

CURRICULUM VITAE

Jing Ma, Ph.D.

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PERSONAL DATA

Place of Birth	Henan, China
Work Address	Fred Hutchinson Cancer Research Center Division of Public Health Sciences 1100 Fairview Ave. N PO Box 19024 - M2-B500 Seattle, WA 98109-1024
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EDUCATION

2006-2010	Fudan University, Shanghai, China, B.S., Mathematics with University Distinction (Highest)
2010-2015	University of Michigan, Ann Arbor, MI, Ph.D., Statistics Advisor: Prof. George Michailidis

POSTGRADUATE TRAINING

2015-2017	Postdoctoral Research Fellow, Department of Biostatistics and Epidemiology & Department of Statistics, University of Pennsylvania. (08/15 - 07/17)
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FACULTY POSITIONS

2017-	Assistant Professor of Biostatistics, Division of Public Health Sciences, Fred Hutchinson Cancer Research Center.
2019-	Affiliated Assistant Professor, Department of Biostatistics, University of Washington.
2019-2020	Assistant Professor, Department of Statistics, Texas A&M University.

AWARDS, HONORS AND SCHOLARSHIPS

A. National Awards

2008	National Merit Scholarship from Ministry of Education of China
2015	Travel Award, National Science Foundation
2018	Travel Award, Data Science Innovation Lab
2018	Travel Award, The Jayne Koskinas Ted Giovanis Foundation for Health and Policy

B. Department/University Awards

2010	College Graduate Excellence Award of Shanghai
2011	Outstanding First Year Ph.D. Student Award
2011-2012	Rackham International Students Fellowship
2012-2013	Outstanding Graduate Student Instructor Award
2012-2015	Rackham School of Graduate Studies Conference Travel Grant

PROFESSIONAL ACTIVITIES

A. Invited Session Organized

2021	ENAR, Baltimore, MD.
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B. Session Chair

2012	<i>Methods for Variable and Model Selection – Contributed Papers</i> , Joint Statistical Meetings, San Diego, CA.
2016	<i>Efficient Methods for Structured Large Genomics Data – Contributed Papers</i> , Joint Statistical Meetings, Chicago, IL.
2017	<i>Understanding the Microbiome Complexity: Genetics and Networks – Invited Papers</i> , ICSA Applied Statistics Symposium, Chicago, IL.
2019	<i>Methodological Innovation in Large-scale Genomics Data Analysis – Invited Session</i> , ICSA China Conference, Tianjin, China.

C. Referee Service

Referee for Bioinformatics, Biometrika, Biometrical Journal, Biometrics, Biostatistics, Electronic Journal of Statistics, Frontiers in Genetics, IEEE Access, Journal of the American Statistical Association - Theory & Methodology, Journal of Machine Learning Research, Journal of Multivariate Analysis, Molecular & Cellular Proteomics, Optimization and Engineering, Scientific Reports (Nature), Statistics in Biosciences, Wiley Interdisciplinary Reviews: Computational Statistics

D. Conference Review

2016	Reviewer for International Conference on Information Systems
2016	Reviewer for Conference on Neural Information Processing Systems (NIPS)
2018	Judge for ASA Section on Genomics and Genetics Student Paper Competition
2018	Reviewer for Conference on Neural Information Processing Systems (NIPS)
2019	Judge for ASA Section on Genomics and Genetics Student Paper Competition
2020	Judge for ASA Section on Genomics and Genetics Student Paper Competition

E. Professional Organizations

2010-	American Statistical Association
2014-	International Chinese Statistical Association
2016-	Eastern North American Region International Biometric Society

TEACHING RESPONSIBILITIES

Instructor at the University of Michigan

- STAT250: Introduction to Statistics and Data Analysis (Lab Instructor). Fall 2010 & Winter 2011

- Applied Qualifying Exam. Summer 2012, 2013 & 2014
- Review of Linear Algebra. Summer 2013 & 2014

Graduate Student Instructor at the University of Michigan

- English Language Institute. Summer 2011
- STAT600: Applied Statistics and Data Analysis. Fall 2011 & 2012
 - GSI Excellence in Teaching Award
- STAT425: Introduction to Probability and Statistics. Fall 2011 & Winter 2012
- STAT601: Multivariate and Categorical Data Analysis. Winter 2012

Instructor at Texas A&M University

- STAT312: Statistics for Biology. Fall 2019

A. Postdoctoral Fellows

2018-2020 Yue Wang, PhD in Biostatistics, UNC Chapel Hill (joint with A. Shojaie).
First position: Assistant Professor of Statistics at Arizona State University.

B. Graduate Students

C. Student Collaborator

2017-2018 Nanxun Ma, UW Biostatistics PhD student, working with M. C. Wu.
2017- Kun Yue, UW Biostatistics PhD student, working with A. Shojaie.
2018- Michael Hellstern, UW Statistics MS student, working with A. Shojaie.

D. MS and PhD Committees in Non-Chair Role

2018-2019 Arjun Sondhi, UW Biostatistics PhD student (advisor: A. Shojaie).
2019-2020 Junsouk Choi, Texas A&M Statistics PhD student (advisor: N. Yang).
2020- Christi Thompson, Texas A&M Statistics PhD student (advisor: R. Carroll).

EDITORIAL RESPONSIBILITIES

None.

SPECIAL NATIONAL RESPONSIBILITIES

None.

SPECIAL LOCAL RESPONSIBILITIES

A. University of Michigan

2011-2012 Coordinator of Reading Group on Statistical Modeling and Analysis of Networks, Department of Statistics.
2011-2013 Co-Chair, Graduate Student Statistical Topics Seminar Series, Department of Statistics.
2012-2013 Student committee member of the Seventh Michigan Student Symposium for Interdisciplinary Statistical Sciences (MSSISS).

B. Fred Hutchinson Cancer Research Center

2018	Organizing committee member of the 2018 Fred Hutch Microbiome Symposium.
2018	Faculty host for University of Washington prospective student visit in March.
2019	Chair, Biostatistics Seminar Series.

C. Texas A&M University

2019-2020	Chair of grants writing committee.
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RESEARCH FUNDING

A. Current

2018-2022	NIH R01 Award Title: Joint Analysis of Microbiome and Other Genomic Data Types FTE: 15% Role: Co-Investigator (PI: M. C. Wu)
2018-2023	NIH U19 Award Title: The Dog Aging Project: The Genetic and Environmental Determinants of Healthy Aging in Companion Dogs FTE: 15% Role: Co-Investigator (PI: D. Promislow)

B. Pending

2021-2025	NIH R01 Award Title: Robust and Efficient Statistical Methods for Microbiome Research Role: Principal-Investigator
2020-2024	NIH R01 Award Title: Novel Statistical Inference for Biomedical Big Data FTE: 15% Role: Co-Investigator (PI: A. Shojaie)

C. Completed

2017-2018	NIH R21 Award Title: DMPA Use and Vaginal Bacterial Diversity among African Women FTE: 4% Role: Co-Investigator (PI: A. Roxby; Sub: D. Fredricks)
2018-2019	NIH R01 Award Title: The Impact of Prenatal Exposure to Persistent Organic Pollutants on Kinetics of Immune Response to Vaccines and Seroprotection in Infants FTE: 10% Role: Co-Investigator (PI: P. Bhatti)

BIBLIOGRAPHY

[* indicates alphabetical ordering authorship.]
 [† indicates corresponding author.]
 [Name underlined indicates student or postdoc mentored.]

A. Publications in Peer-Refereed Journals

1. **Ma, J**, Shojaie, A and Michailidis, G. Network-based pathway enrichment analysis with incomplete network information. *Bioinformatics* 32(20):3165–3174, 2016.
2. **Ma, J** and Michailidis, G. Joint structural estimation of multiple graphical models. *Journal of Machine Learning Research* 17:1–48, 2016.
3. von Rundstedt, F, Kimal, R, **Ma, J**, Arnold, J, Gohlke, J, Putluri, V, Krishnapuram, R, Piyaathna, D, Lotan, Y, Godde, D, Roth, S, Storkel, S, Levitt, J, Michailidis, G, Lerner, S, Coarfa, C, Sreekumar, A, Putluri, N. Integrated pathway analysis of a metabolic signature in bladder cancer - a linkage to The Cancer Genome Atlas project and prediction of survival. *Journal of Urology* 195(6):1911–1919, 2016.
4. *Cai, TT, **Ma, J** and Zhang, L. CHIME: clustering of high-dimensional Gaussian mixtures with EM algorithm and its optimality. *Annals of Statistics*. 47(3):1234–1267, 2019.
 - L. Zhang was a recipient of ASA Biopharmaceutical Section Student Paper Award at the 2017 ICSA Applied Statistics Symposium.
5. *Cai TT, Li H, **Ma J**[†], and Xia Y. Differential Markov random field analysis with applications to detecting differential microbial community networks. *Biometrika* 106(2):401–416, 2019.
6. **Ma J**, Karnovsky A, Afshinnia F, Wigginton J, Feldman H, Rader D, Shama K, Porter A, Rahman M, He J, Hamm L, Shafi T, Pennathur S, Michailidis G. Differential network-based enrichment analysis of lipid pathways altered in Chronic Kidney Disease progression. *Bioinformatics*, 35(18):3441–3452, 2019.
7. Vantaku V, Putluri V, Bader D, Maity S, **Ma J**, . . . , Sreekumar A and Putluri N. Epigenetic loss of AOX1 expression via EZH2 leads to metabolic deregulation in bladder cancer. *Oncogene*, 2019.
8. **Ma J**[†], Shojai A and Michailidis G. A comparative study of topology-based pathway enrichment analysis methods. *BMC Bioinformatics*, 20 (546). 2019
9. Wang Y, Randolph T, Shojai A and **Ma J**[†]. The generalized matrix decomposition biplot and its application to the microbiome data. *mSystems*, 4:e00504-19. 2019
 - Selected as **Editor's pick**.

B. Book Chapters

1. Li, H and **Ma, J** Graphical models in genetics, genomics and metagenomics. In *Handbook of Graphical Models*. Editors: Mathias Drton, Steffen Lauritzen, Marloes Maathuis, Martin Wainwright. Chapman & Hall / CRC, 2018.

C. Other Refereed Scholarly Publications

1. **Ma, J**. Estimation and Inference in High-Dimensional Gaussian Graphical Models with Structural Constraints. University of Michigan. 2015. [PhD Thesis]

D. Manuscripts Submitted/Under Revision

1. **Ma J**. Joint microbial and metabolite network estimation with the censored Gaussian graphical model. Under Revision.
2. Wang Y, Shojai A, Randolph T and **Ma J**. Generalized matrix decomposition regression: estimation and inference for two-way structured data. Under Revision.
3. Yue, K, **Ma, J**, Thornton, T and Shojai, A. REHE: fast variance components estimation for linear mixed models. Under Revision.
4. Hellstern, M, **Ma, J** and Shojai, A. NetGSA: an improved R package for fast computation and visualization of topology-based pathway enrichment analysis.

ORAL PRESENTATIONS

A. Invited Talks at Conferences and Symposia

1. ICSA/KISS Joint Applied Statistics Symposium, Portland, OR; *Pathway enrichment analysis with incomplete network information*. (06/14)
2. ICSA Applied Statistics Symposium, Atlanta, GA; *A zero-inflated Poisson model for abundance quantification from shotgun metagenomic data*. (06/16)
3. ICSA Applied Statistics Symposium, Chicago, IL; *A testing framework for detecting differential microbial communities*. (06/17)
4. Fred Hutch Microbiome Symposium, Seattle, WA; *Inferring differential microbial interactions from co-occurrence data using Markov networks*. (03/18)
5. Data Science Innovation Lab: Mathematical Challenges of Single Cell Dynamics, Bend, OR; *Understanding therapeutic failures through 4D single-cell analysis of metabolic heterogeneity*. (06/18)
6. 12th International Vilnius Conference on Probability Theory and Mathematical Statistics / 2018 IMS Annual Meeting on Probability and Statistics, Vilnius, Lithuania; *Mixed graphical models for joint analysis of microbiome and metabolomic data*. (07/18)
7. Joint Statistical Meetings, Vancouver, Canada; *id.* (07/18)
8. CMStatistics Conference, Pisa, Italy; *Sparse clustering of Gaussian mixtures*. (12/18)
9. The Role of Genomics and Metagenomics in Human Health: Recent Developments in Statistical and Computational Methods, Banff, Canada; *Variance components estimation in linear mixed models*. (02/19)
10. ICSA China Conference, Tianjin, China; *A framework for multi-view analysis of microbiome data*. (07/19)
11. University of Michigan 50th Anniversary Symposium, Ann Arbor, US; *Graphical models and differential networks for microbiome data*. (09/19)
12. CMStatistics Conference, London, UK; *Generalized matrix decomposition: From exploratory analysis to high-dimensional inference*. (12/19)
13. (Cancelled) Conference on Statistical Learning and Data Science, University of California, Irvine, US. (05/20)
14. (Online) Joint Statistical Meetings, Philadelphia, PA; *Fast estimation of change points in regime switching Gaussian graphical models*. (08/20)
15. CMStatistics Conference, London, UK; (12/20)

B. Invited Seminars and Colloquia

15. Department of Mathematics and Statistics, Lancaster University, Lancaster, UK; *Differential network biology*. (10/16)
16. Student Lunch Seminar, Department of Statistics, University of Pennsylvania; *Statistical methods for microbiome data*. (10/16)
17. Department of Statistics, University of Warwick, Coventry, UK; *Differential network biology: testing differences in microbial networks*. (01/17)
18. Li Lab, Department of Biostatistics, University of Pennsylvania; *id.* (02/17)
19. Biostatistics Program, Public Health Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA; *id.* (02/17)

20. Department of Biostatistics, University of Washington, Seattle, WA; *id.* (01/18)
21. Department of Statistics, University of Florida, Gainesville, FL; *id.* (01/18)
22. Biostatistics/ATME Joint Seminar, Public Health Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA; *Network-based enrichment analysis.* (01/18)
23. SLAB Lab Seminar, Department of Biostatistics, University of Washington, Seattle, WA; *Statistical machine learning methods in genetics and genomics.* (02/18)
24. Postdoc Meeting, Public Health Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA; *Statistical methods for microbiome data.* (02/18)
25. Translational Research Program Faculty Meeting, Public Health Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA; *Differential network biology.* (02/18)
26. Department of Statistics, Texas A&M University, College Station, TX; *Differential network biology: testing differences in microbial networks.* (11/18)
27. DAP Science Seminar Series, Texas A&M University, College Station, TX; *Statistical considerations in the Dog Aging Project.* (12/19)

PUBLICLY AVAILABLE SOFTWARE

- **netgsa**: R package for network-based pathway enrichment analysis.
 - Stable release on [CRAN](#).
 - Development version on [GitHub](#).
- **CHIME**: Matlab code for clustering high-dimensional Gaussian mixtures with the EM algorithm. On [GitHub](#).
- **TestBMN**: R package for testing high-dimensional binary Markov networks. On [GitHub](#).
- **GMDcomp**: R package for generalized matrix decomposition (GMD) and GMD-biplots. On [GitHub](#).
- **metaMint**: R package for joint estimation of metabolite and microbial interaction networks.
 - Development version on [GitHub](#).