Mengyuan Kan, Ph.D.

Research Associate

Genetics and Biomedical Informatics, University of Pennsylvania

B301 Richards Building, 3700 Hamilton Walk, Philadelphia, PA 19104, USA

mengykan@pennmedicine.upenn.edu; mengyuankan@gmail.com

Website: https://mengyuankan.github.io/

References

Li Shen, PhD
li.shen@pennmedicine.upenn.edu
Professor
Department of Biostatistics, Epidemiology, and Informatics, University of Pennsylvania

Nuala J. Meyer, MD, MS
Nuala.Meyer@pennmedicine.upenn.edu
Professor
Pulmonary, Allergy, and Critical Care Division, Department of Medicine, University of Pennsylvania

Blanca E. Himes, PhD
blanca.himes@gmail.com
Senior Advisor for Data Science, National Heart, Lung, and Blood Institute
Former Associate Professor, Department of Biostatistics, Epidemiology, and Informatics, University of Pennsylvania

Julie A. Mennella, PhD
mennella@monell.org
Member, Monell Chemical Senses Center

Ann Chen Wu, MD, MPH
ann.wu@genesprout.com
Founder and CEO, GeneSprout Inc.
Former Associate Professor, Department of Population Medicine, Harvard Medical School

Research Interests

Translational bioinformatics, multiomics integration, genetics and pharmacogenomics, open-source tool

Education

2009-2015 Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai, China
Ph.D. in Genetics
Mentor: Dr. Lin He

2011-2013 Center for Statistical Genetics, Baylor College of Medicine, TX

Visiting Ph.D. Student in Statistical Genetics
Mentor: Dr. Suzanne M Leal

2005-2009 East China University of Science and Technology, Shanghai, China
B.S in Biological Science

Employment

2021-present Department of Biostatistics, Epidemiology, and Informatics,
Institutes of Biomedical Informatics, University of Pennsylvania
Research Associate
Supervisor: Dr. Li Shen, Dr. Nuala Meyer & Dr. Blanca E Himes

2016-2021 Department of Biostatistics, Epidemiology, and Informatics,
Institutes of Biomedical Informatics, University of Pennsylvania
Postdoctoral Researcher in Biomedical Informatics
Mentor: Dr. Blanca E Himes

Grants

Colton Autoimmunity Pilot Award
Kan (PI), Li (Multiple PI)
2023-2025
An Integrative Multi-modal Approach to Define and Diagnose Pediatric Autoimmune Neurological Disorders

Global Genomics & Health Equity Pilot Project Award
Himes (PI), Kan (Co-investigator)
2023-2024
The Role of Gene-by-Environment Interactions on Asthma Disparities Among Adults in Philadelphia

Selected Peer-reviewed Publications

Complete List of Published Work in MyBibliography
https://www.ncbi.nlm.nih.gov/myncbi/1fo9lTxHXFLgrb/bibliography/public/

*** indicates co-first authored papers**

Multiomics integration

1. Giannini H, **Kan M***, Cosgriff C, Morley M, Miano T, Narayanan N, Ittner C, Turner A, Esperanza M, Erlich M, et al. Whole blood transcriptomics reveals sepsis mortality-associated changes in neutrophil degranulation. Am J Respir Cell Mol Biol. 2026 Feb 21. Online ahead of print.
2. **Kan M**, Diwadkar AR, Shuai H, Joo J, Wang AL, Ong MS, Sordillo JE, et al. Multiomics analysis identifies BIRC3 as a novel glucocorticoid response-associated gene. J Allergy Clin Immunol. 2022 Jun;149(6):1981-1991.
3. **Kan M**, Sun M, Jiang X, Diwadkar AR, Parikh V, Cao G, Gebski E, Jester W, Lan B, Panettieri RA Jr, Koziol-White C, Lu Q, Himes BE. CEBPD modulates the airway smooth muscle transcriptomic response

to glucocorticoids. Respir Res. 2022 Jul 28;23(1):193.

4. **Kan M**, Koziol-White C, Shumyatcher M, Johnson M, Jester W, Panettieri RA Jr, Himes BE. Airway Smooth Muscle-Specific Transcriptomic Signatures of Glucocorticoid Exposure. Am J Respir Cell Mol Biol. 2019 61(1):110-120.

AI-driven multimodal data integration

5. Wang Z, Zhan Q, Yang S, Zhou Z, **Kan M**, Zhai T, Shen L. An interpretable Graph-Regularized Optimal Transport Framework for Diagonal Single-Cell Integrative Analysis. Gigascience. 2026 Jan 21.

Open-source tools and their applications

6. Lien Y, **Kan M**, Leite R, Garifallou J, Himes B, Winn V, Parry S, Strauss J, Simmons R. Race and fetal sex differences in placental lipid metabolism associated with spontaneous early preterm birth. Biol Reprod. 2025 Apr 17.
7. **Kan M**, Diwadkar AR, Saxena S, Shuai H, Joo J, Himes BE. REALGAR: a web app of integrated respiratory omics data. Bioinformatics. 2022 Sep 15;38(18):4442-4445.
8. Xu Y, Zhang Y, García-Cañaveras JC, Guo L, **Kan M**, Yu S, Blair IA, Rabinowitz JD, Yang X. Chaperone-mediated autophagy regulates the pluripotency of embryonic stem cells. Science. 2020 Jul 24;369(6502):397-403.
9. **Kan M**, Shumyatcher M, Diwadkar AR, Soliman G, Himes BE. Integration of Transcriptomic Data Identifies Global and Cell-Specific Asthma-Related Gene Expression Signatures. AMIA Annu Symp Proc. 2018 Dec 5;2018:1338-1347. **Finalist of AMIA 2018 Student Paper Award.**
10. Diwadkar AR, **Kan M**, Himes BE. Facilitating Analysis of Publicly Available ChIP-Seq Data for Integrative Studies. AMIA Annu Symp Proc. 2020 Mar 4;2019:371-379. **Received AMIA 2019 Distinguished Paper Award**

Genome-wide association studies and pharmacogenomics

11. **Kan M**, Luis R. Saraiva L, Hwang L-D, Lowenthal E, Himes B, Mennella J. Genome-wide Association Study of the Taste and Hedonic Ratings of the Low-Calorie Sweetener Acesulfame Potassium. Sci Rep. 2025 Jul 1;15(1):22121.
12. Mennella JA, **Kan M***, Lowenthal ED, Saraiva LR, Mainland JD, Himes BE, Pepino MY. Genetic Variation and Sensory Perception of a Pediatric Formulation of Ibuprofen: Can a Medicine Taste Too Good for Some?. Int J Mol Sci. 2023 Aug 22;24(17).
13. Joo J, Mak ACY Mak, Xiao S, Sleiman PM, Hu D, Huntsman S, Eng C, **Kan M**, Diwakar AR, et al. Genome-wide association study in minority children with asthma implicates DNAH5 in bronchodilator responsiveness. Sci Rep. 2022 Jul 22;12(1):12514.
14. Dahlin A, Sordillo JE, Ziniti J, Iribarren C, Lu M, Weiss ST, Tantisira KG, Lu Q, **Kan M**, Himes BE, et al. Large-scale, multiethnic genome-wide association study identifies novel loci contributing to asthma susceptibility in adults. J Allergy Clin Immunol 2019 143(4):1633-1635.
15. Panganiban R, Sun M, Dahlin A, Park H, **Kan M**, Himes BE, et al. A functional splicing variant associated with decreased asthma risk abolishes the ability of gasdermin B (GSMDB) to induce epithelial cell pyroptosis. J Allergy Clin Immunol. 2018 142(5):1469-1478.

Immune profiling

16. Espinoza DA, Zrzavy T, Breville G, Thebault S, Marefi A, Mexhitaj I, Yamashita LD, **Kan M**, et al. Paediatric cerebrospinal fluid immune profiling distinguishes paediatric-onset multiple sclerosis from other paediatric-onset acute neurological disorders. EBioMedicine. 2026 Jan:123:106088.

NHLBI Exome Sequencing Project (ESP)

17. **Kan M**, Auer PL, Wang GT, Bucasas KL, Hooker S, Rodriguez A, Li B, Ellis J, Cupples LA, Chen YD, et al. Rare variant associations with waist-to-hip ratio in European-American and African-American women from the NHLBI-Exome Sequencing Project. Eur J Hum Genet. 2016 24(8):1181-7.
18. He Z, O'Roak BJ, Smith JD, Wang G, Hooker S, Santos-Cortez RL, Li B, **Kan M**, Krumm N, Nickerson DA, et al. Rare-variant extensions of the transmission disequilibrium test: application to autism exome sequence data. Am J Hum Genet. 2014 94:33-46.

Cancer genomics and epigenomics

19. Zhang L, **Kan M***, Zhang M, Yu S, Xie H, Gu Z, Wang H, Zhao S, Zhou G, Song H, Zheng C. Multiregion sequencing reveals intratumor heterogeneity of driver mutations in TP53-driven non-small cell lung cancer. Int J Cancer. 2017 140(1):103-10.
20. Liu F, Zhou Y, Zhou D, **Kan M**, Niu X, Zhang Z, Zhang D, Tao L, He L, Zhang L, Liu Y. Whole DNA methylome profiling in lung cancer cells before and after epithelial-to-mesenchymal transition. Diagnosis Pathology. 2014 9:66.

De novo genome sequencing

21. Wu C, Zhang D, **Kan M***, Lv Z, Zhu A, et al. The draft genome of the large yellow croaker reveals well-developed innate immunity. Nat Commun. 2014 5:5227.

Genetic and epigenetic association studies

22. Weng X, Zhang H, **Kan M***, Ye J, Liu F, et al. Leukocyte telomere length is associated with advanced age-related macular degeneration in the Han Chinese population. 2015. Exp Gerontol 69:36-40.
23. **Kan M**, Weng X, Wang T, Liu F, Ye J, et al. No evidence of association between variant rs2075650 in lipid metabolism-related locus APOE/TOMM40 and advanced age-related macular degeneration in Han Chinese population. Exp Biol Med (Maywood). 2015 240:230-234.
24. **Kan M**, Liu F, Weng X, Ye J, Wang T, et al. Association study of newly identified age-related macular degeneration susceptible loci SOD2, MBP, and C8orf42 in Han Chinese population. Diagn Pathol. 2014 9:73.
25. Qian D, **Kan M***, Weng X, Huang Y, Zhou C, et al. Common variant rs10033900 near the complement factor I gene is associated with age-related macular degeneration risk in Han Chinese population. Eur J Hum Genet. 2014 22:1417-1419.
26. Zheng Y, **Kan M***, Yu L, Niu X, Zhou D, He L, Lu S, Liu Y. GPC5 rs2352028 polymorphism and risk of lung cancer in Han Chinese. 2012 Cancer Invest 30:13-19.
27. **Kan MY**, Zhou DZ, Zhang D, Zhang Z, Chen Z, et al. Two susceptible diabetogenic variants near/in MTNR1B are associated with fasting plasma glucose in a Han Chinese cohort. Diabet Med. 2010 27:598-602.

Review

28. **Kan M**, Himes BE. Insights into Glucocorticoid Responses Derived from Omics Studies. Pharmacol Ther. 2021 Feb;218:107674.
29. **Kan M**, Shumyatcher M, Himes B. Using omics approaches to understand pulmonary diseases. Respir Res. 2017 18(1):149.

Book Chapter

Kan M, Himes BE. Genetics and Pharmacogenetics of Asthma. Precision Therapy in Pulmonary, Critical Care and Sleep Medicine. Gomez JL, Himes BE, Kaminski N (eds). 1st ed. Springer, New York, NY. 2020. Chapter 3: 25-37p.

Invited Talks

2021 American Thoracic Society, Mini Symposium: Omics in Asthma and COPD (Virtual)
Multi-Omics Analysis Identifies a Novel Glucocorticoid Response-Associated Locus Near BIRC3

2020 American Thoracic Society, Newman Stephens Memorial Mini Symposium: a Legacy of Science and Success (Virtual)
CEBPD Influences the Airway Smooth Muscle Transcriptomic Response to TNFα and Budesonide Exposure

2018 American Medical Informatics Association Annual Symposia, San Francisco, CA
Integration of Transcriptomic Data Identifies Global and Cell-Specific Asthma-Related Gene Expression Signatures (Finalist of Student Paper Award)

Open-Source Tools

RAVED (https://github.com/HimesGroup/raved) - Reproducible Analysis and Validation of Expression Data
Brocade (https://github.com/HimesGroup/brocade) - Reproducible Analysis of ChIP-Seq Data
REALGAR (http://realgar.org/) - Reducing Associations by Linking Genes And omics Results

Teaching

2021-2025 Guest Lecturer. Genetic Epidemiology (EPID 575), University of Pennsylvania, Philadelphia
Lecture(s): Community Resources for Genetic Studies

2020-2025 Guest Lecturer. Introduction to Biomedical Informatics (BMIN 501), University of Pennsylvania, Philadelphia
Lecture(s): Introduction to bioinformatics

2018-2021 Guest Lecturer. Data Science for Biomedical Informatics (BMIN503), University of Pennsylvania, Philadelphia
Lecture(s): 1) Gene expression data analysis: microarray and RNA-Seq and 2) Functional enrichment analysis.

Lectures by Invitation

2021 Instructor. A Practical, Hands-on Introduction to Genomic Analysis in Pulmonary Medicine (Postgraduate Course 7), American Thoracic Society (Virtual)
Lecture(s): RNA-Seq: Alignment, QC, and Analysis

Journal and Conference Reviewer

AMIA Annual Symposium Proceedings
AMIA Joint Summits on Translational Science
BMC Genomics
Pediatric Pulmonology
Respiratory Research
Scientific Reports