

---

# 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-charles-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 and multi-omics (e.g. genotyping, gene expression, epigenomics, proteomics, etc.)
- Meta-analysis and data integration of omics data and with other data types (e.g. neuroimaging data, real world evidence data, etc.)
- Bayesian hierarchical modeling
- Statistical learning and high-dimensional variable selection
- 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: <sup>^</sup>: co-first author; \*corresponding author; students underlined; Also available at My Google Scholar Page

### 2020

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

---

<sup>0</sup>Last modified: July 24, 2020

2. Lin C, Chang L, **Ma T**, Oh H, Lewis D, and Sibille E. (2020). Older Molecular Brain Aging in Severe Mental Illness. *Molecular Psychiatry*. Accepted.
3. 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.
4. 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.
5. Saegusa T, Zhao Z, Ye Z, Ke H, Xu Z, Chen S and **Ma T\***. (2020). Variable selection in multiple high-dimensional genomic studies with censored survival outcomes. Under revision in *Plos Computational Biology*.
6. Rahman T, Li Y, **Ma T**, Tang L and Tseng GC. (2020). A sparse negative binomial mixture model for clustering RNA-seq count data. Under revision in *Biometrics*.
7. 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. Under revision in *Biostatistics*.
8. 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 C-MET and EGFR Signaling in Human Cancers. Under revision in *Nature Communications*.
9. **Ma T\***, Ren Z and Ke H. (2020+). Robust distance correlation for variable screening. To be submitted.
10. **Ma T**, Rahman T, Zhu L, Zong W, Zeng X, Li JJ and Tseng GC. (2020+). Poorly mimic or greatly mimic? A model-based evaluation with functional characterization for comparison of differential transcriptomic systems across model organisms or across species. To be submitted.
11. Chen S, Liu Q, **Ma T**, Xing Y and Milton D. (2020+). Interconnected Communities in Coexpression Networks. To be submitted.
12. Adenaiye O, Mesquita J, Hong F, German J, Tai S, Youssefi S, Albert, B, **Ma T**, ... and Milton D. (2020+). Tracking Acute Respiratory Infections in A College Resident Community. To be submitted.
13. Khan S, Adenaiye O, **Ma T**, ..., Milton D and Felgner P. (2020+). Subtype-specific IgA antibodies partially mediate influenza immunity following vaccination. To be submitted.
14. Linkov F, Goughnour, S, Vlad A, Elishaev E, **Ma T**, Xu Z, Edwards RP, Ramanathan R, Hamad G and Bovbjerg D. Changes in the endometrial immune markers in women undergoing surgical weight loss. To be submitted.

## 2019

15. 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 distinguished student paper award).
16. 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.
17. **Ma T**<sup>^</sup>, Huo Z<sup>^</sup>, Kuo A<sup>^</sup>, ..., Song C and Tseng GC. (2019). MetaOmics - Comprehensive Analysis Pipeline and Web-based Software Suite for Transcriptomic Meta-Analysis. *Bioinformatics*, 35(9):1597-1599. (^co-first author) PMID: 30518877.
18. 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

19. 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.
20. 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.

21. 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

22. **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)
23. **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)
24. **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.
25. 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.
26. 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.
27. 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.
28. 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.
29. 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

30. 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.
31. 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.
32. 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))
33. 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

34. 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.
35. 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)
  36. 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.
  37. Hou L<sup>^</sup>, **Ma T**<sup>^</sup> 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. (<sup>^</sup>co-first author)

## Book

38. 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.

## 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

### • Guest Lecturer, University of Maryland

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

### • Lecturer, University of Pittsburgh

- BOST2094: Advanced R Computing (with Zhiguang Huo) Spring 2017
- BOST2025: Special Studies in Bayesian Data Analysis (with George Tseng, Zhiguang Huo and Li Zhu) Fall 2016
- BOST2094: Statistical Computing in R Spring 2015

### • Guest Lecturer, University of Pittsburgh

- BOST2078: 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

- BOST 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:

- Hongjie Ke, PhD in STAT-BB 2020-Now
- Erica Lee, MPH in Biostatistics 2020-Now
- Kevin Chuang, MPH in Biostatistics 2019-Now
- John Yee, MPH in Biostatistics 2019-Now
- Megan Gerdes, MPH in Biostatistics 2019-Now
- Eunsol Shim, MPH in Biostatistics 2019-Now
- Zhenyao Ye, MPH in Biostatistics 2018-Now
- Manyun Zhao, MPH in Biostatistics 2018-Now

- PhD dissertation committee:
  - Nicholas Rachmaninoff, PhD in Computational Biology 2020-Now
  - Rosemary Ezeugoh, PhD in Environmental Health Sciences 2020-Now
  - Sarah Irvin, PhD in Epidemiology 2020-Now
  - Yifan Yang, PhD in Statistics 2020-Now
  - Alli Hanley, PhD in Epidemiology 2019-Now
- MPH thesis committee:
  - Samantha Ammons, MPH in Epidemiology 2018-2019
  - Angie Barrall, MPH in Epidemiology 2018-2019
- PhD independent study:
  - 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

---

- **DP1-DA048968-01, NIH National Institute on Drug Abuse (NIDA)**
  - PI: Shuo Chen, University of Maryland Baltimore
  - Role: Co-PI
- **N66001-17-2-4023 and N66001-18-2-4015, Defense Advanced Research Projects Agency (DARPA) BTO**
  - PI: Donald Milton, University of Maryland College Park
  - Role: Statistician and Bioinformatician
- **R01CA221303 - National Cancer Institute**
  - PI: Steffi Oesterreich, University of Pittsburgh Medical Center
  - Role: Statistician
- **R01CA190766 - National Cancer Institute**
  - PI: George Tseng, University of Pittsburgh
  - Role: Statistician
- **R01MH093723 - National Institute of Mental Health**
  - PI: Etienne Sibille, University of Toronto
  - Role: Statistician
- **R01CA163462 - National Cancer Institute**
  - PI: Anda Vlad, University of Pittsburgh Medical Center
  - Role: Statistician

---

## PRESENTATIONS

---

### Talks

- **Invited.** ICSA Xi'an July 2021
  - *A Cox model based two-stage variable selection method for the detection of survival associated biomarkers with multiple genomic studies*
- **Invited.** ICSA Houston Dec 2020

- *Deep learning model using network topology of linkage disequilibrium patterns increases the accuracy of polygenic risk scores*
- **Invited.** WNAR Anchorage June 2020
  - *Deep learning model using network topology of linkage disequilibrium patterns increases the accuracy of polygenic risk scores*
- **Invited.** 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, 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 Liaison 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*
  - *PLOS One*
  - *PLOS Computational Biology*
  - *Genome Medicine*
  - *BMC Bioinformatics*
  - *Journal of Nervous and Mental Disease*

#### **Service to the Profession**

- Chair, 2019 ENAR Spring meeting, session 85: Meta-analysis
- 2016-2018, American Statistical Association Pittsburgh Chapter Student Representative

#### **CONFERENCES AND WORKSHOPS**

---

- 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.