Camille M. Moore, PhD

Camille M. Moore, PhD, is an associate professor at National Jewish Health. Dr. Moore is in the Department of Immunology and Genomic Medicine and Center for Genes, Environment & Health.

Associate Professor

Office of Academic Affairs

Department of Immunology and Genomic Medicine

Center for Genes, Environment & Health

Research Areas

- Analysis of bulk and single cell RNA-sequencing data
- Genetic association studies
- Longitudinal and Correlated Data
- Missing Data

Special Interests

Camille Moore, PhD is an associate professor in the Center for Genes, Environment and Health (CGEH) at National Jewish Health and also holds an appointment in the Department of Biostatistics and Informatics at the University of Colorado Anschutz Medical Campus, where she has taught several graduate level biostatistics courses including Advanced Data Analysis, Statistical Methods for Genetic Association Studies, and Statistical Methods in Genomics. Dr. Moore directs the CGEH Analysis Core, managing a group of 5 biostatisticians and bioinformaticians performing genetic, gene expression, epigenetic, and other ‘omics analyses. She also oversees bioinformatic analysts in the Seibold and Janssen labs and serves as director of the Biostatistics, Bioinformatics and Environmental Sampling Core for the ENIGMA pediatric asthma cohort PPG. Dr. Moore’s research focuses on the development of statistical methods for analyzing bulk and single-cell RNA-sequencing data from longitudinal cohort studies and she has contributed to several RNA-seq analysis R packages. In addition, she has led the genetic analyses in a resequencing study of idiopathic pulmonary fibrosis and has expertise in gene expression network analyses to identify asthma endotypes. Dr. Moore currently serves as a co-investigator on several NIH grants exploring the relationships between bulk and single-cell RNA-sequencing gene expression data and respiratory diseases, including asthma, SARS-CoV-2, acute respiratory distress syndrome, and chronic beryllium disease.

Education

Education

2013 - 2016 Univeristy of Colorado Denver, Aurora, CO

2011 - 2013 University of Colorado Denver, Aurora, CO

2003 - 2007 New York University, New York, NY

1999 - 2003 Cornell University, Ithaca, NY

Academic Affiliations

Clinical Associate Professor

Depatment of Biostatistics and Informatics

University of Colorado Anshutz Medical Campus

Awards & Recognition

2017-2020: Webb-Waring Early Career Investigator, Boettcher Foundation

2015: Strother Walker Award for Outstanding Performance in the Biostatistics PhD Program, University of Colorado Denver, Aurora, CO

2013: Marvin Porter Award for Outstanding Performance in the Biostatistics MS Program, University of Colorado Denver, Aurora, CO

Publications

Moore C, ...Fingerlin TE, Schwartz DA. Resequencing Study Confirms That Host Defense and Cell Senescence Gene Variants Contribute to the Risk of Idiopathic Pulmonary Fibrosis. Am J Respir Crit Care Med2019 Jul 15;200(2):199-208. doi: 10.1164/rccm.201810-1891OC. PubMed PMID: 31034279; PubMed Central PMCID: PMC6635791.

Moore CM, Seibold MA. Possibilities and promise: Leveraging advances in transcriptomics for clinical decision making in allergic diseases. J Allergy Clin Immunol2022 Oct;150(4):756-765. doi: 10.1016/j.jaci.2022.08.016. Epub 2022 Aug 28. Review. PubMed PMID: 36037873.

Vestal BE, Wynn E, Moore CM. lmerSeq: an R package for analyzing transformed RNA-Seq data with linear mixed effects models. BMC Bioinformatics2022 Nov 16;23(1):489. doi: 10.1186/s12859-022-05019-9. PubMed PMID: 36384492; PubMed Central PMCID: PMC9670578.

Wynn EA, Dide-Agossou C, Reichlen M, Rossmassler K, Al Mubarak R, Reid JJ, Tabor ST, Born SEM, Ransom MR, Davidson RM, Walton KN, Benoit JB, Hoppers A, Loy DE, Bauman AA, Massoudi LM, Dolganov G, Strong M, Nahid P, Voskuil MI, Robertson GT, Moore CM, Walter ND. Transcriptional adaptation of Mycobacterium tuberculosis that survives prolonged multi-drug treatment in mice. mBio2023 Oct 31;14(6):e0236323. doi: 10.1128/mbio.02363-23. [Epub ahead of print] PubMed PMID: 37905920; PubMed Central PMCID: PMC10746229.

Moore CM, MaWhinney S, Forster JE, Carlson NE, Allshouse A, Wang X, Routy JP, Conway B, Connick E. Accounting for dropout reason in longitudinal studies with nonignorable dropout. Stat Methods Med Res. 2017 Aug;26(4):1854-1866. doi: 10.1177/0962280215590432. Epub 2015 Jun 15. PubMed PMID: 26078357; PubMed Central PMCID: PMC4679750.

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Locations

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