Yusuph Mavura

Epidemiologist, Biostatistician And Bioinformatician Specializing In Human Genetics.

Genetic epidemiologist, biostatistician and bioinformatician specializing in genomic and real-world data analysis, with focus on health outcomes in diverse populations. Proven track record in securing competitive funding and leading collaborative projects advancing precision medicine and public health.

Contact

Address
San Francisco, CA, 94158

Phone
+1 470 399 1865

E-mail
Yrmavura@gmail.com

Skills

- Exome/Genome sequence data analysis
- Clinical/mendelian genetics
- Complex disease genetics
- Population genetics
- Statistical genetics
- RNASeq data analysis
- Genetic epidemiology
- Causal inference using observational data

Relevant Research Experience

2023-01 - Current

Principal Investigator

University of California San Francisco, San Francisco, CA

- Wrote and secured the highly competitive NHGRI F99/K00 Predoctoral to Postdoctoral Transition Award as Principal Investigator with an exceptional impact score of 10, facilitating dissertation research on "Blood Pressure Polygenic Scores, Target Organ Damage, and Antihypertensive Drug Effects: Insights from Longitudinal Real-World Clinical Data."
- .Designed and executed comprehensive analyses of large-scale genomic and electronic health records (EHR) data to evaluate the clinical utility of polygenic risk scores in an ancestrally diverse real-world cohort.

2019-09 - 2024-12

Junior Principal Investigator

University of California, San Francisco, San Francisco, CA

- Spearheaded a collaborative research project across multiple centers across the US in the $70 million NHGRI clinical sequencing exploratory research (CSER) consortium, focusing on assessment of diagnostic yield from genome and exome sequencing in over 3,000 ancestrally diverse prenatal, Neonatal intensive care unit (NICU), and pediatric cases.
- Analyzed and harmonized genomic, clinical and questionnaire data to demonstrate comparable diagnostic yield across genetic ancestries from exome and genome sequencing for diagnostic testing.
- Primary author to an empirical paper under review presenting primary diagnostic yield findings of CSER, advancing the understanding of genomic diagnostic testing in diverse populations.

2019-09 - 2024-12

PhD Student Researcher

University of California, San Francisco, San Francisco, CA

- Analyzed diagnostic yield of exome sequencing in ancestrally diverse newborns with suspected metabolic disorders as part of the Newborn Sequencing (NBSeqNext) program at UCSF,

- General epidemiology and study design
- Grant writing
- Scientific communication and writing
- Python
- Bash scripting
- R
- Stata
- Perl

Languages

English — Native or Bilingual

Swahili — Native or Bilingual

contributing to the evaluation of genomic sequencing in newborn screening.
- Conducted pan-cancer, cross-tissue transcriptome-wide association study (TWAS) using UKBiobank and Genetic Epidemiology Research on Aging (GERA) cohort data to explore pleiotropic effects in cancer, enhancing understanding of shared genetic architecture across cancer types.
- Spearheaded collaborative study examining genomic rearrangement landscape in localized prostate cancer samples from Nigerian men of African descent, addressing critical gaps in genomic research diversity.

2017-08 - 2018-12

Master's Researcher

Georgia Institute of Technology, Atlanta, GA

- Analysis of mutations in cancer driver genes in matched primary, metastatic and recurrent ovarian cancer whole-exome sequencing samples (WES)

2018-06 - 2018-08

Intern

National Institutes of Health (NIH), Bethesda, MD

- Conducted a Genome-Wide Association study (GWAS) which identified multiple new risk loci for pancreatic cancer in East Asian populations

Education

2019-09 - 2025-03

Ph.D.: Epidemiology and Translational Science

University of California, San Francisco - San Francisco, CA

Advisor: Neil Risch, PhD

- Dissertation: Blood Pressure Polygenic Scores, Target Organ Damage, and Antihypertensive Drug Effects: Insights from longitudinal Real-World Clinical Data.

2017-08 - 2018-12

M.S.: Bioinformatics

Georgia Institute of Technology - Atlanta, GA

2012-05 - 2016-06

B.S.: Biochemistry and Molecular Biology

Jomo Kenyatta University of Agriculture And Technology - Nairobi, Kenya

Publications

- Mavura Y, Song H, Xie J, Tamayo P, Mohammed A, Lawal AT, Bello A, Ibrahim S, Faruk M, Huang FW., Transcriptomic profiling and genomic rearrangement landscape of Nigerian prostate cancer., Prostate., 01/04/23, 10.1002/pros.24471, 36598071

- Kamran SC, Xie J, Cheung ATM, Mavura MY, Song H, Palapattu EL, Madej J, Gusev A, Van Allen EM, Huang FW., Tumor Mutations Across Racial Groups in a Real-World Data Registry., JCO Precis Oncol., 11/01/21, 10.1200/PO.21.00340, 34994651
- Oni-Orisan A, Mavura Y, Banda Y, Thornton TA, Sebro R., Embracing Genetic Diversity to Improve Black Health., N Engl J Med., 03/25/21, 10.1056/NEJMms2031080, 33567186
- Mavura MY, Huang FW., How Cancer Risk SNPs May Contribute to Prostate Cancer Disparities., Cancer Res., 07/15/21, 10.1158/0008-5472.CAN-21-1146, 34266915
- Yusuph Mavura, Nuriye Sahin-Hodoglugil, Ugur Hodoglugil, Mark Kvale, Pierre-Marie Martin, Jessica Van Ziffle, W. Patrick Devine, Sara L. Ackerman, Barbara A Koenig, Pui-Yan Kwok, Mary E. Norton, Anne Slavotinek, Neil Risch., Diagnostic Yield of Exome Sequencing in a Diverse Pediatric and Prenatal Population is not Associated with Genetic Ancestry., medRxiv., 05/24/23, 10.1101/2023.05.19.23290066, In Press at npj Genomic Medicine
- Yusuph Mavura, David Crosslin, Kathleen DM Ferar, John Greally, Lucia Hindorff, Gail P Jarvik, Sara Kalla, Barbara A Koenig, Mark Kvale, Pui-Yan Kwok, Mary Norton, Sharon E. Plon, Bradford C. Powell, Anne Slavotinek, Michelle L Thompson, Alice B Popejoy, Eimear E. Kenny, Neil Risch., Diagnostic yield of genome and exome sequencing in the ancestrally diverse CSER Phase II consortium is not associated with genetic ancestry in a variety of clinical settings., In preparation

Memberships

American Society of Human Genetics (ASHG)
ASHG Career Development Committee 2025-2027