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EMPLOYMENT

Professor	Department of Statistics , Iowa State University	2020-present
Associate Professor	Department of Statistics , Iowa State University	2013-2020
Assistant Professor	Department of Statistics , Iowa State University	2006-2013

EDUCATION

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

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

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

RESEARCH INTERESTS

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

HONORS AND AWARDS

- ◆ 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 College of Agriculture and Life Sciences Team Award, 2015
- ◆ Iowa State University Award for Early Achievement in Research, 2013
- ◆ Graduate School Travel Award and Fellowship, Cornell University, 2005
- ◆ Student Research Grant Award, School of Industrial and Labor Relations, Cornell University, 2004
- ◆ Graduate School Travel Award and Fellowship, Cornell University, 2003
- ◆ Barns Fellowship, Cornell University, 2000
- ◆ Student Research Grant Award of Division of Nutritional Sciences, Cornell University, 2000

REFERRED JOURNAL ARTICLES (bold for Liu and her students, * for corresponding author)

1. J. C. Berry, M. Qi, B. V. Sonawane, A. Sheflin, A. B. Cousins, J. Prenni, D. P. Schachtman, **P. Liu**, R. S. Bart (2022), Increased signal to noise ratios within experimental field trials by regressing spatially distributed soil properties as principal components, [eLife 11:e70056](https://doi.org/10.1162/elife.70056).

2. M. Qi, J. C. Berry, K. Veley, L. O'Connor, O. M. Finkel, I. Salas-González, M. Kuhs, J. Jupe, E. Holcomb, T.G. del Rio, C. Creech, **P. Liu**, S. Tringe, J. L. Dangl, D. Schachtman, R. S. Bart (2022), Identification of beneficial and detrimental bacteria impacting sorghum responses to drought using multi-scale and multi-system microbiome comparisons, *ISME J* <https://doi.org/10.1038/s41396-022-01245-4>
3. M. I. Natukundaa, M. B. Mantilla-Pereza,b, M. A. Grahama,c, **P. Liu**, and M. G. Salas-Fernandez (2022), Dissection of canopy layer-specific genetic control of leaf angle in Sorghum bicolor by RNA sequencing, *BMC Genomics*, 23, 95 <https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12864-021-08251-4>
4. **R. Bi** and **P. Liu** (2021), A Semi-parametric Bayesian Approach for Detection of Gene Expression Heterosis with RNA-Seq Data, *Journal of Applied Statistics*, 2021, DOI: [10.1080/02664763.2021.2004581](https://doi.org/10.1080/02664763.2021.2004581)
5. **E. Goren**, C. Wang, Z. He, A. Sheflin, D. Chiniquy, J. Prenni, S. Tringe, D. Schachtman, **P. Liu*** (2021), Feature selection and causal analysis for microbiome studies in the presence of confounding using standardization. *BMC Bioinformatics* 22, 362. <https://doi.org/10.1186/s12859-021-04232-2>
6. J. Wang, X. Li, T. Guo, M. Dzievit, X. Yu, **P. Liu**, K. P. Price, J. Yu (2021), Genetic Dissection of Seasonal Vegetation Index Dynamics in Maize through Aerial Based High-throughput Phenotyping, *The Plant Genome*, 14(3), e20155, <https://doi.org/10.1002/tpg2.20155>
7. J. Zhao, **Y. Qi**, **P. Liu**, A. Severin, M. Sayadi, I. Paetau-Robinson, W.S. White (2021). Prebiotic Effects of a Cranberry Beverage in a Randomized, Placebo-Controlled, Crossover Clinical Trial. *Current Developments in Nutrition*, 5(2), 1190, https://doi.org/10.1093/cdn/nzab054_045
8. P. Kanodia, V. Paramasivan, R. Srivastava, **R. Bi**, **P. Liu**, W. A. Miller, S. H. Howell (2020), Control of translation during the unfolded protein response in maize seedlings: Life without PERKs, *Plant Direct*, <https://doi.org/10.1002/pld3.241>
9. J. Bao, Y. Yu, H. Li, J. Hawks, G. Szatkowski, B. Dade, **H. Wang**, **P. Liu**, T. Brutnell, B. Spehar, N. Tye-Murray (2020), Evidence for Independent Peripheral and Central Age-Related Hearing Impairment, *Journal of Neuroscience Research*, <https://doi.org/10.1002/jnr.24639>
10. 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 (2019), Molecular signatures of retinal ganglion cells revealed through single cell profiling, *Scientific Reports*, 31;9(1):15778, [doi: 10.1038/s41598-019-52215-4](https://doi.org/10.1038/s41598-019-52215-4)
11. 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*, 3(3): e00122, <https://doi.org/10.1002/pld3.122>
12. 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>

13. L. Dong, 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>
14. 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>
15. **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>
16. 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>
17. 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>
18. 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)
19. 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)
20. 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)
21. C. Zhang, Z. Fei, **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
22. **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)
23. **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)
24. 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)

25. 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)
26. 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)
27. 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)
28. **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)
29. 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)
30. 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)
31. J. E. Koltes, E. Fritz-Waters†, C. J. Eisley, I. Choi, H. Bao, A. Kommadath, N. V. L. Serão, N. J. Boddicker, S. M. Abrams, M. Schroyen, H. Loyd, C. K. Tuggle, G. S. Plastow, L. Guan, P. Stothard, J. K. Lunney, **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)
32. L. Wang, Czedik-Eysenberg, A. Mertz, R. A., **Y. Si**, T. Tohge, A. Nunes-Nesi, S. Arrivault, L. K Dedow, D. W Bryant, **W. Zhou**, J. Xu, S. Weissmann, A. Studer, P. Li, C. Zhang, T. LaRue, Y. Shao, Z. Ding, Q. Sun, R. V Patel, R. Turgeon, X. Zhu, N. J Provart, T. C Mockler, A. R Fernie, M. Stitt, **P. Liu**, and T. P. Brutnell (2014), Exploring the mechanism of C₄ 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)
33. **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)
34. **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)
35. **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 [doi:10.4172/2155-6180.1000204](https://doi.org/10.4172/2155-6180.1000204)

36. 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 C4-related processes, *Journal of Experimental Botany*, 65(13):3543-55
[doi:10.1093/jxb/eru152](https://doi.org/10.1093/jxb/eru152)
37. **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)
38. **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)
39. **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)
40. 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)
41. 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)
42. 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)
43. 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)
44. **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)
45. **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)
46. 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)
47. 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)
48. **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)

49. **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)
50. 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)
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52. 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)
53. 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)
54. 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)
55. G. Li, K. Tivendale, **P. Liu**, Y. Feng, Y. Wannemuheler, W.Cai, P. Mangamele, 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)
56. X. Yu, L. Li, J. Zola, M. Aluru, H. Ye, A. Foudree, H. Guo, S. Anderson, S. Aluru, **P. Liu**, S. Rodermel 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.1365-313X.2010.04449.x](https://doi.org/10.1111/j.1365-313X.2010.04449.x)
57. 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)
58. P. Li, L. Ponnala, N. Gandotra, L. Wang, **Y. Si**, L. Tausta, T. Kebrom, N. Provert, 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)
59. **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

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61. **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)
62. 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)
63. R. J. H. Sawers, **P. Liu**, K. Anufriкова, 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)
64. 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)
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66. J. Ni, **P. Liu**, H. Jia (2000), Binding Properties of M-CAT Element in the Chicken Nicotinic Acetylcholine Receptor γ -Subunit Promoter, *Chinese Journal of Biochemistry and Molecular Biology*, 2000, V16(05): [580-585](#)

BOOK CHAPTERS

67. **P. Liu** and **Y. Si**, Cluster analysis of RNA-sequencing data (2014), in the book of *Statistical Analysis of Next Generation Sequencing Data*, Springer
68. **P. Liu**, **E. Goren**, P. Morris, **D. Walker**, and C. Wang, Statistical Methods for Feature Selection in Microbiome Studies (2021), invited book chapter for *Statistical Analysis of Microbiome Data*, Springer

SUBMITTED PAPERS

69. **Z. Qiao**, E. Barnes, S. Tringe, D. Schachtman, and **P. Liu***, Hurdle Poisson model-based clustering for microbiome data, *revision submitted to Bioinformatics*, 2022
70. **H. Wang**, Y. Qiu*, M. Guo, Y. Yin, **P. Liu***, Constructing Gene Networks by Partial Correlation Graphs with Information Incorporation, *submitted to Bioinformatics*, 2022
71. Qin, X. Wang, X. Tu, D. Tzeng, **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, *revised and submitted to The Plant Journal*, 2021

R PACKAGES FROM MY RESEARCH GROUP

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
6. `PHclust`: model-based clustering with microbiome count data

GRANTS

1. **PI** (sole PI) for Statistical Methods for 'omics Data Analysis
Source of Support: Plant Science Institute, Iowa State University
Total Award Amount: \$ 450,000
Total Award Period Covered: 2/1/2018-6/30/2024
2. **Co-investigator** (sole statistician) for Investigating Obesity-Induced Altered Ovarian Intracellular Signaling, together with Keating (PI)
Source of Support: **NIH** (R01ES030341-01)
Total Award Amount: \$ 2,394,307
Total Award Period Covered: 1/1/2020-10/31/2024
3. **Co-PI** (sole statistician) 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. Dangl (University of North Carolina at Chapel Hill), and A. Cousins (Washington State University)
Source of Support: **DOE** (DE-SC0014395)
Total Award Amount: \$ 13,460,684
Total Award Period Covered: 08/15/2015-07/31/2022
4. **Co-investigator** (sole statistician) for Global Effects of Flavivirus sfRNA on Translation Determined by Ribosome Profiling, together with W.A. Miller (PI, Iowa State University)
Source of Support: **NIH**
Total Award Amount: \$ 391,104
Total Award Period Covered: 6/04/2021 to 05/31/2023
5. **Co-investigator** (sole statistician) for Dietary Intervention Strategies to Support Methyl Group Metabolism in Polycystic Ovary Syndrome, together with K. Schalinske (PI, Iowa State University)
Source of Support: **NIH**
Total Award Amount: \$ 146,551
Total Award Period Covered: 02/25/2019 to 01/31/2020
6. **Co-PI** (sole statistician) for The molecular hallmark of epigenetic control in high-performing yeast, together with Z. Shao (PI, Iowa State University)

Source of Support: Presidential Interdisciplinary Research Seed Grant Program (PIRS), Iowa State University
Total Award Amount: \$ 50,000
Total Award Period Covered: 1/1/2018-12/31/2019

7. **Co-investigator** for Central Plains Research Data Center seed award, together with C. Wang (PI), Z. He, and D-K Lee (Iowa State University)
Source of Support: Central Plains Research Data Center
Total Award Period Covered: 08/16/2018-08/15/2019
8. **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 (Iowa State University)
Source of Support: NIH
Total Award Amount: \$ 1,173,287
Total Award Period Covered: 09/01/2013-05/31/2018
9. **Co-PI** (sole statistician) for GEPR: A Systems Approach to the Development and Function of C4 Photosynthesis, T. Nelson (PI, Yale University), other co-PIs: T. Brutnell (Donald Danforth Plant Science Center) and K. van Wijk (Cornell University)
Source of Support: NSF
Total Award Amount: \$ 8,386,495
Total Award Period Covered: 02/15/2012-01/31/2017
10. **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
Total Award Amount: \$ 4,999,158
Total Award Period Covered: 3/1/2011-2/29/2016
11. **Co-PI** (sole statistician) for GEPR: Comparative analysis of C3 and C4 leaf development in rice, sorghum and maize, T. Nelson (PI, Yale University), other co-PIs: T. Brutnell (Boyce Thompson Institute) and K. van Wijk (Cornell University)
Source of Support: NSF
Total Award Amount: \$ 5,475,676
Total Award Period Covered: 08/01/2007-07/31/2012
12. **Co-PI** (sole statistician) for Host:Pathogen Interactions in Avian Colibacillosis: a Systems-Based, Functional Genomics Approach, together with Nolan (PI), Johnson, Lamont, Kariyawasam and Trampel (Iowa State University)
Source of Support: USDA
Total Award Amount: \$ 955,330
Total Award Period Covered: 02/01/2008-01/31/2012
13. **Co-PI** (sole statistician) for Functional genomics analysis of a highly virulent *Campylobacter jejuni* clone causing sheep abortion, together with Zhang (PI), Yaeger and Sahin (Iowa State University)
Source of Support: USDA

- Total Award Amount: \$ 998,467
Total Award Period Covered: 12/15/09-12/14/12
14. **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
15. **Co-investigator** (sole statistician) 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
16. **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 (Iowa State University)
Source of Support: **NSF**
Total Award Amount: \$ 552,927
Total Award Period Covered: 08/15/2007-08/14/2011
17. **Co-PI** (sole statistician) for Inorganic Carbon Transport and the CO₂-concentrating Mechanism of *Chlamydomonas*, together with Martin Spalding (PI, Iowa State University)
Source of Support: **USDA**
Total Award Amount: \$ 351,000
Total Award Period Covered: 09/01/2007-08/31/2010
18. **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
19. **Statistician** for Identification of Novel APEC Virulence Genes via Functional Genomics, together with Li (PI), Nolan, and Kariyawasam (Iowa State University)
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
- Pending:
20. **Co-PI** (sole statistician) for CRISPR interference to understand microbiome interactions in the rhizosphere, together with Larry Halverson (PI) and Greg Philips
Source of Support: **NSF**
Total Award Amount: \$ 1,229,158
Total Award Period Covered: 05/01/2023-04/30/2026
21. **Co-investigator** (sole statistician) for Resistance exercise to treat major depression via cerebrovascular mechanisms: confirming efficacy and informing precision medicine, together with Jacob Meyer (PI) Nathaniel Wade, Leigh Philips, Wesley Lefferts, and Matthew Herring
Source of Support: **NIH**
Total Award Amount: \$ \$3,605,849
Total Award Period Covered: 7/1/2023-6/30/2028

22. **Co-investigator** (sole statistician) for Targeting cerebral Pulsatility through Aerobic exercise Training in mIddLe agE (PulsATILE Trial), together with Wesley Lefferts (PI)
Source of Support: **NIH**
Total Award Amount: \$2,822,667
Total Award Period Covered: 4/1/2023-3/31/2028

23. **Co-PI** for NSF PGRP: Causes for haploid frailty and pathways to increase haploid vigor in maize, together with Thomas Lubberstedt (PI) and Dior Kelley, Justin Walley, and Baskar Ganapathysubramanian
Source of Support: **NSF**
Total Award Amount:
Total Award Period Covered: 01/01/2023-12/31/2026

STUDENT ADVISING

Graduate students:

- ♦ **Major/Co-Major Professor** for **26** graduate students (**22 graduated**)

PhD students (17):

Current:

1. *Yunhui Qi, Statistics*
2. *Zhili Qiao, Statistics*
3. *David Walker, Statistics*
4. *Hao Wang, Statistics*

Graduated:

5. *Amin Shiraz*, (Co-Major Professor: Yumou Qiu), Statistics
PhD Dissertation (summer, 2022): Power Enhanced Gene Differential Expression Analysis by Incorporating Gene Network Information
currently working at AbbVie
6. *Wenting Zhao* (Co-Major Professor: Yumou Qiu), Statistics
PhD Dissertation (summer, 2022): Statistical methods for conditional dependence and microbiome data analysis
currently working at Zoetis
7. *Emily Goren* (Co-Major Professor: Chong Wang), Statistics
PhD Dissertation (summer, 2019): Statistical methods for ChIP-seq and microbiome studies using next-generation sequencing data
currently working at Cancer Research and Biostatistics (CRAB)
8. *Ran Bi*, Statistics
PhD Dissertation (summer, 2018): Statistical methods for gene expression studies using next-generation sequencing experiments
currently working at Novartis

9. *Chaohui Yuan* (Co-Major Professor: Chong Wang), Statistics
PhD Dissertation (summer, 2018): Statistical methods for microbiome data and antimicrobial resistance analysis
currently working at Eli Lily
10. *Haibo Liu* (Co-Major Professor: Chris Tuggle), Bioinformatics and Computational Biology
PhD Dissertation (spring, 2017): *The swine blood transcriptomics: Application and advancement*
currently working at Iowa State University
11. *Fangfang Liu* (Co-Major Professor: Chong Wang), Statistics
PhD Dissertation (spring, 2015): *Statistical methods in detecting differentially expressed genes, analyzing transposon insertion tolerance for gene, and group selection for survival data*
currently working at Pfizer Inc.
12. *Hye Jin Cho* (Co-Major Professor: Hui-Hsien Chou), Bioinformatics and Computational Biology
PhD Dissertation (summer, 2015): *Computational Prediction, Experiment Design and Statistical Validations of Non-Coding Regulatory RNA*
13. *Ali Berens* (Co-Major Professor: Amy Toth), Bioinformatics and Computational Biology
PhD Dissertation (summer, 2015): *Sociogenomics of social organization: Mechanistic and evolutionary underpinnings of caste development and facial recognition in paper wasps*
14. *Srihari Radhakrishnan* (Co-Major Professor: Nicole Valenzuela), Bioinformatics and Computational Biology
PhD Dissertation (fall, 2015): *On the causes and consequences of sex determination and sex-linkage*
15. *Yaqing Si*, Statistics
PhD Dissertation (summer, 2012): *Statistical analysis of RNA-seq data*
currently an Associate Professor at the School of Statistics, Southwestern University of Finance, Sichuan, China
16. *Megan Orr* (Co-Major Professor: Dan Nettleton), Statistics
PhD Dissertation (summer, 2012): *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
17. *Tieming Ji* (Co-Major Professor: Dan Nettleton, Pat Schnable), Statistics and Bioinformatics and Computational Biology
PhD Dissertation (summer, 2012): *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

MS students (9):

Graduated:

18. *David Walker, Statistics*

Master Creative Component (summer 2021): Developing variational Bayesian inference for applications to gene expression data

19. *Lauren McKeen (Co-major professor: Chong Wang), Statistics*

Master Creative Component (fall 2020): *Simulation studies to assess the power of set testing methods for microbiome data*

20. *Hao Wang (Co-major professor: Yumou Qiu), Statistics*

Master Creative Component (fall 2019): *Gene expression network based on partial correlations*

21. *Ran Bi, Statistics*

Master Creative Component (fall 2014): *Sample size calculation while controlling false discovery rate for differential expression analysis with RNA-seq Data*

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

Master Creative Component (spring 2014): *A Permutation Test of Genetic Association between Salmonella Isolated On-farm and At-abattoir using Amplified Fragment Length Polymorphism*

23. *William Landau, Statistics*

Master Creative Component (spring 2013): *Dispersion Estimation and Its Effect on Test Performance in RNA-seq Data Analysis: A Comparison of Methods*

24. *Yanwen Xiong, Statistics*

Master Creative Component (spring 2012): *Comparison of normalization methods for RNA-seq data analysis*

25. *Vanessa Kvam, Statistics*

Master Creative Component (fall 2011): *A comparison of statistical methods for detecting differentially expressed genes from RNA-seq data*

26. *Hong Hua, Statistics*

Master Creative Component (summer, 2009): *Microarray data analysis for a study of photosynthesis differentiation in maize*

INVITED TALKS

1. Power Multiple Testing in Omics Studies, *Statistical Adjustment for Multiplicity Workshop*, National Cancer Institute, Oct, 2022
2. Model-based Bioclustering Algorithm for Microbiome Data, *CMStatistics*, London UK, Dec 2022
3. Hurdle Poisson Model-based Clustering for Microbiome Data, *ICSA Symposium*, Sep 2021
4. Feature selection for microbiome studies in the presence of confounding using standardization, *JSM*, Aug, 2021

5. A Semi-parametric Bayesian Approach for Detection of Gene Expression Heterosis with RNA-Seq Data, *University of Nebraska, Lincoln*, Oct, 2019
6. Feature selection for microbiome data, *Iowa State University*, Oct, 2019
7. Differential Abundance Analysis of Microbiome Data, *Purdue University*, Sep, 2019
8. Differential Abundance Analysis of Microbiome Data, *Colorado State University*, Sep, 2019
9. Development of Statistical Methods for `omics Data Analysis, PSI Predictive Phenomics Workshop, *Iowa State University*, Apr, 2019
10. A Semi-Parametric Bayesian Approach for Detection of Gene Expression Heterosis with RNA-Seq Data, *University of Delaware*, Nov, 2018
11. Semi-parametric Bayesian approach for differential expression analysis with RNA-sequencing data, *ICSA China Conference*, Qingdao, China, July, 2018
12. Detection of Gene Expression Heterosis with RNA-Sequencing Data, *New York University School of Medicine*, May, 2018
13. Several statistical methods and models in plant genomics studies, PSI Predictive Phenomics Workshop, *Iowa State University*, Oct, 2014
14. Statistical Analysis of RNA-seq Data, Modern Views in Nutrition (MVN) 2014 seminar series, *Iowa State University*, Oct, 2014
15. Statistical Design and Analysis of RNA-seq Data, *Shandong Agricultural University, China*, Jul, 2014
16. An optimal test for detecting differential expression using RNA-seq data, *University of Missouri*, Columbia, Oct, 2012
17. 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
18. Model-Based Clustering for RNA-seq Data, *University of Maryland*, October, 2011
19. Model-Based Clustering for RNA-seq Data, *Conference on Statistical Analyses For Next Generation Sequencing*, *University of Alabama at Birmingham*, Sep 26-27, 2011
20. 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
21. Optimal tests using shrinkage idea with application to high-dimensional gene expression data, *Oklahoma State University*, October, 2010
22. Quick calculation of sample size while controlling false discovery rate with application to microarray, ABG seminar, *Iowa State University*, IA, 2006

23. Empirical Bayes test with application to microarray, *Rutgers University*, NJ, 2006
24. Empirical Bayes test with application to microarray, *University of Texas at Dallas*, TX, 2006
25. Empirical Bayes test with application to microarray, *Iowa State University*, IA, 2006
26. Empirical Bayes test with application to microarray, *Washington University at St. Louis*, MO, 2006
27. Quick calculation of sample size while controlling false discovery rate with application to microarray, *Mayo Clinic*, MN, 2006