

CURRICULUM VITAE

Revised: 09/15/2023

1. **Name:** JINGJING YANG, Ph.D.

2. **Office Address:**

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4. **Current Titles and Affiliations:**

a. Academic Appointments:

i. Primary Appointment:

Assistant Professor, Center for Computational and Quantitative Genetics, Department of Human Genetics, Emory University School of Medicine, 2017 – 2023

Associate Professor, Center for Computational and Quantitative Genetics, Department of Human Genetics, Emory University School of Medicine, 2023 – Present

ii. Secondary Appointment:

Assistant Professor, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2019 – 2023

Associate Professor, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2023 – Present

5. **Education:**

B.S., Computational Mathematics, Jilin University, Jilin Province, China, 2003 – 2007

M.S., Statistics, Clemson University, Clemson, SC, USA, 2008 – 2009

Ph.D., Statistics, Rice University, Houston, TX, USA, 2009 – 2014

6. **Postgraduate Training:**

- a. Postdoctoral Fellow, Center for Statistical Genetics, Department of Biostatistics, University of Michigan School of Public Health, Ann Arbor, Michigan, USA. Advisors: Drs. Gonçalo Abecasis and Xiang Zhou, 2014 – 2017

7. **Continuing Professional Development Activities:**

- a. Completed Mentor Training, implemented by the Emory Chapter of the Atlanta Society of Mentors (ASOM). Certificate attached at the end. Fall 2019.

- b. Completed Junior Faculty Development Courses (JFDC), provided by Emory University School of Medicine, Spring 2022.

8. Committee Memberships:

a. National and International:

- i. Member, Program Committee of American Society of Human Genetics. 2023 – Present

b. Institutional:

- i. Member, Seminar Committee of the Department of Human Genetics, 2018 – 2021
- ii. Member, Written Qualify Exam Committee of Genetics and Molecular Biology (GMB) program, Graduate Division of Biological and Biomedical Sciences (GDBBS), 2020 – 2021
- iii. Member, Education Committee of the Department of Human Genetics, 2021 – Present
- iv. Member, PhD Student Recruitment Committee of GMB, 2021 – Present
- v. Member, Faculty Recruitment Committee of the Department of Human Genetics, 2022 – Present
- vi. Chair, Seminar Committee of the Department of Human Genetics, 2022 – Present
- vii. Member, Faculty Development Advisory Committee (FDAC), School of Medicine, 2022 – Present

9. Peer Review Activities:

a. Grants:

i. National and International:

1. Life Science – Genetics, Bioinformatics and Computational Biology: Genetic Diseases, US-Israel Binational Science Foundation (BSF), Israel, 2018
2. Methodology Research Panel, Medical Research Council (MRC), United Kingdom, 2019
3. Life Sciences and Bio-Medicine, Israel Ministry of Science & Technology, Israel, 2021
4. Genetics, Genomics & Proteomics Panel, Graduate Research Fellowships Program (GRFP), National Science foundation (NSF), USA, 2021
5. Mathematical Science Panel, Graduate Research Fellowships Program (GRFP), National Science foundation (NSF), USA, 2022 – Present
6. Innovative Programs to Enhance Research Training (IPERT) Special Emphasis Panel, NIH/NIGMS, USA, 2022

7. Maximizing Investigators' Research Award A (MRAA) Study Section, NIH/NIGMS, USA, 2022
 8. AGCD-1 K99/R00: Career Development Facilitating the Transition to Independence, NIH/NIA, USA, 2023 – Present
 9. Advancing Genomic Medicine Research R21/R01, NIH/NHGRI, USA, July 2023
- ii. Institutional:
1. Emory Synergy Proposal, Emory University, 2018, 2020
- b. Manuscripts:
- i. Annals of Applied Statistics, 2017 – Present
 - ii. American Journal of Human Genetics, 2017 – Present
 - iii. BioData Mining, 2017 – Present
 - iv. Bioinformatics, 2017 – Present
 - v. Biometrics, 2017 – Present
 - vi. Cell Genomics, 2017 – Present
 - vii. Computational Statistics and Data Analysis, 2017 – Present
 - viii. Computational Statistics, 2017 – Present
 - ix. Frontiers in Genetics, 2017 – Present
 - x. Genes, 2017 – Present
 - xi. Genetics in Medicine, 2017 – Present
 - xii. Genome Biology, 2017 – Present
 - xiii. Genetic Epidemiology, 2017 – Present
 - xiv. Genome Medicine, 2017 – Present
 - xv. International Journal of Statistics in Medical Research, 2017 – Present
 - xvi. Journal of Applied Statistics, 2017 – Present
 - xvii. Human Molecular Genetics, 2017 – Present
 - xviii. Human Genetics and Genomics Advances, 2017 – Present
 - xix. Nature Genetics, 2017 – Present
 - xx. Nature Communications, 2017 – Present
 - xxi. PLOS GENETICS, 2017 – Present
 - xxii. PLOS ONE, 2017 – Present
 - xxiii. PNAS, 2017 – Present
 - xxiv. Statistics in Medicine, 2017 – Present
 - xxv. Statistical Methods in Medical Research, 2017 – Present
 - xxvi. Translational Neurodegeneration, 2017 – Present
 - xxvii. Technometrics, 2017 – Present
 - xxviii. WIREs Computational Statistics, 2017 – Present
 - xxix. eBioMedicine, 2023 – Present
- c. Conference Abstracts:
- i. National and International:
 1. Pacific Symposium on Biocomputing, Big Island of Hawaii, January 2019
 2. American Society of Human Genetics (ASHG) Annual Meeting, Virtual due to COVID-19, October, 2021
 3. American Society of Human Genetics (ASHG) Annual Meeting, Washington DC, 2023

10. Editorships and Editorial Boards:

- a. Guest Associate Editor, PLOS Genetics, 2022 – Present
- b. Associate Editor, Journal of Alzheimer's Disease, 2022 – Present

11. Honors and Awards:

- a. Robert C. Elston Best Paper Award by International Genetic Epidemiology Society (IGES) (Invited to present at 2019 IGES annual meeting, Houston, TX). 2019
- b. 3rd Place Presenter at the 61st McKusick Short Course Virtual Poster Session, The Jackson Laboratory, Bar Harbor, ME. 2020

12. Society Memberships:

- a. American Statistical Association (ASA), 2010 – Present
- b. Eastern North American Region (ENAR) of International Biometric Society, 2010 – Present
- c. American Society of Human Genetics (ASHG), 2014 – Present
- d. International Chinese Statistical Association (ICSA), 2015 – Present

13. Organization of Conferences:

- a. National and International:
 - i. Sessions as Moderator:
 1. *Insights from large-scale studies of diverse phenotypes and populations*. American Society of Human Genetics (ASHG) Annual Meeting, Virtual due to COVID-19, 2021
 2. *High-throughput characterization of coding variants, from benchtop to desktop*. American Society of Human Genetics (ASHG) Annual Meeting, Los Angeles, CA, 2022
- b. Institutional:
 - i. Administrative Positions:
 1. Organizer, Committee Chair, Retreat of Department of Human Genetics, Lake Lanier Resort, Atlanta, GA, 2022
 2. Co-organizer, Clinical Research Bootcamp 101, Emory University School of Medicine, Atlanta, GA, 2023
 3. Organizer, Committee Chair, Retreat of Department of Human Genetics, Lake Lanier Resort, Atlanta, GA, 2023
 4. Organizer, Committee Chair, Stephen T. Warren Distinguished Lecture of Department of Human Genetics, Atlanta, GA, 2023

14. Formal Teaching:

a. Graduate Programs:

i. Master's and PhD Programs:

1. IBS-746: *Graduate Human Genetics*. Graduate course for Graduate Division of Biological and Biomedical Sciences (GDBBS). Instructor of two lectures about Genome-wide Association Study. Gave and graded 2 exam problems. Mentored students' final project. Fall 2018 – Present, 4 contact hours / year
2. BIOS-770: *Advanced Statistical Genetics*. Graduate course for the Department of Biostatistics and Bioinformatics, School of Public Health. Instructor of 4 lectures about Genome-wide Association Study, Spring 2019, 8 contact hours / year. Co-Course Organizer, instructor of 5 lectures about Genome-wide Association Study and Transcriptome-wide Association Study, attended student final project presentation during 3 lectures, Spring 2022 – Present, 16 contact hours / year.
3. IBS-500R: *Introduction to Data Analytics*. Graduate course for GDBBS. Instructor of two lectures about permutation test and machine learning, Fall 2021, 4 contact hours / year
4. BIOS-516: *Introduction to Large-Scale Biomedical Data Analysis*. Graduate course for the Department of Biostatistics and Bioinformatics, School of Public Health. Instructor of 1 lecture about Genome-wide Association Study, Fall 2021 – Present, 2 contact hours / year
5. IBS-538: *Design and Analysis of Experiments*. Graduate course for GDBBS. Instructor of two lectures about multivariate analysis and machine learning, Spring 2022, 6 contact hours / year
6. IBS-519: *Introduction to data analysis: Statistical Rigor, Reproducibility, and Experimental Design for Biomedical Data Analysis*. Graduate course for GDBBS. Co-Course Organizer, Fall 2022 – Present. 15 contact hours / year

b. Other Categories:

1. Genetic Epidemiology Journal Club. Present once per semester from 2018 – Present, 2 contact hours / year.
2. Bi-weekly meeting with trainees in my lab (~1hr / trainee / two-week). Discuss research projects. ~200 contact hours / year, 2018 – Present.

15. Supervisory Teaching:

a. PhD Students Directly Supervised:

- i. Qile Dai, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, Fall 2020 – Present
- ii. Shizhen Tang, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, Fall 2021 – Present
- iii. Randy Parrish, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, Fall 2022 – Present

b. Postdoctoral Fellows Directly Supervised:

- i. Justin Lunningham, Ph.D., 2018 – 2020. Currently Tenure-Track Assistant Professor at the University of North Texas, Health Science Center at Fort Worth.

- c. Thesis Committees:
- i. Biao Zeng, Ph.D. program in the School of Biological Sciences, Georgia Institute of Technology, 2018.
 - ii. Janise Kuehner, Ph.D. program in Genetics and Molecular Biology (GMB), GDBBS, Emory University, 2018 – 2023.
 - iii. Nikhil Tao Ramgiri, B.S. of Biology with honor's thesis, Emory College, 2019.
 - iv. Sini Nagpal, Ph.D. in Bioinformatics in the School of Biological Sciences, Georgia Institute of Technology, 2022.
 - v. Ye Zheng, Ph.D. program in the Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2022 – 2023
 - vi. Cynthia Perez, Ph.D. program in Genetics and Molecular Biology (GMB), GDBBS, Emory University, 2022– Present.
 - vii. Taylor Head, Ph.D. program in the Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2022 – Present
 - viii. Junyu Chen, Ph.D. program in the Department of Epidemiology, Emory University School of Public Health, 2022 – Present
 - ix. Shijia Bian, Ph.D. program in the Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2023 – Present
 - x. Jared Collins, M.S. program in the School of Biological Sciences, Georgia Institute of Technology, 2023
 - xi. Jing Huang, M.S. program in Genetics and Molecular Biology (GMB), GDBS, Emory University, 2023
- d. Other:
- i. Sini Nagpal, M.S., Summer Intern, Georgia Institute of Technology, 2018. Currently post-doctoral fellow at Georgia Institute of Technology.
 - ii. Raymond Jiang, Summer High School Intern, Walton High School, 2018. Currently college student at Georgia Institute of Technology.
 - iii. Tianhui Mao, B.S. of Quantitative Theory and Methods (QTM), Emory College, 2018 – 2019. Currently Data Science Analyst at McKinsey & Company.
 - iv. Junyu Chen, M.S., Research Specialist, Emory University School of Medicine, 2018 – 2020. Currently PhD student of Epidemiology, Emory University School of Public Health.
 - v. Xiaoran Meng, M.S., Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2018 – 2019. Currently Data Scientist in China.
 - vi. Lei Wang, MSPH, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2021 – 2022. Currently PhD Student of Biostatistics, University of Colorado School of Medicine.
 - vii. Kevin Johnson, MSPH, Department of Epidemiology, Emory University School of Public Health, 2021 – 2022. Currently CDC ORISE fellow.
 - viii. Tingyang Hu, MSPH, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2021 – 2022. Research Scientist, Department of Human Genetics, Emory University School of Medicine, 2022 – 2023.
 - ix. Xizhu Liu, B.S. of Quantitative Theory and Methods (QTM), with Highest Honor for Thesis Project, Emory College, 2021 – 2022. Currently Master Student of Biostatistics, Yale University School of Public Health.
 - x. Rebecca Yu, Summer High School Intern, Milton High School, 2021 – 2023. Currently College Student at Columbia University with Egleston Scholarship.
 - xi. Shuyi Guo, MSPH, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2022 – 2023
 - xii. Yingte Liu, MSPH, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2023 – Present

16. Lectureships, Seminar Invitations, and Visiting Professorships:

- a. National and International:
 - i. *Integrating Functional data in Genome-wide Association Studies with Applications on Studies of Age-related Macular Degeneration and Alzheimer's Disease* (Invited Seminar). Seminar at the School of Life Science, Chongqing University, Chongqing, China. March 2018.
 - ii. *Scalable Bayesian Method for Functional Genome-wide Association Studies* (Invited Seminar). Department of Mathematics, University of North Texas, Dallas, TX. November, 2018.
 - iii. *OTTERS: A Powerful Framework Integrating Summary-level Molecular QTL Data with GWAS Data* (Invited Seminar). Department of Public Health Sciences, Penn State College of Medicine, Hershey, PA. March 2023.
- b. Regional:
 - i. *Bayesian Approaches to Functional Integration of Genomic Data* (Invited Seminar), Center for Integrative Genomics, School of Biological Sciences, Georgia Institute of Technology. Atlanta, GA. February 2018.
- c. Institutional:
 - i. *Scalable Bayesian Functional Genome-wide Association Study Method using Summary Statistics with Application on Age-related Macular Degeneration* (Invited Seminar). Seminar at the Population Biology, Ecology, and Evolution (PBEE) Graduate Program, Emory University. Atlanta, GA. October 2017.
 - ii. *Novel Bayesian Methods for Transcriptome-wide Association Studies* (Invited Seminar). Seminar at the Genetics and Molecular Biology (GMB) Graduate Program, Emory University, Atlanta, GA. March 2019.

17. Invitations to National/International, Regional, and Institutional Conferences:

- a. National and International:
 - i. *TIGAR: An Improved Bayesian Tool for Transcriptomic Data Imputation Enhances Gene Mapping of Complex Traits*. East North American Region (ENAR) International Biometric Society Spring Meeting, Virtual through Zoom due to COVID-19, 2020.
 - ii. *Scalable Bayesian Functional GWAS Method Accounting for Multiple Quantitative Functional Annotations*. 4th International Conference on Econometrics and Statistics (EcoSta) 2021, Virtual due to COVID-19, HKUST, Hong Kong. June 2021.
 - iii. *Novel Variance-Component TWAS Method for Studying Alzheimer's Disease Dementia*. Annual Meeting of Religious Orders Study (ROS) and Memory and Aging Project (MAP), Rush University, Chicago, IL. Virtual due to COVID-19. May 2021.
 - iv. *Bayesian Genome-wide TWAS method integrating both cis- and trans- eQTL with GWAS summary statistics*. International Chinese Statistical Association Annual Meeting 2021, Virtual due to COVID-19. September 2021.
 - v. *OTTERS: A Powerful TWAS Framework Leveraging Summary-level Reference Data*. Plant & Animal Genome Conference (PAG 30), San Diego, CA. January, 2023.
 - vi. *SR-TWAS: Leveraging Multiple Reference Panels to Improve TWAS Power by Ensemble Machine Learning*. East North American Region (ENAR) International Biometric Society Spring Meeting, Nashville, TN. March 2023.
 - vii. *A Scalable Bayesian Functional GWAS Method Accounting for Multivariate Quantitative Functional Annotations*. Joint Statistical Meetings (JSM), Toronto, Canada. August 2023.

18. Abstract Presentations at National/International, Regional, and Institutional Conferences (* denotes the presenter, under line denotes the trainee I advise):

- a. National and International:
 - i. **J. Yang*** and D. Scott, *Robust Fitting of a Weibull Model with Optional Censoring*, Joint Statistical Meetings (JSM), Montreal, Canada, August 2013. (Oral)
 - ii. **J. Yang***, H. Zhu, D. Cox, *Smoothing Functional Data with a Bayesian Hierarchical Model*, ENAR Spring Meetings. Baltimore, MD, March 2014. (Oral)
 - iii. **J. Yang***, X. Zhou, G. Abecasis, *A Scalable Bayesian Method for Integrating Functional Annotations in Genome-wide Association Studies*, American Society of Human Genetics 2015 Annual Meeting, Baltimore, MD, October 2015. (Poster)
 - iv. **J. Yang***, S. Chen, G. Abecasis. *Improved Score Statistics for Meta-analysis in Single-variant and Gene-level Association Studies*, American Society of Human Genetics 2016 Annual Meeting, Vancouver, Canada, October 2016. (Oral)
 - v. **J. Yang***, X. Zhou, G. Abecasis. *Scalable Bayesian Functional Genome-wide Association Study Method with Summary Statistics*. American Society of Human Genetics 2017 Annual Meeting, Orlando, FL. October 2017. (Poster)
 - vi. **J. Yang***, S. Nagpal, M.P. Epstein, A. Tsoi, M. Patrick, A.P. Wingo, T.S. Wingo. *Integrative functional genomics analysis of neuropathologic features of Alzheimer's Disease and related cognition decline reveals novel insights on previously identified loci*. American Society of Human Genetics 2018 Annual Meeting, San Diego, CA. October 2018. (Poster)
 - vii. J.N. Kuehner*, E.C. Bruggeman⁺, J. Chen⁺, F. Wang, C. Xu, Z. Wen, **J. Yang**, B. Yao. *Genome-wide 5hmC dynamics during human organoid development and its dysregulation in Alzheimer's disease*. American Society of Human Genetics 2019 Annual Meeting, Houston, TX. October 2019. (Poster)
 - viii. **J. Yang***, J. Luningham, J. Chen, S. Tang, D.A. Bennett, P.L. De Jager, A. Buchman. *Novel Bayesian Genome-Wide TWAS method to leverage both cis- and trans- eQTL information through summary statistics*. The 61st McKusick Short Course Virtual Poster Session, Virtual due to COVID-19. August 2020. (Poster)
 - ix. **J. Yang***, J. Luningham, J. Chen, S. Tang, D.A. Bennett, P.L. De Jager, A. Buchman. *Bayesian Genome-Wide TWAS method to leverage both cis- and trans-eQTL information through summary statistics*. American Society of Human Genetics 2020 Annual Meeting, Virtual due to COVID-19. October 2020. (Poster)
 - x. S. Tang*, D.A. Bennett, P.L. De Jager, A. Buchman, **J. Yang**. *Powerful variance-component method for TWAS identifies novel and known risk genes for Alzheimer's dementia*. American Society of Human Genetics 2020 Annual Meeting, Virtual due to COVID-19. October 2020. (Poster)
 - xi. **J. Yang***, R. Parrish, Greg Gibson, M.P. Epstein. *TIGAR-V2: Efficient TWAS Tool with Nonparametric Bayesian eQTL Weights of 49 Tissue Types from GTEx V8*. American Society of Human Genetics 2021 Annual Meeting, Virtual due to COVID-19. October 2021. (Poster)
 - xii. R. Parrish*, A. Buchman, P.L. De Jager, D.A. Bennett, M.P. Epstein, **J. Yang**. *SR-TWAS: Leveraging multiple reference panels to improve TWAS power by ensemble machine learning*. American Society of Human Genetics 2021 Annual Meeting, Virtual due to COVID-19. October 2021. (Oral)
 - xiii. S. Tang*, D.A. Bennett, P.L. De Jager, A. Buchman, Q. Zheng, **J. Yang**. *Novel Global Quantile Regression Based Method for Differential Gene Expression Analysis of Quantitative traits*. American Society of Human Genetics 2021 Annual Meeting, Virtual due to COVID-19. October 2021. (Poster)
 - xiv. Q. Dai*, L. Franke, U. Vosa, G.C. Gibson, M.P. Epstein, **J. Yang**. *Novel Bayesian TWAS method using eQTL summary statistics*. American Society of Human Genetics 2021 Annual Meeting, Virtual due to COVID-19. October 2021. (Poster)

19. Research Focus:

Quantitative genomics studies for complex traits and diseases, including integrating functional information in genome-wide association studies (GWAS), integrative multi-omics data analysis, disease risk prediction, and sequence data analysis. My work includes statistical methods/tools development, and applying Machine Learning and Deep Learning methods to biomedical studies.

20. Grant Support

a. Active Support:

i. Federally Funded:

1. R01 DK125187 (MPI: Y. Sun and V.C. Marconi) 08/2020 – 03/2025
NIH/NIDDK
Title: *Multi-omic Predictors of Renal Function among HIV-infected Individuals of African Ancestry*
Total Direct Cost: \$1,941,038
Role: Co-Investigator (4.7% Effort)
2. R35 GM138313-01 (PI: J. Yang) 09/2020 – 06/2025
NIH/NIGMS (Maximizing Investigators' Research Award for Early Stage Investigators, MIRA for ESIs)
Title: *Novel Bayesian statistical tools for integrating multi-omics data to help elucidate the genomic etiology of complex phenotypes.*
Total Direct Cost: \$1,168,937
Role: PI (51% Effort)
3. R01 DE030342-01A1 (PI: E. Leslie) 09/2021 – 05/2026
NIH/NIDCR
Title: *Genomics of Cleft Palate.*
Total Direct Cost: \$2,599,505
Role: Co-Investigator (5% Effort)

ii. Private Foundation Funded:

1. 2022 Research Professorship (PI: M. Torres) 07/2022 – 06/2027
American Society of Clinical Oncology Foundation
Title: *Genetic Determinants of Treatment-Related Comorbidities, Poor Treatment Adherence*
Total Direct Cost: \$327,654
Role: Co-Investigator (1% Effort)
2. AWS Promotional Cloud Credit (PI: J. Yang) 07/2022 – 08/2024
Amazon Web Service Public Sector
Title: *WebTIGAR: AWS based webtool for TWAS*
Total Credit: \$12,563
Role: PI

iii. Contracts:

1. Rush University Medical Center (**PI: J. Yang**) 01/2020-12/2024
 Title: *Develop risk prediction models for Alzheimer's disease using data from Rush Religious Orders Study and Rush Memory and Aging Project (ROSMAP)*
 Total Direct Cost: \$102,850
 Role: PI (20% Effort)
- b. Previous Support:
 - i. R01-AG056533 (PI: A.P. Wingo) 10/2017-12/2017
 Title: *Psychological risk modifiers of Alzheimer's disease*
 Role: Co-Investigator (20% Effort)
 - ii. Atlanta VA Medical Center IPA Award (PI: J. Yang) 01/2018 - 12/2018
 Title: *Integrative analysis of the genome-wide genotyping, transcriptomic, and global microRNA sequencing data (Project ID 00072165).*
 Role: PI (20% Effort)
 - iii. Emory University School of Medicine I³ (Imagine, Innovate and Impact) Award (MPI: J. Yang, B. Yao, Z. Wen) 04/2019-03/2020
 Title: *Studying the mechanisms of individual variation in antidepressant response for precision medicine.*
 Role: MPI (3% Effort)
 - iv. Emory University Start-up (PI: J. Yang) 10/2017-09/2021
 Title: *Startup fund provided by the Center for Computational and Quantitative Genetics, Department of Human Genetics, Emory University School of Medicine.*
 Total Direct Cost: \$600,000
 Role: PI
 - v. R21 AG070659-01A1 (MPI: Q. Zheng, D. Wang, J. Yang) 09/2021 – 05/2023
 NIH/NIA
 Title: *"Global significance test based on quantile regression with applications to genomic studies of Alzheimer's disease."*
 Direct Cost: \$70,380 (Emory Subaward)
 Role: MPI (15.1% Effort)

21. Bibliography:

- a. Published and Accepted Research Articles (clinical, basic science, other) in Refereed Journals: (*: Correspondence Author; +: Co-first Author; Under Line: trainees I advise)
 - i. **Yang, J.** and Scott, D.W. *Robust Fitting of a Weibull Model with Optional Censoring.* Computational Statistics & Data Analysis, 2013. 1(67), 149-161. PMID: 23888090
 - ii. **Yang, J.**, Zhu, H., Choi, T., and Cox, D.D. *Smoothing and Mean-Covariance Estimation of Functional Data with a Bayesian Hierarchical Model.* Bayesian Analysis, 2016. 11(3), 649-670. PMID: 28395117
 - iii. **Yang, J.**, Cox, D.D., Lee, J.S., Ren, P., and Choi, T. *Efficient Bayesian Hierarchical Functional Data Analysis with Basis Function Approximations Using Gaussian-Wishart Processes.* Biometrics, 2017. 73: 1082-1091. doi:10.1111/biom.12705. PMID: 28395117
 - iv. **Yang, J.**, Fritsche, L.G., Zhou, X., Abecasis, G., International Age-Related Macular Degeneration Genomics Consortium. *A Scalable Bayesian Method for Integrating Functional Information in Genome-wide Association Studies.* American Journal of Human Genetics (Impact Factor 10.5), 2017. 101(3), 404-416. PMID: 28844487

- v. Tsoi, L.C., **Yang, J.**, Liang, Y., Sarkar, M.K., Xing, X., Beamer, M.A., Aphale, A., Raja, K., Kozlow J., Getsios, S., Voorhees, J.J., Kahlenberg, J.M., Elder, J.T., Gudjonsson, J.E. *Transcriptional Determinants of Individualized Inflammatory Responses at Anatomically Separate Sites*. *Journal of Allergy and Clinical Immunology* (Impact Factor 10.79), 2018. 141(2):805-808. doi: 10.1016/j.jaci.2017.07.054. PMID: 29031600
- vi. **Yang, J.***, Chen, S., Abecasis, G, IAMDCG. *Improved Score Statistics for Meta-Analysis in Single-Variant and Gene-Level Association Studies*. *Genetic Epidemiology* (Impact Factor 2.13), 2018. 42(4): 333-343. DOI: 10.1002/gepi.22123. PMID: 29696691. (Selected for the the Robert C. Elston Best Paper Award 2019 by IGES).
- vii. Patrick, M.T., Stuart, E.P., Raja, K., Gudjonsson, E.J., Tejasvi, T., **Yang, J.**, Ghandran, V., Das, S., Callis-Duffin, K., Ellinghaus, E., Enerback, C., Esko, T., Franke, A., Kang, H.M., Krueger, G., Rahman, P., Rosen, C., Weidinger, S., Weichenthal, M., Wen, X., Voorhees, J., Abecasis, G., Gladman, D., Nair, R., Elder, J., Tsoi, L.C. *Genetic signature to provide robust risk assessment of psoriatic arthritis development in psoriasis patients*. *Nature Communications* (Impact Factor 14.92), 2018. 9 (1), 2018: 4178. PMID: 30301895.
- viii. Nagpal, S.*, Meng, X.*, Epstein, M.P., Tsoi, T.C., Patrick, M., Gibson, G., De Jager, P., Bennett, D.A., Wingo, A.P., Wingo, T.S., **Yang J.*** *TIGAR: An Improved Bayesian Tool for Transcriptomic Data Imputation Enhances Gene Mapping of Complex Traits*. *American Journal of Human Genetics* (Impact Factor 10.5), 2019. 105 (2), 258-266. PMID: 31230719. (Honorably mentioned by the Editors' Corner).
- ix. **Yang, J.*** and Ren, P. *BFDA: A MATLAB Toolbox for Bayesian Functional Data Analysis*. *Journal of Statistical Software* (Impact Factor 11.66), 2019. 89(2): 1548-7660. DOI: 10.18637/jss.v089.i02.
- x. Brieger, K., Zajac, G., Pandit, A.*, Foerster, J., Li, K., Annis, A., Schmidt, E., Clark, C., McMorrow, K., Zhou, W., **Yang, J.**, Kwong, A, Boughton, A., Wu, J., Scheller, C., Parikh, T., De la Vega, A., Brazel, D., Frieser, M., Rea-Sandin, G., Fritsche, L., Vrieze, S., Abecasis, G.* *Genes for Good: Engaging the Public in Genetics Research via Social Media*. *American Journal of Human Genetics* (Impact Factor 10.5). 2019. 105(1):65-77. DOI: 10.1016/j.ajhg.2019.05.006. PMID: 31204010.
- xi. Clever, F., Cho, I.K., **Yang, J.** and Chan, A.*. *Progressive Polyglutamine Repeat Expansion in Peripheral Blood Cells and Sperm of Transgenic Huntington's Disease Monkeys*. *Journal of Huntington's disease*, 2019. 8(4), pp.443-448.
- xii. Xing, Y., Chen, J., Hilley, H., Steele, H., **Yang, J.** and Han, L.*. *Molecular signature of pruriceptive MrgprA3+ neurons*. *Journal of Investigative Dermatology* (Impact Factor 10.79), 2020. 140(10), 2041-2050. DOI: doi.org/10.1016/j.jid.2020.03.935.
- xiii. Wingo, T.S., **Yang, J.**, Fan, W., Canon, S.M., Gerasimov, E.S., Lori, A., Logsdon, B., Yao, B., Seyfried, N.T., Lah, J.J., Levey, A.I., Boyle, P.A., Schneider J.A., De Jager, P.L., Bennett, D.A., Wingo, A.P.*. *Brain microRNAs associated with late-life depressive symptoms are also associated with cognitive trajectory and dementia*. *NPJ Genomic Medicine* (Impact Factor 7.22), 2020. 5(1), pp.1-8.
- xiv. Zhang, J., Guo, X., Gonzales, S., **Yang, J.**, & Wang, X. *TS: a powerful truncated test to detect novel disease associated genes using publicly available gWAS summary data*. *BMC bioinformatics* (Impact Factor 3.16), 2020. 21, 1-15.
- xv. Waldman, I.D.*, Poore, H.E., Luningham, J.M., **Yang, J.** *Testing Structural Models of Psychopathology at the Genomic Level*. *World Psychiatry* (Impact Factor 49.55), 2020. 19:1-10. DOI: 10.1002/wps.20772.
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b. Manuscripts Submitted:

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- ii. **Yang J***, Liu X, Oveisgharan S, Zammit AR, Nag S, Bennett DA, Buchman AS. *Inferring Alzheimer's disease pathologic traits from clinical measures in living adults*. medRxiv. 2023 Jan 1. DOI: <https://doi.org/10.1101/2023.05.08.23289668>. (Under Review with Journal of Alzheimer's Disease)
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