

Curriculum Vitae

Zhijin Wu, Ph.D.

Professor
Department of Biostatistics
Brown University

ADDRESS

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EDUCATION

1997	B.S.	Biochemistry and Molecular Biology	Peking University
2000	M.S.	Molecular Biology	University of Southern California
2005	Ph.D.	Biostatistics	Johns Hopkins University

Dissertation: *Probe Level Models for DNA Microarrays*
Advisor: Rafael A. Irizarry

ACADEMIC APPOINTMENTS

July, 2005 – June, 2012	Assistant Professor , Department of Biostatistics (Tenure Track), Brown University
July, 2012 – June, 2019	Associate Professor , Department of Biostatistics (Tenured), Brown University
July, 2019 –	Professor , Department of Biostatistics (Tenured), Brown University

OTHER ACADEMIC AND PROFESSIONAL POSITIONS

July, 2005 – present	Faculty, Center for Statistical Sciences, Brown University
Dec, 2011 – June, 2012	Director, Master's Program in Biostatistics, Department of Biostatistics, Brown University
July, 2012 – present	Director, PhD Program in Biostatistics, Department of Biostatistics, Brown University

ACADEMIC HONORS & AWARDS

2005	Margaret Merrell Award for outstanding research Department of Biostatistics Johns Hopkins Bloomberg School of Public Health
2011	CAREER Award, National Science Foundation

MEMBERSHIP IN PROFESSIONAL SOCIETIES

American Statistical Association
International Biometric Society (ENAR)
International Chinese Statistics Association

PUBLICATIONS (students marked with * and corresponding author indicated with †)

A. Peer-reviewed publications

1. Viswanath V, **Wu Z**, Fonck C, Wei Q, Boonplueang R and Andersen JK. (2000). Transgenic mice neuronally expressing baculoviral p35 are resistant to diverse types of induced apoptosis, including seizure – associated neurodegeneration. *Proceedings of the National Academy of Sciences* 97(5):2270 –5.
2. Peng J, **Wu Z**, Wu Y, Hsu M, Stevenson FF, Boonplueang R, Roffler–Tarlov SK and Andersen JK (2002). Inhibition of caspases protects cerebellar granule cells of the weaver mouse from apoptosis and improves behavioral phenotype. *Journal of Biological Chemistry* 277(46):44285–91.
3. Wu, Z, **Wu, Z**, Wiegandt, DA and Nassar, CR (2003). High–performance 64–QAM OFDM via carrier interferometry spreading codes. *Vehicular Technology Conference, 2003 IEEE 58th* 1:557-561.
4. Irizarry RA, Ooi SL, **Wu Z** and Boeke J (2003). Use of mixture models in a microarray – based screening procedure for detecting differentially represented yeast mutants. *Statistical Applications in Genetics and Molecular Biology* 2(1).
5. Cope LM, Irizarry RA, Jaffee H, **Wu Z** and Speed TP (2003). A benchmark for Affymetrix genechip expression measures. *Bioinformatics* 20: 323–331.
6. **Wu Z**, Irizarry RA, Gentleman R, Martinez Murillo F and Spencer F (2004). A model based background adjustment for oligonucleotide expression arrays. *Journal of the American Statistical Association*, 99(468):909–917.
7. **Wu Z** and Irizarry RA (2004). Preprocessing of oligonucleotide array data. *Nature Biotechnology* 22: 656–658. [PMID: 15175677]
8. **Wu Z** and Irizarry RA (2005). Stochastic models inspired by hybridization theory for short oligonucleotide arrays. *Journal of Computational Biology*, 12(6) 882–893. [PMID: 16108723]
9. Irizarry RA, Cope L, **Wu Z** (2006). Feature – level exploration of the Choe et al. Affymetrix GeneChip control dataset. *Genome Biology*, 2006, 7:404. [PMID: 16953902]
10. Irizarry RA, **Wu Z** and Jaffee H (2006). Comparison of affymetrix genechip expression measures. *Bioinformatics* 22(7):789–794. [PMID: 16410320]
11. **Wu Z**† and Irizarry RA (2007). A statistical frame work for the analysis of microarray probe – level data. *Annals of Applied Statistics*. 1(2) 333–357.
12. Sui Y* and **Wu Z**† (2007). Alternative statistical parameter for high – throughput screening assay quality assessment. *Journal of Biomolecular Screening* 12(2):229–234. [PMID: 17218666]
13. Yegnasubramanian S, Haffner MC, Zhang Y, Gurel B, Cornish TC, **Wu Z**, Irizarry RA, Morgan J, Hicks J, DeWeese TL, Isaacs WB, Bova GS, De Marzo AM, Nelson WG (2008). DNA hypomethylation arises later in prostate cancer progression than CpG island hypermethylation and contributes to metastatic tumor heterogeneity. *Cancer Research*. 68(21):8954–67.
14. Santiago Jr RB, **Wu Z**, Zhang L, and Widmer G (2008). Identification of growth inhibiting compounds in a giardia lamblia high-throughput screen. *Molecular & Biochemical Parasitology*. 162(2):149–54.

15. Miselis N, **Wu Z**, Rooijen NV and Agnes KB (2008). Targeting tumor-associated macrophages in an orthotopic murine model of diffuse malignant mesothelioma. *Molecular Cancer Therapeutics* 7(4):788–799.
16. **Wu Z**[†], Liu D and Sui Y* (2008). Quantitative assessment of hit detection and confirmation in single and duplicate HTS screenings. *Journal of Biomolecular Screening*. 13(2):159–167.
17. **Wu Z**[†] A review of statistical methods for preprocessing oligonucleotide microarrays (2009). *Statistical Methods in Medical Research*, 18 (6), 533–541.
18. Paruthiyil S, Cvorovic A, Zhao X, **Wu Z**, Sui Y and others (2009). Drug and cell type-specific regulation of genes with different classes of estrogen receptor β -selective agonists. *Public Library of Science One*. 4(7): e6271.
19. Sui Y*, Zhao X, Speed TP and **Wu Z**[†]. Background Adjustment for DNA Microarrays Using a Database of Microarray Experiments (2009). *Journal of Computational Biology*. 16(11): 1501–1515.
20. Irizarry RA, Ladd-Acosta C, Wen B, **Wu Z**, Montano C, Onyango P, Cui H, Gabo K, Rongione M, Webster M, Ji H, Potash JB, Sabuncuyan S, Feinberg AP (2009). The human colon cancer methylome shows similar hypo- and hypermethylation at conserved tissue-specific CpG island shores. *Nature Genetics*. 41(2):178–86.
21. **Wu Z**, Li X, Husnay R, Chakravarthy V, Wang B and Wu Z (2009). A novel highly accurate log skew normal approximation method to lognormal sum distributions. *Wireless Communications and Networking Conference IEEE 2009*. 1–6.
22. **Wu Z**[†], Jenkins BD, Rynears TA and others (2010). Empirical bayes analysis of sequencing-based transcriptional profiling without replicates. *BMC Bioinformatics*. 11:564.
23. Miselis N, Lau BW, **Wu Z**, Kane AB (2010). Kinetics of host cell recruitment during dissemination of diffuse malignant peritoneal mesothelioma. *Cancer Microenvironment* 4(1): 39–50.
24. **Wu Z**[†] and Aryee M. (2010) Subset quantile normalization using negative control features. *Journal of Computational Biology*, 17(10):1385–1395.
25. Champion SN, Houseman EA, Sandrof MA, Hensley JB, Sui Y, Gaido KW, **Wu Z** and Boekelheide K (2010). Suppression of radiation-induced testicular germ cell apoptosis by 2, 5-hexanedione pretreatment. II. Gene array analysis reveals adaptive changes in cell cycle and cell death pathways. *Toxicological Sciences* 117(2):457–465.
26. Ghosh M, Fahey JV, Shen Z, Lahey T, Cu-Uvin S, **Wu Z**, Mayer K, Wright PF, Kappes JC, Ochsenbauer C and Wira CR* (2010). Anti-HIV activity in cervical-vaginal secretions from HIV-positive and -negative women correlate with innate antimicrobial levels and IgG antibodies. *Public Library of Science One*. 5(6):e11366.
27. Hansen KD, **Wu Z**, Irizarry RA and Leek JT (2011). Sequencing technology does not eliminate biological variability. *Nature Biotechnology* 29:572–573.
28. Yegnasubramanian S, **Wu Z**, Haffner MC, Esopi D, Aryee MJ, Badrinath R and others (2011). Chromosome-wide mapping of DNA methylation patterns in normal and malignant prostate cells reveals pervasive methylation of gene-associated and conserved intergenic sequences. *BMC Genomics* 12(1):313–332.

29. Aryee, M, **Wu Z**, Ladd-Acosta C, Herb B, Feinberg Ap, Yegnasubramanian S and Irizarry R (2011). Accurate genome-scale percentage DNA methylation estimates from microarray data. *Biostatistics* 12(2):197–210.
30. Faghiri Z, Bonilla Santiago R, **Wu Z**, and Widmer G (2011). High-throughput screening in sub-optimal growth conditions identifies agonists of *Giardia lamblia* proliferation. *Parasitology* 138(2):194–200.
31. Gong J, Campos H, McGarvey S, **Wu Z**, Goldberg R and Baylin A (2011). Adipose tissue palmitoleic acid and obesity in humans: does it behave as a lipokine? *The American Journal of Clinical Nutrition* 93(1):186–191.
32. Gong J, Campos H, McGarvey S, **Wu Z**, Goldberg R and Baylin A (2011). Genetic variation in stearoyl-CoA desaturase 1 is associated with metabolic syndrome prevalence in Costa Rican adults. *The Journal of Nutrition*:141(12) 2211-2218.
33. DeLong AK, Wu M, Bennett D, Parkin N, **Wu Z**, Hogan JW and Kantor R (2011). SQUAT (Sequence Quality Analysis Tool) for protease and reverse transcriptase. *AIDS Research and Human Retroviruses* 27. PMID: 21916749
34. Li X, **Wu Z**, Chakravarthy V and Wu Z (2011). A low complexity approximation to lognormal sum distributions via transformed log skew normal distribution. *IEEE Transactions on Vehicular Technology*. 60(8):4040-4045.
35. Hansen KD, Irizarry RA and **Wu Z**[†] (2012). Removing technical variability in RNA-seq data using conditional quantile normalization. *Biostatistics*, 13(2):204-216.
36. Champion SN, Catlin N, Houseman EA, Hensley J, Sui Y, Caido KW, **Wu Z** and Boekelheide K (2012) Molecular alterations underlying the enhanced disruption of spermatogenesis by 2,5-hexanedione and carbendazim co-exposure. *Reproductive Toxicology* 33 (3): 382-389.
37. Dyhrman ST, Jenkins BD, Rynearson TA, Saito MA, Mercier ML, Harriet Alexander H, Whitney LP, Drzewianowski A, Bulygin VV, Bertrand EM, **Wu Z**, Benitez-Nelson C, Heithoff A (2012). The transcriptome and proteome of the diatom *thalassiosira pseudonana* reveal a diverse phosphorus stress response. *PLoS ONE*, 7.3 (2012):e33768.
38. Wu H, Wang C and **Wu Z**[†] (2013). A new shrinkage estimator for dispersion improves differential expression detection in RNA-seq data. *Biostatistics* 14 (2), 232-243.
39. Austin A*, Linkletter C and **Wu Z** (2013). Covariate-defined latent space random effects model. *Social Networks*, 35(3):338-346.
40. Dunn CW, Luo X, **Wu Z** (2013). Phylogenetic analysis of gene expression. *Integrative and Comparative Biology* 53 (5), 847-856. PMID: 23748631
41. Srivatsan A, Jenkins S, Jeon M, **Wu Z**, Kim C, Chen J and Pandey R (2014). Gold nanocage-photosensitizer conjugates for dual-modal image-guided enhanced photodynamic therapy. *Theranostics* 2014; 4(2):163-174.
42. Wu H, Chi Wang and **Wu Z**[†] (2015). PROPER: comprehensive power evaluation for differential expression using RNA-seq. *Bioinformatics* 31 (2): 233-241.
43. Mossman JA, Tross JG, Li N, **Wu Z**, Rand DM (2016). Mitochondrial-nuclear interactions mediate sex-specific transcriptional profiles in *Drosophila*. *Genetics* 204(2):613-630.

44. Li M, Tucker LD, Asara JM, Cheruiyot CK, Lu H, **Wu Z**, Newstein MC, Dooner MS, Friedman J, Lally MA, Ramratnam B (2016). Stem-loop binding protein is a multifaceted cellular regulator of HIV-1 replication. *The Journal of clinical investigation*. 26(8):3117-29.
45. Mossman JA, Tross JG, Jourjine NA, Li N, **Wu Z**, Rand DM (2017). Mitonuclear interactions mediate transcriptional responses to hypoxia in Drosophila. *Molecular Biology and Evolution*, 34(2): 447-466.
46. Huang Y-T, Zhang Y, **Wu Z** and Michaud DS (2017). Genotype-based gene signature of glioma risk identified by integrative genome-wide association study. *Neuro Oncology* 19(7):940-950.
47. Li N, McCall MN & **Wu Z**[†] (2017). Establishing informative prior for gene expression variance from public databases. *Statistics in Biosciences*, 9(1):160-177.
48. **Wu Z**[†], Zhang Y*, Stitzel ML, and Wu H. (2018) Two-phase differential expression analysis for single cell RNA-seq. *Bioinformatics*, 34(19): 3340-3348. PMID: 29688282
49. Yanagi KS, **Wu Z**, ..., Hart AC. Meta-analysis of genetic modifiers reveals candidate dysregulated pathways in Amyotrophic Lateral Sclerosis (2019). *Neuroscience*, 396(1):A3-A20. PMID: 30594291
50. Li Z, **Wu Z**, Jin P and Wu H. Dissecting differential signals in high-throughput data from complex tissues (2019) *Bioinformatics*, doi: 10.1093/bioinformatics/btz196 PMID: 30903684
51. **Wu Z**[†], Wu H. Accounting for cell-type hierarchy in evaluating single cell RNA-seq clustering (2020) *Genome Biology*, (2020)21:123 doi:10.1186/s13059-020-02027-x PMID: 32450895
52. Su, K., **Wu, Z.**, & Wu, H. (2020). Simulation, Power Evaluation, and Sample Size Recommendation for Single Cell RNA-seq. *Bioinformatics* doi:10.1093/bioinformatics/btaa607 PMID: 32614380
53. Wu X, Wu H, and **Wu Z**[†] (2021) Penalized Latent Dirichlet Allocation Model in Single-Cell RNA Sequencing. *Statistics in Biosciences* [Online]. Available: <https://doi.org/10.1007/s12561-021-09304-8>
54. **Wu Z**[†], Su K, Wu H. Non-linear Normalization for Non-UMI Single Cell RNA-Seq. *Frontiers in genetics*. 2021 Apr 9;12:452.

B. Book Chapters

1. Bolstad BM, Irizarry RA, Gautier L and **Wu Z**. Low-level analysis and pre-processing of Affymetrix GeneChip data. *Bioinformatics and Computational Biology Solutions Using R and Bioconductor*. Springer 2005
2. **Wu Z**[†] and Wu Z. Exploration, visualization and preprocessing of high- dimensional data. *Statistical Methods in Molecular Biology*. Humana Press 2010
3. **Wu Z**[†] and Wu H. Experimental design and power calculation for RNA-seq experiments. *Statistical Genomics: Methods and Protocols, Methods in Molecular Biology*. Springer 2016

C. Non-Peer Reviewed Publications

1. Wang K, Liu X, Guo Y, **Wu Z**, Zhi D, Ruan J, Zhao Z. The International Conference on Intelligent Biology and Medicine (ICIBM) 2018: systems biology on diverse data types. (2018) *BMC Systems Biology* 12 (Suppl 8) :125

2. Liu X, Xie L, **Wu Z**, Wang K, Zhao Z, Ruan J, Zhi D. The International Conference on Intelligent Biology and Medicine (ICIBM) 2018: bioinformatics towards translational applications (2018) : BMC Bioinformatics **19 (Suppl 17)** :492
3. **Wu Z**, Yan J, Wang K, Liu X, Guo Y, Zhi D, Ruan J, Zhao Z. The International Conference on Intelligent Biology and Medicine (ICIBM) 2018: genomics with bigger data and wider applications (2019) *BMC Genomics*: 20 (Suppl 1) :80
4. Zhi D, Zhao Z, Li F, **Wu Z**, Liu X, Wang K. The International Conference on Intelligent Biology and Medicine (ICIBM) 2018: genomics meets medicine. (2019) *BMC Medical Genomics*: 12 (Suppl 1) :20

D. Invited Lectures (Since 2012)

1. June 2012. Normalizing RNA-seq data using conditional quantile normalization. ICSA Applied Statistical Symposium. Boston, MA.
2. Nov 2012. A new shrinkage estimator for dispersion improves differential expression detection in RNA-seq data. University of Texas MD Anderson Cancer Center.
3. Dec 2012. Differential expression in RNA-seq data. Correlated and high dimensional data seminar. Harvard University, Department of Biostatistics.
4. June 2013. Simulation based power computation in RNA-seq. ICSA Joint Statistics Conference. Bethesda, MD
5. July 21 2015. Gene set analysis for large and sparse effects BioC 2015, Bioconductor Annual Conference. Seattle, WA.
6. Aug 5 2015 Gene set analysis for large and sparse effects. Joint Statistical Meeting. Seattle, WA.
7. Nov 20 2015 Gene set analysis for large and sparse effects. Boston University.
8. June 2016 Normalization issues in scRNAseq data. ICSA 2016 Symposium. Atlanta, Georgia.
9. Sept 2016. Single cell RNA sequencing. Penn State University.
10. Dec 2016. Analyzing heterogeneity in single cell RNA-sequencing. ICSA 2017 International Conference. Shanghai, China.
11. May 2017. The two phases in single cell RNA-sequencing. Workshop in Statistical Challenges in Single-Cell Biology. Ascona, Switzerland .
12. Aug 2017. Normalization and reproducibility in single cell RNA-seq. Joint Statistical Meeting. Baltimore, MD.
13. March 2018. Normalization and reproducibility in single cell RNA-seq. ENAR. Atlanta, GA
14. Aug 2018. Power Analysis for RNA-seq in single cells. Joint Statistical Meeting 2018. Vancouver, Canada.
15. Aug 2018. The two phases in single cell RNA-sequencing. Keynote speaker. International Conference on Bioinformatics and Neurosciences (ICoBN 2018). Las Vegas, NV.
16. Sept 2018. Differential expression in single cells. University of California Berkeley. Computational Biology Program.
17. Sept 2018. Differential expression in two phases in single cell RNA-seq. The fourth annual Single Cell Analysis USA Congress. Boston, MA.

18. Feb 2019. Penalized Latent Dirichlet Allocation in Single Cell RNA Sequencing. Frontiers in Single-cell Technology, Applications and Data Analysis, Banff International Research Station for Mathematical Innovation and Discovery (BIRS) Banff, Canada
19. March 2019. Evaluation of Cell Clustering in Single Cell Data. ENAR 2019 Philadelphia, PA
20. July 2019. Evaluation of Cell Clustering in Single Cell Data. ICSA 2019. Tianjin, China
21. Aug 2019. Evaluation of Cell Clustering in Single Cell Data. JSM 2019. Denver, CO
22. September 2019. Finding biological signal in single cell RNA sequencing data. Department of Statistics, University of Virginia.
23. October 2019. Finding biological signal in single cell RNA sequencing data. Department of Biostatistics & Informatics. University of Colorado Denver.

E. Contributed Papers and Abstracts Presented (abstracts presented by others not listed)

1. Using sequence information to improve RNA expression measures. Joint Statistical Meetings 2003, San Francisco
2. Stochastic models inspired by hybridization theory for short oligonucleotide arrays. RECOMB 2004, San Diego

RESEARCH GRANTS AND CONTRACTS: ACTIVE

Statistical Methods

1. **Dissecting epitranscriptomic signal from complex tissues** (1R01GM141392-01)
 Role: subcontract PI
 Agency: NIH/NIGMS
 Period: 09/2021 – 08/2025

Interdisciplinary Collaborations

2. **COBRE Center for Computational Biology of Human Disease** (Phase II) (P20 GM109035)
 Role: Core B co-director, mentor
 PI: David Rand
 Agency: NIGMS
 Period: 09/01/21 – 08/31/26
3. **Novel Markers of Exposure and Pathways of Response to Chromium** (R01 ES027981)
 Role: Co – Investigator
 PI: Bernardo Lemos
 Agency: NIGMS/Harvard
 Period: 02/01/18-01/31/23
4. **Salivary Extracellular Vesicles as Biomarkers for Alzheimer's Disease and Related Disorders**
 Role: Co – Investigator
 PI: Kreiling, Jill
 Agency: NIGMS/RIH
 Period: 06/01/22-03/31/26

Training Grants

1. **Predocutorial Training Program in Biological Data Science at Brown University**

(1T32GM128596-01)

Role: Co-PI
PI: Sohini Ramachandran
Agency: NIH/NIGMS
Period: 09/01/18-08/31/23

RESEARCH GRANTS AND CONTRACTS: COMPLETED

1. **Statistical Methods for Single-Cell RNA-Seq (R01GM122083-01)**

Role: subcontract PI
Agency: NIH/NIGMS
Period: 08/15/2016 – 07/31/2021

2. **COBRE Center for Computational Biology of Human Disease (Phase I) (P20 GM109035)**

Role: Core B co-director, mentor
PI: David Rand
Agency: NIGMS
Period: 09/01/16 – 08/31/21

3. **COBRE Center for Central Nervous System Function (Phase II) (P20 GM109035)**

Role: Core director
PI: Jerome Sanes
Agency: NIGMS
Period: 09/1/18 – 08/31/22

4. **Statistical and Computational Methods for RNA-seq data**

Role: PI
Agency: NSF
Period: 05/01/11- 04/30/16

5. **Nuclear-Mitochondrial Fitness Interactions in Drosophila (multiple PI with David Rand)**

Role: co-PI
Agency: NIH/NIGMS
Period: 8/01/12 - 7/31/16

6. **CFAR Developmental Award: Novel statistical methodology for the design and analysis of High Throughput Screening (HTS) experiments**

Role: PI
Agency: NIH/The Miriam Hospital Subcontract
Period: 12/01/2006 -01/15/2008

7. **Effects of Tissue Heterogeneity on Gene Expression Measures in Tumor Samples**

Role: PI
Period: 1/1/07-12/31/08

8. **Gene Networks in Peri – pubertal Sertoli Cell Injury**

Role: Co – Investigator
Project PI: Mary Hixon
Agency: NIH (R01 ES01 5704 – 01)
Period: 8/1/2007 – 7/31/2011

9. **HCV in Alcoholics**

Role: Co – Investigator
Project PI: Jack Wands
Agency: NIH/Rhode IslandHospital subcontract

- Period: 12/01/99 - 08/31/11
10. **High-throughput screening for new inhibitors of Giardia lamblia**
 Role: Co – Investigator
 Project PI: Giovannj Widmer
 Agency: NIH/Tufts University Subcontract
 Period: 07/21/09- 06/30/11
11. **Manufactured Nanomaterials: Physico-chemical Principles of Biocompatibility and Toxicity**
 Role: Co – Investigator
 Project PI: Agnes Kane
 Agency: NIEHS
 Period: 10/01/07 – 09/30/11
12. **Preprocessing and Analysis Tools for Contemporary Microarray Applications**
 Role: Co – PI
 Project PI: Rafael Irizarry
 Agency: NIH/Johns Hopkins University Subcontract
 Period: 09/24/2007 – 8/31/2012
13. **Reuse in RI: A State-Based Approach To Complex Exposures**
 Role: Co-Director of Analytical Core
 Project PI: Kim Boekelheide
 Agency: NIH
 Period: 04/18/05 - 03/31/14
14. **COBRE for Perinatal Biology**
 Role: Consultant
 Project PI: James Padbury
 Agency: NIH
 Period: 4/01/08 - 3/31/13
15. **Lifespan/Tufts/Brown Center for AIDS Research (Biostatistics Core)**
 Role: Co – Investigator
 Project PI: Charles C. J. Carpenter
 Agency: NIH/NIAID (P30 AI 42853)
 Period: 07/01/07 - 06/30/12
13. **COBRE Center for Central Nervous System Function (Phase I) (P20 GM109035)**
 Role: Core director
 PI: Jerome Sanes
 Agency: NIGMS
 Period: 08/15/13 – 07/31/18

PROFESSIONAL LEADERSHIP AND SERVICE

National-International

- **NIH BMRD study section 2022**
- **NSF Grant Review Panelist 2009/2011 /2013/2015**
- **Associate Editor (2018- 2020)**
 The Journal of the American Statistical Association (JASA)

- **Journal Reviewer** *Science, Annals of Applied Statistics, The Journal of the American Statistical Association, Nucleic Acid Research, BiomedCentral, Nature Biotechnology, Journal of Bioinformatics and Computational Biology, Proceedings of the National Academy of Sciences, Bioinformatics, Statistical Applications in Genetics and Molecular Biology, Journal of Computational Biology, Biometrical Journal, American Journal of Clinical Nutrition, Scientific Report*
- **Publications Officer** (2015-2017)
ASA Section on Statistics in Genomics and Genetics Publications Officer
- **Publication Committee Chair** (2018)
International Conference on Intelligent Biology and Medicine (ICIBM 2018)

Brown University

- Director of PhD Program in Biostatistics 2012-
- Biostatistics Recruitment and Admissions committee 2012-
- Director of Master's Program in Biostatistics 2011-2012
- Faculty Executive Committee 2013 Spring
- Member of the Data Science Initiative's Campus Advisory Board 2017-2019

ADVISING

PhD Thesis Directed

Yunxia Sui, Ph.D. in Biostatistics 2010
Robust Gene Expression Measure using Databases of Microarrays
Current position: Statistician at AbbVie

Andrea Austin, Ph.D. in Biostatistics 2013
Latent class social network models and application in genomics
Current position: Research Scientist at Dartmouth College

Yi Zhang, Ph.D. in Biostatistics 2018
Pathway Analysis of Genomic Data
Current position: Statistician at Google

Xiaotian Wu, Ph.D. in Biostatistics 2020
Statistical Methods for Single Cell RNA Sequencing
Current position: Statistician at Google

Xiaoyu Wei, Ph.D. in Biostatistics 2022
Current position: Statistician at Amazon

Postdoctoral advisee

Nan Li, postdoctoral fellow
Statistical and computational methods for RNAseq data
Current position: Statistical Analyst at St. Jude Children's Research Hospital

Thesis Committee

Devin Koestler, Ph.D. Biostatistics, Aug 2011
Chui Sun Yap, Ph.D. Molecular, Cellular Biology and Biochemistry, 2008
Jian Gong, Ph.D. Epidemiology, 2010
Bahar Erar, Ph.D. Biostatistics, Aug 2016
Hsin-Ta Wu, Ph.D. Computer Science, May 2016

Jun Ke, Ph.D. Biostatistics, 2020
Nichlas Skvir, Ph.D. Computational Biology, 2022