
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, Statistical 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. epigenetic regulation of genes, 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

Under revision, Ready to submit

⁰Last modified: December 10, 2021

1. Zong W, Rahman T, Zhu L, Zeng X, Zhang Y, Zou J, Liu S, Ren Z, Litman D, Li JJ, Osterreich S, **Ma T*** and Tseng GC*. (2021+). CAMO: A molecular congruence analysis framework for evaluating model organisms. Under revision in *Nature Methods*.
2. Ye Z[^], Mo C[^], Ke H[^], Yan Q, Chen C, Chen S* and **Ma T***. (2021+). Meta-analysis of transcriptome-wide association studies across 13 brain tissues identified novel clusters of genes associated with nicotine addiction. Under revision in *Genes*.
3. Mo C[^], Ye Z[^], Hatch K, Zhang Y, Wu Q, Liu S, Kochunov P, **Ma T*** and Chen S*. (2021+). Genetic Fine-mapping with Dense Linkage Disequilibrium Blocks: genetics of nicotine dependence. Under revision in *BMC Bioinformatics*.
4. Wu Q, Zhang Y, **Ma T**, Kochunov P and Chen S. (2021+). A multivariate to multivariate approach for voxel-wise genome-wide association analysis. Under revision in *Biometrics*.
5. Chen C, Shen B, **Ma T**, Wang M and Wu R. (2021+). A statistical framework for recovering pseudo-dynamic networks from static data. Under revision in *Bioinformatics*.
6. Belus J, Ke H, **Ma T**, Regenauer K, Myers B and Magidson J. (2021+). Testing Alcohol and HIV Stigmas as Mechanisms of Change in a Behavioral Treatment for Substance Use and ART Adherence for People Living with HIV in Cape Town, South Africa. Under revision in *Journal of the International AIDS Society*.
7. Kochunov P, Ma Y, Hatch K, Jahanshad N, ..., **Ma T**, ..., Nichols T and Hong E. (2021+). Brain-Wide vs. Genome-Wide Vulnerability Biomarkers for Severe Mental Illnesses. Under revision in *Biological Psychiatry*.
8. Hanley A, Nguyen Q, Badawi D, Chen J, **Ma T** and Slopen N. (2021+). Timeliness in Autism Diagnosis and Intervention Among Three Birth Cohorts of Children, 2016-2018. Under revision in *Pediatrics*.
9. Xing Y, Du Y, Kochunov P, Erp TV, **Ma T** and Calhoun V. (2021+). A novel feature selection method using multi-granularity weighted neighborhood rough set combined with entropy to identify biomarkers of mental disorders. Under revision in *Expert Systems with Applications*.
10. **Ma T***, Ke H and Ren Z*. (2021+). Robust distance correlation for variable screening. Ready to submit.
11. Ke H, Ren Z, Chen S, Tseng G, Qi J and **Ma T***. (2021+). A fast and robust variable screening method for detecting genome-wide epigenetic regulators of gene expression. Ready to submit.
12. Ye Z[^], Mo C[^], Liu S, Gao S, Zhao B, Canida T, Wu Y, ..., Chen S* and **Ma T***. Evaluating the causal effects of blood pressures on white matter integrity: a Mendelian Randomization study using UK Biobank data. Ready to submit.
13. 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. Ready to submit.
14. Khan S, Adenaiye O, **Ma T**, ..., Milton D and Felgner P. (2021+). Subtype-specific IgA antibodies partially mediate in uenza immunity following vaccination. Ready to submit.
15. 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. Ready to submit.

2021

Methodology work:

16. Ye Z[^], Mo C[^], Liu S[^], Hatch K, Gao S, ..., Kochunov P*, Chen S* and **Ma T***. (2021). White matter integrity and nicotine dependence: evaluating vertical and horizontal pleiotropy. *Frontiers in Neuroscience*, 15.
17. Ye Z[^], Ke H[^], 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*, 12.
18. Saegusa T, Zhao Z, Ke H, Ye Z, Xu Z, Chen S and **Ma T***. (2021). Detecting survival-associated

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- biomarkers from heterogeneous populations. *Scientific Reports*, 11(1): 1-12.
19. Wu Q, **Ma T**, Liu Q, Milton D, Zhang Y and Chen S. (2021). ICN: extracting interconnected communities in gene co-expression networks. *Bioinformatics*. In press. (a preliminary version won the student paper award of American Statistical Association (ASA) Statistics in Imaging Section).
 20. Li Y, Rahman T, **Ma T**, Tang L and Tseng GC. (2021). A sparse negative binomial mixture model for clustering RNA-seq count data. *Biostatistics*. In press.
 21. Mo C[^], Ye Z[^], Ke H[^], Lu T, Canida T, ..., Hong E, Kochunov P, **Ma T*** and Chen S*. (2021). A new Mendelian Randomization method to estimate causal effects of multivariate brain imaging exposures. *Pacific Symposium on Biocomputing (PSB) 2022*. Accepted.

Application work:

22. 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. *AIDS and Behavior*. Accepted.
23. Gao S, Donohue B, Hatch K, Chen S, **Ma T**, ..., Nichols T and Kochunov P. (2021+). Comparing Empirical Kinship Derived Heritability for Imaging Genetics Traits in UK Biobank and Human Connectome Project. *NeuroImage*. Accepted.
24. Adenaiye O, Lai J, Bueno de Mesquita PJ, Hong F, ..., **Ma T** and Milton D. (2021). Infectious SARS-CoV-2 in Exhaled Aerosols and Efficacy of Masks During Early Mild Infection. *Clinical Infectious Diseases*. Accepted.
25. Hanley A, Nguyen Q, Badawi D, Chen J, **Ma T** and Slopen N. (2021). The Diagnostic Odyssey of Autism: A Cross-Sectional Study of 3 Age Cohorts of Children from the 2016-2018 National Survey of Children's Health. *Child and Adolescent Psychiatry and Mental Health*. Accepted.
26. Kochunov P, Ma Y, Kvarita M, ..., **Ma T**, Chen S, Nichols T and Hong E. (2021). Separating Clinical and Subclinical Depression by Big Data Informed Structural Vulnerability Index and Its impact on Cognition: ENIGMA Dot Product. Pacific Symposium on Biocomputing (PSB) 2022. Accepted.
27. Cruz-Cano R, **Ma T**, Yu Y, Lee M and Liu H. (2021). Forecasting COVID-19 Cases based on Social Distancing in Maryland, U.S.A.: A Time Series Approach. *Disaster Medicine and Public Health Preparedness*, 1-4.

2020

Methodology work:

28. **Ma T**, Ren Z and Tseng GC. (2020). Variable screening with multiple studies. *Statistica Sinica*, 30(2): 925-953.
29. Wu Q, Milton D, Xing Y, **Ma T**, Zhang Z and Chen S. (2020). Link predictions for incomplete network data with outcome misclassification. *Statistics in Medicine*, 40(6): 1519-1534. (a preliminary version won the student paper award at 2020 Statistical Methods in Imaging (SMI) conference).
30. 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*, 12(3): 376-398.
31. 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*, 11(6): 696.

Application work:

32. 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*, 1-11.

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33. 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*, 40 (6), 1064-1076.

2019

34. **Ma T**[^], Huo Z[^], Kuo A[^], ..., Song C and Tseng GC. (2019). MetaOmics - Comprehensive Analysis Pipeline and Web-based Software Suite for Transcriptomic Meta-Analysis. *Bioinformatics*, 35(9): 1597-1599. PMID: 30518877.
35. Zhu L, Huo Z, **Ma T** and Tseng G. (2019). Bayesian indicator variable selection model with multi-layer overlapping groups. *Annals of Applied Statistics*, 13(4): 2611-2636. (a preliminary version won the ENAR 2018 distinguished student paper award).
36. 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*, 12(1): 1-22.
37. Grabosch S, Bulatovic M, Zeng F, **Ma T**, ..., Edwards R and Vlad A. Cisplatin-induced immune modulation in ovarian cancer mouse models with distinct inflammation profiles. *Oncogene*, 38(13): 2380-2393. PMID: 30518877.

2018

38. Fang Z, **Ma T**, Zhu L, ..., Tang G and Tseng GC. (2018). A Bayesian Model for Integrating High-Throughput Multi-Omics Data with Missingness Handling. *Bioinformatics*, 34(22):3801-3808. PMID: 30184058.
39. 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.
40. 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

41. **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)
42. **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)
43. **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.
44. 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.
45. 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.
46. 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.
47. 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.
48. 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

49. 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.
50. 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.
51. 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))
52. 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

53. 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.
54. 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)
55. Suryawanshi S, Huang X, Elishaev E, Budi 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.
56. Hou L[^], **Ma T**[^] 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.

Book

57. 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 2022.

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, 2021
- EPIB664: Missing Data Analysis Fall 2019, Spring 2022
- 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; 16 students) 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, PhD in STAT-BB:
 - Travis Canida 2021-Now
 - Hongjie Ke 2020-Now
- Academic advisor and thesis/project committee chair, MPH in Biostatistics:
 - Soroor Saidian 2021-Now
 - Ameri Mahsa 2020-Now
 - Amanda Behdin 2020-Now
 - Boao Zhao 2020-Now
 - Erica Lee 2020-Now
 - Kevin Chuang (current position: Research Assistant II at Henry Jackson Foundation) 2019-2021
 - John Yee (current position: Statistician, U.S Census Bureau) 2019-2020
 - Megan Gerdes (current position: ORISE fellow, CDC) 2019-2020
 - Eunsol Shim (current position: Statistician, U.S Census Bureau) 2019-2020
 - Zhenyao Ye (current position: PhD candidate in Human Genetics, University of Maryland) 2018-2020
 - Manyun Zhao (current position: Biostatistician at Northwestern University) 2018-2020
- PhD dissertation committee:
 - Tong Lu, PhD in STAT-BB 2021-Now
 - 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-Now

- Alli Hanley, PhD in Epidemiology 2019-2021
- Jun Chu, PhD in Health Service 2020-Now
- Nicholas Rachmaninoff, PhD in Computational Biology 2021-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 STAT-BB Fall 2020
 - Yifan Yang, PhD in Statistics Spring
 - Yunjiang Ge, PhD in STAT-BB 2019-Now
 - William Evans, PhD in Kinesiology 2019-Now

RESEARCH SUPPORT

Active:

- **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
 - Total direct costs: \$100,000
 - Role: PI
- **1DP1DA048968-01, NIH/NIDA, PI: Shuo Chen**
 - A Multivariate Mediation and Deep Learning Framework for Genome-Connectome-Substance Use Research.
 - Period: 09/1/19-8/31/24
 - Total direct costs: \$463,500
 - Role: Site PI
 - Efforts: 30%
- **R34MH122268, NIH/NIMH, PI: Jessica Magidson**
 - Training CHWs to Support Re-Engagement in TB/HIV Care in the Context of Depression and Substance use.
 - Period: 07/30/20-05/31/23
 - Total direct costs: \$689,139
 - Role: Co-I
 - Efforts: 5%
- **R01AG062315-01A1, NIH/NIA, PI: Jie Chen**
 - Effect of Hospital and Community Care Coordination on Health Care Quality and Equity among Individuals with Risk Factors or Diagnosis of ADRD.
 - Period: 03/01/21-02/28/24
 - Total direct costs: \$1,233,474
 - Role: Co-I
 - Efforts: 5%
- **20216801533435, USDA-NIFA, PI: Hee-Jung Song**

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- Effects of an integrated system approach on hypertension management in community dwelling older adults.
 - Period: 10/01/20-09/30/23
 - Total direct costs: \$553,285
 - Role: Co-I
 - Efforts: 5%

- **1U19AI162130-01, NIH/NIAID, PI: Donald K. Milton**

- Evaluating Modes of Influenza Transmission using a Randomized Controlled Trial (EMIT-2-RCT).
- Period: 09/01/21-05/31/26
- Total direct costs: \$2,287,150
- Role: Co-I
- Efforts: 5%

Pending:

- **R21, NIH/NIDA, PI: Tianzhou Ma**

- A novel gene-to-imaging study that integrates GWAS, multi-omics QTL and brain imaging data to unveil the neurogenetic mechanism of nicotine addiction.
- Period: 09/01/22-08/31/24
- Total direct costs: \$275,000
- Role: PI
- Efforts: 25%

- **R01, NIH/NIBIB, PI: Peter Kochunov**

- Solar-Eclipse Computational Tools for Imaging Genetics.
- Period: 09/01/21-08/31/25
- Total direct costs: \$451,230
- Role: Site PI
- Efforts: 15%

- **Breakthrough Award, DoD, PI: Joanne Dorgan**

- Physiologic estrogens and biomarkers of breast cancer recurrence following neoadjuvant aromatase inhibitor therapy.
- Period: 09/30/22-09/29/25
- Total direct costs: \$80,942 (UMCP portion)
- Role: Site PI
- Efforts: 15%

- **75N93021C00014, NIH/NIAID, PI: Donald K. Milton**

- NIAID Centers of Excellence for Influenza Research and Response (CEIRR).
- Period: 04/01/2021-03/31/2028
- Role: Co-I
- Efforts: 13%

Past:

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

- Contagious Phenotypes of Acute Respiratory Infection: Identification, Characterization, and Biomarkers.
- Period: 10/01/2018 – 12/31/2020
- Role: Statistician and Bioinformatician

- Efforts: 25%
- Faculty-student research award AY20-21, University of Maryland
 - Novel statistical methods for long non-coding RNA biomarker detection using RNA-Seq data.
 - Period: 09/01/2020 - 08/31/2021
 - Total direct costs: \$10,000
 - Role: PI
- Faculty start-up fund, University of Maryland Department of Epidemiology and Biostatistics
 - Period: 08/23/2021 - Present
 - Total direct costs: \$30,000

PRESENTATIONS

Talks

- **Invited.** ICSA 2022 China Conference, Xi'an, China July 2022
 - *A Cox model based two-stage variable selection method for the detection of survival associated biomarkers with multiple genomic studies.*
- **Invited.** ICSA Symposium 2022 , Gainesville, Florid June 2022
 - *A fast and robust variable screening method for detecting genome-wide epigenetic regulators of gene expression.*
- **Invited.** Department of Mathematics, University of Maryland Oct 2021
 - *Novel variable screening methods for omics data integration.*
- **Invited** (Virtual). UM Greenebaum Comprehensive Cancer (UMGCCC), University of Maryland School of Medicine 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** (Cancelled). WNAR, Anchorage June 2020
 - *Deep learning model using network topology of linkage disequilibrium patterns increases the accuracy of polygenic risk scores.*
- **Invited** (Cancelled). University of Maryland School of Medicine May 2020
 - *Poorly mimic or greatly mimic? A model-based evaluation with functional characterization for comparison of differential transcriptomic systems across model organisms.*
- **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.*
- 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.** Department of Epidemiology and Biostatistics, University of Maryland College Park Dec 2017
 - *Differential expression analysis in multiple omics studies.*

- **Invited.** Department of Epidemiology and Biostatistics, University of Southern Carolina Feb 2018
– *Differential expression analysis in multiple omics studies.*
- **Invited.** Department of Epidemiology and Biostatistics, University of Arizona Feb 2018
– *Differential expression analysis in multiple omics studies.*
- **Invited.** Department of Mathematics and Statistics, University of Vermont Feb 2018
– *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 Francisco, 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 Pan-cancer analysis.*

Posters

- Poster (Selected; Virtual). 2021 NIDA GECCRT Meeting, National Institute of Health (NIH) March 2021
– *White matter integrity and nicotine dependence in smokers: evaluating vertical and horizontal pleiotropy.*
- 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

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- MPower BHHP seed grant, University of Maryland Mar 2021
 - 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), TTK Faculty Search Committee (2020.10-2021.06), PTK Faculty Search Committee (Chair, 2021.01-2021.07)
- 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 (2019-2021)

PROFESSIONAL SERVICE

Editorial Service

- Guest Editor, *Frontiers in Genetics*: New analytical methods and applications for brain imaging genetics, 2021.11-
- Editorial Board, *NeuroImage: Reports*, 2021.12-

Grant Review Service

- NIH ad-hoc reviewer for Behavioral Genetics and Epidemiology study section (BGES), meeting on Feb 8-9th, 2022.

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*
- *Communications in Statistics - Theory and Methods*
- *Journal of Statistical Planning and Inference*
- *Nature Communication*
- *Bioinformatics*
- *Genome Medicine*
- *BMC Bioinformatics*
- *BMC Medical Research Methodology*
- *PLOS Computational Biology*
- *PLOS One*
- *Scientific Reports*
- *Human Brain Mapping*
- *NeuroImage*
- *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

- 2021 ASHG Annual Meeting.
- 2020 ICSA Symposium.
- 2016-2017, 2019 JSM.
- 2014-2017, 2019 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 Francisco, CA. Feb 2017
- Optimization Opening Workshop, SAMSI, Research Triangle Park, NC. Aug 2016
- 5th Annual WCRC Retreat, Nemaquin 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 basketball and soccer.