CURRICULUM VITAE

Revised: *06/19/2025*

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 – 2025
  ii. Chair, Organization Committee of a 5-day workshop at Banff International Research Station. 2024-2025

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 – 2024
  iv. Member, PhD Student Recruitment Committee of GMB/GDBBS, 2021 – 2023
  v. Member, Faculty Development Advisory Committee (FDAC), School of Medicine, 2021 – 2024
  vi. Member, Faculty Recruitment Committee of the Department of Human Genetics, 2022 – 2024
  vii. Chair, Seminar Committee of the Department of Human Genetics, 2022 – 2025
  viii. Member, PhD Student Recruitment Committee of PBEE/GDBBS, 2023 – Present
  ix. Member, DEI Committee of the Department of Human Genetics, 2025 – present

9. Peer Review Activities:

a. Grants:

  i. National and International:

    1. Life Science – Genetics, Bioinformatics and Computational Biology: Genetic Diseases, US-Isreal 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

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

9. Advancing Genomic Medicine Research R21/R01, NIH/NHGRI, USA, July 2023

10. Bioengineering, Biodata, and Biomodelling Technologies (BBBT-02) R21/R01, NIH, USA, November 2023; November 2024

11. Aging, Injury, Musculoskeletal, Rheumatologic, and Dermatologic disorders (AIMR) Study Section, NIH, March 2024; April 2025

12. Genetics of Health and Disease (GHD) Study Section, NIH, June 2024

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. Computational Statistics and Data Analysis, 2017 – Present
vii. Computational Statistics, 2017 – Present
viii. Frontiers in Genetics, 2017 – Present
ix. Genes, 2017 – Present
x. Genetics in Medicine, 2017 – Present
xi. GENETICS, 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. Biostatistics, 2022 – Present
        xxx. Cell Genomics, 2012 – Present
        xxxi. Journal of Genetics and Genomics, 2022 – Present
        xxxii. Journal of the American Statistical Association, 2022 – Present
        xxxiii. Journal of Alzheimer’s Disease, 2023 – Present
        xxxiv. eBioMedicine, 2023 – Present
        xxxv. Cell & Bioscience, 2025 – Present
        xxxvi. NAR Cancer, 2025 – 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 Meetings, 2023-2025

10. Editorships and Editorial Boards:

    a. Guest Associate Editor, PLOS Genetics, 2022 – 2024

    b. Associate Editor, Journal of Alzheimer’s Disease, 2022 – Present

    c. Associate Editor, PLOS Genetics, 2024 – 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

    c. Emory School of Medicine Researcher Appreciation Day Recognition, Atlanta, GA. 2024.

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 Chair:
    1. Chair of Organization Committee, Banff International Research Station (BIRS) 5-day workshop entitled “*Novel Statistical Approaches for Studying Multi-omics Data*”, 2025

ii. 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 – 2025
    2. Co-organizer, Clinical Research Bootcamp 101, Emory University School of Medicine, Atlanta, GA, 2023
    3. Organizer, Committee Chair, Stephen T. Warren Distinguished Lecture of Department of Human Genetics, Atlanta, GA, 2023 – 2025
    4. Organizer, Committee Chair, Conversation with Emory Leaders, Department of Human Genetics, Atlanta, GA, 2023 – 2025

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 – 2024, 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 – 2023, 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 – 2025
   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
   iv. Qiang Liu, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, Fall 2025 – Present

b. Postdoctoral Fellows Directly Supervised:
   i. Justin Luningham, 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– 2025.
   vii. Taylor Head, Ph.D. program in the Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2022 – 2024
   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 – 2025
   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. Currently PhD student of Biostatistics program at Pennsylvania State University.
    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. Currently PhD student of Biostatistics at UT Health Houston.
    xii. Yingte Liu, MSPH, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2023 – 2024.
    xiii. Qiang Liu, MSPH, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2023 – 2025.
    xiv. Qiuzi (Coco) Wu, B.S. of Quantitative Science with a focus on Neurobiology. Research project, 2024 – 2025.
    xv. Arpit Ramani, Summer High School Intern, Wheeler High School, 2024 – Present.
    xvi. Siyang Shen, MSPH, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2024 – 2025.
    xvii. Bo Shen, MSPH, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2024 – Present.
    xviii. Conglin Bao, MSPH, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2024 – Present.
    xix. Ruilong Chen, MSPH, Department of Biostatistics and Bioinformatics, Emory University School of Public Health, 2025 – 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* (<u>Invited Seminar</u>). 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. *Scalable Bayesian Functional GWAS Method Accounting for Multiple Quantitative Functional Annotations* (Invited Seminar). Department of Genetics, University of North Carolina at Chapel Hill, Chapel Hill, NC. August 2021.
- iv. *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.
- v. *Methods for Integrating Summary-level Methylation QTL Data with GWAS data of PTSD* (Invited Seminar). Psychiatric Genomics Consortium for PTSD, Virtually on Zoom. February 2024.
- vi. *Epigenetics and Gene Regulation Module (five 90-minute lectures).* Bruce Weir Summer Institute in Statistical Genetics (SISG), Georgia Tech, Atlanta, GA. 2024 – Present.
- vii. *SR-TWAS: Leveraging Multiple Reference Panels to Improve TWAS Power by Ensemble Machine Learning* (Invited Seminar). Division of Epidemiology, Department of Medicine, Vanderbilt University Medical Center. Virtually on zoom. June 2024.
- viii. *Imputing AD Pathologies using Clinical Variables*. Rush Alzheimer's Disease Center, Rush University Medical Center. Virtually on zoom, July 2024.
- ix. *Advanced TWAS/PWAS Tools Improve Gene Mapping in Alzheimer's Disease Dementia* (Invited Seminar). Novartis, Biomedical Research, Cambridge, MA, July 2025.

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.
  - iii. *SR-TWAS: Leveraging Multiple Reference Panels to Improve TWAS Power by Ensemble Machine Learning*. Seminar at the Genetic Epidemiology Journal Club at Emory University, Atlanta, GA. April 2024.

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.

viii. *SR-TWAS: Leveraging Multiple Reference Panels to Improve TWAS Power by Ensemble Machine Learning*. Statistical, Computational, Translational, and Ethical Challenges in Biobank Analysis 5-day Workshop at Banff International Research Station. July 2024.

ix. *Integrating Spatial Transcriptomics and snRNA-seq Data Enhances Studies of Alzheimer's Disease.* MCBIOS. Salt Lake City, UT. March 2025

x. *Cell-type-specific Transcriptomic-wid eAssociation Studies Detected 80 Independent Risk Genes for Alzheimer's Disease Dimentia.* FunGen-AD xQTL Symposium, San Francisco, CA. Virtual Presentation by Zoom. May 2025

xi. *Unveiling Cell-type-specific Risk Genes for Alzheimer's Disease Dementia by Integrating Large-scale snRNA-Seq Data from Prefrontal Cortex Tissue with GWAS Summary Data.* The 10th Workshop on Biostatistics and Bioinformatics, Georgia State University, Atlanta, GA. May 2025

xii. *Integrating spatial transcriptomic and snRNAseq data enhances the studies of AD*. ROSMAP Annual Meeting, Rush University Medical Center. Chicago, IL, May 2025.

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, Platform Presentation, top 10%. (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. 3rd Place Best Presentation. (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. Reviewers' Choice, top 10%. (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. Platform Presentation, top 5%. Selected as Predoctoral Semifinalist for the 2021 Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research. (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. Reviewers' Choice, top 10%. (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)

xv. S. Tang*, A. Buchman, D.A. Bennett, Y. Wang, Q. Zheng, **J. Yang**. *Differential gene expression analysis based on linear mixed model corrects false positive inflation for studying quantitative trait.* American Society of Human Genetics 2022 Annual Meeting, Los Angeles, CA. October 2022. (Poster)

xvi. R. Parrish*, A. Buchman, Y. Wang, P.L. De Jager, D.A. Bennett, M.P. Epstein, **J. Yang**. *Leveraging multiple reference panels by stacked regression TWAS identifies 6 novel independent risk genes for Parkinson's disease.* American Society of Human Genetics 2022 Annual Meeting, Los Angeles. October 2022. (Poster)

xvii. T. Hu*, R.L. Parrish, A.S. Buchman, N.T. Seyfried, P.L. De Jager, D.A. Bennett, M.P. Epstein, **J. Yang**. Omnibus proteome-wide association study (PWAS) method identified 28 novel risk genes for Alzheimer's disease. American Society of Human Genetics 2022 Annual Meeting, Los Angeles. October 2022. (Poster)

xviii. Q. Dai*, G. Zhou, H. Zhao, U. Vosa, A. Battle, A. Teumer, L. Lehtimaki, O. Raitakari, T. Esko, M.P. Epstein, **J. Yang**. *OTTERS: A powerful TWAS framework leveraging summary-level reference data.* American Society of Human Genetics 2022 Annual Meeting, Los Angeles. October 2022. (Poster)

xix. Q. Dai*, M.P. Epstein, **J. Yang**. STDCC: Supervised Tensor Decomposition tool for studying Cell-cell Communication using single-cell RNA-seq data. American Society of Human Genetics 2023 Annual Meeting, Washington D.C. November 2023. Reviewers' Choice, top 15%. (Poster)

xx. S. Guo*, **J. Yang**. *Bayesian genome-wide TWAS with reference transcriptomic data of brain and blood tissues identified 93 risk genes for Alzheimer's disease dementia.*

American Society of Human Genetics 2023 Annual Meeting, Washington D.C. November 2023. (Poster)

xxi. S. Tang*, A.S. Buchman, P.L. Jager, D.A. Bennett, S. Tasaki, J. Hu, **J. Yang**. *Deconvoluting Bulk RNA-seq Data of 1200 samples of Dorsolateral Prefrontal Cortex tissue using reference single nucleus RNAseq data of 400 samples for Cell-Type-Specific TWAS of AD Dementia.* American Society of Human Genetics 2023 Annual Meeting, Washington D.C. November 2023. (Poster)

xxii. T. Hu*, Q. Dai, M.P. Epstein, **J. Yang**. *PWAS with summary-level pQTL reference data of brain, CSF, and plasma tissues identifies 23 risk genes for Alzheimer's disease dementia.* American Society of Human Genetics 2023 Annual Meeting, Washington D.C. November 2023. Platform Presentation, top 10%. (Oral)

xxiii. S. Tang*, A.S. Buchman, D.A. Bennett, P.L. De Jager, J. Hu, **J. Yang**. *Combining spatial transcriptomic with snRNA-seq data enhances differential gene expression analyses.* American Society of Human Genetics 2024 Annual Meeting, Denver, CO. November 2024. Platform Presentation, top 10%. (Oral)

xxiv. Q. Dai*, S. Tang, J. Hu, P. De Jager, D. Bennett, A. Buchman, **J. Yang**, M.P. Epstein. *Cell-Cell Communication Patterns in Alzheimer's Disease Dementia and Mild Cognitive Impairment Vary by Cortical Layers.* American Society of Human Genetics 2024 Annual Meeting, Denver, CO. November 2024. Platform Presentation. Selected as Predoctoral Semifinalist for the 2024 Trainee Research Excellence Awards (top 60 out of 800 applications) for the 2024 Annual Meeting of the American Society of Human Genetics. (Oral)

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 sequencing 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. 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)

2. 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)

3. R01 HL173002-01 (PI: L. Han; **Emory Subaward PI: J. Yang**) 04/2024 – 03/2027
   NIH/NHLBI
   Title: *RNAseq and ATACseq analysis of sensory neurons*.

Total Direct Cost for Emory Subaward: $87,668
Role: Co-Investigator (5% Effort in Y1-3)

4. R01 R01AG089703-01A1 (**PI: J. Yang**) 06/2025 – 03/2030
NIH/NIA
Title: *Investigating Cis- and Trans-Genetic Regulation of Brain Transcriptomics and Proteomics Associated with AD/ADRD.*
Total Direct Cost: $ 2,040,381
Role: PI (36% 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)

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 I^3 (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)

vi. 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

vii. 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)

viii. Radiology-Pathology-Informatics Seed Grant (MPI: Li, **J. Yang**, H. Trivedi, G. Prada)
Emory University School of Medicine 09/2023 – 09/2024
Title: *Develop novel breast cancer risk biomarkers combining transcriptomic, clinicopathologic, and pathology profiles*
Total Direct Cost: $25,000
Role: MPI

ix. Radiology+Pathology+Informatics Seed Grant (MPI: Li, **J. Yang**, H. Trivedi, G. Prada)
Emory University School of Medicine 11/2023 – 11/2024
Title: *Develop biomarkers to predict which patients with triple negative breast cancer will respond to therapies*
Total Direct Cost: $66,667
Role: MPI (4% Effort)

x. 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)

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, IAMDGC. *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.

xvi. Luningham, J.M., Chen, J., Tang, S., De Jager, P., Bennett, D.A., Buchman, A.S. and **Yang, J.***. *Bayesian transcriptome-wide association study method leveraging both cis- and trans-eQTL information through summary statistics.* 2020. Am J Hum Genet (Impact Factor 10.5). 2020 Oct 1. 107(4):714-726. doi: 10.1016/j.ajhg.2020.08.022. PMID: 32961112; PMCID: PMC7536614

xvii. Hwang, H., Liu, R., Maxwell, J.T., **Yang, J.***, Xu, C.*. *Machine learning identifies abnormal Ca2+ transients in human induced pluripotent stem cell derived cardiomyocytes.* NPJ Scientific Report (Impact Factor 4.37). 2020. 10, 16977. DOI: 10.1038/s41598-020-73801-x. PMID: 33046816.

xviii. Tang, S., Buchman, A.S., De Jager, P., Bennett, D.A., Epstein, M.P. and **Yang, J.***. *Novel Variance-Component TWAS method for studying complex human diseases with applications to Alzheimer's dementia.* PLoS Genetics (Impact Factor 5.91), 2021. *17(4)*, p.e1009482.. DOI: https://doi.org/10.1371/journal.pgen.1009482.

xix. Kuehner, J.N.[+], Chen, J.[+], Bruggeman, E.C., Wang, F., Li, Y., Xu, C., McEachin, Z.T., Li, Z., Chen, L., Hales, C.M. and Wen, Z.*, **Yang, J.***, Yao B.*. 5-*hydroxymethylcytosine is dynamically regulated during forebrain organoid development and aberrantly altered in Alzheimer's disease.* Cell Reports (Impact Factor 9.42)*, 2021. 35(4), p.10904.*

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xxii. Yan, L. [+], Song, H. [+], Guo, Y., Ren, P., Zhou, W., Li, S., **Yang, J.***, Shen, X.*. *HLDnet: Novel deep learning based Artificial Intelligence tool fuses acetic acid and Lugol's iodine cervicograms for accurate pre-cancer screening.* Biomedical Signal Processing and Control (Impact Factor 3.88), 2022. *71*, p.103163.

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xxiv. **Yang, J.***, Oveisgharan, S., Liu, X., Wilson, R.S., Bennett, D.A. and Buchman, A.S. *Risk models based on non-cognitive measures may identify presymptomatic Alzheimer's disease*. Journal of Alzheimer's Disease, 2022. Vol. 89, no. 4, pp. 1249-1262. DOI: 10.3233/JAD-220446.

xxv. Chen, J., Wang, L., S., De Jager, P., Bennett, D.A., Buchman, A.S., and **Yang, J.***. *A scalable Bayesian functional GWAS method accounting for multivariate quantitative functional annotations with applications for studying Alzheimer's disease*. Human Genetics and Genomics Advances, 2022. 3(4), p.100143. DOI: https://doi.org/10.1016/j.xhgg.2022.100143.

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xxviii. Shams, M., Laney, D.A., Jacob, D.A., **Yang, J.**, Dronen, J., Logue, A., Rosen, A. and Riedl, M. *Validation of a suspicion index to identify patients at risk for hereditary angioedema.* Journal of Allergy and Clinical Immunology: Global, 2023, 2(1), pp.76-78.

xxix. **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.* Journal of Alzheimer's Disease Preprint (2023): 1-13.

xxx. Lobel, C.J., Laney, D.A., **Yang, J.**, Jacob, D., Rickheim, A., Ogg, C.Z., Clynes, D. and Dronen, J. *FDrisk: development of a validated risk assessment tool for Fabry disease utilizing electronic health record data.* Journal of Rare Diseases, 2024, 3(1), pp.1-10.

xxxi. Guo, S. and **Yang, J.***. *Bayesian genome-wide TWAS with reference transcriptomic data of brain and blood tissues identified 93 risk genes for Alzheimer's disease dementia.* Alzheimer's Research & Therapy 16, no. 1 (2024): 120.

xxxii. Head ST, Dezem F, Todor A, **Yang J**, Plummer J, Gayther S, Kar S, Schildkraut J, Epstein MP*. *Cis-and trans-eQTL TWASs of breast and ovarian cancer identify more than 100 susceptibility genes in the BCAC and OCAC consortia.* The American Journal of Human Genetics. 2024 Jun 6;111(6):1084-99.

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b. Manuscripts Submitted:

i. **Yang, J.***, Epstein, M.P.* and DAI, Q. *STACCato: Supervised Tensor Analysis tool for studying Cell-cell Communication using scRNA-seq data across multiple samples and conditions. bioRxiv 2023.12.15.571918; doi: https://doi.org/10.1101/2023.12.15.571918*. (Under Review)

ii. Liu Q, Parrish RL, Tang S, Tasaki S, Bennett DA, Seyfried NT, De Jager PL, Menon V, Buchman AS, **Yang J*.** *Cell-type-specific Transcriptomic-wide Association Studies Detected 91 Independent Risk Genes for Alzheimer's Disease Dementia*. medRxiv. 2025:2025-05.

c. Published Abstracts:

i. 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. *Determinants of Intra-Individual Transcriptional Homogeneity in Inflammatory Responses at Anatomically Separate Sites*. Journal of Investigative Dermatology, 2017. 137(5), Supplement 1, Page S90.

ii. Patrick, M.T., Stuart, E.P., Raja, K., **Yang, J.**, Zawistowski, M., Voorhees, J.J., Tejasvi, T., Gudjonsson, J.E., Chandran, V., Rahman, P., Nair, R.P., Gladman, D.D., Elder, J.T., Tsoi, L.C. 746 *Challenges and opportunities for integrating genetics and health records in risk assessment for psoriasis subtypes*. Journal of Investigative Dermatology, 2018. 138 (5), S127.

iii. Patrick, M.T., Stuart, E.P., **Yang, J.**, Raja, K., Yang, Y., Madu, D., Tejasvi, T., Voorhees, J.J., Kang H.M., Gudjonsson, J.E., Abecasis, G., Nair, R.P., Wen X., Elder J.T., Tsoi, L.C. *Identification of psoriasis-associated genes using genetically predicted transcriptomes.* Journal of Investigative Dermatology, 2018. 138 (5), S126.

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v. Li, S., Yan, L., **Yang, J.***, Shen, X.*, Guo, Y., Ren, P. *Multi-state data fusion for recognition of cervical precancerous lesions.* Proceedings-2020 Chinese Automation Congress, CAC. 2020. 3597-3601.

vi. Song, H., Yan, L., **Yang, J.***, Shen, X.*, Guo, Y., Ren, P. *Multi-model data fusion for cervical precancerous lesions detection.* Proceedings-2020 Chinese Automation Congress, CAC. 2020. 4462-4467.