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**RESEARCH POSITIONS**

**Professor of Biostatistics (with tenure), 07/24 – present**  
The University of Chicago, Department of Public Health Sciences

**Associate Professor of Biostatistics (with tenure), 07/17 – 06/24**  
The University of Chicago, Department of Public Health Sciences

**Assistant Professor of Biostatistics, 08/10 – 06/17**  
The University of Chicago, Department of Public Health Sciences

**Postdoctoral Research Associate, 07/08 – 07/10**  
Fred Hutchinson Cancer Research Center  
Advisor: Drs. Ross L. Prentice and Li Hsu

**Postdoctoral Research Associate, 02/08 – 07/08**  
Lewis-Sigler Institute for Integrative Genomics, Princeton University  
Advisor: Dr. John D. Storey

**EDUCATION AND BACKGROUND**

**Ph.D., Biostatistics, 06/03 – 01/08**  
Department of Biostatistics, University of Washington  
Thesis Title: Causal Modeling in Quantitative Genomics (Advisor: Dr. John D. Storey)

**B. S., 09/98 – 06/02**  
School of Economics, Peking University, Beijing, China

**PUBLICATIONS**

\* Corresponding author.

1. Yihao Lu, Meritxell Oliva, Brandon L. Pierce, Jin Liu\* and **Lin S. Chen\***. (2024) Integrative cross-omics and cross-context analysis elucidates molecular links underlying genetic effects on complex traits. *Nature Communications*, volume 15, Article number: 2383. PMID: 38493154 PMCID: PMC10944527

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2. Fan Yang\*, Lin S. Chen\*, Shahram Oveisgharan, Dawood Darbar and David A. Bennett. (2024) Integrating Mendelian Randomization with causal mediation analysis for characterizing direct and indirect exposure-to-outcome effects. *Annals of Applied Statistics*, accepted.
  3. Yihao Lu, Ke Xu, Bowei Kang, Brandon L. Pierce, Fan Yang\* and Lin S. Chen\*. (2024) An integrative multi-context Mendelian randomization method for identifying risk genes across human tissues. *The American Journal of Human Genetics*, in minor revision.
  4. Oliva M\*, Demanelis K, Lu Y, Chernoff M, Jasmine F, Ahsan H, Kibriya MG, **Chen LS\***, Pierce BL\*. (2023) DNA methylation QTL mapping across diverse human tissues provides molecular links between genetic variation and complex traits. *Nature Genetics*, 55, 112–122. PMID: 36510025
  5. Cheng Q, Zhang X, **Chen LS\***, Liu J\* (2022) Mendelian randomization accounting for complex correlated horizontal pleiotropy while elucidating shared genetic etiology. *Nature Communications*. 13: 6490. PMID: 36310177. PMCID: PMC9618026.
  6. Gleason KJ, Yang F\*, **Chen LS\***. (2021) A robust two-sample transcriptome-wide Mendelian Randomization method integrating GWAS with multi-tissue eQTL summary statistics. *Genetic Epidemiology*. 45(4):353-371.  
❖ The Best Paper in Genetic Epidemiology Award for the Year 2021.
  7. Yang F, Gleason KJ, Wang J, Duan J, He X, Pierce BL, **Chen LS\*** (2021) CCmed: Cross-condition mediation analysis for identifying robust trans-associations mediated by cis-gene. *Bioinformatics*. 37(17):2513-2520.
  8. Gleason KJ<sup>1</sup>, Yang F<sup>1</sup>, Pierce BL, He X, **Chen LS\***. (2020) Primo: integration of multiple GWAS and omics QTL summary statistics for elucidation of molecular mechanisms of trait-associated SNPs and detection of pleiotropy in complex traits. *Genome Biology*. 21: Article 236. PMID: 32912334
  9. Demanelis K, Jasmine F, **Chen LS**, Chernoff M, Tong L, Delgado D, Zhang C, Shinkle J, Sabarinathan M, Lin H, Ramirez E, Oliva M, Kim-Hellmuth S, Stranger BE, Lai TP, Aviv A, Ardlie K, Aguet F, Ahsan H, GTEx Consortium, Doherty JA, Kibriya M, Pierce BL. (2020) Determinants of telomere length across human tissues. *Science*. 369, eaaz6876. PMID: 32913074
  10. Cai M, **Chen LS**, Liu J, Yang C. (2020) Quantifying the impact of genetically regulated expression on complex traits and disease. *Nucleic Acid Research Genomics and Bioinformatics*. 2(1). PMCID: PMC7034630. PMID: 32118202
  11. Song X, Ji J, Gleason KJ, Yang F, Martignetti JA, **Chen LS\***, Wang P\*. (2019) Insights into impact of DNA copy number alteration and methylation on the proteogenomic

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- landscape of human ovarian cancer via a multi-omics integrative analysis. *Molecular & Cellular Proteomics*, **18(8S1)**: S52-65.
12. Wang J, Wang P, Hedeker D, **Chen LS.\*** (2019) Using multivariate mixed-effects selection models for analyzing batch-processed proteomics data with non-ignorable missingness. *Biostatistics*. 20(4):648-665. PMID: 29939200
  13. Ma WP, **Chen LS**, Ozbek U, Han SW, Lin C, Paulovich AG, Zhong H, Wang P. (2019) Integrative proteo-genomic analysis to construct CNA-protein regulatory map in breast tumors. *Molecular & Cellular Proteomics*, **18(8S1)**: S66-81.
  14. Clark DJ, ... others, **Chen LS**, ... others, Nesvizhskii AI, Wang P, Zhang H, and the NCI CPTAC Investigators. (2019) Integrated proteogenomic characterization of clear cell renal cell carcinoma. *Cell*, 9:180(1):207. PMID: 31923397.
  15. Pierce BL, Tong L, Argos M, Jasmine F, Zaman R, Islam T, Rahman M, Baron JA, Kibriya MG, **Chen LS**, Ahsan H. (2018) Co-occurring eQTLs and mQTLs: evidence for shared causal variants and shared causal mechanisms. *Nature Communications*, **9**: 804.
  16. Wang J, Liu Q, Pierce BL, Huo D, Olopade OI, Ahsan H, **Chen LS.\*** (2018). A meta-analysis approach with filtering for identifying gene-level gene-environment interactions. *Genetic Epidemiology*, 42(5):434-446. PMID: 29430690 PMCID: PMC6013347
  17. Bryan MS, Argos M, Andrulis IL, Hopper JL, Chang-Claude J, Malone KE, John EM, Gammon MD, Daly NB, Terry MB, Buys SS, Huo D, Olopade OI, Genkinger JM, Whittemore AS, Jasmine F, Kibriya MG, **Chen LS**, Ahsan H. (2018) Germline variation and breast cancer incidence: A gene-based association study and whole-genome prediction of early onset breast cancer. *Cancer Epidemiology, Biomarkers & Prevention*, 27(9):1057-1064.
  18. Yang F, Wang J, the GTEx consortium, Pierce BL, **Chen LS\***. (2017) Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis. *Genome Research*, **27 (11)**: 1859-1871.
  19. **Chen LS**, Wang J, Wang X, Wang P. (2017) A mixed-effects model for incomplete data with batch-level abundance-dependent missing-data mechanism. *Annals of Applied Statistics*, **11(1)**: 114-138.
  20. GTEx Consortium. (2017) Genetic effects on gene expression across human tissues. *Nature*, 550: 204-213. PMID: 29022597 PMCID: PMC5776756.
  21. Dean SG, Zhang C, Gao J, Roy S, Shinkle J, Sabarinathan M, Argos M, Tong L, Ahmed A, Islam MT, Islam T, Rakibuz-Zaman M, Sarwar G, Shahriar H, Rahman M, Yunus M,

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- Graziano JH, **Chen LS**, Jasmine F, Kibriya MG, Ahsan H, Pierce BL. (2017) The association between telomere length and mortality in Bangladesh. *Aging*, 9(6):1537-1551.
22. Bryan MS, Argos M, Andrulis IL, Hopper JL, Chang-Claude J, Malone K, John EM, Gammon MD, Daly M, Terry MB, Buys SS, Huo D, Olopade O, Genkinger JM, Jasmine F, Kibriya MG, **Chen L**, Ahsan H. (2017) Limited influence of germline genetic variation on all-cause mortality in women with early onset breast cancer: evidence from gene-based tests, single-marker regression, and whole-genome prediction. *Breast Cancer Res Treat*, 164(3):707-717.
23. Liu Q, **Chen LS\***, Nicolae DL, Pierce BL. (2016) A unified set-based test with adaptive filtering for gene-environment interaction analyses in association studies. *Biometrics*. **72(2)**:629-638. PMID: 26496228.
24. Wang J, Gamazon ER, Pierce BL, Stranger BE, Im HK, Gibbons RD, Cox NJ, Nicolae DL, **Chen LS\***. (2016) Imputing gene expression in uncollected tissues within and beyond GTEx. *The American Journal of Human Genetics*, **98 (4)**: 697-708.
25. Huo D, ... others, **Chen LS**, ... others, Haiman CA. (2016) Genome-wide association studies in women of African ancestry identified 3q26.21 as a novel susceptibility locus for oestrogen receptor negative breast cancer. *Hum Mol Genet*, **25(21)**:4835-4846.
26. Sighoko D, Ogundiran T, Ademola A, Adebamowo C, **Chen L**, Odedina S, Anetor I, Ndom P, Gakwaya A, Ojenbede O, Huo D, Olopade OI. (2015) Breast cancer risk after full-term pregnancies among African women from Nigeria, Cameroon, and Uganda. *Cancer*, **121 (13)**: 2237-2243.
27. Argos M, **Chen L**, Jasmine F, Tong L, Pierce BL, Roy S, Paul-Brutus R, Gamble MV, Harper KN, Parvez F, Rahman M, Rakibuz-Zaman M, Slavkovich V, Baron JA, Graziano JH, Kibriya MG, Ahsan H. (2015) Gene-specific differential DNA methylation and chronic arsenic exposure in an epigenome-wide association study of adults in Bangladesh. *Environ Health Perspect*, **123(1)**: 64-71.
28. **Chen LS**, Prentice RL and Wang P. (2014) A penalized EM algorithm for multivariate Gaussian data with non-ignorable missing data. *Biometrics*. **70(2)**: 312-322. PMCID: PMC4061266.
29. Pierce BL, Tong T, **Chen LS**, Rahaman R, Argos M, Jasmine F, Roy S, Paul-Brutus R, Westra HJ, Franke L, Esko T, Zaman R, Islam T, Rahman M, Baron JA, Kibriya MG, Ahsan H. (2014) Mediation analysis demonstrates that trans-eQTLs are often explained by cis-Mediation: A genome-wide analysis among 1,800 South Asians. *PLoS Genetics*. **10(12)**:e1004818. PMCID: PMC4256471.

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30. Liu Q, Nicolae DL\* and **Chen LS\***. (2013) Marbled inflation from population structure in gene-based association studies with rare variants. *Genet Epidemiology*, **37(3)**: 286-292.
  31. **Chen LS\***, Hsu L, Gamazon E, Cox NJ and Nicolae DL. (2012) An exponential combination procedure for set-based association test in sequencing studies. *The American Journal of Human Genetics*, **91(6)**: 977-986.
  32. **Chen LS\***. (2012) Using eQTLs to reconstruct gene regulatory networks. *Quantitative Trait Loci (QTL)*, **1**:175-189.
  33. Hutter CM, ...others, **Chen LS**, ...others, Peters U. (2012) Characterization of gene-environment interactions for colorectal cancer susceptibility loci. *Cancer Research*, **72(8)**: 2036-2044.
  34. Peters U, ...others, **Chen L**, ...others, Potter JD, Casey G. (2012) Meta-analysis of new genome-wide association studies of colorectal cancer risk. *Hum Genet.*, **131**: 217-234.
  35. **Chen LS**, Paul D, Prentice RL and Wang P. (2011) A regularized Hotelling's  $T^2$  test for pathway analysis in proteomics studies. *Journal of the American Statistical Association*, **106(496)**: 1345-1360.
  36. **Chen LS**, Hutter CM, Potter JD, Liu Y, Prentice RL, Peters U and Hsu L. (2010) Insights into colon cancer etiology using a regularized approach to gene set analysis of GWAS data. *The American Journal of Human Genetics*. **86 (6)**: 860-871.
  37. Prentice RL, Paczesny S, Aragaki A, Amon L, **Chen L**, Pitteri S, McIntosh M, Wang P, Busald TB, Hsia J, Jackson R, Rossouw JE, Manson JE, Johnson K, Eaton C, Hanash SM. (2010) Novel proteins associated with risk for coronary heart disease or stroke among postmenopausal women identified by in-depth plasma proteome profiling. *Genome Medicine*, **2(7)**: 48.
  38. Pitteri SJ, Hanash SM, Aragaki A, Amon L, **Chen L**, Buson TB, Paczesny S, Katayama H, Wang H, Johnson MM, Zhang Q, McIntosh M, Wang P, Kooperberg C, Rossouw JE, Jackson R, Manson JE, Hsia J, Liu S, Martin L and Prentice RL. (2009) Postmenopausal estrogen and progestin effects on the serum proteome. *Genome Medicine*, **1(12)**: 121.
  39. **Chen LS** and Storey JD. (2008) Eigen- $R^2$  for dissecting the variation of high-dimensional studies, *Bioinformatics*, **24 (19)**: 2260-2262.
  40. **Chen LS**, Emmert-Streib F, and Storey JD. (2007) Harnessing naturally randomized transcription to infer regulatory relationships among genes. *Genome Biology*, **8**: R219.
  41. **Chen L** and Storey JD. (2006) Relaxed significance criteria for linkage analysis. *Genetics*, **173**: 2371-2381.

**SOFTWARE DEVELOPMENT**

- CCmed: Gleason KJ, Yang F, Chen LS (2020) Mediation analysis across conditions
- MrMrRobin: Gleason KJ, Yang F, Chen LS (2020) Mr.MtRobin: Multi-tissue transcriptome-wide Mendelian Randomization method
- Primo: Gleason KJ, Yang F, Chen LS (2019) Package in R for Integrative Multi-Omics analysis. <https://github.com/kjgleason/primo>
- GMAC: Yang F, Wang J, and **Chen LS** (2017), an R software package for genomic mediation analysis with adaptive confounding adjustment, available through CRAN.
- mvMISE: Wang J and **Chen LS** (2017), an R software package for a general framework of multivariate mixed-effects selection models. Currently available at <https://github.com/lschen-stat/mvMISE>, and will be available through CRAN.
- ofGEM: Wang J and **Chen LS** (2017), an R software package for a meta-analysis approach with filtering for identifying gene-level gene-environmental interactions with genetic association data. Current available at <https://github.com/lschen-stat/ofGEM>, and will be available through CRAN.
- mixEMM: **Chen LS**, Wang P, and Wang J (2017), an R software package for a mixed-effects model for analyzing cluster-level non-ignorable missing data, available through CRAN.
- MixRF: Wang J and **Chen LS**. (2016), an R software package for imputing clustered incomplete data using a random-forest approach, available through CRAN.
- PEMM: **Chen LS** and Pei Wang (2014), an R software package for analyzing abundance-dependent incomplete data in proteomics studies, available through CRAN.
- Trigger: **Chen LS**, Sangurdekar D and Storey JD (2011), an R software package that guides an integrative genomic analysis, available through Bioconductor.
- RHT: **Chen LS** (2011), an R software package for pathway analysis in omics data, available through CRAN.
- SNPath: **Chen LS** (2010), an R package for pathway analysis in association study. Available at <https://github.com/lschen-stat/SNPath>.

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EigenR2: **Chen LS** and Storey JD (2008), an R software package for dissecting variation in high-dimensional data. Available at <https://github.com/lischen-stat/eigenR2>.

## FUNDING

### (a) Current and pending:

1. NIH 1R01GM154421-01. PI: Chen. **My role: single PI.** Title: "Integrative multivariate association and genomic analyses". Proposed project period: 04/01/2024-03/31/2028. Total direct cost: \$1,459,322. Pending, scored at 5% (impact score 22).
2. NIH 1U01MH139345-01. PI: Chen. My role: **single PI.** Title: "Integrative Analysis Methods for the dGTE<sub>x</sub> Initiative". Proposed project period: 07/01/2024-06/30/2027. Total direct cost \$1,159,099 for 3 years. Pending, impact score 26, RFA no percentile.
3. NIH 1R01AG087616-01. PI: Chen. **My role: single PI.** Title: "Integrative genomic analysis with causal inference in multi-ethnic studies". Proposed project period: 04/01/2023-03/31/2028. Total direct cost: \$1,512,726. Pending, scored at 26% (impact score 38).
4. NIH 2R01 GM108711. PI: Chen. **My role: single PI.** Title: "Integrative multivariate association and genomic analyses". Project period: 09/01/2019-05/31/2023. No-cost extension will continue effort at 51% FTE through 05/31/2024. Total cost: \$ 1,497,936.
5. NIH R35 ES028379. PI: Pierce. **My role: Co-I.** Title: "Arsenic and the Human Genome: susceptibility and response to exposure". Project period: 09/2017-07/2025. 10% FTE.
6. NIH 1R01 CA229618. PI: Stranger and Huang. **My Role: Co-I and U Chicago Site PI.** Title: "Genetic mechanisms underlying sexual dimorphism in cancer and response to therapy". Project period: 12/01/2019-05/31/2024. 8% FTE.
7. NIH U24 HG012339 PI: Piece. **My role: co-I.** Title: "A data resource for studying DNA methylation in diverse human tissue types". 10% FTE projected.

### (b) Past:

8. NIH U24 CA210993-01. PI: Wang and Schadt. **My role: Co-I and U Chicago Site PI.** Title: "Systems biology based proteogenomic translator for cancer marker discovery towards precision medicine". Total direct costs (UC site): \$428,179. Project period: 09/19/16-08/31/2021.
9. NIH R03 CA174984-02. PI: **Chen.** **My role: PI.** Title: "Multivariate functional analysis of the genetic basis of cancer". Project period: 03/07/13-02/28/15.
10. NIH R01 GM108711. PI: **Chen.** **My role: PI.** Title: "Integrative multivariate association and genomic analyses". Project period: 01/2013-08/2019.

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11. NIH R01 MH101820. PI: Nicolae, Cox. **My role: Co-I.** Title: "Harnessing GTEx to Create Transcriptome Knowledge and Inform Disease Biology". Project period: 08/01/13-07/31/17.
  12. NIH U01 CA161032. PI: Olopade, Huo, White. **My role: Co-I.** Title: "Using Genomics to Reduce Breast Cancer Disparities in the African Diaspora". Project period: 07/19/12-12/31/16.
  13. NIH R01 ES023834. PI: Pierce. **My role: Co-I.** Title: "Genetics of arsenic metabolism: fine-mapping and rare variant analysis". Project period: 06/06/14-03/31/18.
  14. NIH U01 HG007601. PI: Pierce. **My role: Co-I.** Title: "Telomere length and chromosomal instability across various tissue types". Project period: 08/01/14-05/31/18.
  15. Department of Defense (DoD) W81XWH-14-1-0529. PI: Pierce. **My role: Co-I.** Title: "Identifying DNA methylation features that underlie prostate cancer disparities". Project period: 09/30/14-09/29/17.

### TEACHING EXPERIENCE

1. Instructor for PBHS 32700 Biostatistical Methods, University of Chicago, Jan-March 2018, 2021, 2022, 2023
2. Instructor for PBHS/STAT 22400 Applied Regression Analysis, University of Chicago, Sept-Dec, 2011, 2012, 2013, 2016, 2017, 2018, 2019
3. Instructor for PBHS 32100 Introduction to Biostatistics, University of Chicago, July-August, 2011, 2012, 2014
4. Instructor for HGEN 47100 Introductory Statistical Genetics, University of Chicago, Jan-March, 2015 (with Novembre J and Pierce BL)
5. Instructor for PBHS 33200 Statistical Analysis with Missing Data, University of Chicago, Jan-March, 2016
6. Instructor for Quantitative Biology (Qbio) bootcamp, September, 2020, 2021, 2022.

### INVITED SPEAKING

- |      |   |
|------|---|
| 2008 | Seminar, Department of Statistics, Carnegie Mellon University, PA   |
| 2008 | Seminar, Department of Statistics, Purdue University, IN  |
| 2008 | Seminar, Department of Statistics, University of California, Irvine, CA   |
| 2008 | Seminar, Fred Hutchinson Cancer Research Center, WA   |
| 2009 | Invited talk, ENDGAME meeting, University of Michigan, Ann Arbor, MI  |
| 2009 | Invited talk, ENAR (The International Biometrics Society Eastern North American Region) annual meeting, San Antonio, TX |
| 2010 | Seminar, Department of Biostatistics, Emory University, GA  |
| 2010 | Seminar, Department of Biostatistics, New York University, NY   |
| 2010 | Seminar, Fred Hutchinson Cancer Research Center, WA   |
| 2010 | Invited talk, WNAR (The International Biometrics Society Western North American Region) annual meeting, Seattle, WA     |
| 2011 | Invited talk, ENAR annual meeting, Miami, FL  |



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- 2011 Invited talk, IMS (The International Biometrics Society) -China International conference on Statistics and Probability, Xi'An, China
- 2011 Seminar, Department of Statistics, Penn State University, PA
- 2011 Seminar, Department of Epidemiology and Biostatistics, School of Public Health, University of Illinois at Chicago, Chicago, IL
- 2012 Invited talk, ENAR annual meeting, Washington DC
- 2012 Invited talk, 2nd IMS Asia Pacific Rim Meeting, Tsukuba, Japan
- 2013 Invited talk, ENAR annual meeting, Orlando, FL
- 2013 Invited talk, IMS-China International conference on Statistics and Probability, Chengdu, China
- 2013 Seminar, Department of Biostatistics and Medical Informatics, University of Wisconsin, Madison, WI
- 2014 Invited talk, the 6<sup>th</sup> International Forum on Statistics, Renmin University, Beijing, China
- 2014 Invited talk, Joint Statistical Meeting, Boston, MA
- 2015 Invited talk, ENAR annual meeting, Miami, FL
- 2015 Invited talk, International Chinese Statistical Association Annual meeting (ICSA), Fort Collins, CO
- 2015 Invited talk, American Public Health Association annual meeting, Chicago, IL
- 2015 Seminar, Department of Genetics and Genomics Sciences, Mt Sinai Hospital, New York, NY
- 2015 Seminar, Department of Preventive Medicine – Biostatistics, Northwestern University, Chicago, IL
- 2015 Seminar, Department of Biostatistics, School of Public Health, Yale University, New Haven, CT
- 2015 Seminar, Division of Epidemiology and Biostatistics, School of Public Health, University of Illinois at Chicago, Chicago, IL
- 2016 Invited talk, Joint Statistical Meeting, Chicago, IL
- 2016 Invited talk, The 9th International Conference of the ERCIM WG on Computational and Methodological Statistics (CMStatistics), Seville, Spain
- 2016 Invited talk, The 10th ICSA international conference, Shanghai, China
- 2017 Seminar, Duke-NUS Medical School, Singapore
- 2017 Selected talk, GETx community meeting, Barcelona, Spain
- 2017 Invited talk, ICSA annual meeting, Chicago, IL
- 2017 Invited talk, The 10th International Conference of CMStatistics, London, UK
- 2018 Invited talk, Hangzhou International Conference on Frontiers of Data Science, Hangzhou, China
- 2018 Seminar, Department of Biostatistics, University of Michigan.
- 2018 Seminar, Lawrence University in Appleton, Wisconsin.
- 2018 Seminar, Department of Mathematics, The Hong Kong University of Science and Technology.
- 2019 Seminar, Bioinformatics and Computational Biology Graduate Program, University of Idaho.
- 2019 Seminar, Fred Hutchinson Cancer Research Center.
- 2019 Seminar, Department of Biostatistics & Bioinformatics, Duke University.
- 2019 Seminar, Department of Biostatistics, School of Medicine, Indiana University.
- 2020 Seminar, Department of Biostatistics, University of Pittsburgh.
- 2020 Seminar, Department of Biostatistics, University of Pennsylvania.

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2020	Seminar, Department of Statistics and Probability, Michigan State University
2021	Seminar, Division of Biostatistics, School of Public Health, University of Minnesota
2021	Invited talk, International Indian Statistical Association (IISA)
2021	Invited talk, Joint Statistical Meeting, Seattle, Washington (virtual)
2021	Invited talk, WNAR annual meeting, virtual
2022	Invited talk, IMS workshop, Statistical Methods in Genetic/Genomic Studies
2022	Invited talk, ENAR annual meeting, virtual
2022	Seminar, Department of Mathematics and Statistics at Washington State University
2022	Invited talk, The Robert Elston award presentation for the best paper in Genetic Epidemiology in 2021, IGES annual meeting, Paris, France
2022	Seminar, the Quantitative Issues in Cancer Research Working Seminar at Harvard School of Public Health, Harvard University
2023	Seminar, Department of Biostatistics, Columbia University
2024	Seminar, Department of Biostatistics and Data Sciences, the University of Texas Health Science Center at Houston, School of Public Health Sciences
2024	Seminar, Department of Preventive Medicine, Division of Biostatistics, Northwestern University

**DEPARTMENT AND UNIVERSITY SERVICE**

Department graduate student admission committee member in multiple years 2010-2019

Department curriculum committee member in multiple years, 2010-2019

Department qualify exam committee member in Year 2020-2023

Instructor for Quantitative Biology (Qbio) bootcamp, a weeklong bootcamp for new graduate student of Biological Science Division, September, 2020, 2021, 2022.

**EXTRAMURAL SERVICE****Grant Review:**

2022-2024	Regular member of NIH study section Analytics and Statistics for Population Research panel A (ASPA), co-chair for the Feb and Oct panels in 2023
2020-2022	Regular member of NIH study section Biostatistical Methods and Research Design (BMRD)
Various	Ad hoc grant reviewer for NIH BMRD in June 2013, December 2013, February 2014, June 2014, February 2015, and March 2018, February 2019, June 2019.
2020/8	Ad hoc grant reviewer for Emerging Technologies and Training in Neurosciences (ETTN), Special Emphasis Panel/Scientific Review Group
2016	Ad hoc grant reviewer for NIH Avenir Award Program for Genetics or Epigenetics of Substance Abuse (DP1)

Editorial service:

2018-present Associate Editor, *Biometrics*

2023-present Associate Editor, *PLoS Genetics*

2011-2012 Guest Editor, *Frontier in Genetics*

2012-2015 Associate Editor, Academic Editor, *PLoS One*

2015, 20-21 Guest Associate Editor, *PLoS Genetics*

Various Manuscript reviewer for *Science*, *Nature Genetics*, *Journal of American Statistical Association*, *Annals of Statistics*, *Biometrika*, *Nature Biotechnology*, *Nature Communications*, *The American Journal of Human Genetics*, *PLoS Genetics*, *Biometrics*, *Biostatistics*, *Annals of Applied Statistics*, *Genome Biology*, *Bioinformatics*, *BMC Bioinformatics*, *BMC Genetics*, *BMC System Biology*, *Journal of Biopharmaceutical Statistics*, *PLoS ONE*, *Statistics and Its Interface*, *Statistical Applications in Genetics and Molecular Biology*

Service:

2021-2022 Program Chair for the Section on Statistics in Genomics and Genetics. American Statistical Association (ASA)

Various Invited/contributed session organizer or session chair, ENAR annual meeting, WNAR annual meeting, JSM, ICOSA, and other IMS meetings.

2016-2017 Organizing committee member for 2017 International Chinese Statistical Association symposium, Chicago, IL

**GRADUATE STUDENT ADVISING**

(a) Primary thesis advisor for:

1. Yihao Lu, 2019-2024, Ph.D. in Biostatistics (my role: advisor)
2. Bowei Kang, Ph.D. student in Biostatistics (my role: advisor). Expected 2027
3. Kevin Gleason, 2016-2020, Ph.D. in Biostatistics (my role: advisor). Received NIH F31 award, 1F31CA239557-01A1.
4. Jiebiao Wang, 2012-2017, Ph.D. in Biostatistics (my role: primary advisor, co-advised with Dr. Robert Gibbons), **The Departmental Best Dissertation Award 2017-2018**; currently an Assistant Professor in the Department of Biostatistics, University of Pittsburgh as a tenure-track assistant professor in 2019.
5. Qianying Liu, 2010-2014, Ph.D. in Biostatistics (my role: primary advisor, co-advised with Dr. Dan Nicolae)
6. Ke Xu, (2021-2023) Master's in Statistics (my role: advisor)
7. Jason Lin, 2020-2021, Master's in Statistics (my role: advisor)
8. Yuqing He, 2019-2020, Master's in Statistics (my role: advisor)

(b) Committee member for:

9. Stephanie Melkonian, 2011-2013, Ph.D. in Epidemiology (my role: committee member)
10. Chenan Zhang, 2013-2016, Ph.D. in Epidemiology (my role: committee member)
11. Molly Scannell Bryan, 2013-2016, Ph.D. in Epidemiology (my role: committee member)
12. Dayana Delgado, 2016-2022, Ph.D. in Epidemiology (my role: committee member)

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13. Meytal Chernoff, 2016-2022, Ph.D. in Epidemiology (my role: committee member)
  14. Lizeth Tamayo, 2020-present, Ph.D. in Epidemiology (my role: committee member)
  15. James Li, 2023-present, Ph.D. in Epidemiology (my role: committee member)
  16. Skowron, Kinga. A MSCP student. Graduated 2021. (my role: statistical advisor)
  17. Jodi Mayfield, MD, 2013-2014, Master's in health studies (my role: statistical advisor)
  18. William Conte, MD, 2018-present, Master's in Public Health Sciences (my role: statistical advisor)