INTERNATIONAL GENETIC
EPIDEMIOLOGY SOCIETY

Save The Date: Monday, February 23, 2026
11 am (EST), 8 am (PST) and 5 pm (CET)

Dear IGES members,

IGES hosts regular virtual journal clubs throughout the year to increase IGES members' familiarity with emerging and classic literature in genetic epidemiology and to foster discussion and networking among members. This month’s journal club features a study of over 230,000 whole genomes from the *All of Us* Research Program demonstrating that self-identified race and ethnicity align with continuous, rather than discrete, genetic variation. Proper adjustment for both genome-wide and locus-specific ancestry is necessary to prevent false associations and to ensure rigor in genetic studies. Make plans to attend our next meeting!

Title: "Integrating Population Genetics and Genetic Epidemiology to Unravel Complex Traits”

***Am J Hum Genet*. 2025 Jun 5;112(6):1286-1301.**

Article: https://doi.org/10.1016/j.ajhg.2025.04.012

Given the complementary content, the following paper will also be presented:

***Nat Commun*. 2023 Nov 7;14(1):6802.**

Article: https://doi.org/10.1038/s41467-023-42491-0

Abstract (adapted from the original abstract):

While U.S. populations are widely recognized as stratified and admixed at the continental level, subcontinental ancestry is rarely incorporated into genetic studies. This omission can

lead to residual genome-wide and locus-specific confounding, biasing association analyses and the development of polygenic risk scores. In addition, the extent to which U.S. Census-based self-identified race and ethnicity relates to genetic diversity at continental and subcontinental scales remains unclear.

To address these gaps, we analyzed approximately two million common variants from 230,016 unrelated whole genomes in the *All of Us* Research Program, integrating classical population genetic approaches with global reference panels. We further examined subcontinental European admixture by incorporating genome-wide data from ~19,000 individuals representing 79 European populations and five European American cohorts.

Our analyses reveal that self-identified race and ethnicity groups form continuous gradients of genetic variation rather than discrete clusters, with substantial heterogeneity across regions. Hispanic/Latino participants exhibited a broad spectrum of ancestries and accounted for over 90% of individuals not identifying within race categories. Ancestry was significantly associated with BMI and height. Notably, adjustment for both genome-wide and locus-specific ancestry eliminated false-positive associations at highly differentiated loci, underscoring the necessity of accounting for subcontinental ancestry in genetic association studies.

Registration Link:

https://msm-edu.zoom.us/meeting/register/OjM24iOFQmy-EpO9Ar7IZg

After registering, you will receive a confirmation email containing information about joining the meeting.

Bio:

Dr. Mateus Gouveia is originally from Brazil, where he earned his M.Sc. and Ph.D. in Population Genetics and Genomics/ Bioinformatics from the Federal University of Minas Gerais, with part of his doctoral research conducted at the National Cancer Institute (NCI). Mateus completed his postdoctoral training at the Brazilian National Health Institute (Fiocruz) and the National Human Genome Research Institute (NHGRI), where he later served as a Research Fellow at the Center for Research on Genomics and Global Health (CRGGH). At CRGGH, he led large-scale genomic studies using supercomputing and cloud-based platforms, including the *All of Us* Research Program. Mateus' research focuses on population genomics, genetic epidemiology with expertise in large-scale and biobank-based ancestry and association analyses. He received an NIH K99/R00 award to investigate how subcontinental ancestry influences genetic association studies; work featured in *Science* and NHGRI press releases. Mateus has authored over 40 high-profile peer-reviewed publications and recently joined Morehouse School of Medicine as an Assistant Professor of Genetics in the Department of Public Health Education. Dr. Gouveia's Lab takes an integrative approach to population genetics and genetic epidemiology to advance precision medicine in populations with broad ancestral backgrounds.

Do you have any suggestions for interesting topics, papers, or presenters for further talks? Or would you like to support us in organizing the Journal Club? Please contact Dr. Silke Szymczak (silke.szymczak@uni-luebeck.de)

On behalf of the organizing team of the IGES Journal Club,
Silke Szymczak
Heejong Sung
Cheryl Cropp