Use of Race, Ethnicity, and Ancestry as Population Descriptors in Genomics Research

Public Workshop: June 14, 2022

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TUESDAY, JUNE 14, 2022 12:30 – 5 PM ET

12:30–12:40 PM ET   **Welcome and Goals for the Workshop**
Charmaine Royal, *Committee Co-Chair*
Robert O. Keohane Professor of African & African American Studies, Biology, Global Health, and Family Medicine & Community Health
Director, Duke Center on Genomics, Race, Identity, Difference and Duke Center for Truth, Racial Healing & Transformation
Duke University

Aravinda Chakravarti, *Committee Co-Chair*
Director, Center for Human Genetics and Genomics Muriel G & George W Singer
Professor of Neuroscience & Physiology
New York University Grossman School of Medicine

SESSION I: EXAMINING USE OF POPULATION DESCRIPTORS IN GENOMICS RESEARCH

Moderator: John Novembre, University of Chicago

Objectives
• To explore what types of population descriptors are needed for genetics and genomics studies
  • What is a genetics study trying to accomplish?
  • Who is sampled? Why are they sampled? What are participants called, and why?
• To examine how and why genetics studies should or should not incorporate social categories and environmental factors

12:40–12:45 PM   **Brief Introduction to the Session**
John Novembre
Professor, Department of Human Genetics, Department of Ecology & Evolution
University of Chicago

12:45–1:45 PM   **Speakers' Talks**
Gil McVean
Professor of Statistical Genetics
Director, Big Data Institute
Fellow of Linacre College
University of Oxford

Akinyemi Oni-Orisan
Assistant Professor, Department of Clinical Pharmacy
University of California, San Francisco School of Pharmacy

Nancy Cox
Director, Vanderbilt Genetics Institute
Director, Division of Genetic Medicine
Mary Phillips Edmonds Gray Professor of Genetics
Vanderbilt University

Graham Coop
Professor, Department of Evolution and Ecology and Center for Population Biology
University of California, Davis

1:45–2:25 PM	**Q&A with speakers**
2:25–2:40 PM	**Break**

SESSION II: USE OF POPULATION DESCRIPTORS BY BIOBANKS AND OTHER RESEARCH CONSORTIA

Moderator: Ann Morning, New York University

Objectives

- To examine how and why biobanks use taxonomies currently, especially in areas of large diversity
- To explore how legacy data might be managed and merged with future data
- To learn how large-scale data collection projects are designed

2:40–2:45 PM **Brief Introduction to the Session**
Ann Morning
Associate Professor, Department of Sociology
Academic Director, 19 Washington Square North (NYU Abu Dhabi in NY)
New York University

2:45–3:30 PM **Speakers' Talks**
Phil Tsao
Professor (Research), Medicine – Cardiovascular Medicine
Stanford University

Alice Popejoy
Assistant Professor, Department of Public Health Sciences
University of California, Davis

Mashaal Sohail
Associate Professor, Center for Genomic Sciences
National Autonomous University of Mexico

3:30–4:00 PM **Q&A with Speakers**

4:00–4:10 PM **Break**

SESSION III: COMMUNITY INPUT ON POPULATION DESCRIPTORS IN GENOMICS RESEARCH

Moderator: Charmaine Royal, Duke University

Objective	• To hear from a variety of interested parties on the following topics:
	  • What works and doesn't work about the current population descriptors used in genomics research?
	  • What could be improved in current use of population descriptors in genomics research?

4:10–4:15 PM

Introduction to the Session
Charmaine Royal
Robert O. Keohane Professor of African & African American Studies, Biology, Global Health, and Family Medicine & Community Health
Director, Duke Center on Genomics, Race, Identity, Difference and Duke Center for Truth, Racial Healing & Transformation
Duke University

4:15–4:55 PM

Speakers' Comments
Jennifer Webster
Senior Director, Precision Medicine RWE Lead
Pfizer

Santiago Molina
Postdoctoral Fellow, Sociology/Science in Human Culture
Department of Sociology
Weinberg College of Arts & Sciences
Northwestern University

Norbert Tavares
Program Manager, Cell Biology
Chan-Zuckerberg Initiative

King Jordan
Professor, School of Biological Sciences
Director, Bioinformatics Graduate Program
Georgia Institute of Technology

Dianalee McKnight
Medical Affairs Director, Emerging Clinical Omics
Invitae

Ramya M. Rajagopalan
Associate Director, Training, Evaluation, and Qualitative Research
Center for Empathy and Technology, T. Denny Sanford Institute for Empathy and Compassion
University of California, San Diego

Stacy Christiansen
Managing Editor, *JAMA*
Chair, *AMA Manual of Styles*

Hannah Wand
Director, Preventive Genomics Program

Genetics Counselor
Stanford Health Care

4:55–5:00 PM   **Concluding Remarks**

5:00 PM   **Adjourn**