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HONGMEI ZHANG

University Address

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Education

Ph.D.	Statistics	Iowa State University, Ames, IA
M.S.	Statistics	Iowa State University, Ames, IA
M.S.	Mathematics	Truman State University, Kirksville, MO
M.S.	Electronic Engineering	Nanjing Research Institute of Technology, Nanjing, China

Professional Experience

2023 – present	Interim Director, Division of Health System Management and Policy, University of Memphis, TN
2017 – present	Professor (tenured) and Bruns Endowed Professor Division of Epidemiology, Biostatistics, and Environmental Health Sciences, University of Memphis, Memphis, TN
2016 – present	Director, Division of Epidemiology, Biostatistics, and Environmental Health Sciences, University of Memphis, Memphis, TN
2013 – 2023	Program Coordinator (Biostatistics), Division of Epidemiology, Biostatistics, and Environmental Health Sciences, University of Memphis, Memphis, TN
2017 – present	Professor, Department of Mathematical Sciences, University of Memphis, TN (affiliated faculty)
2017– present	Professor, Bioinformatics in the Department of Biology, University of Memphis, TN (affiliated faculty)
2013 – 2017	Associate Professor (tenured) Division of Epidemiology, Biostatistics, and Environmental Health Sciences, University of Memphis, Memphis, TN
2013 – 2017	Associate Professor, Department of Mathematical Sciences, University of Memphis, TN (affiliated faculty)
2013 – 2017	Associate Professor, Bioinformatics in the Department of Biology, University of Memphis, TN (affiliated faculty)
2012 – 2013	Associate Professor (tenured) Department of Epidemiology and Biostatistics, University of South Carolina, Columbia, SC
2007 – 2012	Assistant Professor Department of Epidemiology and Bio-statistics, University of South Carolina, Columbia, SC

2003 – 2007	Assistant Professor Department of Mathematics and Statistics, University of West Florida Pensacola, FL
2003 – 2007	Statistical consultant Department of Mathematics and Statistics, University of West Florida Pensacola, FL
2001– 2002	Research Assistant, Laurence H. Baker Center in Biological Statistics Ames, IA
1999 – 2001	Research Assistant, Statistical Computing Section, Department of Statistics, Iowa State University, Ames, IA.
1990 – 1994	Technician, Nanjing Research Institute of Electronic Technology, Nanjing, China

Recent Memberships and Professional Services

Memberships

1999 – present	American Statistical Association (ASA) (2021: Fellow) Citation: *For outstanding service and leadership in biostatistics education; for extensive collaborative efforts in epidemiological and medical research; and for notable contributions to variable selection and clustering methods and practice*
2020 – present	Selected as senior member of Sigma Xi Honor Society
2004 – 2005	Mathematical Association of America (MAA)

Professional Services

2023	Section Chair (invited), Invited Overview Lecture, JSM 2023
2022	Nominated as the 2024 Chair-elect of the ASA Council of Chapters Governing Board
2022, 2023	Section Chair (invited), contributed section organized by RAS, JSM 2022
2021 – present	2022 Chair-Elect, Risk Analysis Section (RAS), ASA
2020	Nominated as the Chair-elect of the ASA Risk Analysis section
2020 – 2022	President of the ASA West Tennessee Chapter Officers
2017 – 2019	Supervise newly elected ASA West Tennessee Chapter Officers
2009 – 2013	Secretary/Treasurer of the ASA South Carolina Chapter
2007	Vice president of the ASA Florida Chapter
2005 – 2007	Secretary/Treasurer of the ASA Florida Chapter
2016 – 2017	Funder and Organizer of the Division of Epidemiology, Biostatistics, and Environmental Health Colloquium. University of Memphis, Memphis, TN
2014	Section Chair of the “Bayesian Nonparametric Methods and Some Applications” at the 2014 Joint Statistical Meeting, Boston MA
2012	Organizer of the ASA South Carolina Chapter 2013 Meeting
2007 – 2010	Organizer of the BIOS Forum, University of South Carolina
2007	Chair of the ASA Florida Chapter 2005 Meeting organizing committee
2006	Section Chair of the “Bayesian Statistics” at the International Conference, Statistics, Mathematics, and Related fields, Hawaii
2005	Section Chair of the “DNA Data and Microarray Measurements” at the 2005 Joint Statistical Meeting, Minneapolis, Minnesota.

Referee/Reviewer for funding agencies

2023	NIH/NIAID P01 review panel NIH/NIAID U01 review panel NIH/NIEHS U24 review panel NSF Statistics panel United States Department of Veterans Affairs NURR
2022	NIH/NIAID IRAP review panel NIH/NIAID Special emphasis panel NIH/NIAID U19 review panel NIH/NIEHS U24 review panel United States Department of Veterans Affairs NURR
2021	NIH/NIAID U19 review panel (temporary) NIH/NHLBI DCC review panel (temporary)
2020	Dutch Research Council (NWO) review panel NIH/NIAID Special emphasis panel
2016 – 2021	NIH/NIEHS P30 review panel (standing member) NIH/NIEHS Training grants review panel (standing member)
2016 – 2018	NIH KNOD Research Initiative review panel (temporary) NIH/NICHD P01 review panel (temporary) NIH/NHLDB secondary data analyses review panel (R21) (temporary)
2015	NIH/ Children's Environmental Health & Disease Prevention Research Centers (Special panel)
2015	NIH KNOD Research Initiative review panel (temporary)
2013	NIH/NIAID IRAP Research Initiative review panel (temporary)
2012	Health Effects Institute, USA
2011	Medical Research Council (MRC), United Kingdom
2008	Reviewer for the 2008 Arnold School of Public Health Seed Grant Applications

Reviewer for Journals

Journals in Statistics/Biostatistics: Biometrics; Biostatistics; Journal of Agricultural, Biological, and Environmental Statistics (JABES); Computational Statistics and Data Analysis; Statistics in Medicine; Contemporary Clinical Trials; American Journal of Biostatistics; Environmental and Ecological Statistics, JRSS-C; Journal of Applied Statistics, Mathematical Bioscience Engineering.

Journals in genetic/epigenetic statistics: Mathematical Biosciences; Briefings in Bioinformatics; Bioinformatics; BMC in Bioinformatics; GENE; Journal of Genetics; Proceedings of the National Academy of Sciences (PNAS); Journal of Genetica; The Journal of Applications in Genetics and Molecular Biology; Journal of Evolutional Biology; PLosOne; Epigenomics; Epigenome, Clinical Epigenetics, Frontiers in Bioinformatics,

Journals in the applied field (allergy, asthma, and immunology): The Journal of Allergy and Clinical Immunology (JACI), Journal of Smoke Cessation, Pediatric Allergy and Immunology, American Journal of Respiratory and Critical Care medicine/AJRCCM, Genomics, World Allergy Organization Journal, Open Life Sciences, BMC Medicine, Biology, Journal of Inflammation Research, Pediatric and Perinatal Epidemiology.

Reviewer for publishers

2017 – 2021	CRC Press, LCC

Editorial Board

American Journal of Biostatistics (member), Computational and Mathematical Methods in Medicine (guest editor), Epigenomes (Editorial Board Member since May 2023)

Awards and Honors

2021-2024	University Research Professorship Award University of Memphis, Memphis, TN
2018	PI Millionaire University of Memphis, Memphis, TN
2010	Promising Investigator Research Award University of South Carolina, Columbia, SC
2006	Collaborative Research Award University of West Florida, Pensacola, FL
2006	University Summer Research Award University of West Florida, Pensacola, FL
2004	University Summer Research Award University of West Florida, Pensacola, FL
2003	The George W. Snedecor Award in Statistics Iowa State University, Ames, IA
2003	Vince Sposito Computing Excellence Award, Iowa State University, IA
2002	Vera David Fellowship, Iowa State University, IA

Research grant applications

Funded projects (sorted by starting year and ending year):

Active grants:

1) Title: Clusters of Epigenetic Networks at Birth and Asthma Incidence in Children
    PI: Zhang
    Funding Source: NIH/NIAID
    Amount funded: $393,981
    Duration: 10/1/2023 – 9/30/2025
    Role and % effort: PI (10%)
2) Title: Surface exosome integrin profiling to predict organotropic metastasis of breast cancer
    PIs: Huang, Hoang
    Funding Source: NIH/NCI
    Amount funded: $300,000
    Duration: 7/1/2023 – 6/30/2026
    Role and % effort: Co-I (5%)
3) Title: Public Health Informatics, Data, Equity, Analytics, and Systems (PH-IDEAS) approach to strengthen Shelby County Health Department Infrastructure, Workforce, and Data Systems
    PIs: Taylor, Joshi
    Funding Source: CDC
    Amount funded: $8,739,721.00
    Duration: 12/01/2022-11/30/2027
    Role and % effort: Co-I (10%)

Completed grants:

4) Title: Single exosome protein profiling with surface enhanced Raman scattering imaging
    PIs: Huang, Hoang

Funding Source: NIH/NCI
Amount funded: $300,000
Duration: 4/1/2020 – 3/30/2023
Role and % effort: Co-I (5%)

5) Title: Does epigenetic methylation explain the gender-switch in adolescent asthma?
PI: Hongmei Zhang
Funding Source: NIAID/NIH
Amount funded: $3,036,427
Duration: 01/01/2016 – 12/31/2022 (NCE)
Role and % effort: PI (20%)
6) Title: Effect of Prenatal Compounds on Adult Lung Function via Neonatal DNA
PI: Wilfried Karmaus
Funding Source: NHLBI/NIH
Amount funded: $3,282,776
Duration: 09/01/2016 – 08/31/2022 (NCE)
Role and % effort: Co-I (10% on average)
7) Title: Epigenetics of severe asthma
PIs: Arshad, Peters, Vijay
Funding Source: NHLBI/NIH
Amount funded: $2,712,390
Duration: 04/01/2017 – 03/31/2022 (NCE)
Role and % effort: Co-I (3%)
8) Title: Epigenome-wide association study of childhood asthma
PIs: Arshad, Peters, Vijay
Funding Source: NIAID/NIH
Amount funded: $3,875,019
Duration: 09/01/2016 – 08/31/2021
Role and % effort: Co-I (5%)
9) Title: Examining Resilience in Youth Exposed to Maternal Intimate Partner Violence Substance Use, and HI
PI: Howell
Funding Source: NICHD/NIH
Amount funded: $416,009
Duration: 3/2017 – 2/2020
Role and % effort: Co-I (5%)
10) Title: Joint patterns of multi-genetic/epigenetic factors via non-parametric clustering and their association with allergic diseases
PI: Meredith Ray
Funding Source: NIAID/NIH
Amount funded: $140,000
Duration: 01/2018 – 12/31/2019
11) Title: Does epigenetic methylation explain the gender-switch in adolescent asthma?
PI: Hongmei Zhang
Funding Source: Asthma and Allergy Foundation of America
Amount funded: $40,000
Duration: 08/07/2015 – 08/06/2017
Role and % effort: PI (10%)
12) Title: Patterns of infant feeding and child's health at six years of age
PI: Wilfried Karmaus
Funding Source: CDC HRSA R40
Amount funded: $100,000

Duration: 04/01/2016 – 03/31/2017
Role and % effort: Co-I (5%)

13) Title: Phenomics: Joint clustering to associate changes in allergy and asthma over time (R21)
PI: Hongmei Zhang
Funding Source: NIAID/NIH
Amount funded: $372,111.00
Duration: 1/15/2013 – 1/14/2016 (no cost extension)
Role and % effort: PI (25%)
14) Title: Transgenerational epigenetic inheritance of allergy in a multigenerational cohort (R01)
PI: Wilfried Karmaus
Funding Source: NIAID/NIH
Amount funded: $2,676,923.00
Duration: 1/2011–12/2015
Role and % effort: Co-I and lead statistician (20% with a support of graduate assistants for all years and a Post-Doc for years 3 to 5)
15) Title: Vitamin D and Related Genes, Race, and Prostate Cancer Aggressiveness
PI: Susan Steck
Funding Source: DOD
Amount funded: $713,828
Duration: 1/2011–12/2015 (no cost extension)
Role and % effort: Co-I and lead statistician (7% on average. The 3rd year is no-cost extension)
16) Title: South Carolina Cancer Disparities Community Network – II
PI: James Hebert
Funding Source: NIH
Amount funded: $4,778,222.00
Dates: 07/2010 – 06/2015
Role and % effort: Co-I and lead statistician (5% on years 1 to 4, and 15% on year 5)
17) Title: Data analysis on sleep disruption as a risk factor of cancer among veterans
PI: Hongmei Zhang
Funding source: Department of Veteran's Affairs, Health Services Research & Development
Amount funded: $35,000.00
Duration: 09/01//2012 – 08/31/2013
Role and % effort: PI (10%)
18) Title: Use of a Community-University Partnership to Eliminate Environmental Stressors (P50)
PI: Sacoby Wilson
Funding source: NIH
Amount funded: 1,215,541.00
Duration: 9/2009 – 6/2013
Role and % effort: Co-I and lead statistician (10%)
19) Title: Sleep Disruption among Veterans: Implications for Cancer Risk
PI: Jim Burch
Funding source: Department of Veteran's Affairs, Health Services Research & Development
Amount funded: $99,529.00
Duration: 03/2011 – 02/2012
Role and % effort: Co-I and lead statistician (10%)
20) Title: Multiple Modes of Infant Feeding and Trajectories Influencing Infant Health
PI: Wilfried Karmaus
Funding Source: HSRA
Amount funded: $100,000.00
Duration: 02/2010 – 01/2011
Role and % effort: Co-I and lead statistician (10%)

21) Title: Joint Clustering Methods Through Quantile Regression
    PI: Hongmei Zhang
    Funding Source: Office of Research and Graduate Education, University of South Carolina
    Amount funded: $10,000.00
    Duration: 4/2010 – 7/2011
    Role and % effort: PI (10%, no salary support but with student and local travel support)
22) Title: Measuring gene expression in epithelial duct cells collected from breast milk
    PI: Wilfried Karmaus
    Funding Source: USC Medical School - The Interdisciplinary Conference on Pregnancy and the Health of Women and Children
    Total Amount: $3,000
    Dates: 01/2009 – 04/2009
    Role and % effort: Co-I and lead statistician (no salary release)
23) Title: Epidemiology of asthma: risk & prognosis in a cohort from birth to adolescence
    PI: Wilfried Karmaus (USC subcontract)
    Funding source: NIH
    Amount funded: $236,000.00
    Duration: 6/2009 – 5/2012
    Role and % effort: Co-I and lead statistician (20% with support of graduate assistants for all years)
24) Title: Evaluate Micronutrient Effect to The Prevention of South Carolina Neural Tube Defect Accommodating Measurement Errors and Bias
    PI: Hongmei Zhang
    Funding Source: Research Opportunity Program, University of South Carolina
    Amount funded: $9,000.00
    Duration: 05/2008 – 08/2009
    Role and % effort: PI (10%, no salary support but with student and local travel support)
25) Title: Summer Research on False Positive Quad Screening Tests
    PI: Hongmei Zhang
    Funding Source: USC Medical School - The Interdisciplinary Conference on Pregnancy and the Health of Women and Children
    Total Amount: $3,000
    Dates: 05/2008 – 8/2008
    Role and % effort: PI (10%, no salary support but with student support)
26) Title: The Influence of Gender on Molecular Signatures of Fibrotic Lung Disease
    PI: Hongmei Zhang (MPI with Tara Sabo-Attwood)
    Funding Source: NIH
    Amount funded: $140,040.00
    Duration: 9/2008 – 8/2010 (extended to 8/2011)
    Role and % effort: PI (10%)
27) Title: Stress, endocrine disruption, and adverse pregnancy outcomes
    PI: Wilfried Karmaus
    Funding source: GEAR, EPSCoR/IDeA
    Amount funded: $36,000.00
    Duration: 12/2008 – 04/2009
    Role and % effort: Co-I and lead statistician (2.5%)
28) Title: Combinatorial and Statistical Problems in Genomics
    Co-PI: Hongmei Zhang, Rohan Hemasinha
    Funding Source: NSF
    Total Amount: $110,000.00
    Dates: 05/2007 – 08/2008

Role and % effort: Co-PI (10%)

29) Title: Sampling Design in Biological Area and Phylogenetic Analysis in Genetics
PI: Hongmei Zhang
Funding Source: University of West Florida
Amount funded: $6,250.00
Duration: 05/2006 –11/2006
Role and % effort: PI (20%)

30) Title: Future Sampling Plan for Unseen Species with Finite Population
PI: Hongmei Zhang
Funding Source: University of West Florida
Amount funded: $6,250.00
Duration: 05/2004 – 11/2004
Role and % effort: PI (20%)

Publications

Book:

H Zhang. Analyzing High-dimensional Gene Expression and DNA Methylation Data with R. CRC Press; 2020 May 14. ISBN-13: 978-0367495169. ISBN-10: 0367495163.

**: co-authors are students/post-docs under my supervision, or I was the corresponding author. Other students/Post-docs as the first author or a co-author are underlined.*

Article accepted or in press

Statistical Methods:

Statistical Applications:

1. G Seumois, …, **H Zhang**, …, P Vijayanand. *Cytotoxic CD4+ tissue-resident memory T cells are associated with asthma severity*. Med (accepted).

Article published

Statistical Methods:

2. **H Zhang**, X Huang, H Arshad. *Comparing Dependent Undirected Gaussian Networks.* Bayesian Analysis. **2022** Jan;1(1):1-26.
3. X Mou, **H Zhang***, H Arshad. *Identifying intergenerational patterns of correlated methylation sites*. Annals of Applied Statistics. **2022** Mar;16(1):521-36.
4. X Huang, **H Zhang**. *Tests for differential Gaussian Bayesian networks based on quadratic inference functions.* Computational Statistics & Data Analysis. **2021** Jul 1;159:107209.
5. X Huang, **H Zhang**. *Corrected score methods for estimating Bayesian networks with error-prone nodes*. Statistics in Medicine. 40: 2692– 2712. https://doi.org/10.1002/sim.8925, **2021**.
6. J Wang*, S Han, **H Zhang***. *A Nested Clustering Method to Detect and Cluster Transgenerational DNA Methylation Sites Via Beta Regressions* in Modern Statistical Methods for Health Research, edited by Y Zhao, D Chen, Springer, **2021**.
7. **H Zhang**, X Huang, …, JW Holloway. *Gaussian Bayesian network comparisons with graph ordering unknown*. Computational Statistics and Data Analysis. **2021** May 1;157:107156.
8. MA Ray*, D Bowman, R Csontos, RV Arsdale, **H Zhang**. *A Matrix-Variate Dirichlet Process to Model Earthquake Hypocenter Temporal Patterns*. Statistical Modeling: an International Journal. https://doi.org/10.1177/1471082X20939767, **2020**.

9. J Ren, F Zhou, X Li, Q Chen, **H Zhang**, S Ma, Y Jiang, C Wu. *Semi-parametric Bayesian variable selection for gene-environment interactions*. Statistics in Medicine. DOI:10.1002/sim.8434. **2019**.
10. Y Jiang, **H Zhang***, SV Andrews, H Arshad, S Ewart, JW Holloway, MD Fallin, KM Bakulski, W Karmaus. *Estimation of Eosinophil Cells in Cord Blood with References Based on Blood in Adults via Bayesian Measurement Error Modeling*. Bioinformatics. https://doi.org/10.1093/bioinformatics/btz839, **2019**.
11. S Han*, **H Zhang**, W Sheng & H Arshad. *The nested joint clustering via Dirichlet process mixture model*, Journal of Statistical Computation and Simulation, 89:5, 815-830, DOI: 10.1080/00949655.2019.1572756. **2019**.
12. M Ray*, J Kang, and **H Zhang**, *Detecting Spatial Clusters via a Mixture of Dirichlet Processes*, Journal of Probability and Statistics, vol. 2018, Article ID 3506794, 12 pages, **2018.** https://doi.org/10.1155/2018/3506794.
13. **H Zhang**, Y Zou*, W Terry*, W Karmaus, H Arshad. *Joint clustering with correlated variables, The American Statistician, DOI: 10.1080/00031305.2018.1424033.* **2018.**
14. A Kaushal*, **H Zhang**, W Karmaus, M Ray, MA Torres, AK Smith, S Wang. *Comparison of different cell type correction methods for genome-scale epigenetics studies.* BMC Bioinformatics. Vol. 18, 216. **2017.**
15. W Terry*, **H Zhang**, A Maity, H Arshad, W Karmaus. *Unified Variable Selection in Semi-parametric Models*. Statistical Methods in Medical Research. **2017** Dec;26(6):2821-31.
16. S Han*, **H Zhang**, W Karmaus, G Roberts, H Arshad. *Adjusting background noise in cluster analyses of longitudinal data.* Computational Statistics and Data Analysis. DOI: 10.1016/j.csda.2016.11.009. **2016.**
17. M Ray*, X Tong*, GA Lockett, **H Zhang**, W Karmaus. *An efficient approach to screening epigenome-wide data.* BioMed Research International. Vol. 2016, Article ID 2615348, 16 pages. **2016**.
18. S Han*, **H Zhang**, R Homayouni, W Karmaus. *An efficient Bayesian approach for Gaussian Bayesian network structure learning.* Communications in Statistics - Simulation and Computation. 10.1080/03610918.2016.1143103. **2016**.
19. M Ray*, J Kang, **H Zhang**, *Identifying Activation Centers with Spatial Cox Point Processes Using FMRI Data*, in IEEE/ACM Transactions on Computational Biology and Bioinformatics, Vol. 13, 1130-1141. **2016**.
20. **H Zhang**, X Huang, J Gan*, W Karmaus, T Sabo-Attwood. *A Two-component G-prior for Variable Selection*. Bayesian Analysis. Vol. 11: 353-80. **2016.**
21. **H Zhang**, A Maity, H Arshad, J Holloway, W Karmaus. *Variable selection in semi-parametric models*. Statistical Methods in Medical Research. **2016** Aug;25(4):1736-52.
22. S Han*, **H Zhang**, G Lockett, N Mukherjee, J Holloway, W Karmaus, *Identifying heterogeneous transgenerational DNA Methylation Sites via Clustering in Beta Regression.* Annals of Applied Statistics. Vol. 9: 2052-2072. **2015**.
23. X Huang, **H Zhang**. *Variable selection in linear measurement error models via penalized score functions*. Journal of Statistical Planning and Inference. Vol. 143: 2101-2111. **2013.**
24. B Omolo, **H Zhang**, W Karmaus. *Cautions of Using Allele-Based Tests Under Heterosis.* International Journal of Statistics in Medical Research. Vol. 2: 47-54. **2013**.
25. **H Zhang**, J Gan*. *A reproducing kernel-based spatial model in Poisson regression.* International Journal of Biostatistics. Vol. 8, pages 28. **2012**.
26. H He*, **H Zhang**, A Maity, Y Zou, J Hussey, W Karmaus. *Power of a reproducing kernel-based method for testing the joint effect of a set of single-nucleotide polymorphisms.* Genetica. DOI 10.1007/s10709-012-9690-5. **2012**.
27. **H Zhang**, K Ghosh, and P Ghosh. *Sampling designs via a multivariate hypergeometric-Dirichlet process model for a multi-species assemblage with unknown heterogeneity*. Computational Statistics and Data Analysis. Vol. 56: 2562-2573. **2012**.

28. D Rahardja, Y Zhao, and **H Zhang**. *Bayesian credible sets for a binomial proportion based on one-sample binary data subject to one type of misclassification.* Journal of Data Science. Vol. 10: 51-59. **2012**.
29. J Gan*, **H Zhang**, R Best. *Mixture of measurement errors and their impact on parameter Inferences.* Journal of Statistical Computing and Simulation. Vol. 83: 613-626. **2011.**
30. **H Zhang**, W Karmaus, J Gan*, W Bao*, Y Zhao, D Rahardja, J Holloway, M Scott, and SH Arshad. *Adjusting wheal size measures to correct atopy misclassification*. International Journal of General Medicine. Vol. 4: 597-606, **2011**.
31. M Dey, H Stern, and **H Zhang**. *Information Content in Small and Large Trades*. Economic Notes. Vol. 40: 45-74, **2011**.
32. D Rahardja, Y Zhao, and **H Zhang**. *Maximum Likelihood Estimation of Odds Ratios in Misclassified Binary Data with a Validation Substudy*. Model Assisted Statistics and Applications. Vol. 6: 121-125, **2011**.
33. **H Zhang**[1], and J Zhang[2]. *A Semiparametric Bayesian Estimation Method of the Accelerated Failure Time Model.* Advances and Applications in Statistical Sciences, Vol. 1: 125-143, **2010**. [1,2]Equal contribution.
34. H Luo[1], **H Zhang**[2], RA Long, and R Benner. *Depth Distributions of Alkaline Phosphatase and Phosphonate Utilization Genes in the North Pacific Subtropical Gyre*. Aquatic Microbial Ecology. Vol. 62: 61–69, **2010**. [1,2]Equal contribution
35. **H Zhang**, R Hemasinha, X Gu. A Statistical Model and Algorithm for Genome Phylogeny Accommodating Lateral Gene Transfer, The International Journal of Systems and Synthetic Biology. Vol. 1: 241-253, **2010**.
36. **H Zhang**. *Designing sampling plans to capture rare objects*. Canadian Journal of Statistics, Vol. 37: p417-434, **2009**.
37. **H Zhang**, H Stern. *Sample size calculation for finding unseen species.* Bayesian Analysis, Vol. 4. 763 – 792, **2009**.
38. **H Zhang**, Y Zhong, B Hao, and X Gu. *A Simple Method for Phylogenomic Inference Using the information of Gene-Content of Genomes,* Gene, 441: p163-8. doi:10.1016/j.gene.2008.07.008, **2009**.
39. **H Zhang** and H Stern. *Inferences for genotyping error rate in ancestry identification from simple sequence repeat marker profiles*, JABES, Vol. 14: p170-187, **2009**.
40. **H Zhang**. *Inferences on the Number of Unseen Species and the Number of Abundant/Rare Species*, Journal of Applied Statistics, Vol. 34: 725-40, **2007**.
41. **H Zhang** and H Stern. *Assessment of ancestry probabilities in the presence of genotyping errors*. Theoretical and Applied Genetics, Vol. 112: 472-482, **2006**.
42. **H Zhang** and H Stern. *An investigation of a generalized multinomial model for species data*, J. Statistical Computing and Simulation, Vol. 75: 347-362, **2005**.
43. X Gu and **H Zhang**. *Genome Phylogenetic Analysis Based on Extended gene contents.* Molecular Biology and Evolution, Vol. 21: 1401-1408, **2004**.
44. **H Zhang** and X Gu. *Maximum Likelihood for Genome Phylogeny on Gene Content.* Statistical Applications in Genetics and Molecular Biology, Vol. 3: Article 31, **2004**.
45. **H Zhang**, A Nitzman, and T Royappa. *Statistical Modeling and Sizing Determination Guidelines*. J. TAPPI, Vol. 3: 3-8, **2004**.

Statistical Applications:

46. SY Ngo, C Venter, WC Anderson III, K Picket, **H Zhang**, SH Arshad, RJ Kurukulaaratchy. *Clinical Features and Later Prognosis of Replicable Early-Life Wheeze Clusters from 2 Birth Cohorts 12-years Apart.* Pediatric Allergy and Immunology. **2023** Jul;34(7):e13999.

47. L Kadalayil, …, **H Zhang**, … JW Holloway. *Analysis of DNA methylation at birth and in childhood reveals changes associated with season of birth and latitude*. Clinical Epigenetics. **2023** Dec;15(1):1-23.
48. A Farhan, …, **H Zhang**, H Arshad. *Prediction of Adult Asthma-risk in early childhood using novel adult asthma predictive risk scores.* Allergy. **2023** Sep 3, https://doi.org/10.1111/all.15876.
49. PK Rahimabad, AD Jones, **H Zhang**, …, Wilfried Karmaus. Polymorphisms in Glutathione S-Transferase (*GST*) Genes Modify the Effect of Maternal Smoking in Pregnancy on Offspring DNA Methylation. Genes. **2023** Aug 18;14(8):1644.
50. A Budu-Aggrey, A Kilanowski, …, **H Zhang**, …, M Nelis. *European and multi-ancestry genome-wide association meta-analysis of atopic dermatitis highlights importance of systemic immune regulation.* Nature Communications. **2023** Oct 4;14(1):6172.
51. A Rathod*, R Melaram*, **H Zhang***, …, JW Holloway. The association of DNA methylation at birth with adolescent asthma is mediated by atopy, Clinical and Experimental Allergy. **2023** Aug 28. Rathod and Melaram are equal contributors.
52. J Hu, X Xu, J Li, Y Jiang, X Hong, KM Rexrode[1], G Wang, FB Hu, **H Zhang**, WJ Karmaus, X Wang, L Liang. *Sex Differences in the Intergenerational Link Between Maternal and Neonatal Whole Blood DNA Methylation: A Genome-wide Analysis in the Boston Birth Cohort*. Clinical Epigenetics. **2023** Mar 25;15(1):51
53. VD Janjanam, S Ewart, **H Zhang**, Y Jiang, H Arshad, AH Ziyab, W Karmaus. *Offspring epigenetic markers at birth related to gestational BMI predict offspring BMI-trajectories from infancy to 26 years*. Obesity Science & Practice. **2023**, 1-11. DOI: 10.1002/osp4.660.
54. KD Amrhein, M Taylor, RE Wilson Jr., CE Gallops, A Annamer, V Vinduska, EA Kwizera, **H Zhang**, Y Wang, TB Hoang, X Huang. *Dual Imaging Single Vesicle Surface Protein Profiling and Early Cancer Detection.* ACS, Applied Materials and Interfaces. **2023**, 15(2): 2679-92. Wang, Hoang, and Huang equally contributed.
55. A Ziyab, JW Holloway, Y Ali, **H Zhang**, W Karmaus. *Eczema among adolescents in Kuwait: prevalence, severity, sleep disturbance, antihistamine use, and risk factors*. World Allergy Organization Journal. **2023** Jan 1: 16(1): 100731.
56. SH Arshad, L Wheatley, JW Holloway, …, **H Zhang**, A Togias. *The Role of Epigenetics in Multi-generational Transmission of Asthma: an NIAID Workshop Report-based narrative review.* Clinical & Experimental Allery. **2022** Nov;52(11):1264-75.
57. A Kilanowski, …, **H Zhang**, …, Anke Hüls, *Methylation risk scores for childhood aeroallergen sensitization: Results from the LISA birth cohort.* Allergy. **2022** Apr 19.
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157. A Ziyab, W Karmaus, RJ Kurukulaaratchy, **H Zhang**, SH Arshad. *Developmental trajectories of body mass index from infancy to 18 years of age: prenatal determinants and health consequences*. Journal of Epidemiology & Community Health. doi:10.1136/jech-2014-203808. **2014**.
158. R Kurukulaaratchy, **H Zhang**, A Raza, V Patil, W Karmaus, S Ewart, and SH Arshad. *The diversity of young adult wheeze: a cluster analysis in a longitudinal birth cohort*. Clinical & Experimental Allergy. Vol. 44: 724-735, **2014**.
159. A Ziyab, W Karmaus, **H Zhang**, J Holloway, S Steck, S Ewart, HS Arshad. *Allergic sensitization and filaggrin variants predispose to the comorbidity of eczema, asthma, and rhinitis: results from the Isle of Wight birth cohort.* Clinical and Experimental Allergy. doi: 10.1111/cea.12321. Epub ahead of print. **2014**.
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161. L Rice, C Jiang, SM Wilson, K Burwell-Naney, A Samantapudi, **H Zhang**. *Use of Segregation Indices, Townsend Index, and Air Toxics Data to Assess Cancer Risk Disparities in Metropolitan Charleston, South Carolina*. International Journal of Environmental Research and Public Health. Vol. 11: 5510-5526. **2014**.
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164. K Burwell, **H Zhang**, A Samantapudi, C Jiang, L Dalemarre, L Rice, E Williams, S Wilson. *Spatial Disparity in the Distribution of Superfund Sites in South Carolina: An Ecological Study.* Environmental Health. Vol. 12: 96. **2013**.
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168. J Runkle, **H Zhang**, K Wilfried, A Brock-Martin, E Svendsen. *Long term Impact of Environmental Public Health Disaster on Health System Performance: Experiences from the Graniteville, South Carolina Chlorine Spill.* Southern Medical Journal. 106: 74-81. **2013**.
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function growth: a birth cohort study. BMC Pulmonary Medicine. 13:56. doi:10.1186/1471-2466-13-56. **2013**.

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179. MG Hill, S Menon, S Smith, **H Zhang**, X Tong*, P Browne. *Sexual health disparities in a pregnant population in Columbia, South Carolina.* Journal of the South Carolina Medical Association. Vol. 109: page 9. **2013.**
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186. J Ritchey, W Karmaus, T Sabo-Attwood, S Steck, **H Zhang**. *A Cross-Sectional Study of the Association of Age, Race and Ethnicity, and Body Mass Index with Sex Steroid Hormone Marker Profiles among Men in the National Health and Nutrition Examination Survey (NHANES III).* BMJ Open. Vol. 2(5). DOI: 10.1136/bmjopen-2012-001315. **2012**.

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189. SH Arshad, W Karmaus, A Raza, RJ Kurukulaaratchy, SM Matthews, JW Holloway, A Sadeghnejad, **H Zhang**, G Roberts, SL Ewart. *The effect of parental allergy on childhood allergic diseases depends on the sex of the child.* Journal Allergy and Clinical Immunology. Vol. 130: 427-434. **2012**.
190. N Soto-Ramírez, W Karmaus, M Yousefi, **H Zhang**, J Liu, and V Gangur. *Maternal immune markers in serum during gestation and in breast milk and the risk of asthma-like symptoms at ages 6 and 12 months: a longitudinal study*. Allergy, Asthma and Clinical Immunology. Vol.8, doi:10.1186/1710-1492-8-11. **2012**.
191. K Hanjangsit, W Karmaus, P Dimitrov, **H Zhang**, J Burch, S Tzolova, V Batuman. *The role of a parental history of Balkan endemic nephropathy in the occurrence of BEN: a prospective study.* International journal of nephrology and renovascular disease. Vol. 5: 61-68. **2012**.
192. LW Chu, R Ritchey, SS Devesa, SM Quraishi, **H Zhang**, and AW Hsing. *Prostate Cancer Incidence Rates in Africa*. Prostate Cancer. doi:10.1155/2011/947870. **2011**.
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194. M Wirth, J Burch, J Violanti, C Burchfiel, D Fekedulegn, M Andrew, **H Zhang**, DM Miller, JR Hebert, and J Vena. *Shiftwork Duration and the Awakening Cortisol Response among Police Officers*. Chronobiology International. Vol. 28: 446-457, **2011**.
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197. A Ziyab, A Raza, W Karmaus, N Tongue, **H Zhang**, S Matthews, SH Arshad, and G Roberts. *Trends in eczema in the first 18 years of life: results from the Isle of Wight 1989 birth cohort study.* Clinical and Experimental Allergy. Vol. 40, No. 12, 1776-1784, **2010**.
198. JE Arruda, **H Zhang**, RT Amoss, KL Coburn, and WR Aue. *Rhythmic oscillations in quantitative EEG measured during a continuous performance task.* Applied Psychophysiology and Biofeedback, 34:7–16, DOI 10.1007/s10484-008-9071-0, **2009**.
199. J Guess, J Burch, K Ogoussan, C Armstead, **H Zhang,** S Wagner, JR Hebert, P Wood, SD Youngstedt, LJ Hofseth, UP Singh, D Xie, and WJM Hrushesky. *Circadian Disruption, Per3,and Human Cytokine Secretion*, Integrative Cancer Therapies. Vol.8, 329-336, **2009**.
200. IU Ogbuanu, **H Zhang**, and W Karmaus. *Can we apply the Mendelian randomization methodology without considering epigenetic effects?* Emerging Themes in Epidemiology, 6:3, **2009**.
201. M Lott, M Manning, J Singh, **H Zhang**, H Singh, and D Marcus. *23-Gauge Vitrectomy in 100 Eyes: Short-term Visual Outcomes and Complications,* Journal of Retinal and Vitreous Diseases, Vol. 28, No. 9, p1193-1200, doi: 10.1097/IAE.0b013e31817c5a28, **2008**.

202. J Wei, R Randy, and **H Zhang**. *Life Cycle Pattern Study on Malicious Codes*, International Journal of Information Privacy and Security, Vol 2: p26-41, **2008**.
203. J Wei, J Zhuo, and **H Zhang**. *Development of a Mobile Learning Model for Online Education*, International Journal of Mobile Learning and Organization. Vol. 2: p28-44, **2008**.

Statistical software:

204. M Ray*, X Tong*, **H Zhang**. ttScreening: *Genome-wide DNA methylation sites screening by use of training and testing samples.* R Core Team. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL: http://www.R-project.org. **2014.**
205. W Bao*, X Tong*, M Ray*, **H Zhang**. RegClust: *Cluster analysis via regression coefficients*. R Core Team. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL: http://www.R-project.org. **2014**.
206. X Gu, W Huang, D Xu, and **H Zhang**. *GeneContent: Software for Whole-Genome Phylogenetic Analysis*, Bioinformatics. Vol. 21: 1713-1714, **2004**.

Advising

Post-doctoral fellow

2022 – present	Rajesh Melaram
2019 – 2021	Yu-Sheng Lee
2013 – 2015	Shengtong Han

Students (Ph.D.)

Students under supervision at the University of Memphis

2023 – present	Nahid Sultana (Epidemiology)
2023 – present	Shengqiang Chen (Biostatistics)
2023 – present	Michael Ofori (Biostatistics)
2022 – present	Siyao Liu (Biostatistics; part-time)
2022 – present	Naznin Alam (Biostatistics)
2021 – present	James Adefisoye (Biostatistics)
2018 – 2021	Liang Li (Epidemiology)
2018 – 2021	Rutu Patel (Epidemiology)
2018 – 2021	Aniruddha Rathod (Epidemiology)
2018 – 2021	Jiajing Wang (Statistics)
2018 – 2020	Farnaz Solatikia (Statistics)
2017 – 2021	Shadia Khan Sunny (Epidemiology)
2016 – present	Luhang Han (Statistics; part-time)
2014 – 2017	Akhilesh Kaushal (Epidemiology)

Students under supervision at the University of South Carolina

2012 – 2014	Meredith Ray
2011 – 2014	Xin Tong
2010 – 2013	Yubo Zou
2007 – 2010	Jianjun Gan

Students (MS or MPH)

Students under supervision at the University of Memphis

2018 – 2021	Jiasong Duan (Biostatistics, MS)
2018 – 2019	Farnaz Solatikia (Biostatistics, MS)
2015 – 2016	Lee Curbo (Biostatistics concentration, MPH)

2014 – 2015	Bilal Mohammed Quraishi (Biostatistics concentration, MPH)
2013 – 2015	Will Terry (Statistics, MS)
2013 – 1/2014	Elliott Cole (Biostatistics concentration, MPH)

Students under supervision at the University of South Carolina (Biostatistics, MSPH)

2011 – 2012	Genevieve Ray
2010 – 2012	Hong He
2010 – 2011	Xin Tong
2008 – 2010	Weichao Bo

Students under supervision at the University of West Florida (Statistics, MS)

2007	Joshua Kelly
2005	Chirstel Chancey
2005	Sue Dickerson

Research Staff supervisions

Research supervision at the University of Memphis

2013 – 2014	Meredith Ray
2013 – 1/2014	Wenhui Sheng

Graduate Assistant (GA) supervisions (Hired graduate research assistants. Most were funded by research grants)

GA supervision at the University of South Carolina

2011 – 2013	Ashok Varma Samantapudi
2012 – 2013	Meredith Ray
5/2011 – 2012	Genevieve Ray
2010 – 2013	Xin Tong
2010 – 2011	Yubo Zou
2010 – 2011	He Hong
2007 – 2010	Jianjun Gan
2008 – 2010	Weichao Bao
Fall 2007	Ju Qiu

GA supervision at the University of Memphis

2023 – present	Nahid Sultana (Epidemiology)
2023 – present	Shengqiang Chen (Biostatistics)
2022 – present	Naznin Alam (Biostatistics)
2021 – present	James Adefisoye (Biostatistics)
2021 – 2022	Yojitha Dasari
2018 – 2021	Jiasong Duan (Biostatistics, MS)
2018 – present	Liang Li (Epidemiology)
2018 – present	Rutu Patel (Epidemiology)
2018 – present	Aniruddha Rathod (Epidemiology)
2018 – 2020	Farnaz Solatikia (Statistics)
2017 – 2021	Shadia Khan Sunny (Epidemiology)
2016 – 2020	Luhang Han (Statistics)
2014 – 2017	Akhilesh Kaushal (Epidemiology)
2013 – 2015	Will Terry (Statistics, MS)

Academic supervisions (Academic Advisor)

Academic supervision at the University of Memphis

2023 – present	Nahid Sultana, Shengqiang Chen, Michael Ofori
2022 – present	Siyao Liu, Naznin
2021 – present	James Adefisoye
2018 – 2021	Liang Li, Rutu Patel, Aniruddha Rathod
2018 – 2021	Jiasong Duan
2017 – 2021	Shadia Sunny
2015 – 2016	Lee Curbo
2014 – 2015	Sohely Perven

Academic supervision at the University of South Carolina

2010 – 2014	Meredith Ray
2010 – 2013	Yubo Zou
2009 – 2012	Hong He
2008 – 2010	Jianjun Gan

Abstracts/Presentations

The first author is the presenter. Only conferences, at which I was the presenter or students under my supervision were the presenters, were included. Presentations, which I was involved as a co-author but I did not participate in the conference, are not included.

Conference/Workshop presentations:

09/2023 (Invited)	H Zhang. Gaussian network comparisons and applications to epigenetic data. 75th Anniversary Research Conference, Department of Statistics, Iowa State University, Ames, IA.
08/2023	JO Adefisoye, H Zhang. A composite likelihood approach to Gaussian network differentiation, Joint Statistical Meeting, Toronto, CA.
08/2022	C Wu, X Mou, H Zhang. Identifying differentially methylated CpG sites and regions in the human genome based on the generalized beta regression. Joint Statistical Meeting, Washington DC.
06/2022	H Zhang, H Arshad, X Huang. Comparing dependent undirected Gaussian networks. ISBA 2022, Montreal, Canada.
08/2021	H Zhang, X Huang, S Han, F Rezwan, W Karmaus, H Arshad, J Holloway. Gaussian Bayesian network comparisons with graph ordering unknown. JSM, Online.
03/2021	J Duan. H Zhang. An Assessment of a novel clustering approach applied to multi-dimensional data. Memphis Data Conference, Online
03/2021	R Patel, M Ray, H Zhang, F Mzayek. Risk factors of myocardial infarction at later ages in healthy middle-aged men. Memphis Data Conference, Online
03/2021	M Ray, D Bowman, R Csontos, R vanArsdale, H Zhang, Application of the Dirichlet process to model earthquake hypocenter temporal patterns. Memphis Data Conference, Online
08/2020	J Wang, H Zhang, J Holloway, SH Arshad, W Karmaus. A Nested Clustering Method to Detect and Cluster Transgenerational DNA Methylation Sites via Beta Regressions. JSM, Online.
06/2020	A Rathod, J Duan, H Zhang, JW Holloway, S Ewart, SH Arshad, W Karmaus. Interweaving between genetic and epigenetic studies on asthma. EAACI, 2020, Online
05/2020	A Rathod, H Zhang, SH Arshad, S Ewart, W Karmaus, JW Holloway. DNA Methylation at Birth is Associated with Asthma Acquisition from Pre- to Post-Adolescence Mediated by Atopy. American Thorax Society, 2020, Online

05/2020	R. Patel , F Solatikia, H. Zhang, A Wolde, W Karmaus, SL Ewart, C Relton, S Ring, J Henderson, SH Arshad, JW Holloway, The Association of Asthma Acquisition with DNA Methylation Changes During Adolescence Is Gender-Specific, A Genome-Wide Epigenetic Study. American Thorax Society, 2020, Online
05/2020	R Patel, H Zhang, W Karmaus, S Ewart, SH Arshad, JW Holloway**.** Association of BMI trajectory at earlier childhood with lung function at adulthood is mediated by DNA methylation. American Thorax Society, 2020, Online
08/2019	J Wang, H Zhang, J Holloway, SH Arshad, W Karmaus. A Bayesian method to identify CpG sites exhibiting transgenerational effects on DNA methylation and their heterogeneity via nested clustering in Beta regression. JSM, July 27-August 1st, 2019, Denver, CO.
08/2019	M Ray, L Sobral, SH Arshad, J Holloway, W Karmaus, H Zhang. Identifying patterns of multi-genetic/epigenetic factors via non-parametric clustering. JSM, July 27-August 1st, 2019, Denver, CO.
02/2019	J Wang, H Zhang et al., *DNA Methylation Predicts BMI Status Change from Pre-Adolescence to Post-Adolescence*, AAAAI, San Francisco.
07/2018 (Invited)	H Zhang, *Differential Bayesian Network Testing.* ICSA-Qingdao.
12/2017 (Invited)	H Zhang. *From variable selection to differential Bayesian networks*. American Statistical Association Western TN Chapter meeting. Memphis, TN.
08/2017	H Zhang, S Han, W Sheng, W Karmaus, H Arshad. *The joint clustering via Dirichlet process mixture model on longitudinal data.* Joint Statistical Meeting, Baltimore, MD.
06/2017 (Invited)	H Zhang. *Gender and epigenetic differences, from the Isle of Wight study birth cohort and beyond*. NIH/NIAID Asthma Gender Shifting Workshop, Rockville MD.
05/2017	L Han, H Zhang, SP Oggu, A Kaushal, H Arshad, W Karmaus, JW Holloway, S Ewart. *Identifying stable and dynamic CpG sites pre- and post-adolescence transition via a longitudinal genome-scale study.* ATS, Washington DC.
09/2016	Three students presented at the European Respiratory Society (ERS 2016) annual conference held in London, UK. The projects were on association studies between DNA methylation and allergic diseases.
08/2016	H Zhang, X Huang, S Han, W Karmaus. *Bayesian method for testing differential directed acyclic graphs*. Joint Statistical Meeting, Chicago.
12/2015	H Zhang, X Huang, S Han, W Karmaus. *Bayesian method for testing differential directed acyclic graphs*. Singapore.
08/2015	Y Zou, H Zhang, W Terry, W Karmaus, H Arshad. *Joint cluster with correlated variables via a semi-parametric Bayesian model.* Joint Statistical Meeting, Seattle, WA.
02/2015	B Quraishi and A Kaushal both orally presented at the AAAAI (Feb. 20-24, Houston, TX) meeting on applications of random forest and robust regressions in studies related to allergic disease (Quraishi) and arsnic exposure (Kaushal).
10/2014 (Invited)	H Zhang, Y Zou, W Karmaus, G Roberts, H Arshad, *Joint Clustering on Correlated Variables*. West Tennessee ASA Chapter monthly meeting.
08/2014	H Zhang, X Huang, J Gan, W Karmaus, T Sabo-Attwood. *A two-component G prior for variable selection*. Joint Statistical Meeting, Boston, MA.
08/2014	S Han, H Zhang, G Lockett, N Mukherjee, J Holloway, W Karmaus. *Identifying Heterogeneous Transgenerational DNA Methylation Sites via Clustering in Beta Regression*. Joint Statistical Meeting, Boston, MA.
08/2014	M Ray, H Zhang, J Kang. *Clustering fMRI Metadata to Identify Significant Regions of Brain Activation*. JSM annual meeting, Boston, MA.
06/2014	H Zhang, Y Zou, W Karmaus, G Roberts, H Arshad, *Joint Clustering on Correlated Variables*. WNAR annual statistic meeting. Honolulu, HI.

06/2014	H Zhang, S Han, GA Lockett, N Mukherjee, JW Holloway, W Karmaus. *Identifying Heterogeneous Transgenerational DNA Methylation Sites via Clustering in Beta Regression*. The third Joint Biostatistics Symposium. Chengdu, China.
09/2013	H Zhang. *Burden Disparities in Air Toxic Exposure and Cancer Risks*. Charleston Area Environmental Justice and Health Summit.
05/2013	H Zhang, et al. *Interaction Between DNA Methylation And Genotype In Th2 Pathway Genes, Association With Asthma And Adolescent Transition Of Asthma Between Ages 10 And 18 Years*. ATS, Philadelphia.
12/2013	H Zhang. *Bayesian Variable Selection in Linear and Semi-parametric Models*. The 9th ICSA International Conference: Challenges of Statistical Methods for Interdisciplinary Research and Big Data. Hong Kong, China.
09/2012 (Invited)	H Zhang. *Methylation data, pre-processing, data mining and analysis*. International Society for Environmental Epidemiology, Columbia, SC.
08/2012	H Zhang, X Huang, J Gan, W Karmaus, T Sabo-Attwood. *Variable adaptive calibration and variable selection in linear models with mis-measured covariates*. Joint Statistical Meeting, San Diego, CA.
06/2012 (Invited)	H Zhang, K Ghosh, P Ghosh, *Capturing species at a certain abundance level in a multi-species assemblage with unknown heterogeneity*. Southern Regional Council of Statistics, Jekyll Island, GA.
05/2012 (Invited)	H Zhang. *Mis-measurement model*. Bioinformatics and Biostatistics Workshop. Atlanta, GA.
08/2011	Y Zou, H Zhang, W Karmaus, and H Arshad, *A Bayesian Approach for Joint Clustering Through a Dirichlet Process*. Joint Statistical Meeting, Miami, FL.
03/2011	H Zhang, X Huang, W Karmaus, J Gan, T Sabo-Attwood. *Bayesian Adaptive Calibration and Variable Selection in Linear Models with Mis-measured Covariates.* Eastern North American Region (ENAR) conference, FL.
12/2010 (invited)	H Zhang, H Stern. *Inferences for the Genotyping Error Rate from Ancestry Identification Data.* The 25th International Biometric Conference, Brazil.
06/2010	H Zhang, W Karmaus, W Bao, J Gan, M Scott, SH Arshad. *Correcting Atopy Misclassification through Wheal Size Adjustment* (poster). The 29th Congress of the European Academy of Allergy and Clinical Immunology, UK.
04/2010	J Gan, H Zhang. *Semi-parametric Measurement Error Modeling in Logistic Regression, with application to Survey Data.* American Statistical Association South Carolina Chapter meeting, SC.
04/2010	W Bao, H Zhang. *Clustering Analysis of Zernike Coefficients from High Order Aberration Patient.* American Statistical Association South Carolina Chapter meeting, SC.
03/2010	H Zhang, K Ghosh, P Ghosh. *Bayesian Species Clustering via DP and Sampling Designs via Monte Carlo.* Eastern North American Region conference, LA.
03/2010	J Gan, H Zhang. *Semi-parametric Measurement Error Modeling in Logistic Regression.* Eastern North American Region conference, LA.
03/2009	J Gan, H Zhang. *Impact of Multi-level Measurement Errors in Survey Data.* Eastern North American Region conference, TX.
05/2008 (invited)	H Zhang, H Stern. *An Approximated Likelihood Approach for Genotyping Error Rate Estimation When Assessing Ancestry Probabilities.* International Conference on BioMedical Engineering and Informatics, China.
03/2008	H Zhang. *Joint Effect from Environmental and Behavior Risk Factors to Cancer Death Rates using Bayesian Multi-level Modeling.* Eastern North American Region conference, TX.
02/2007 (invited)	H Zhang, H Stern. *Future Sampling Designs to Capture Animals from Rare Species.* American Statistical Association Florida Chapter meeting, FL.

02/2006	H Zhang, X Gu. *Inference on the Number of Unseen Species and the Number of Abundant/Rare Species.* American Statistical Association Florida Chapter meeting, FL.
01/2006	H Zhang. *Inferences on the Number of Species and the Number of Abundant/Rare Species.* Hawaii International Conference on Statistics, Mathematics and Related Fields, Honolulu, HI.
08/2005	H Zhang. *Inferences on the Number of Species and the Number of Abundant/Rare Species.* Joint Statistical Meeting, Minneapolis, MN.
03/2005	H Zhang. *Genome Phylogenetic tree Analysis Based on Extended gene contents.* Eastern North American Region conference, Austin, TX.
02/2005	H Zhang. *Inferences on the Number of Species and the Number of Abundant/Rare Species.* American Statistical Association Florida Chapter meeting, FL.
05/2004	H Zhang, X Gu. *Genome Phylogenetic tree Analysis Based on Extended gene contents.* Interface 2004: Computational Biology and Bioinformatics, Baltimore, MD.
02/2004	H Zhang, H Stern. *Sample size calculation for finding unseen species.* American Statistical Association Florida Chapter meeting, FL.

Seminars/Symposiums at institutions (Presenter: Hongmei Zhang)

03/2022	Gaussian directed and undirect network comparisons. Invited by the Department of Biomedical Engineering, University of Memphis, Memphis, TN.
11/2019 (invited)	Network Comparisons via Bayesian Inferences. University of Arkansas of Medical Sciences, Little Rock, AK.
04/2019 (invited)	*Bayesian network selection with ordered data.* University of Tennessee Health Science Center, Memphis, TN
11/2018 (invited)	*Analytical methods in transgenerational epigenetics studies, what we have and what we need,* NIH/NIAID workshop, Rockville, MD
02/2018 (invited)	*From variable selection to Bayesian differential networks*, Vanderbilt University, Nashville, TN
04/2015 (invited)	*A two-component G prior for variable selection*. Department of Mathematical Sciences. University of Memphis, Memphis, TN
04/2015 (invited)	*Joint cluster with correlated variables via a semi-parametric Bayesian model*. Bioinformatics seminar, University of Memphis, Memphis, TN.
04/2014 (invited)	*Variable selection in semi-parametric models.* Bioinformatics seminar, University of Memphis, Memphis, TN.
02/2013 (Invited)	*Bayesian variable selection in linear and semi-parametric models.* Medical University of South Carolina, Charleston, SC.
10/2010 (invited)	*Correcting Atopy Misclassification through Wheal Size Adjustment.* Department of Clinical Sciences and Simmons Cancer Center, University of Texas Southwestern Medical Center at Dallas, TX.
09/2010 (invited)	*Capturing Species at A Certain Abundance Level from A Population with Unknown Heterogeneity.* Department of Statistics, University of South Carolina, SC.
10/2009	*The Impact of Risk Factors on Cancer Incidences with Random Spatial Effect Adjusted Using Kernel Machines.* Department of Epidemiology and Biostatistics, University of South Carolina, SC.
01/2008 (invited)	*Ancestry Identification, Genotyping Error, and Its Impact.* Medical University of South Carolina, SC.
10/2007	*Inferences for Genotyping Error Rate in Ancestry Identification From SSR Marker Profiles.* Bioinformatics Group, University of South Carolina.
01/2005	*Constructing Phylogenies.* Department of Mathematics and Statistics, University of West Florida, FL.

03/2004 (invited)	*Sample size calculation for finding unseen species.* Department of Statistics, Florida State University.
11/2003	*Applications of Microarray data.* Department of Mathematics and Statistics, University of West Florida.

Teaching Experience

Courses taught at the University of Memphis
Graduate courses in Biostatistics:

PUBH 7/8305 Quantitative Method Review of Research
Textbook: Borenstein, M., Hedges, L. V., Higgins, J. P., Rothstein, H. R. R. (2009). *Introduction to Meta-Analysis*. New York: John Wiley. ISBN 978-0-470-05724-7.

PUBH 7310/8310 Mixed modeling
Textbook: West, B.T., Welch, K.B., and Galecki, A.T. Linear Mixed Models: A Practical Guide Using Statistical Software. Boca Raton: Chapman & Hall/CRC.

PUBH 7153/8153 Biostatistics in Bioinformatics.
Textbooks: 1) Gentleman, V.J. Carey, W. Huber, R.A. Irizarry, S. Dudoit. Bioinformatics and Computational Biology Solutions Using R and Bioconductor (recommended).
2) H Zhang. Analyzing High-dimensional Gene Expression and DNA Methylation Data with R (recommended).

Graduate courses in genetic statistics:
PUBH 7455/8455 Genetic and Epigenetic Epidemiology
Textbook: Andreas Ziegler and Inke König A statistical Approach to Genetic Epidemiology.

Course taught at the University of South Carolina:
Graduate courses in Biostatistics:
BIOS 700 Introduction to Biostatistics.
Textbook: Marcello Pagano and Kimberlee Gauvreau, Principles of Biostatistics (2nd edition).

BIOS 701 Concepts and Methods of Biostatistics.
Textbook: Marcello Pagano and Kimberlee Gauvreau, Principles of Biostatistics (2nd edition).

BIOS 757 Intermediate Biometrics.
Textbook: Kleinbaum, Kupper, Muller, and Nizam, Applied Regression Analysis and Multivariate Methods (4th edition).

BIOS 775 Biostatistical Aspects of Bioinformatics.
Textbooks: 1) Maria Rizzo, Statistical Computing with R.
2) R. by Gentleman, V.J. Carey, W. Huber, R.A. Irizarry, S. Dudoit, Bioinformatics and Computational Biology Solutions Using R and Bioconductor.

Graduate courses in genetic statistics:
EPID 777 Genetic and Epigenetic Epidemiology
Reading material: Andreas Ziegler and Inke König, A statistical Approach to Genetic Epidemiology.

EPID894 Genetic Epidemiology

Textbook: Andreas Ziegler and Inke König, A statistical Approach to Genetic Epidemiology.

Courses taught at the University of West Florida:

Undergraduate courses in Statistics:
Sta2023 Essentials of Statistics.Text book: Essentials of Statistics by *Mario Triola.*
Sta4173 Biostatistics. Text Book: Biostatistical Analysis (4th edition) by *Jerrold Zar*

Graduate courses in Statistics:
Sta5176 Biostatistics.
Text Book: Jerrold Zar, Biostatistical Analysis (4th edition).

Sta5166 Applied Statistics.
Text Book: *McClave and Sincich*, Statistics

Sta5206 Analysis of Variance.
Text Book: Neter,Kutner, Nachtsheim, and Li, Applied Linear Models (5th edition).

Sta5207 Applied Linear Regression Models.
Text Book: Neter,Kutner, Nachtsheim, and Li, Applied Linear Models (5th edition).

Sta6246 Experimental Design.
Text Book: Douglas Montgomery, Design and analysis of experiments (5th Edition).

Sta6507 Nonparametric Data Analysis.
Text Book: W.J. Conover, Practical Nonparametric Statistics (3rd edition).

Courses taught at the Iowa State University:

Stat 227 (2002-2003) Introduction to Business Statistics

Courses taught at the Truman State University:

College Algebra (1999), Summer course for the SEE (Scholastic Enhancement Experience) program

Guest lectures and short courses

2017	Short course to graduate students in the Psychology Department, University of Memphis, Memphis
2014	Guest lecture on semi-parametric variable selection, University of Memphis, Memphis (BINF 7980).
2012	Guest lecture on path analysis, University of South Carolina, Columbia (EPID 845)
2010, 2011	Guest lecture on biostatistician in grant proposal writing (EPID 801), University of South Carolina, Columbia
2010, 2011, 2012	Guest lecture on bioinformatics in public health (EPID 758), University of South Carolina, Columbia
2008, 2009	Guest lecture on gene-gene and gene-environmental interaction, University of South Carolina, Columbia (EPID 801)
Dec., 2008	Guest lecture on measurement error, University of South Carolina, Columbia (EPID 845)
Dec. 14, 2007:	Short course in Statistics to OB/GYN Doctors, University of South Carolina, Columbia