.org/10.1371/journal.pone.0081415)
30. Q. Xia, W. T. Muraola, Z. Shen, O. Sahin, H. Wang, Z. Wu, **P. Liu**, and Q. Zhang (2013), Adaptive mechanisms of *Campylobacter jejuni* to erythromycin treatment, *BMC Microbiology*, 13:133. [doi:10.1186/1471-2180-13-133](https://doi.org/10.1186/1471-2180-13-133)

31. X. Chen, **P. Liu**, H-H. Chou (2013), Whole-genome thermodynamic analysis reduces siRNA off-target effects, *PLoS ONE* 8(3): e58326. [doi:10.1371/journal.pone.0058326](https://doi.org/10.1371/journal.pone.0058326)
32. Z. Wu, O. Sahin, Z. Shen, **P. Liu**, W. G. Miller and Q. Zhang (2013), Multi-omics approaches to deciphering a hypervirulent strain of *Campylobacter jejuni*, *Genome Biology and Evolution*, 5(11):2217-30, [doi: 10.1093/gbe/evt172](https://doi.org/10.1093/gbe/evt172)
33. H. Hao, Z. Yuan, Z. Shen, J. Han, O. Sahin, **P. Liu**, Q. Zhang (2013), Mutational and transcriptomic changes involved in the development of macrolide resistance in *Campylobacter jejuni*, *Antimicrobial Agents and Chemotherapy*, 57(3):1369, [doi: 10.1128/AAC.01927-12](https://doi.org/10.1128/AAC.01927-12)
34. **M. Orr**, **P. Liu** and D. Nettleton (2012), Estimating the Number of Genes that are Differentially Expressed in Both of Two Independent Experiments, the *Journal of Agricultural, Biological, and Environmental Statistics*, 17(4): 583-600. [doi: 10.1007/s13253-012-0108-8](https://doi.org/10.1007/s13253-012-0108-8)
35. **P. Liu\*** and C. Wang (2012), An optimal semi-parametric testing procedure for normal means, *invited article for Journal of Probability and Statistics*, Volume 2012, Article ID 913560, [doi:10.1155/2012/913560](https://doi.org/10.1155/2012/913560)
36. H. Lin, C. Wang, **P. Liu**, D.J. Holtkamp (2012), Construction of Disease Risk Scoring Systems using Logistic Group Lasso: Application to Porcine Reproductive and Respiratory Syndrome Survey Data, *Journal of Applied Statistics*, 40(4): 736-746. [doi:10.1080/02664763.2012.752449](https://doi.org/10.1080/02664763.2012.752449)
37. W. Fang, **Y. Si**, S. Douglass, D.C. Diaz-Cano, S. Merchant, M. Pellegrini, **P. Liu** and M. Spalding (2012), Global Changes in *Chlamydomonas* Gene expression Regulated by Carbon Dioxide and CIA5/CCM1, *The Plant Cell*, 24(5):1876-93, [doi/10.1105/tpc.112.097949](https://doi.org/10.1105/tpc.112.097949)
38. **T. Ji**, **P. Liu** and D. Nettleton (2012), Borrowing Information Across Genes and Experiments for Improved Residual Variance Estimation in Microarray Data Analysis, *Statistical Applications in Genetics and Molecular Biology*, 11: 3, Article 12, [doi: 10.1515/1544-6115.1806](https://doi.org/10.1515/1544-6115.1806)
39. **V. M. Kvam**, **P. Liu\*** and **Y. Si** (2012), A comparison of statistical methods for detecting differentially expressed genes from RNA-seq data, *invited article for American Journal of Botany*, 99(2): 248-256. [doi/10.3732/ajb.1100340](https://doi.org/10.3732/ajb.1100340)
40. E. E. Sandford, **M. Orr**, X. Li, H. Zhou, T. J. Johnson, S. Kariyawasam, **P. Liu**, L. K. Nolan and S. J. Lamont (2012), Strong Concordance Between Transcriptomic Patterns of Spleen and Peripheral Blood Leukocytes in Response to Avian Pathogenic *Escherichia coli*, *Avian Diseases*, 56(4):732-736, [doi: 10.1637/10261-060512-Reg.1](https://doi.org/10.1637/10261-060512-Reg.1)
41. T. Luangtongkum, Z. Shen, V. W. Seng, O. Sahin, B. Jeon, **P. Liu**, Q. Zhang (2012), Impaired fitness and transmission of macrolide-resistant *Campylobacter jejuni* in its natural host, *Antimicrobial Agents and Chemotherapy* 56(3): 1300-1308, [doi: 10.1128/AAC.05516-11](https://doi.org/10.1128/AAC.05516-11)
42. E. E. Sandford, **M. Orr**, M. Shelby, X. Li, H. Zhou, T. J. Johnson, S. Kariyawasam, **P. Liu**, L. K. Nolan and S. J. Lamont (2012), Leukocyte Transcriptome from Chickens Infected with Avian Pathogenic *Escherichia coli* Identifies Pathways Associated with Resistance, *Results in Immunology* 2: 44-53. [doi:10.1016/j.rinim.2012.02.003](https://doi.org/10.1016/j.rinim.2012.02.003)

43. L. Wang, **Y. Si**, L. K. Dedow, Y. Shao, **P. Liu**, T. Brutnell (2011), A Low-Cost Library Construction Protocol and Data Analysis Pipeline for Illumina-Based Strand-Specific Multiplex RNA-Seq, *PLoS ONE* 6(10): e26426. [doi:10.1371/journal.pone.0026426](https://doi.org/10.1371/journal.pone.0026426)
44. E. E. Sandford, **M. Orr**, E. Balfanz, N. Bowerman, X. Li, H. Zhou, T. J. Johnson, S. Kariyawasam, **P. Liu**, L. K. Nolan and S. J. Lamont (2011) Spleen transcriptome response to infection with avian pathogenic *Escherichia coli* in broiler chickens, *BMC genomics*, 12:469 [doi:10.1186/1471-2164-12-469](https://doi.org/10.1186/1471-2164-12-469)
45. G. Li, K. Tivendale, **P. Liu**, Y. Feng, Y. Wannemuheler, W. Cai, P. Mangiamale, T. Johnson, C. Penn and L.K. Nolan (2011) Transcriptome Analysis of Avian Pathogenic *Escherichia coli* O1 in Chicken Serum Reveals Adaptive Responses to Systemic Infection, *Infection and Immunity*, 79: 1951-1960; [doi:10.1128/IAI.01230-10](https://doi.org/10.1128/IAI.01230-10)
46. X. Yu, L. Li, J. Zola, M. Aluru, H. Ye, A. Foudree, H. Guo, S. Anderson, S. Aluru, **P. Liu**, S. Rodermeier and Y. Yin (2011) A brassinosteroid transcriptional network revealed by genome-wide identification of *bes1* target genes in *Arabidopsis thaliana*, *The Plant Journal*, 65(4):634-46 [doi: 10.1111/j.1365-3113.2010.04449.x](https://doi.org/10.1111/j.1365-3113.2010.04449.x)
47. J. T. G. Hwang and **P. Liu** (2010) Optimal tests shrinking both means and variances applicable to microarray data analysis, *Statistical Applications in Genetics and Molecular Biology*, 9:1 article 36, [doi: 10.2202/1544-6115.1587](https://doi.org/10.2202/1544-6115.1587)
48. P. Li, L. Ponnala, N. Gandotra, L. Wang, **Y. Si**, L. Tausta, T. Kebrom, N. Provart, R. Patel, C.R. Myers, E.J. Reidel, R. Turgeon, **P. Liu**, Q. Sun, T. Nelson, and T. Brutnell (2010) The developmental dynamics of the maize leaf transcriptome as revealed through ultra high-throughput sequencing, *Nature Genetics*, 42(12): 1060-1067, [doi:10.1038/ng.703](https://doi.org/10.1038/ng.703)
49. **M. Orr** and **P. Liu\*** (2009) Sample size estimation while controlling false discovery rate for microarray experiments using the ssize.fdr package, *R Journal*, [1\(1\) 47-53](https://doi.org/10.18637/rj.1001)
50. S. Covshoff, W. Majeran, **P. Liu**, K. J. M. Kolkman, K. J. van Wijk, T. Brutnell (2008) De-regulation of maize C<sub>4</sub> photosynthetic development in a mesophyll cell defective, *Plant Physiology*, 146: 1469-1481, [doi: 10.1104/pp.107.113423](https://doi.org/10.1104/pp.107.113423)
51. **P. Liu\*** and J. T. G. Hwang (2007) Quick estimation of sample size while controlling false discovery rate and application to microarray analysis, *Bioinformatics*, 23: 739-746, [doi: 10.1093/bioinformatics/btl664](https://doi.org/10.1093/bioinformatics/btl664)
52. X. Zheng, H-C Huang, W. Li, **P. Liu**, Q-Z Li, Y. Liu (2007) Modeling nonlinearity in dilution design microarray data, *Bioinformatics*, 23: 1339-1347, [doi:10.1093/bioinformatics/btm002](https://doi.org/10.1093/bioinformatics/btm002)
53. R. J. H. Sawers, **P. Liu**, K. Anufrikova, Q. Sun, G. Olsefski, J. T. G. Hwang, T. Brutnell (2007) A multi-treatment experimental system to examine photosynthetic differentiation in the maize leaf, *BMC genomics*, 8:12, [doi:10.1186/1471-2164-8-12](https://doi.org/10.1186/1471-2164-8-12)
54. S. A. Jesch, **P. Liu**, X. Zhao, M. T. Wells, and S. A. Henry (2006) Multiple endoplasmic reticulum-localized protein complexes respond to phospholipid metabolism and regulate gene expression by distinct mechanisms, *Journal of Biological Chemistry*, 281: 24070 – 24083, [doi: 10.1074/jbc.M604541200](https://doi.org/10.1074/jbc.M604541200)



55. T. N. Soon, N. Shaw, N. Vinckenbosch, **P. Liu** (equally contributed first authors), et al., (2002) Selective cooperation between fatty acid-binding proteins and peroxisome proliferator-activated receptors in regulating transcription, *Molecular and Cellular Biology*, 22: 5114-5127, [doi: 10.1128/MCB.22.14.5114-5127.2002](https://doi.org/10.1128/MCB.22.14.5114-5127.2002)
56. J. Ni, **P. Liu**, H. Jia (2000), Binding Properties of M-CAT Element in the Chicken Nicotinic Acetylcholine Receptor  $\gamma$ -Subunit Promoter, *Chinese Journal of Biochemistry and Molecular Biology*, 2000, V16(05): [580-585](#)

## PUBLISHED BOOK CHAPTER

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57. **P. Liu**, Cluster analysis of RNA-sequencing data (2014), in the book of *Statistical Analysis of Next Generation Sequencing Data*, Springer

## SUBMITTED PAPERS

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58. **R. Bi** and **P. Liu**, Invariant Semi-parametric Bayesian approach (iSBA) for differential expression analysis with RNA-Sequencing data, *submitted*
59. **E. Goren**, C. Wang, Z. He, A. Sheflin, D. Chiniquy, J. Prenni, S. Tringe, D. Schachtman, **P. Liu**, Feature selection and causal analysis for microbiome studies in the presence of confounding using standardization, *submitted*
60. **C. Yuan**, **P. Liu**, and C. Wang, A Bayesian approach based on a hierarchical Poisson hurdle model for differential abundance analysis of microbiome data, *submitted*
61. L. A. Laboissonniere, J. J. Goetz, G. M. Martin, **R. Bi**, T. J.S. Lund, L. Ellson, M. R. Lynch, B. Mooney, H. Wickham, A. Mani, **P. Liu**, G. W. Schwartz, and J. M. Trimarchi, Genetic signatures of retinal ganglion cells revealed through single cell profiling, *submitted*, 2019
62. L. Qin, L. Dong, X. Tu, D. Tzeng, X. Wang, **R. Bi**, Z. Ding, **P. Liu**, G. Li, Y. Chen, T. Brutnell, S. Zhong, and P. Li, The LIGULELESS2 (LG2) regulatory network in the maize leaf, *submitted*, 2019

## R PACKAGES FROM MY RESEARCH GROUP

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1. `Ssize.fdr`: sample size calculation for t- and F-tests while controlling FDR
2. `AMAP.Seq`: empirical Bayes test to detect differentially expressed genes with RNA-seq data
3. `MBCluster.Seq`: model-based clustering with RNA-seq data
4. `ssizeRNA`: sample size calculation while controlling FDR for RNA-seq experiment
5. `BinQuasi`: Joint analysis of biological replicates for ChIP-sequencing data

## GRANTS

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Awarded:

1. **Co-PI** for Systems Analysis of the Physiological and Molecular Mechanisms of Sorghum Nitrogen Use Efficiency, Water Use Efficiency, and Interactions with the Soil Microbiome, D. Schachtman (PI, University of Nebraska-Lincoln), with other co-PIs: M. Harrison (Boyce Thompson Institute), S. Kresovich (Clemson University); J. Prenni (Colorado State University),

R. Bart, A. Eveland, and T. Mockler (Donald Danforth Plant Science Center), S. Tringe (Lawrence Berkeley National Laboratory–DOE Joint Genome Institute), I. Dweikat and A. Zygielbaum (University of Nebraska–Lincoln), J. Dangi (University of North Carolina at Chapel Hill), and A. Cousins (Washington State University)

Source of Support: DOE

Total Award Amount: \$ 13,460,684

Total Award Period Covered: 08/15/2015-08/14/2020

2. **Co-PI** for The molecular hallmark of epigenetic control in high-performing yeast, together with Shao (PI)

Source of Support: Presidential Interdisciplinary Research Seed Grant Program (PIRS), Iowa State University

Total Award Period Covered: 1/1/2018-12/31/2019

3. **Co-investigator** for Central Plains Research Data Center seed award, together with C. Wang (PI), Z. He, and D-K Lee

Source of Support: Central Plains Research Data Center

Total Award Period Covered: 08/16/2018-08/15/2019

4. **Co-investigator** for Hierarchical Modeling and Parallelized Bayesian Inference for the Analysis of RNAseq Data, together with D. Nettleton (PI), J. Niemi and P. Schnable

Source of Support: NIH

Total Award Amount: \$ 1,173,287

Total Award Period Covered: 09/01/2013-05/31/2018

5. **Co-PI** for GEPR: A Systems Approach to the Development and Function of C4 Photosynthesis, T. Nelson (PI) from Yale University, other co-PIs: T. Brutnell from Donald Danforth Plant Science Center and K. van Wijk from Cornell University

Source of Support: NSF

Total Award Amount: \$ 8,386,495

Total Award Period Covered: 02/15/2012-01/31/2017

6. **Co-PD** for Improving nutrient utilization and feed efficiency through research and extension to enhance pig industry sustainability and competitiveness, together with Patience (PD) and Anderson, Campbell, Dekkers, DeRouchey, Gabler, Gilbert, Johnson, Kerr, Lonergan, Lonergan, Mabry, Nettleton, Rothschild, Rowland, Tokach, Tuggle, van Kessel, Weber

Source of Support: USDA AFRI

Total Award Amount: \$ 4,999,158

Total Award Period Covered: 3/1/2011-2/29/2016

7. **Co-PI** for GEPR: Comparative analysis of C3 and C4 leaf development in rice, sorghum and maize, T. Nelson (PI) from Yale University, other PIs: T. Brutnell from Boyce Thompson Institute and K. van Wijk from Cornell University

Source of Support: NSF

Total Award Amount: \$ 5,475,676

Total Award Period Covered: 08/01/2007-07/31/2012

8. **Co-PD** for Host:Pathogen Interactions in Avian Colibacillosis: a Systems-Based, Functional Genomics Approach, together with Nolan (PI), Johnson, Lamont, Kariyawasam and Trampel

Source of Support: USDA

Total Award Amount: \$ 955,330

Total Award Period Covered: 02/01/2008-01/31/2012

9. **Co-PD** for Functional genomics analysis of a highly virulent *Campylobacter jejuni* clone causing sheep abortion, together with Zhang (PI), Yaeger and Sahin from Iowa State University  
Source of Support: USDA  
Total Award Amount: \$ 998,467  
Total Award Period Covered: 12/15/09-12/14/12
10. **Co-investigator** for Integration of quantitative genetics, statistics, and computational biology for animal genetic improvement, together with Dekkers and Lamont Iowa State University  
Source of Support: USDA CSREES  
Total Award Amount: \$ 258,000  
Total Award Period Covered: 1/1/2010-12/31/2012
11. **Co-investigator** for PSI Healthy Carbohydrate Project  
Source of Support: Plant Sciences Institute, Iowa State University  
Total Award Amount: \$ 250,000  
Total Award Period Covered: 2011-2012
12. **Co-PI** for Development of high-dimensional data analysis methods for the identification of differentially expressed gene sets, together with D. Nettleton (PI), S. X. Chen, J. Dekkers and C. Tuggle from Iowa State University  
Source of Support: NSF  
Total Award Amount: \$ 552,927  
Total Award Period Covered: 08/15/2007-08/14/2011
13. **Co-PI** for Inorganic Carbon Transport and the CO<sub>2</sub>-concentrating Mechanism of *Chlamydomonas*, together with Martin Spalding (PI) from Iowa State University  
Source of Support: USDA  
Total Award Amount: \$ 351,000  
Total Award Period Covered: 09/01/2007-08/31/2010
14. **Participant** for Approaching crops as ecosystems (ACE): Complex biotic interactions affecting plant health  
Source of Support: Plant Sciences Institute, Iowa State University  
Total Award Amount: \$ 40,000  
Total Award Period Covered: 2011-2012 (1-year)
15. **Statistician** for Identification of Novel APEC Virulence Genes via Functional Genomics, together with Li (PI), Nolan, and Kariyawasam  
Source of Support: USDA Formula Funds Grant from Iowa State University  
Total Award Amount: \$ 20,000  
Total Award Period Covered: 11/01/2007-10/31/2009

## STUDENT ADVISING

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Graduate students:

- ♦ Advisor/co-advisor for **19** graduate students (**16 graduated, 13 in statistics**)

*PhD students (12):*



*Current:*

1. *Emily Goren, Statistics*
2. *Wenting Zhao, Statistics*

*Graduated:*

3. *Ran Bi, Statistics*  
PhD Dissertation (Aug, 2018): Statistical methods for gene expression studies using next-generation sequencing experiments  
currently working at FDA
4. *Chaohui Yuan (Co-Major Professor: Chong Wang), Statistics*  
PhD Dissertation (July, 2018): Statistical methods for microbiome data and antimicrobial resistance analysis  
currently working at Eli Lilly
5. *Fangfang Liu (Co-Major Professor: Chong Wang), Statistics*  
PhD Dissertation: *Statistical methods in detecting differentially expressed genes, analyzing transposon insertion tolerance for gene, and group selection for survival data*  
currently working at Pfizer Inc.
6. *Yaqing Si, Statistics*  
PhD Dissertation: *Statistical analysis of RNA-seq data*  
currently an Associate Professor at the School of Statistics, Southwestern University of Finance, Sichuan, China
7. *Megan Orr (Co-Major Professor: Dan Nettleton), Statistics*  
PhD Dissertation: *Assessing differential expression when the distribution of effect sizes is asymmetric and evaluating concordance of differential expression across multiple gene expression experiments*  
currently a tenure-track Assistant Professor at the North Dakota State University
8. *Tieming Ji (Co-Major Professor: Dan Nettleton, Pat Schnable), Statistics and Bioinformatics and Computational Biology*  
PhD Dissertation: *Borrowing information across genes and experiments for improved error variance estimation in microarray data analysis and statistical inferences for gene expression heterosis*  
currently a tenure-track Assistant Professor at the University of Missouri
9. *Haibo Liu (Co-Major Professor: Chris Tuggle), Bioinformatics and Computational Biology*
10. *Hye Jin Cho (Co-Major Professor: Hui-Hsien Chou), Bioinformatics and Computational Biology*  
PhD Dissertation: *Computational Prediction, Experiment Design and Statistical Validations of Non-Coding Regulatory RNA*
11. *Ali Berens (Co-Major Professor: Amy Toth), Bioinformatics and Computational Biology*  
PhD Dissertation: *Sociogenomics of social organization: Mechanistic and evolutionary underpinnings of caste development and facial recognition in paper wasps*

12. *Srihari Radhakrishnan* (Co-Major Professor: Nicole Valenzuela), Bioinformatics and Computational Biology

*MS students (7):*

*Current:*

13. *Hao Wang*, Statistics

*Graduated*

14. *Ran Bi*, Statistics

Master Creative Component: *Sample size calculation while controlling false discovery rate for differential expression analysis with RNA-seq Data*, M.S. in Statistics, graduated in Fall 2014

15. *Yingzhou Du* (Co-Major Professor: Chong Wang), Statistics

Master Creative Component: *A Permutation Test of Genetic Association between Salmonella Isolated On-farm and At-abattoir using Amplified Fragment Length Polymorphism*, M.S. in Statistics, graduated in Spring 2014

16. *William Landau*, Statistics

Master Creative Component: *Dispersion Estimation and Its Effect on Test Performance in RNA-seq Data Analysis: A Comparison of Methods*, M.S. in Statistics, graduated in Spring 2013

17. *Yanwen Xiong*, Statistics

Master Creative Component: *Comparison of normalization methods for RNA-seq data analysis*, M.S. in Statistics, graduated in Spring 2012  
currently a Senior Research Associate at the Pioneer Hi-Bred

18. *Vanessa Kvam*, Statistics

Master Creative Component: *A comparison of statistical methods for detecting differentially expressed genes from RNA-seq data*, M.S. in Statistics, graduated in Fall 2011

19. *Hong Hua*, Statistics

Master Creative Component: *Microarray data analysis for a study of photosynthesis differentiation in maize*, M.S. in Statistics, graduated in Summer, 2009  
currently a Senior Business analyst at Hewlett-Packard in China

- ♦ Program of Study (POS) committee member (not major professor) for another >80 graduate students (60 completed)
- ♦ Rotation advisor for 3 students in the Program of Bioinformatics and Computational Biology, ISU

Research Assistants that I supported:

1. Megan Orr (05/08-12/10, and 05/11-07/12)
2. Yaqing Si (07/09-07/12)
3. Dason Kurkiewicz (05/11-12/12)

4. Wen Zhou (07/12-5/13, and 1/14-5/2014)
5. Fangfang Liu (01/13-5/13, and 8/13-12/13)
6. Yinan Fang (08/13-12/13)
7. Ran Bi (5/2014-8/2018)
8. Emily Goren (5/2015-5/2017, 1/18-4/19)
9. Chaohui Yuan (8/2016-5/2017)
10. Wenting Zhao (5/18-present)
11. Hao Wang (5/19-present)

#### Other students

- ◆ Co-Mentor (with Dan Nettleton) for Alliance students Jared Mills and Katrina Williams, summer, 2010

#### INVITED TALKS

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1. A Bayesian approach based on a hierarchical Poisson hurdle model for differential abundance analysis of microbiome data, University of Delaware, Nov, 2018
2. Semi-parametric Bayesian approach for differential expression analysis with RNA-sequencing data, ICSA China Conference, July, 2018
3. Detection of Gene Expression Heterosis with RNA-Sequencing Data, New York University School of Medicine, May, 2018
4. Several statistical methods and models in plant genomics studies, PSI Predictive Phenomics Workshop, Iowa State University, Oct, 2014
5. Statistical Analysis of RNA-seq Data, Modern Views in Nutrition (MVN) 2014 seminar series, Iowa State University, Oct, 2014
6. Statistical Design and Analysis of RNA-seq Data, Shandong Agricultural University, China, Jul, 2014
7. An optimal test for detecting differential expression using RNA-seq data, *University of Missouri*, Columbia, Oct, 2012
8. An optimal test with maximum average power while controlling FDR with application to RNA-seq data, *ICSA 2012 Applied Statistics Symposium*, Boston, Jun 23-26, 2012
9. Model-Based Clustering for RNA-seq Data, *University of Maryland*, October, 2011
10. Model-Based Clustering for RNA-seq Data, *Conference on Statistical Analyses For Next Generation Sequencing*, University of Alabama at Birmingham, Sep 26-27, 2011
11. Optimal tests using shrinkage idea with application to high-dimensional gene expression data, *Symposium on Innovations in Design, Analysis, and Dissemination: Frontiers in Biostatistical Methods*, Kansas City, Missouri, April, 2011
12. Optimal tests using shrinkage idea with application to high-dimensional gene expression data, *Oklahoma State University*, October, 2010

13. Quick calculation of sample size while controlling false discovery rate with application to microarray, ABG seminar, *Iowa State University*, IA, 2006
14. Empirical Bayes test with application to microarray, *Rutgers University*, NJ, 2006
15. Empirical Bayes test with application to microarray, *University of Texas at Dallas*, TX, 2006
16. Empirical Bayes test with application to microarray, *Iowa State University*, IA, 2006
17. Empirical Bayes test with application to microarray, *Washington University at St. Louis*, MO, 2006
18. Quick calculation of sample size while controlling false discovery rate with application to microarray, *Mayo Clinic*, MN, 2006

## TEACHING EXPERIENCES

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- ♦ **Instructor for STAT 500:** Statistical Methods I, Iowa State University, Fall, 2018  
Teaching evaluation: 4.5/5.0
- ♦ **Instructor for STAT 516:** Statistical Design and Analysis for Microarray Experiments, Iowa State University, Spring, 2009  
Teaching evaluation: 4.5/5.0
- ♦ **Instructor for STAT 104:** Introduction to Statistics, Iowa State University, Fall 2008, Spring 2010  
Teaching evaluation: 3.8/5.0
- ♦ **Instructor for STAT 402:** Statistical Design, Iowa State University, Spring of 2011, 2012, 2013, 2014, 2019, and Fall of 2013, 2014, 2015, 2016, 2017  
Teaching evaluation: 4.1-4.5/5.0
- ♦ **Instructor for STAT 416:** Statistical Design and Analysis for Microarray Experiments, Iowa State University, Spring of 2007, 2008, 2011, 2012, 2013, 2014, 2015, 2017, 2018  
Teaching evaluation: 4.2-5.0/5.0

## EDITORIAL ACTIVITIES

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- ♦ *Associate Editor of BMC Bioinformatics, Jan 2012 to present*

## HONORS AND AWARDS

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- ♦ Iowa State University Plant Sciences Institute Scholar, 2018 – present
- ♦ College of Liberal Arts and Sciences Award for Mid-Career Achievement in Research, 2018
- ♦ Iowa State University Award for Early Achievement in Research, 2013

## PROFESSIONAL MEMBERSHIPS

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- ♦ American Statistical Association (ASA)
- ♦ International Chinese Statistical Association (ICSA)