
TIANZHOU (CHARLES) MA

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

(301)-405-6421 ✦ tma0929@umd.edu

<https://matianzhou.github.io/>

EDUCATION

University of Pittsburgh,

Pittsburgh, PA, US

- Ph.D. in Biostatistics, *April 2018*
 - GPA: *3.98/4.00*
 - 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*
 - GPA: *Honors*
 - 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*
 - GPA: *3.93/4.00*
 - *with High Distinction (Summa Cum Laude)*

RESEARCH INTEREST

My research interest lies in the intersection between statistical methodology and its applications to multi-omics (e.g. genotyping, gene expression, epigenomics, proteomics, etc.) and bioinformatics. In particular, I am interested in omics data integration and meta-analysis, Bayesian modeling, high-dimensional variable selection, general statistical learning, and software development for general bioinformatic problems. In addition to methodology development, I have also collaborated with researchers in the cancer field (e.g. breast cancer and ovarian cancer), psychiatry and epidemiology for data analysis and motivation of new methodology.

PROFESSIONAL EXPERIENCE

- **Assistant Professor**

Aug 2018 ~ Now

- Department of Epidemiology and Biostatistics, University of Maryland College Park

PUBLICATIONS

2018

1. **Tianzhou Ma**, Zhao Ren and George C. Tseng. (2018). Variable screening with multiple studies. *Statistica Sinica*. Accepted.
2. 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.

⁰Last modified: October 25, 2018

3. **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).
4. 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*. Accepted.
5. Li Zhu, Zhiguang Huo, **Tianzhou Ma**, George Tseng. (2018). Bayesian indicator variable selection model with multi-layer overlapping groups. Under revision in *Annals of Applied Statistics*. (a preliminary version won the ENAR distinguished student paper award).
6. Zhiguang Huo, Li Zhu, **Tianzhou Ma**, Hongcheng Liu, Song Han, Daiqing Liao, Jinying Zhao and George Tseng. (2018). Two-way Horizontal and Vertical Omics Integration for Disease Subtype Discovery. Under revision in *Statistics in Biosciences*.
7. 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. Submitted to *Cancer*.
8. 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

9. **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)
10. **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)
11. **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.
12. 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.
13. 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.
14. 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.
15. 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.
16. 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.
17. 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

18. 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.
19. 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.
20. 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))
21. Sanei-Moghaddam A, **Ma T**, Goughnour SL, Edwards RP, Lounder 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

22. 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.
23. 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)
24. 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.
25. 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)

Ready to submit, In preparation

26. **Tianzhou Ma**, Tanbin Rahman, Li Zhu, Xiangrui Zeng, Jingyi J. Li and George C. Tseng. (2018). Poorly mimic or greatly mimic? A model-based evaluation with functional characterization for comparison of differential transcriptomic systems across model organisms or across species. Ready to submit.
27. Zhou Fang, Chien-wei Lin, Xiangrui Zeng, **Tianzhou Ma**, George C. Tseng. (2018). Comparative Pathway Integrator: a framework of meta-analytic integration of multiple transcriptomic studies for consensual and differential pathway analysis. Ready to submit.
28. Tanbin Rahman*, **Tianzhou Ma*** and George C. Tseng. (2018). Penalized likelihood approach for the clustering of RNA-seq count data. Ready to submit. (*co-first author).
29. Lin C, Chang L, **Tianzhou Ma**, Oh, H, Lewis D, Tseng GC and Sibille E. (2018). Genetic Modulation of Brain Molecular Aging. In preparation.
30. Seney M, French B, **Ma T**, Tseng G, Sibille E and Lotrich F. (2018). Interferon-alpha can

worsen anhedonic behavior, with correlated changes in transcripts related to mTOR signaling. In preparation.

Book

31. 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 2008-2010
 - Three consecutive years' recipient of University College Scholarship

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

PRESENTATIONS

Talks

- 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.
- The 5th Annual Women's Cancer Research Center (WCRC) Retreat, Nemaquin Woodlands Resort, 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?

PROFESSIONAL SERVICE

Referee of Journals

- *American Statistician, Journal of Biopharmaceutical Statistics, Neural Computation, Computational Statistics and Data Analysis, PLOS One, PLOS Computational Biology, Annals of Applied Statistics, Genome Medicine, BMC Bioinformatics*

Service to the Profession

- 2016-2018, American Statistical Association Pittsburgh Chapter Student Representative

CONFERENCES AND WORKSHOPS

- 2016-2017 JSM.
- 2014-2017 ENAR Spring meeting.
- 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.