

---

# TIANZHOU (CHARLES) MA

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

(301)-405-6421 [◇ tma0929@umd.edu](mailto:tma0929@umd.edu)

<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
- 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 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

---

### 2019

1. Li Zhu, Zhiguang Huo, **Tianzhou Ma**, George Tseng. (2019). Bayesian indicator variable selection model with multi-layer overlapping groups. *Annals of Applied Statistics*. Tentatively accepted. (a preliminary version won the ENAR distinguished student paper award).
2. Zhiguang Huo, Li Zhu, **Tianzhou Ma**, Hongcheng Liu, Song Han, Daiqing Liao, Jinying Zhao and George Tseng. (2019). Two-way Horizontal and Vertical Omics Integration for Disease Subtype Discovery. Minor revision in *Statistics in Biosciences*.

---

<sup>0</sup>Last modified: April 6, 2019

3. Takumi Saegusa, **Tianzhou Ma**, Mei-Ling Ting Lee, Gang Li, Ying Qing Chen. (2019+). Variable selection in censored threshold regression model with applications to HIV drug adherence data. To be submitted.
4. Shuo Chen, Qingzhi Liu, **Tianzhou Ma**, Yishi Xing and Donald Milton. (2019+). Interconnected Communities in Coexpression Networks. To be submitted.
5. **Tianzhou Ma**, Tanbin Rahman, Li Zhu, Xiangrui Zeng, Jingyi J. Li and George C. Tseng. (2019+). 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.
6. Tanbin Rahman\*, **Tianzhou Ma**\* and George C. Tseng. (2019+). Penalized likelihood approach for the clustering of RNA-seq count data. To be submitted. (\*co-first author).
7. Lin C, Chang L, **Tianzhou Ma**, Oh, H, Lewis D, Tseng GC and Sibille E. (2019+). Genetic Modulation of Brain Molecular Aging. To be submitted.

## 2018

8. **Tianzhou Ma**, Zhao Ren and George C. Tseng. (2018). Variable screening with multiple studies. *Statistica Sinica*. Accepted.
9. Zhou Fang, **Tianzhou Ma**, Li Zhu, Qi Yan, Wei Chen, Gong Tang and George C. Tseng. (2018). A Bayesian Model for Integrating High-Throughput Multi-Omics Data with Missingness Handling. *Bioinformatics*. Accepted.
10. **Tianzhou Ma**\*, Zhiguang Huo\*, Anche Kuo\*, Li Zhu, Zhou Fang, Xiangrui Zeng, Chien-Wei Lin, Silvia Liu, Lin Wang, Peng Liu, Tanbin Rahman, Lun-Ching Chang, Sunghwan Kim, Jia Li, Yongseok Park, Chi Song and George C. Tseng. (2018). MetaOmics - Comprehensive Analysis Pipeline and Web-based Software Suite for Transcriptomic Meta-Analysis. *Bioinformatics*. Accepted. (\*co-first author).
11. Xiangrui Zeng, Zhou Fang, **Tianzhou Ma**, Chien-wei Lin and George C. Tseng. (2018). Comparative Pathway Integrator: a framework of meta-analytic integration of multiple transcriptomic studies for consensual and differential pathway analysis. *bioRxiv*, 444604. pdf
12. Grabosch S, Bulatovic M, Zeng F, **Ma T**, Zhang L, Ross M, Brozick J, Fang Y, Tseng G, Kim E, Gambotto A, Elishaev E, Edwards R and Vlad, A. Cisplatin-induced immune modulation in ovarian cancer mouse models with distinct inflammation profiles. *Oncogene*: 1.
13. Andersen CL, Boisen MM, Sikora MJ, **Ma T**, Tseng G, Suryawanshi S, Vlad AM, Elishaev E, 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.
14. Luo J, Liu S, Tao J, Ren B, Chen Z, Li F, Nalesnik M, **Ma T**, Cieply K, Cheng S, Chen Q, Michalopoulos GK, Nelson JB, Hamilton R, Bhargava R, Pennathur A, Luketich JD, Monga SP, Tseng G and Yu Y. (2018). Oncogenic Gene Fusion and Chromosome Rearrangement of *Pten-NOLC1* in Human Cancers. Submitted to *Science*.

## 2017

15. **Tianzhou Ma**, Faming Liang and George C. Tseng. (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)
16. **Tianzhou Ma**, Faming Liang, Steffi Oesterreich and George C. Tseng. (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)
17. **Tianzhou Ma**, Chi Song and George C. Tseng. (2017). Discussant paper on "Statistical contributions to bioinformatics: Design, modelling, structure learning and integration". *Statistical Modelling*, 17(4-5): 305-315.

18. Scifo E, Pabba M, Kapadia F, **Tianzhou Ma**, Lewis DA, Tseng GC and Sibille E. (2017). Sustained molecular pathology across episodes and remission in depression. *Biological Psychiatry*, 83(1): 81-89.
19. Andersen CL, Sikora MJ, Boisen MM, **Ma T**, Christie A, Tseng G, Park Y, Luthra S, Chandran U, Haluska P, Mantia-Smaldone GM, Odunsi K, McLean K, Lee AV, Elishaev E, 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.
20. Linkov F, Goughnoura SL, **Ma T**, Xu Z, Edwards RP, Lokshin AE, Ramanathan RC, Hamad GG, McCloskey C and Bovbjerg DH. (2017). Changes in inflammatory endometrial cancer-associated biomarkers in individuals undergoing surgical weight loss. *Gynecologic Oncology*. Accepted. PMID: 28797697.
21. French L, **Tianzhou Ma**, 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.
22. 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.
23. Grabosch S, Tseng G, Edwards RP, Lankes HA, Moore K, Odunsi K, Vlad A, **Ma T**, Strange M, Brozick J, Lugade A, Omilian A, Bshara W, Stuckey AR, 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

24. Silvia Liu, Wei-Hsiang Tsai, Ying Ding, Rui Chen, Zhou Fang, Zhiguang Huo, SungHwan Kim, **Tianzhou Ma**, Ting-Yu Chang, Nolan Michael Priedigkeit, Adrian V. Lee, Jianhua Luo, Hsei-Wei Wang, I-Fang Chung, George C. Tseng. (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.
25. Zhang L, **Ma T**, Brozick J, Babalola K, Budiu R, 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.
26. 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))
27. Sanei-Moghaddam A, **Ma T**, Goughnour SL, Edwards RP, Louder PJ, Ismail N, Comerci JT, 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

28. Mony JT, Zhang L, **Ma T**, Grabosch S, Tirodkar TS, Brozick J, Tseng G, Elishaev E, Edwards RP, 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.
29. Liao S, Hartmaier RJ, McGuire KP, Puhalla SL, Luthra S, Chandran UR, **Ma T**, Bhargava R, Davidson NE, Benz S, Lee AV, 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)
30. Suryawanshi S, Huang X, Elishaev E, Budiu RA, Zhang L, Kim S, Donnellan N, Mantia-Smaldone G, **Ma T**, Tseng G, Lee T, Mansuria S, 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.
31. Lin Hou\*, **Tianzhou Ma**\* and Hongyu Zhao. (2014). Incorporating functional annotation information in prioritizing disease associated SNPs from genome wide association studies. *Science China Life Sciences*, 57(11), 1072-1079. (\*co-first author)

## Book

32. George C. Tseng, Zhiguang Huo and **Tianzhou Ma**. Foundations for High-Throughput Omics Data Analysis: Methods, Theories and Applications. *Chapman & Hall/CRC*. In preparation and expected in 2018.

## AWARDS

### Student Awards

- Delta Omega Honorary Society in Public Health Apr 2018
  - Delta Omega Membership
- ASA Section on Bayesian Statistical Science (SBSS) Aug 2017
  - Student Paper Award
- American Statistics Association (ASA) Pittsburgh chapter Apr 2017
  - Student of the Year
- Dahshu Data Science Symposium: Computational Precision Health 2017 Feb 2017
  - Best Paper Award
- Department of Biostatistics, University of Pittsburgh
  - Best Student Presentation Award Apr 2017
  - Outstanding Graduate Student Researcher Award Apr 2016
- Graduate School of Public Health, University of Pittsburgh Apr 2015
  - Dean's Day Poster Competition Award
- Faculty of Arts and Science, University of Toronto
  - Three consecutive years on Dean's list 2008-2010
- University College, University of Toronto
  - Three consecutive years' recipient of University College Scholarship 2008-2010

### Travel Awards

- SAMSI, Research Triangle Park, NC.
  - Travel Award to attend "Optimization Opening Workshop" Aug 2016

## TEACHING EXPERIENCE

- **Lecturer, University of Maryland**
  - EPIB661: Applied Multivariate Data Analysis Spring 2019
  - EPIB662: Missing Data Analysis Fall 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; 23 students) Fall 2016
  - BIOST2094: Statistical Computing in R (21 students) 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 ADVISING

---

- PhD dissertation committee:
  - Alli Hanley 2019-Now
- MPH thesis committee:
  - Samantha Ammons 2018-Now
  - Angie Barrall 2018-Now
- Academic advisor:
  - Zhenyao Ye 2018-Now
  - Manyun Zhao 2018-Now

## RESEARCH SUPPORT

---

- **“Contagious Phenotypes of Acute Respiratory Infection: Identification, Characterization, and Biomarkers”, funded by US Defense Advanced Research Projects Agency**
  - 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.** 2019 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.
- 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?

---

## DEPARTMENTAL SERVICE

- EPIB Graduate Student Recruitment/Admissions Committee
- Department Liason to the University Library System

---

## PROFESSIONAL SERVICE

### Journal Referee

- *Annals of Applied Statistics*
- *Computational Statistics and Data Analysis*
- *American Statistician*
- *Journal of Biopharmaceutical Statistics*
- *Neural Computation*

- *PLOS One, PLOS Computational Biology*
- *Genome Medicine*
- *BMC Bioinformatics*

### 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 JSM.
- 2014-2017, 2019 ENAR Spring meeting.
- 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
- 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 basketball and soccer.