TIANZHOU (CHARLES) MA

2234M School of Public Health Bldg, College Park, MD 20742

(301)-405-6421 ⋄ tma0929@umd.edu

https://sph.umd.edu/people/tianzhou-ma ⋄ https://matianzhou.github.io/

EDUCATION

University of Pittsburgh,   Pittsburgh, PA, US

- Ph.D. in Biostatistics,   *Apr 2018*
  - Thesis: *Differential expression and feature selection in the analysis of multiple omics studies.*
  - Advisors: George C. Tseng, ScD and Zhao Ren, PhD

Yale University,   New Haven, CT, US

- M.S. in Biostatistics,   *May 2013*
  - Thesis: *Incorporating functional annotation information in prioritizing disease associated SNPs from genome wide association studies.*
  - Advisor: Hongyu Zhao, PhD

University of Toronto,   Toronto, ON, Canada

- Honours B.Sc. in Genes, Genetics and Biotechnology (specialist),   *June 2010*
  - *with High Distinction (Summa Cum Laude)*

RESEARCH INTERESTS

- Bioinformatics, genetics (GWAS and post-GWAS fine mapping) and multi-omics (e.g. expression of both coding and noncoding RNA, epigenomics, proteomics, etc.)

- Meta-analysis and data integration of omics data and with other data types (e.g. imaging-genetics)

- Statistical learning and high-dimensional variable selection

- Bayesian hierarchical modeling

- Survival data analysis

- Application of statistical and machine learning methods in cancer, psychiatry, infectious disease and epidemiology fields

PROFESSIONAL EXPERIENCE

- **Assistant Professor**   Aug 2018 ∼ Now
  - Department of Epidemiology and Biostatistics, University of Maryland, College Park, MD
- **UMD Affiliate**   Dec 2018 ∼ Now
  - Maryland Population Research Center, University of Maryland, College Park, MD

PUBLICATIONS

Notes: ^: co-first author; *corresponding author; students underlined; Also available at My Google Scholar Page

2021

---

1. Cruz-Cano R, **Ma T**, Yu Y, Lee M and Liu H. Forecasting COVID-19 Cases based on Social Distancing in Maryland, U.S.A.: A Time –Series Approach. (2021). *Disaster Medicine and Public Health Preparedness*. Accepted.

2. Saegusa T, <u>Zhao Z</u>, <u>Ke H</u>, <u>Ye Z</u>, Xu Z, Chen S and **Ma T***. (2021). Detecting survival-associated biomarkers from heterogeneous populations. *Scientific Reports*, 11(1): 1-12.

3. Wu Q, **Ma T**, Liu Q, Milton D, Zhang Y and Chen S. (2021). Extracting Interconnected Communities in Gene Co-expression Networks. *Bioinformatics*. Accepted.

4. <u>Ye Z^</u>, <u>Ke H^</u>, Chen, S, Cruz-Cano, R, He, X, Zhang, J, Dorgan J, Milton D and **Ma T***. (2021). Biomarker categorization in transcriptomic meta-analysis by concordant patterns with application to Pan-cancer studies. *Frontiers in Genetics*. Accepted.

5. Rahman T, Li Y, **Ma T**, Tang L and Tseng GC. (2021). A sparse negative binomial mixture model for clustering RNA-seq count data. Under revision in *Biostatistics*.

6. Rose A, Belus J, **Ma T**, Lee J, Wan C, Reyes A, Joska J, Andersen L, Myers B and Magidson J. (2021+). An event-level analysis of the relationship between harmful alcohol use and anti-retroviral treatment non-adherence in people accessing HIV treatment in Cape Town, South Africa. Under revision in *AIDS and Behavior*.

7. **Ma T***, <u>Ke H</u> and Ren Z*. (2021+). Robust distance correlation for variable screening. To be submitted.

8. Zong W, Rahman T, Zhu L, Zeng X, Zhang Y, Zou J, Liu S, Li JJ, **Ma T*** and Tseng GC*. (2021+). Congruence evaluation for model organisms in transcriptomic response. To be submitted.

9. Adenaiye O, Mesquita J, Hong F, German J, Tai S, Youssefi S, Albert, B, **Ma T**, ... and Milton D. (2021+). Tracking Acute Respiratory Infections in A College Resident Community. To be submitted.

10. Khan S, Adenaiye O, **Ma T**, ..., Milton D and Felgner P. (2021+). Subtype-specific IgA antibodies partially mediate influenza immunity following vaccination. To be submitted.

11. Linkov F, Goughnour, S, Vlad A, Elishaev E, **Ma T**, Xu Z, Edwards RP, Ramanathan R, Hamad G and Bovbjerg D. (2021+). Changes in the endometrial immune markers in women undergoing surgical weight loss. To be submitted.

12. Gao S, Donohue B, Hatch K, Chen S, **Ma, T**, ..., Nichols T and Kochunov P. Comparing Empirical Kinship Derived Heritability for Imaging Genetics Traits in UK Biobank and Human Connectome Project. To be submitted.

2020

13. **Ma T**, Ren Z and Tseng GC. (2020). Variable screening with multiple studies. *Statistica Sinica*, 30(2): 925–953.

14. Lin C, Chang L, **Ma T**, Oh H, French, B, ..., Tseng G and Sibille E. (2020). Older Molecular Brain Aging in Severe Mental Illness. *Molecular Psychiatry*. Accepted.

15. Saegusa T, **Ma T**, Lee MT, Li G and Chen Y. (2020). Variable selection in censored threshold regression model with applications to HIV drug adherence data. *Statistics in Biosciences*. Accepted.

16. Zeng X, Zong W, Lin C, Fang Z, Li Y, **Ma T**, Lewis D, Enwright J and Tseng GC. (2020). Comparative Pathway Integrator: a framework of meta-analytic integration of multiple transcriptomic studies for consensual and differential pathway analysis. *Genes*. Accepted.

17. Wu Q, Milton D, Xing Y, **Ma T**, Zhang Z and Chen S. (2020). Predicting Latent Contacts from Self-reported Social Network Data via Outcome Misclassification Adjustment. *Statistics in Medicine*. Accepted.

18. Yu Y, Liu S, Tao J, Ren B, Chen Z, Li F, Nalesnik M, **Ma T**, ..., Tseng G and Luo J. (2020). Pten-NOLC1 fusion promotes cancers involving MET and EGFR signalings. *Oncogene*. Accepted.

19. <u>Ye Z^</u>, Mo C^, Hatch K, Liu S, Gao S, Hong E, Kochunov P*, Chen S* and **Ma T***. White matter integrity and nicotine dependence in smokers: evaluating vertical and horizontal pleiotropy. *bioRxiv* (2020).

20. Mo C^, <u>Ye Z^</u>, Hatch K, Zhang Y, Wu Q, Liu S, Kochunov P, **Ma T*** and Chen S*. Genetic

Fine-mapping with Dense Linkage Disequilibrium Blocks: genetics of nicotine dependence. *bioRxiv* (2020).

2019

21. Zhu L, Huo Z, **Ma T** and Tseng G. (2019). Bayesian indicator variable selection to incorporate hierarchical overlapping group structure in multi-omics applications. *Annals of Applied Statistics*, 13(4): 2611-2636. (a preliminary version won the ENAR distinguished student paper award).

22. Huo Z, Zhu L, **Ma T**, ..., Zhao J and Tseng G. (2019). Two-way Horizontal and Vertical Omics Integration for Disease Subtype Discovery. *Statistics in Biosciences.* In press.

23. **Ma T**$^\wedge$, Huo Z$^\wedge$, Kuo A$^\wedge$, ..., Song C and Tseng GC. (2019). MetaOmics - Comprehensive Analysis Pipeline and Web-based Software Suite for Transcriptomic Meta-Analysis. *Bioinformatics*, 35(9):1597-1599.($^\wedge$co-first author) PMID: 30518877.

24. Grabosch S, Bulatovic M, Zeng F, **Ma T**, ..., Edwards R and Vlad A. (2019). Cisplatin-induced immune modulation in ovarian cancer mouse models with distinct inflammation profiles. *Oncogene*, 38(13):2380-2393. PMID: 30518877.

2018

25. Fang Z, **Ma T**, Zhu L, ..., Tang G and Tseng GC. (2018). Bayesian integrative model for multi-omics data with missingness. *Bioinformatics*, 34(22):3801-3808. PMID: 30184058.

26. Andersen CL, Boisen MM, Sikora MJ, **Ma T**, ..., Edwards RP and Oesterreich S. (2018). The evolution of estrogen receptor signaling in the progression of endometriosis to endometriosis-associated ovarian cancer. *Hormones and Cancer*, 9(6): 399-407. PMID: 30302736.

27. Scifo E, Pabba M, Kapadia F, **Ma T.**, Lewis DA, Tseng GC and Sibille E. (2018). Sustained molecular pathology across episodes and remission in depression. *Biological Psychiatry*, 83(1): 81-89. PMID: 28935211.

2017

28. **Ma T**, Liang F and Tseng GC. (2017). Biomarker detection and categorization in ribonucleic acid sequencing meta-analysis using Bayesian hierarchical models. *Journal of the Royal Statistical Society: Series C*, 66(4): 847-867. (won ASA Section on Bayesian Statistical Science (SBSS) student paper award to attend 2017 JSM, reported on RNA-Seq Blog)

29. **Ma T**, Liang F, Oesterreich S and Tseng GC. (2017). A Joint Bayesian Model for Integrating Microarray and RNA Sequencing Transcriptomic Data. *Journal of Computational Biology*, 24(7): 647-662. (selected to present at Dahshu Data Science Symposium: Computational Precision Health 2017 and won the best paper award)

30. **Ma T**, Song C and Tseng GC. (2017). Discussant paper on "Statistical contributions to bioinformatics: Design, modelling, structure learning and integration". *Statistical Modelling*, 17(4-5): 305-315.

31. Andersen CL, Sikora MJ, Boisen MM, **Ma T**, ..., Edwards RP and Oesterreich S. (2017). Active estrogen receptor-alpha signaling in ovarian cancer models and clinical specimens. *Clinical Cancer Research*, 23(14): 3802-3812. PMID: 28073843.

32. Linkov F, Goughnoura SL, **Ma T**, Xu Z, ..., McCloskey C and Bovbjerg DH. (2017). Changes in inflammatory endometrial cancer-associated biomarkers in individuals undergoing surgical weight loss. *Gynecologic Oncology.* Accepted. PMID: 28797697.

33. French L, **Ma T**, Oh H, Tseng GC and Sibille E. (2017). Age-related gene expression in the frontal cortex suggests synaptic function changes in specific inhibitory neuron subtypes. *Frontiers in aging neuroscience*, 9: 162. PMID: 28611654.

34. Pabba M, Scifo E, Kapadia F, Nikolova YS, **Ma T**, Mechawar N, Tseng GC and Sibille E. (2017). Resilient protein co-expression network in male orbitofrontal cortex layer 2/3 during human aging. *Neurobiology of Aging*, 58: 180-190. PMID: 28750307.

35. Grabosch S, Tseng G, Edwards RP, Lankes HA, Moore K, Odunsi K, Vlad A, **Ma T**, ..., Walker JL and Birrer M. (2017). Multiplex profiling identifies distinct local and systemic alterations during intraperitoneal chemotherapy for ovarian cancer: An NRG Oncology/Gynecologic Oncology Group Study. *Gynecologic Oncology*, 146(1):137-145. PMID: 28483269.

2016

36. Liu S, Tsai W, Ding Y, Chen R, Fang Z, Huo Z, Kim S, **Ma T**, ..., Chung I and Tseng GC. (2016). Comprehensive evaluation of fusion transcript detection algorithms and a meta-caller to combine top performing methods in paired-end RNA-seq data. *Nucleic Acids Research*, 44(5):e47. PMID: 26582927.

37. Zhang L, **Ma T**, ..., Tseng G and Vlad AM. (2016). Effects of Kras activation and Pten deletion alone or in combination on MUC1 biology and epithelial to mesenchymal transition in ovarian cancer. *Oncogene*, 35(38): 5010-20. PMID: 26973247.

38. Chen CY, Logan RW, **Ma T**, Lewis DA, Tseng GC, Sibille E and McClung CA. (2016). Effects of aging on circadian patterns of gene expression in the human prefrontal cortex. *Proceedings of the National Academy of Sciences*, 113(1): 206-21. PMID: 26699485. (High Attention Paper, 99th percentile, News on National Public Radio (NPR))

39. Sanei-Moghaddam A, **Ma T**, ..., Mansuria SM and Linkov F. (2016). Changes in hysterectomy trends after the implementation of a clinical pathway. *Obstetrics & Gynecology*, 127(1), 139-147. PMID: 26646126.

2015 and before

40. Mony JT, Zhang L, **Ma T**, ..., Huang X and Vlad AM. (2015). Anti-PD-L1 prolongs survival and triggers T cell but not humoral anti-tumor immune responses in a human MUC1-expressing preclinical ovarian cancer model. *Cancer Immunology, Immunotherapy*, 64(9):1095-108. PMID: 25998800.

41. Liao S, Hartmaier RJ, McGuire KP, Puhalla SL, Luthra S, Chandran UR, **Ma T**, ..., Tseng GC and Oesterreich S. (2015). The molecular landscape of premenopausal breast cancer. *Breast Cancer Research*, 17(1): 1-13. PMID: 26251034. (discussed in an interview; *Nature*, 527: S108-109)

42. Suryawanshi S, Huang X, Elishaev E, Budiu RA, Zhang L, Kim S, Donnellan N, Mantia-Smaldone G, **Ma T**, ..., Edwards RP and Vlad AM. (2014). Complement Pathway Is Frequently Altered in Endometriosis and Endometriosis-Associated Ovarian Cancer, *Clinical Cancer Research*, 20(23): 6163-6174. PMID: 25294912.

43. Hou L$^\wedge$, **Ma T**$^\wedge$ and Zhao H. (2014). Incorporating functional annotation information in prioritizing disease associated SNPs from genome wide association studies. *Science China Life Sciences*, 57(11), 1072-1079. ($^\wedge$co-first author)

Book

44. Tseng GC, Huo Z and **Ma T**. Foundations for High-Throughput Omics Data Analysis: Methods, Theories and Applications. *Chapman & Hall/CRC*. In preparation and expected in 2021.

ABSTRACTS

1. Hatch K, Donohue B, **Ma T**, Chen S, Ma Y, Gao S, Hong E, Jahanshad N, Thompson P, Kochunov P. Novel Application of Algorithmic Approaches and Parallel GPU Computing for Voxel-wise Heritability and Voxel-wise Genome-Wide Association Studies. *OHBM 2021*, virtual.

2. Belus J, Ke, H, **Ma T**, Rose A, Regenauer K, Andersen L, Joska J, Safren S, Myers B and Magidson J. Alcohol-specific reward as a mediator of a behavioral activation intervention to reduce problematic substance use in people living with HIV in South Africa. *ABCT 2021*, New Orleans, LA.

3. Adenaiye O, Lai J, Hong F, Tai S, German J, Youssefi S, Mesquita P, Albert B, **Ma T**, Weston S, Frieman M and Milton D. Viral Shedding from Persons Infected with SARS-CoV02: Aerosols, Droplet Spray, and Fomites. AAAR 2021, Albuquerque, NM.

TEACHING

- **Lecturer, University of Maryland**

  - EPIB652: Categorical Data Analysis   Fall 2020
  - EPIB664: Missing Data Analysis   Fall 2019

- EPIB661: Applied Multivariate Data Analysis   Spring 2019, 2020, 2021

- **Guest Lecturer, University of Maryland**

    - EPIB633: Health Survey Design and Analysis *Missing data imputation using SAS*   Oct 2019

- **Lecturer, University of Pittsburgh**

    - BIOST2094: Advanced R Computing (with Zhiguang Huo)   Spring 2017
    - BIOST2025: Special Studies in Bayesian Data Analysis (with George Tseng, Zhiguang Huo and Li Zhu)   Fall 2016
    - BIOST2094: Statistical Computing in R   Spring 2015

- **Guest Lecturer, University of Pittsburgh**

    - BIOST2078: Introductory high-throughput genomic data analysis II: theories and algorithms: *Selected Bayesian Methods in Genomic Studies*   Dec 2015

- **Teaching Assistant, University of Pittsburgh and Yale University**

    - BIOST 2078: Introductory high-throughput genomic data analysis II: theories and algorithms   Fall 2015
    - IMED 645: Introduction to Biostatistics, Yale University School of Medicine   Summer 2012

STUDENT MENTORING

- Academic advisor and thesis/project committee chair:

    - Travis Canida, PhD in STAT-BB   2021-Now
    - Hongjie Ke, PhD in STAT-BB   2020-Now
    - Soroor Saidian, MPH in Biostatistics   2021-Now
    - Ameri Mahsa, MPH in Biostatistics   2020-Now
    - Amanda Behdin, MPH in Biostatistics   2020-Now
    - Boao Zhao, MPH in Biostatistics   2020-Now
    - Erica Lee, MPH in Biostatistics   2020-Now
    - Kevin Chuang, MPH in Biostatistics   2019-2021
    - John Yee, MPH in Biostatistics   2019-2020
    - Megan Gerdes, MPH in Biostatistics   2019-2020
    - Eunsol Shim, MPH in Biostatistics   2019-2020
    - Zhenyao Ye, MPH in Biostatistics   2018-2020
    - Manyun Zhao, MPH in Biostatistics   2018-2020

- PhD dissertation committee:

    - Yujiang Ge, PhD in STAT-BB   2020-Now
    - Yiming Chen, PhD in STAT-BB   2020-Now
    - Yifan Yang, PhD in Statistics   2020-Now
    - Jianyu Lai, PhD in Epidemiology   2021-Now
    - Lakeshia Watson, PhD in Epidemiology   2020-Now
    - Julia Callaway, PhD in Epidemiology   2020-Now
    - Sarah Irvin, PhD in Epidemiology   2020-2021
    - Alli Hanley, PhD in Epidemiology   2019-2021
    - Jun Chu, PhD in Health Service   2020-Now
    - Nicholas Rachmaninoff, PhD in Computational Biology   2020-Now
    - Rosemary Ezeugoh, PhD in Environmental Health Sciences   2020-Now

- MPH thesis committee:

    - Samantha Ammons, MPH in Epidemiology   2018-2019

- – Angie Barrall, MPH in Epidemiology 2018-2019
- PhD independent study:
  - – Wing Yan Yuen , PhD in STAT-BB Fall 2020
  - – Jianyu Lai , PhD in Epidemiology Spring 2020
  - – William Evans, PhD in Kinesiology Spring 2020
  - – Yifan Yang, PhD in Statistics Fall 2019
  - – Yunjiang Ge, PhD in STAT-BB Fall 2019

RESEARCH SUPPORT

Current:

- **MPower BHHP seed grant, UMD, PI: Tianzhou Ma, Peter Kochunov**
  - – Genetic risk factors of accelerated brain aging in severe mental illness: an imaging genetics approach.
  - – Period: 04/01/2021 - 03/31/2022
  - – Role: Principal Investigator
  - – Total direct costs: $100,000

- **R01A5-204062, NIH, PI: Jie Chen**
  - – Effect of Hospital and Community Care Coordination on Health Care Quality and Equity among Individuals with RiskFactors or Diagnosis of ADRD
  - – Period: 03/01/2021 - 02/28/2024
  - – Role: Co-Investigator (Efforts: 5%)

- **20216801533435, USDA-NIFA, PI: Hee-Jung Song**
  - – Effects of an integrated system approach on hypertension management in community dwelling older adults.
  - – Period: 10/01/2020 - 09/30/2023
  - – Role: Co-Investigator (Efforts: 5%)
  - – Total direct costs: $ 553,285.35

- **R34MH122268, NIMH, PI: Jessica Magidson**
  - – Training CHWs to Support Re-Engagement in TB/HIV Care in the Context of Depression and Substance use.
  - – Period: 07/07/2020 - 05/31/2023
  - – Role: Co-Investigator (Efforts: 5%)

- **FSRA Award 2020-21, UMD, PI: Tianzhou Ma**
  - – Novel statistical methods for long non-coding RNA biomarker detection using RNA-Seq data.
  - – Period: 09/2020-08/2021
  - – Role: Principal Investigator
  - – Total direct costs: $10,000

- **1DP1DA048968-01, NIDA, PI: Shuo Chen**
  - – A Multivariate Mediation and Deep Learning Framework for Genome-Connectome-Substance Use Research
  - – Period: 09/01/2019 - 08/31/2024
  - – Role: Subcontract PI (Efforts: 30%)
  - – Total direct costs: $1,500,000

- **75N93021C00014, NIAID-CRIP, PI: Donald Milton**

- NIAID Centers of Excellence for Influenza Research and Response (CEIRR)
- Period: 04/01/2021 - 03/31/2028
- Role: Co-Investigator (Efforts: 8%)
- Total direct costs: $1,400,000

Past:

- **N66001-17-2-4023 and N66001-18-2-4015, DARPA BTO, PI: Donald Milton**

  - Contagious Phenotypes of Acute Respiratory Infection: Identification, Characterization, and Biomarkers.
  - Period: 10/31/2018 - 08/31/2020
  - Role: Statistician and Bioinformatician (Efforts: 25%)

- **R01CA221303 - National Cancer Institute**

  - PI: Steffi Oesterreich, University of Pittsburgh Medical Center
  - Role: Statistician
  - 2017/09 - 2018/07

- **R01CA190766 - National Cancer Institute**

  - PI: George Tseng, University of Pittsburgh
  - Role: Statistician
  - 2017/09 - 2018/07

- **R01MH093723 - National Institute of Mental Health**

  - PI: Etienne Sibille, University of Toronto
  - Role: Statistician
  - 2014/01 - 2017/08

- **R01CA163462 - National Cancer Institute**

  - PI: Anda Vlad, University of Pittsburgh Medical Center
  - Role: Statistician
  - 2013/09 - 2017/08

PRESENTATIONS

Talks

- **Invited**. ICSA Xi'an   July 2022
  - *A Cox model based two-stage variable selection method for the detection of survival associated biomarkers with multiple genomic studies*
- **Invited**. UM Greenebaum Comprehensive Cancer (UMGCCC), University of Maryland Baltimore June 2021
  - *Congruence evaluation for model organisms in transcriptomic response*
- **Invited** (Virtual). Department of Biostatistics and Bioinformatics, Georgetown University   Dec 2020
  - *High-dimensional variable screening: from single study to multiple studies*
- **Invited** (Canceled). WNAR Anchorage   June 2020
  - *Deep learning model using network topology of linkage disequilibrium patterns increases the accuracy of polygenic risk scores*
- **Invited**. The 11th ICSA International Conference, Hangzhou, China   Dec 2019
  - *Variable screening with multiple studies and its application in survival analysis.*
- **Invited**. JSM 2019, Denver, CO   Aug 2019
  - *Variable screening with multiple studies and its application in survival analysis.*
- **Invited**. The 2nd Conference on Lifetime Data Science, Pittsburgh, PA   May 2019

- - *Variable selection in censored threshold regression model with applications to HIV drug adherence data.*
- ENAR 2019 Spring meeting, Philadelphia, PA   March 2019
  - *Variable screening with multiple studies.*
- **Invited**. School of Public Health, University of Maryland College Park   Oct 2018
  - *Statistical and computational methods for the meta-analysis and resemblance analysis of transcriptomic studies.*
- **Invited** (Withdrawl). Department of Epidemiology and Biostatistics, University of Southern Carolina   Feb 2018
  - *Differential expression analysis in multiple omics studies.*
- **Invited** (Withdrawl). Department of Epidemiology and Biostatistics, University of Arizona Feb 2018
  - *Differential expression analysis in multiple omics studies.*
- **Invited** (Withdrawl). Department of Mathematics and Statistics, University of Vermont   Feb 2018
  - *Differential expression analysis in multiple omics studies.*
- **Invited**. Department of Epidemiology and Biostatistics, University of Maryland College Park Dec 2017
  - *Differential expression analysis in multiple omics studies.*
- JSM 2017, Baltimore, MD   Aug 2017
  - *Biomarker detection and categorization in RNA-seq meta-analysis using Bayesian hierarchical model.*
- ENAR 2017 Spring meeting, Washington, DC   March 2017
  - *Biomarker detection and categorization in RNA-seq meta-analysis using Bayesian hierarchical model.*
- Dahshu Data Science Symposium: Computational Precision Health 2017, San Franscisco, CA Feb 2017
  - *A joint Bayesian modeling for integrating microarray and RNA-seq transcriptomic data.*
- JSM 2016, Chicago, IL   Aug 2016
  - *Biomarker detection and categorization in RNA-seq meta-analysis using Bayesian hierarchical model.*
- **Invited**. Statistical Genetics/Genomes Lab, University of Pittsburgh   Dec 2015
  - *A Bayesian hierarchical model for RNA-seq meta-analysis and biomarkers categorization by study heterogeneity.*
- **Invited**. The 5th Annual Women's Cancer Research Center (WCRC) Retreat, Farmington, PA Nov 2015
  - *Immune gene signature pairs predict survival in immune-reactive cancer patients: a Pancancer analysis.*

Posters

- Poster (Selected). 2021 NIDA GECCRT Meeting, National Institute of Health (NIH) March 2021
  - *White matter integrity and nicotine dependence in smokers: evaluating vertical and horizontal pleiotropy (Virtual)*
- Poster, ASA Spring Banquet, Pittsburgh, PA   April 2016
  - *A Bayesian hierarchical model for RNA-seq meta-analysis and biomarkers categorization by study heterogeneity.*
- Poster, GSPH Dean's day competition, University of Pittsburgh   April 2016
  - *Disrupted circadian rhythms at the molecular level in Bipolar disorder (BP) and Schizophrenia (SCZ).*
- Poster, ENAR 2017 Spring meeting, Austin, TX   March 2016
  - *A Bayesian hierarchical model for RNA-seq meta-analysis and biomarkers categorization by study heterogeneity.*

- Poster, GSPH Dean's day competition, University of Pittsburgh   April 2015
  - *Cross-species Gene Expression Analysis: In what functional domains do mouse models predict human disease on a molecular basis?*

AWARDS

- Faculty-student research award AY20-21, University of Maryland   Dec 2019
- Delta Omega Membership, Delta Omega Honorary Society in Public Health   Apr 2018
- Student Paper Award, ASA Section on Bayesian Statistical Science (SBSS)   Aug 2017
- Student of the Year, American Statistics Association (ASA) Pittsburgh chapter   Apr 2017
- Best Paper Award, Dahshu Data Science Symposium: Computational Precision Health 2017 Feb 2017
- Best Student Presentation Award, Department of Biostatistics, University of Pittsburgh   Apr 2017
- Travel Award to attend "Optimization Opening Workshop", SAMSI Research Triangle Park Aug 2016
- Outstanding Graduate Student Researcher Award, Department of Biostatistics, University of Pittsburgh   Apr 2016
- Dean's Day Poster Competition Award, GSPH, University of Pittsburgh   Apr 2015
- Three consecutive years on Dean's list, Faculty of Arts and Science, University of Toronto 2008-2010,
- Three consecutive years' recipient of University College Scholarship, University College, University of Toronto,   2008-2010

EVENT ORGANIZING

- First UMD-SPH Conference on Big Data in Public Health, University of Maryland College Park, 02/28/2020
  - · >200 attendees from 35 different institutions and organizations.
  - · See news report on UMD-SPH website.

DEPARTMENTAL/SCHOOL/UNIVERSITY SERVICE

- Department: EPIB Graduate Student Recruitment/Admissions Committee (2018-present), EPIB Executive Committee (2019-present), EPIB Curriculum Committee (2019-present)

- School: Undergraduate Degree Program Task Force Committee (2019-present)

- University: Department Liason to the University Library System (2018-present), University Academic Standards And Procedures (APAS) Committee (2019-present)

PROFESSIONAL SERVICE

Journal Referee

- *Annals of Applied Statistics*

- *Computational Statistics and Data Analysis*

- *American Statistician*

- *Journal of Biopharmaceutical Statistics*

- *Neural Computation*

- *Statistical Analysis and Data Mining*

- *Statistics and Its Interface*

- *The American Statistician*
- *Statistics and Its Interface*
- *Communications in Statistics – Theory and Methods*
- *Journal of Statistical Planning and Inference*
- *Bioinformatics*
- *Genome Medicine*
- *BMC Bioinformatics*
- *BMC Medical Research Methodology*
- *Scientific Reports*
- *PLOS One*
- *PLOS Computational Biology*
- *Human Brain Mapping*
- *Aging*
- *Journal of Nervous and Mental Disease*

Service to the Profession

- Organizer, 2020 ICSA Houston, session 43: Recent advances in statistical methods for big biomedical data integration
- Chair, 2019 ENAR Spring meeting, session 85: Meta-analysis
- 2016-2018, American Statistical Association Pittsburgh Chapter Student Representative

CONFERENCES AND WORKSHOPS

- 2020 ICSA Symposium
- 2016-2017, 2019 JSM.
- 2014-2017, 2019, 2021 ENAR Spring meeting.
- The 11th ICSA International Conference, Hangzhou, China.   Dec 2019
- The 2nd Conference on Lifetime Data Science, Pittsburgh, PA.   May 2019
- NIDA and NIAAA Genetics and Epigenetics Research Meeting, Rockville, MD.   Jan 2019
- 2017 Summer Short Course on Causal Discovery and Datathon, Pittsburgh, PA.   June 2017
- 3rd Annual Statistical Methods in Imaging Conference, Pittsburgh, PA.   May 2017
- Computational Precision Health 2017, San Franscisco, CA.   Feb 2017
- Optimization Opening Workshop, SAMSI, Research Triangle Park, NC.   Aug 2016
- 5th Annual WCRC Retreat, Nemacolin Woodlands Resort, PA.   Nov 2015

PROGRAMMING AND SOFTWARES

- R, SAS, Stata, C++, Python, UNIX shell scripting and others.

MEMBERSHIP

- Member of American Statistical Association   *Sep 2013 ∼ Now*
- Member of Eastern North American Region International Biometric Society   *Sep 2013 ∼ Now*
- Member of International Chinese Statistical Association   *Mar 2015 ∼ Now*

HOBBIES

Writing, Playing baskeball and soccer.