

# Population Descriptors in Genomic Research: Applying the NASEM Recommendations

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*Moderated by*  
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# Using Population Descriptors in Genetics and Genomics Research

*A New Framework For An Evolving Field*

**Presentation to the CERA ELSI Friday Forum**

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# Statement of Task

The committee's work included:

- **Assessing use of race, ethnicity, and other population descriptors** in the basic science of genetics and genomics, health risk as a function of our genomes, and health disparities
- **Developing “best practice” approaches** for the appropriate use of population descriptors
- **Discussing obstacles to adoption and implementation** of best practices
- **Proposing potential implementation strategies** to help enhance the adoption of best practices by the research community
- **Out of scope:** use of race and ethnicity in clinical care and biomedical research generally; racism in science and genomics; providing policy recommendations to NIH and government agencies

# Problems with the Current Use of Population Descriptors

## 1. Continuing use of race as a measure of human genetic variation

- Scientific problem: Racial groupings do not map on to or capture complex patterns of human genetic variation, so they make for a poor tool or proxy for biological difference

# Problems with the Current Use of Population Descriptors

## 1. Continuing use of race as a measure of human genetic variation

- Scientific problem: Racial groupings do not map on to or capture complex patterns of human genetic variation, so they make for a poor tool or proxy for biological difference
- Social problem: Using racial groupings in genomic research sends the erroneous message that these socially constructed groups (e.g., OMB categories) are objective and discrete entities that reflect innate, fixed, and meaningful biological differences
- Such “typological thinking”
  - facilitates ongoing beliefs in racial hierarchies
  - takes observed racial differentials (e.g. in health outcomes or education) to be inevitable rather than responsive to changes in policy or practice

# Problems with the Current Use of Population Descriptors

2. **The failure to realize that population differences reflect differences in environmental exposures as well as genetic variant frequencies**
  
3. **The variable, inconsistent, and unreflective use of population descriptors such as race and ethnicity within and across studies**
  - Ex: Referring to “race,” “ethnicity,” and “ancestry” interchangeably
  
  - Ex: Mixing different types of group labels within a single study, such as “African American” (ethnic label), “Finnish” (national or ethnic label), “Jewish” (religious or ethnic label), “White” (racial label) and “East Asian” (geographic label)

# What is a Population Descriptor?

... a **concept of difference or classification scheme** that categorizes individuals into groups or “populations” based on a perceived characteristic or dimension of interest.

**Descent-associated population descriptors** classify populations whose members are thought to share some characteristic deriving from their common origin. Human beings across the globe have devised a family of descent-associated categorization systems (e.g., clan, caste, tribe, ancestry, ethnicity, indigeneity, race, etc.).

**Group labels**—such as “French” or “Yoruba”—are then applied to the populations identified.

# Population Descriptors Considered in the Report

## Ancestry

A person's origin or descent, lineage, "roots," or heritage

## Genetic ancestry

The paths through an individual's family tree by which they have inherited DNA from specific ancestors

## Geography

Spatial location or geography can be measured by various indicators, such as an individual's birthplace, current place of residence, or series of previous residences

## Ethnicity

Classifies human beings according to claims of shared heritage, often based on perceived cultural similarities (e.g., language, religion, foodways, dress, norms)

## Indigeneity

Emphasizes a group's enduring tie to a particular geographic location as well as shared culture and traditions

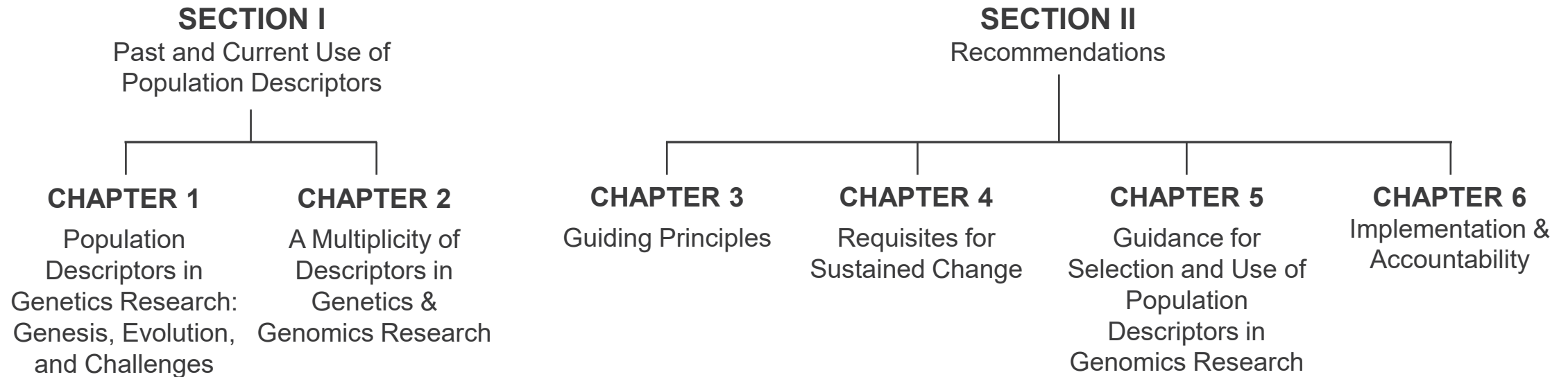
## Race

Classifies—and often ranks—human beings according to claims of shared ancestry based on perceived innate biological similarities

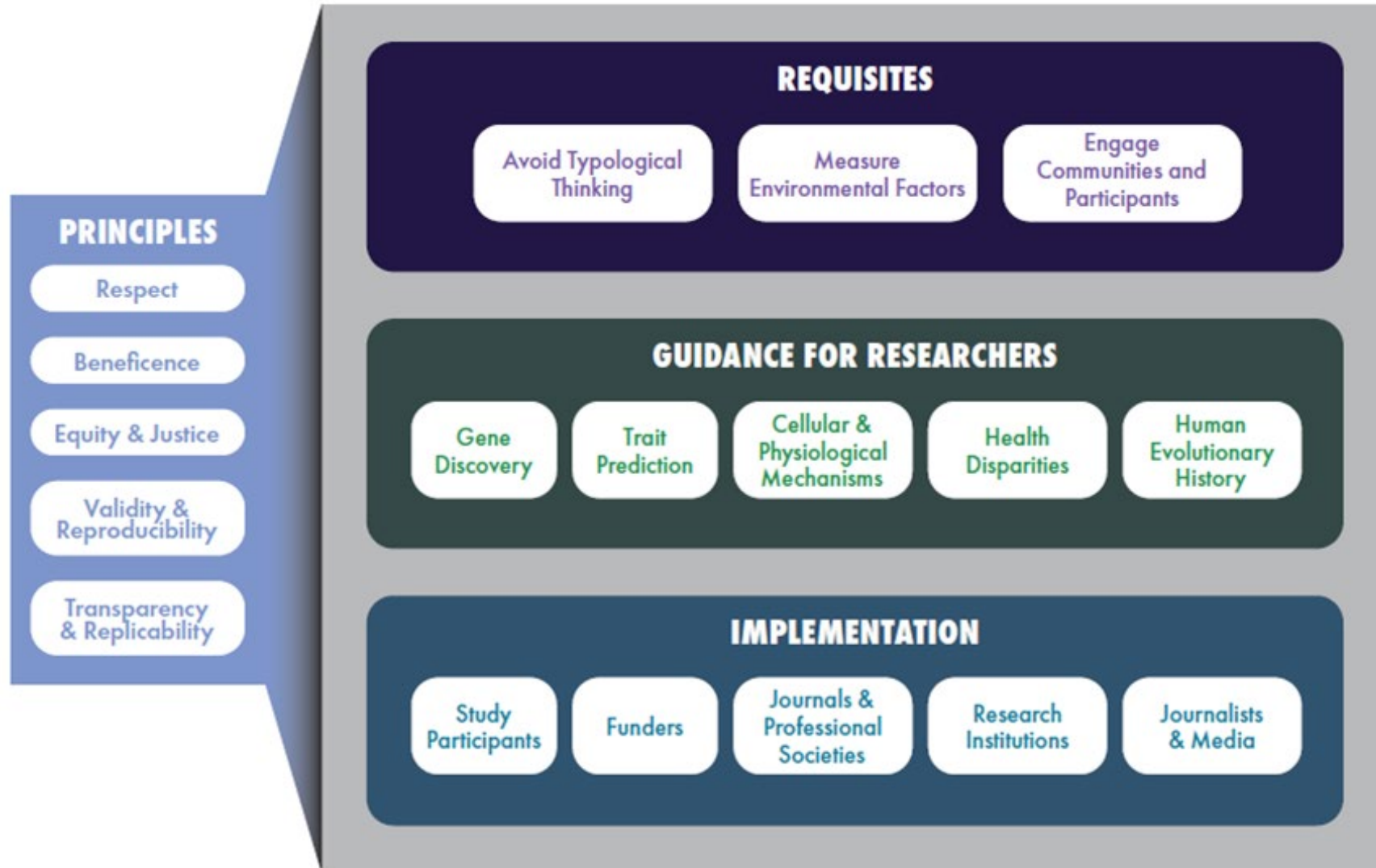


# Using Population Descriptors in Genetics & Genomics Research

## A New Framework for an Evolving Field



# What Makes this Report Unique?



# Requisites to Sustain Change

## Avoid typological thinking

- There is a misconception that humans can be grouped into discrete, innate biological categories
- Patterns of human genetic variation are complex
- Researchers should avoid the inaccurate assumptions of typological thinking
- **See Recommendations 1-3**

## Measure environmental factors

- Virtually all phenotypes result from interplay between genetic and environmental factors
- Descent-associated population descriptors are not good proxies for environmental effects
- Researchers should use variables that more precisely capture the information needed
- **See Recommendation 4**

## Engage communities and participants

- Misperceptions about human genetic variation and group identities can have negative impacts on individuals and communities and can impede research
- Research teams should include experts in community engagement to integrate perspectives from these communities throughout the research process
- **See Recommendation 5**

# Overview of Recommendations

The committee developed 13 recommendations that fall into three categories

## Requisites

- **Recommendations 1-5**
- For a general audience
- Overarching approaches important for the long-term success of this effort

## Guidance for Researchers

- **Recommendations 6-8**
- 16 best practices for different types of genomics studies
- For researchers using genetics and genomics data

## Implementation & Accountability

- **Recommendations 9-13**
- For selected key players in the research ecosystem
- To support researchers implementing these recommendations and best practices



# Guidance for Researchers

Researchers should tailor their use of population descriptors to the type and purpose of the study

- There are many types of genetics and genomics studies
- There is no one-size-fits-all solution
- Researchers are decision-makers about how population descriptors are used in research. The report charges researchers to be active participants in deciding whether to use population descriptors and, if so, which ones
- Researchers should be transparent and report their decisions about population descriptors and group labels
- **See Recommendations 6-8**

## *Types of Genomics Studies*

Gene Discovery –  
Mendelian

Trait Prediction –  
Mendelian

Gene Discovery –  
Complex Traits

Trait Prediction –  
Complex Traits


Cellular &  
Physiological  
Mechanisms


Health Disparities


Human  
Evolutionary  
History




































## LEGEND

 Preferred population descriptor(s)

 Should not be used

 In some cases; refer to Ch. 5 text and the decision tree in Appendix D

 Descriptors could be used if appropriate proxies for environmental, not genetic, effects

GENOMICS STUDY TYPE	Race	Ethnicity/ Indigeneity	Geography	Genetic Ancestry	Genetic Similarity	Notes
<b>1:</b> Gene Discovery - Mendelian Traits						Similarity suffices as a genetic measure; at fine-scale, other variables may be useful
<b>2:</b> Trait Prediction - Mendelian Traits						No population descriptors may be necessary for analysis
<b>3:</b> Gene Discovery - Complex Traits						Similarity suffices as a genetic measure
<b>4:</b> Trait Prediction - Complex Traits						Similarity suffices as a genetic measure
<b>5:</b> Cellular and Physiological Mechanisms						No population descriptors may be necessary for analysis
<b>6:</b> Health Disparities with Genomic Data						Not all health disparities studies rely on descent-associated population groupings, so none may be necessary for analysis
<b>7:</b> Human Evolutionary History						Reconstructing genetic ancestry may be of central interest

# Implementation & Accountability

The research ecosystem has many players who individually and collectively share responsibility for making changes and helping researchers implement these recommendations

Study participants

Funders of genomics  
research

Research institutions

Journals & professional  
societies

Journalists & media

**See Recommendations 9-13**

# Acknowledgements

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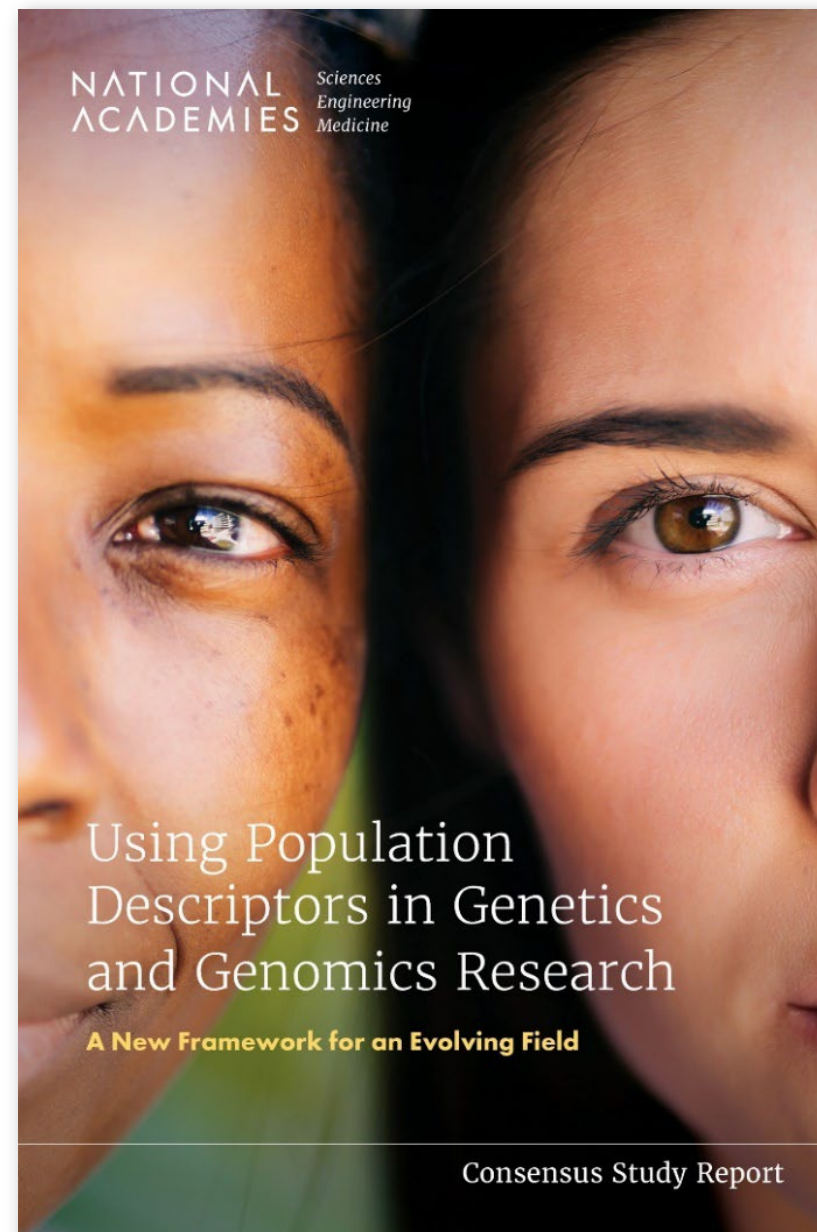
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Full report at  
<http://www.nap.edu>





# Save the Date!

ELSI Friday Forum resumes for a session on...

**Fair Access and Equity of Individualized  
Interventions for Ultrarare Genetic Conditions**

**September 8, 2023 at 12pm ET/9am PT**