

Peng Liu

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Iowa State University

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EMPLOYMENT

Associate Professor	Department of Statistics , Iowa State University	2013-present
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. **Basic Medical Sciences**, Peking University Health Science Center (previously known as Beijing Medical University), Beijing, China, 7/1998

RESEARCH INTERESTS

- ◆ Statistical Genomics, Bioinformatics, Biostatistics
- ◆ Statistical Inference for High-dimensional Data
- ◆ Bayesian Statistics

REFEREED JOURNAL PUBLICATIONS

1. R. Srivastava, Z. Li, G. Russo, J. Tang, **R. Bi**, U. Muppirala, S. Chudalayandi, A. Severin, M. He, S. Vaitkevicius, C. Lawrence-Dill, **P. Liu**, A.E. Stapleton, D. Bassham, F. Brandizzi, S. Howell (2018), Persistent ER stress in maize seedlings engages ZmIRE1 in a multiphasic process that transitions from prosurvival activities to cell death, *accepted by The Plant Cell*,
2. **E. Goren**, **P. Liu**, C. Wang, and C. Wang (2018), BinQuasi: a peak detection method for ChIP-seq data with biological replicates, *published online by Bioinformatics*
3. 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, *accepted by the Journal of Integrative Plant Biology*
4. He, M., **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*, *in press*, <https://doi.org/10.1016/j.cpb.2017.12.003>
5. 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)

6. 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)
7. 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)
8. C. Zhang, S. Fei, **P. Liu**, T. Ji, J. Peng, U. Frei, 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
9. **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)
10. **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)
11. 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)
12. 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)
13. 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)
14. 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)
15. **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)
16. 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)
17. 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)

18. 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)
19. L. Wang, Czedik-Eysenberg, A. Mertz, R. A., **Y. Si**, ..., **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)
20. **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)
21. **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)
22. **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
23. 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)
24. **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)
25. **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)
26. **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)
27. 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)
28. 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)
29. 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)
30. 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):1369-1378, [doi: 10.1128/AAC.01927-12](https://doi.org/10.1128/AAC.01927-12)

31. **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)
32. **P. Liu*** and C. Wang (2012), Robust Semiparametric Optimal Testing Procedure for Multiple 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)
33. 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)
34. W. Fang, **Y. Si**, S. Douglass, D. Casero, S. Merchant, M. Pellegrini, I. Ladunga, **P. Liu** and M. Spalding (2012), Transcriptome-Wide Changes in *Chlamydomonas reinhardtii* Gene Expression Regulated by Carbon Dioxide and the CO₂-Concentrating Mechanism Regulator CIA5/CCM1, *The Plant Cell*, 24(5):1876-1893, [doi/10.1105/tpc.112.097949](https://doi.org/10.1105/tpc.112.097949)
35. **T. Ji, P. Liu** and D. Nettleton (2012), Borrowing Information Across Genes and Experiments for Improved Error 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)
36. **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)
37. 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* Infection, *Avian Diseases*, 56(4):732-736, [doi: 10.1637/10261-060512-Reg.1](https://doi.org/10.1637/10261-060512-Reg.1)
38. 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)
39. 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.rnim.2012.02.003](https://doi.org/10.1016/j.rnim.2012.02.003)
40. 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)
41. 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)
42. G. Li, K. Tivendale, **P. Liu**, Y. Feng, Y. Wannemuheler, W. Cai, P. Mangiamale, T. Johnson, C. Constantinidou, 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(5): 1951-1960; doi:10.1128/IAI.01230-10

43. 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):634-646 doi: 10.1111/j.1365-313X.2010.04449.x
44. 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
45. 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, *Nature Genetics*, 42(12): 1060-1067, doi:10.1038/ng.703
46. **M. Orr** and **P. Liu*** (2009) Sample size estimation while controlling false discovery rate for microarray experiments using the ssize.fdr package, *The R Journal*, 1(1): 47-53
47. S. Covshoff, W. Majeran, **P. Liu**, J. M. Kolkman, K. J. van Wijk, T. Brutnell (2008) Deregulation of maize C₄ photosynthetic development in a mesophyll cell-defective mutant, *Plant Physiology*, 146: 1469-1481, doi: 10.1104/pp.107.113423
48. **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(6): 739-746, doi: 10.1093/bioinformatics/btl664
49. X. Zheng, H-C Huang, W. Li, **P. Liu**, Q-Z Li, Y. Liu (2007) Modeling nonlinearity in dilution design microarray data, *Bioinformatics*, 23(11): 1339-1347, doi:10.1093/bioinformatics/btm002
50. 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
51. S. A. Jesch, **P. Liu**, X. Zhao, M. T. Wells, and S. A. Henry (2006) Multiple Endoplasmic Reticulum-to-Nucleus Signaling Pathways Coordinate Phospholipid Metabolism with Gene Expression by Distinct Mechanisms, *Journal of Biological Chemistry*, 281: 24070 – 24083, doi: 10.1074/jbc.M604541200
52. N.-S. Tan, 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(14): 5114-5127, doi: 10.1128/MCB.22.14.5114-5127.2002
53. 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

PUBLISHED BOOK CHAPTER

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

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

GRANTS

Awarded:

1. **PI** for Systems Analysis of the Physiological and Molecular Mechanisms of Sorghum Nitrogen Use Efficiency, Water Use Efficiency, and Interactions with the Soil Microbiome, other PIs include D. Schachtman (leading PI, University of Nebraska-Lincoln), M. Harrison (Boyce Thompson Institute), S. Kresovich (Clemson University); J. Prenni (Colorado State University), R. Bart, T. Brutnell, D. Chitwood, 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
Total Award Amount: \$ 13,460,684
Total Award Period Covered: 08/15/2015-07/14/2020
2. **PI** for PSI faculty scholar of Plant Phenomics
Source of Support: Plant Sciences Institute, Iowa State University
Total Award Amount: \$ 225,000
Total Award Period Covered: 2/1/2018-1/31/2021
3. **Co-investigator** 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 Amount: \$ 50,000
Total Award Period Covered: 1/1/2018-12/31/2019
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. **PI** for GEPR: A Systems Approach to the Development and Function of C4 Photosynthesis, other PIs include T. Nelson (leading PI) from Yale University, 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-investigator** 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. **PI** for GEPR: Comparative analysis of C3 and C4 leaf development in rice, sorghum and maize, other PIs include T. Nelson (leading PI) from Yale University, 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-investigator** 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-investigator** 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-investigator** 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-investigator** for Inorganic Carbon Transport and the CO₂-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

Pending:

16. **Co-investigator** for The molecular hallmark of epigenetic control in high-performing yeast, together with Shao (PI)
Source of Support: NSF
Total Award Amount: \$ 2,000,000
Total Award Period Covered: 1/1/2019-12/31/2022
17. **Co-investigator** for The molecular hallmark of epigenetic control in high-performing yeast, Huang (PI), submitted to the LAS signature research incubator, Iowa State University
18. **Co-investigator** for Dietary Intervention Strategies to Support Methyl Group Metabolism in Polycystic Ovary Syndrome, together with Schalinske (PI)
Source of Support: NIH
Total Award Amount: \$ 146,551
Total Award Period Covered: 1/1/2019-12/31/2020
19. **Collaborator** for Disruption of methyl group metabolism by diabetes in the brain: impact on neurotransmitter imbalance and associated depression, together with Schalinske (PI)
Source of Support: NIH
Total Award Period Covered: 1/1/2019-12/31/2020

STUDENT ADVISING

Graduate students:

- ◆ Advisor/co-advisor for **17** graduate students (**14 graduated**)

PhD students (11):

Current:

1. *Ran Bi*, Statistics
2. *Emily Goren*, Statistics
3. *Chaohui Yuan* (Co-Major Professor: Chong Wang), Statistics

Graduated:

4. *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.
5. *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
6. *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
7. *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
8. *Haibo Liu* (Co-Major Professor: Chris Tuggle), Bioinformatics and Computational Biology
9. *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*
10. *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*
11. *Srihari Radhakrishnan* (Co-Major Professor: Nicole Valenzuela), Bioinformatics and Computational Biology

MS students (6):

Graduated

12. *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
currently a PhD student at Iowa State University
13. *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
currently a PhD student at Iowa State University

14. *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
currently a PhD student at Iowa State University

15. *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

16. *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
currently a biostatistician at AT Still University

17. *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

SELECTED INVITED TALKS

1. Semi-parametric Bayesian approach for differential expression analysis with RNA-sequencing data, ICSA China Conference, July, 2018
2. Detection of Gene Expression Heterosis with RNA-Sequencing Data, New York University School of Medicine, May, 2018
3. Several statistical methods and models in plant genomics studies, PSI Predictive Phenomics Workshop, Iowa State University, Oct, 2014
4. Statistical Analysis of RNA-seq Data, Modern Views in Nutrition (MVN) 2014 seminar series, Iowa State University, Oct, 2014
5. Statistical Design and Analysis of RNA-seq Data, Shandong Agricultural University, China, Jul, 2014
6. An optimal test for detecting differential expression using RNA-seq data, *University of Missouri*, Columbia, Oct, 2012
7. 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

8. Model-Based Clustering for RNA-seq Data, *University of Maryland*, October, 2011
9. Model-Based Clustering for RNA-seq Data, *Conference on Statistical Analyses For Next Generation Sequencing*, University of Alabama at Birmingham, Sep 26-27, 2011
10. 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
11. Optimal tests using shrinkage idea with application to high-dimensional gene expression data, *Oklahoma State University*, October, 2010

INVITED LECTURES

12. Statistical analysis for RNA-seq data, BCB570, Bioinformatics IV: Functional Genomics and Systems Biology, *Iowa State University*, 2014
13. Statistical analysis for RNA-seq data, BCB570, Bioinformatics IV: Functional Genomics and Systems Biology, *Iowa State University*, 2013
14. Statistical analysis for RNA-seq data, BCB570, Bioinformatics IV: Functional Genomics and Systems Biology, *Iowa State University*, 2011
15. Experimental Design and statistical analysis of microarrays, NSF REU summer program on Bioinformatics, *Iowa State University*, 2010
16. Designing and Analyzing Microarray Experiment, Microbiology 604, *Iowa State University*, IA, 2007

TEACHING EXPERIENCES

- ◆ **Instructor for STAT 516:** Statistical Design and Analysis for Microarray Experiments
- ◆ **Instructor for STAT 104:** Introduction to Statistics, Iowa State University
- ◆ **Instructor for STAT 402:** Statistical Design
- ◆ **Instructor for STAT 416:** Statistical Design and Analysis for High-dimensional Gene Expression Experiments

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EDITORIAL ACTIVITIES

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

HONORS AND AWARDS

- ◆ College of Liberal Arts and Sciences, Award for Mid-Career Achievement in Research, 2018
- ◆ Iowa State University Award for Early Achievement in Research, 2013
- ◆ Graduate School Travel Award and Fellowship, Cornell University, 3/2005 and 8/2005
- ◆ Research Grant, 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