

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.
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FACULTY POSITIONS

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

RESEARCH FUNDING

A. Current projects as Principal Investigator

2021-2022	Fred Hutch Pathogen-Associated Malignancies Integrated Research Center / Microbiome Research Pilot Award Title: Statistical Methods for Network-based Analysis of the Colorectal Cancer Microbiome
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B. Current projects as Co-Investigator

- 2018-2022 NIH R01 Award (PI: M. C. Wu)
Title: Joint Analysis of Microbiome and Other Genomic Data Types
- 2018-2023 NIH U19 Award (PI: D. Promislow)
Title: The Dog Aging Project: The Genetic and Environmental Determinants of Healthy Aging in Companion Dogs
- 2020-2024 NIH R01 Award (PI: A. Shojaie)
Title: Novel Statistical Inference for Biomedical Big Data

C. Pending

- 2022-2027 NIH R01 Award
Title: Statistical Methods for Network-based Integrative Analysis of Microbiome Data
Role: Principal-Investigator

D. Completed

- 2017-2018 NIH R21 Award
Title: DMPA Use and Vaginal Bacterial Diversity among African Women
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
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, Piyaathana, 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**[†], Shojaie A and Michailidis G. A comparative study of topology-based pathway enrichment analysis methods. *BMC Bioinformatics*. 20 (546). 2019
9. Wang Y, Randolph T, Shojaie 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**.

10. **Ma J**. Joint microbial and metabolite network estimation with the censored Gaussian graphical model. *Statistics in Biosciences*. 13:351–372, 2021.
11. Hellstern, M, **Ma, J**, Yue, K and Shojaie, A. netgsa: Fast computation and interactive visualization for topology-based pathway enrichment analysis. *PLoS Computational Biology*. To appear, 2021

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.
2. **Ma, J**, Yue, K and Shojaie, A. Networks for compositional data. In *Statistical Analysis of Microbiome Data*. Editors: Subharup Guha, Somnath Datta. Springer, 2020

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. Preprints

1. Yue, K, **Ma, J**, Thornton, T and Shojaie, A. REHE: fast variance components estimation for linear mixed models. *Submitted to Genetic Epidemiology*. <https://www.biorxiv.org/content/10.1101/2021.02.03.429643v1>
2. Wang Y, Shojaie A, Randolph T and **Ma J**. Generalized matrix decomposition regression: estimation and inference for two-way structured data. *Submitted to Journal of the Royal Statistical Society, Series B (Statistical Methodology)*. <https://arxiv.org/abs/2104.08408>

ORAL PRESENTATIONS

A. Invited Talks at Conferences and Symposia

- 06/14 International Chinese Statistical Association/Korean International Statistical Society Joint Applied Statistics Symposium, Portland, OR
Title: "Pathway enrichment analysis with incomplete network information."
- 06/16 International Chinese Statistical Association Applied Statistics Symposium, Atlanta, GA
Title: "A zero-inflated Poisson model for abundance quantification from metagenomic data."
- 06/17 International Chinese Statistical Association Applied Statistics Symposium, Chicago, IL
Title: "Differential network biology: testing differences in microbial networks."

- 03/18 Fred Hutch Microbiome Symposium, Seattle, WA
Title: "Inferring differential microbial interactions from co-occurrence data using Markov networks."
- 06/18 Data Science Innovation Lab: Mathematical Challenges of Single Cell Dynamics, Bend, OR
Title: "Understanding therapeutic failures through 4D single-cell analysis of metabolic heterogeneity."
- 07/18 The 12th International Vilnius Conference on Probability Theory and Mathematical Statistics / 2018 IMS Annual Meeting on Probability and Statistics, Vilnius, Lithuania
Title: "Mixed graphical models for joint analysis of microbiome and metabolomic data."
- 07/18 Joint Statistical Meetings, Vancouver, Canada; id.
- 12/18 The 11th International Conference of the ERCIM WG on Computational and Methodological Statistics, Pisa, Italy
Title: "Sparse clustering of Gaussian mixtures."
- 02/19 The Role of Genomics and Metagenomics in Human Health: Recent Developments in Statistical and Computational Methods, Banff, Canada
Title: "Variance components estimation in linear mixed models."
- 07/19 International Chinese Statistical Association Conference, Tianjin, China
Title: "A framework for multi-view analysis of microbiome data."
- 12/19 The 12th International Conference of the ERCIM WG on Computational and Methodological Statistics, London, UK
Title: "Generalized matrix decomposition: From exploratory analysis to high-dimensional inference."
- 08/20 Joint Statistical Meetings, Philadelphia, PA (Virtual)
Title: "Fast estimation of change points in regime switching Gaussian graphical models."
- 07/21 International Chinese Statistical Association Conference, Xi'an, China; (rescheduled to 07/22)

B. Invited Seminars and Colloquia

- 10/16 Department of Mathematics and Statistics, Lancaster University, Lancaster, UK
Title: "Differential network biology: testing differences in microbial networks."
- 01/17 Department of Statistics, University of Warwick, Coventry, UK; id.
- 02/17 Biostatistics Program, Public Health Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA; id.
- 01/18 Department of Biostatistics, University of Washington, Seattle, WA; id.
- 01/18 Department of Statistics, University of Florida, Gainesville, FL
Title: "Graphical models and differential networks for microbiome data."
- 01/18 Biostatistics/ATME Joint Seminar, Public Health Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA
Title: "Network-based enrichment analysis."
- 02/18 Statistical Learning Applied to Biology Lab Seminar, Department of Biostatistics, University of Washington, Seattle, WA
Title: "Statistical machine learning methods in genetics and genomics."
- 02/18 Translational Research Program, Public Health Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA
Title: "Differential network biology."
- 11/18 Department of Statistics, Texas A&M University, College Station, TX
Title: "Graphical models and differential networks for microbiome data."

- 09/19 University of Michigan 50th Anniversary Symposium, Ann Arbor, US
Title: "Graphical models and differential networks for microbiome data."
- 12/19 (Virtual) The Dog Aging Project Science Seminar Series, Texas A&M University, College Station, TX
Title: "Statistical considerations in the Dog Aging Project."
- 10/20 (Virtual) Hanash Lab Meeting, The University of Texas MD Anderson Cancer Center
Title: "Machine learning tools for omics data analysis."
- 01/21 (Virtual) Gut Origins of Latino Diabetes (GOLD) Monthly Meeting, Albert Einstein College of Medicine, New York, NY
Title: "Statistical methods for microbiome data analysis."
- 03/21 (Virtual) Translational Data Science Seminar Series, Fred Hutchinson Cancer Research Center, Seattle, WA
Title: "Systems biology approaches for microbiome data analysis."
- 11/21 Biostatistics Seminar Series, Fred Hutchinson Cancer Research Center, Seattle, WA
Title: TBD.
- 11/21 ASA Section of Statistics in Genomics and Genetics (SSGG) Webinars
Title: TBD.

AWARDS, HONORS AND SCHOLARSHIPS

A. National Awards

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| 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

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| 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

B. Session Chair

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| 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 Annals of Applied Statistics, Bioinformatics, Biometrika, Biometrical Journal, Biometrics, Biostatistics, Electronic Journal of Statistics, Frontiers in Genetics, IEEE Access, Journal of Computational Biology, Journal of the American Statistical Association – Applications & Case Studies, Journal of the American Statistical Association – Theory & Methodology, Journal of Machine Learning Research, Journal of Multivariate Analysis, Molecular & Cellular Proteomics, Optimization and Engineering, PLoS Computational Biology, Scientific Reports (Nature), Statistics in Biosciences, Statistics in Medicine, 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. Grant Review

2020	FHCRC Translational Data Science Integrated Research Center Pilot Grant
2020	UW ITHS Research Innovation Award
2020	FHCRC Division of Public Health Sciences Bid & Proposal Projects
2021	FHCRC Translational Data Science Integrated Research Center Pilot Grant

F. Professional Organizations

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

TEACHING RESPONSIBILITIES

A. 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

B. 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

C. Instructor at Texas A&M University

- STAT312: Statistics for Biology. Fall 2019

ADVISING AND MENTORING

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.
2021 - Ilias Moysadis, PhD in Statistics, Pennsylvania State University.

B. Graduate Students

- 2021- Zifan Yu, UW Biostatistics MS Capstone student.
2021- Anh-Minh Nguyen, UW Biostatistics MS Capstone student.

C. Student Collaborator

- 2017-2018 Nanxun Ma, UW Biostatistics PhD student, working with M. C. Wu.
2017-2020 Kun Yue, UW Biostatistics PhD student, working with A. Shojaie.
2018-2020 Michael Hellstern, UW Statistics MS student, working with A. Shojaie.
2021- Lakshin Kumar, UW Biochemistry undergraduate student, working with D. Promislow.

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- Elizabeth Thompson, Texas A&M Statistics PhD student (advisor: R. Carroll).

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 UW Biostatistics Prospective PhD Student Visit Days.
2019 Chair, Biostatistics Seminar Series.
2021 Faculty host for UW Biostatistics Prospective PhD Student Visit Days.

C. Texas A&M University

- 2019-2020 Chair of grants writing committee.

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](#).
- **DNEA**: R code for differential network-based enrichment analysis. 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. On [GitHub](#).
- **TestBMN**: R package for testing high-dimensional binary Markov networks. On [GitHub](#).