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An Overview of the NHGRI Office of Communications

The power of inclusive, fact-driven communications about genomics

Sarah Bates, Communications Director

September 2023



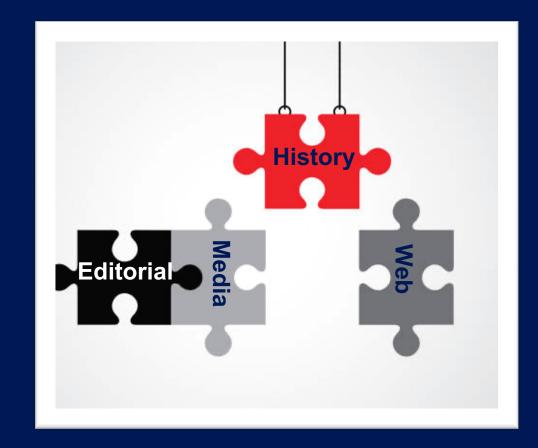


Guiding principles & values

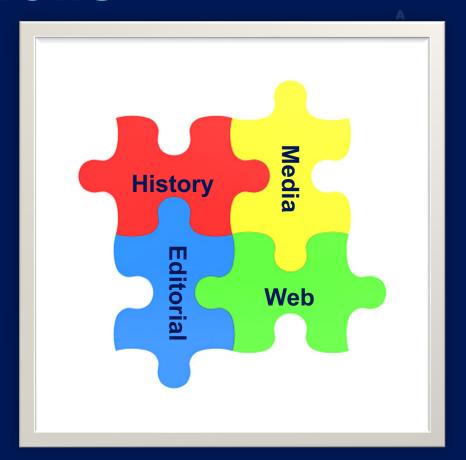
- Communications is integral to NHGRI strategy and operations
- Social, historical and ethical context is critical
- New tools and their changing uses and audiences continue to alter the science communications landscape
- Collaboration between researchers and science communicators is vital



Office of Communications







Now



Outline

- Overview of the Office of Communications (15 mins)
 Sarah Bates, NHGRI
- History of Genomics Program (15 mins)
 Christopher Donohue, NHGRI
- Information Science Research Talk Based upon NHGRI Archive (15 mins)

Spencer Hong & Thomas Stoeger, Northwestern

10 mins for Q&A



NHGRI Office of Communications

Sarah Bates

Director

Britny Kish

Deputy Director

Yewande Komolafe

Operations Coordinator

Editorial Team	Creative Team	History Team	Web Team	Public Affairs Team
Sonja Soo	Darryl Leja	Christopher Donohue	Radwan Kakar	Mauresa Pittman
Science Writer	Graphic Designer	Historian	Lead Web Developer	Lead Public Affairs Specialist
		Zach Utz		
Anna Rogers	Ernesto Del Aguila	Archivist	Kenya Smith	Jenn Montooth
Science Writer	Digital Arts Specialist		Midlevel Web Developer	Social Media Specialist
		Nicola Sugden		
		IRTA Fellow		
Theo Tiffney	Alvaro Encinas		Ellaha Sadat	Mukul Nerurkar
Communications Specialist	Videographer	Liz Dietz	Frontend Designer	Digital Information Specialist
		IRTA Fellow	, and the second	
	Julia Fekecs	Kris Wetterstrand		
	Digital Arts Specialist	Scientific Laiason to the Director for Extramural Activities		

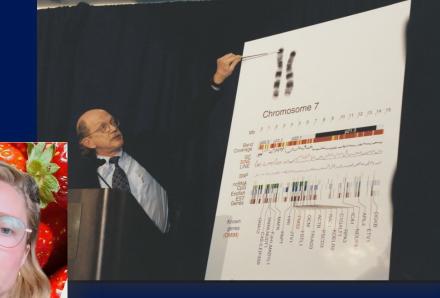




Now



The modern era of scicomm





Squishy sea creature vomits aging cells

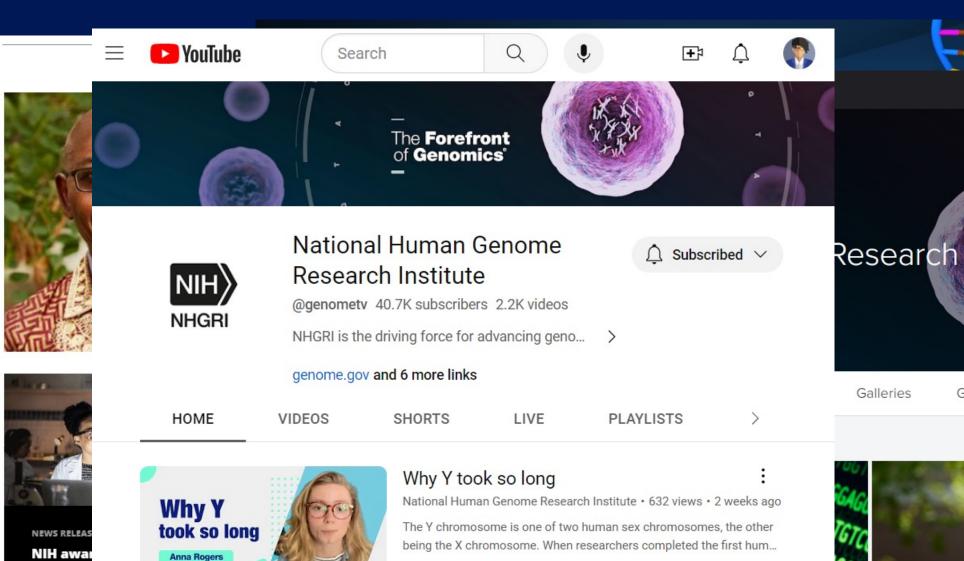
Anna RogersScience writer

basket of strawberries from the grocery store, and they look

Interdisciplinary



Engaging





Groups

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NHGRI's Oral History Collection

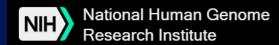
create go science (for early research

NIH

NHGRI



NHGRI's Oral History Collection features discussions with influential figures in the field of genomics Aneuploidy

















...Begin your search here

SEPTEMBER 18, 2023

National Advisory Council for Human Genome Research

Watch the live webcast of the Open Session from 10:30 a.m. to 6:00 p.m. ET.

Webcast

Agenda

NEWS RELEASE

NIH awards \$50.3 million for "multi-omics" research on human health and disease

THE GENOMICS LANDSCAPE

Human Genome Project leaders release video of virtual reunion



ABOUT NHGRI

2020 NHGRI Strategic Vision





In the Multimedia category, Prabarna Ganguly and Harriet Bailey earned top prize for their video "The Human <u>Pangenome</u>," published by the National Human Genome Research Institute. "Explaining DNA is never easy, so I was impressed by their mastery of blending animation and strong writing to effectively tell a story," said one judge.









Group Awards

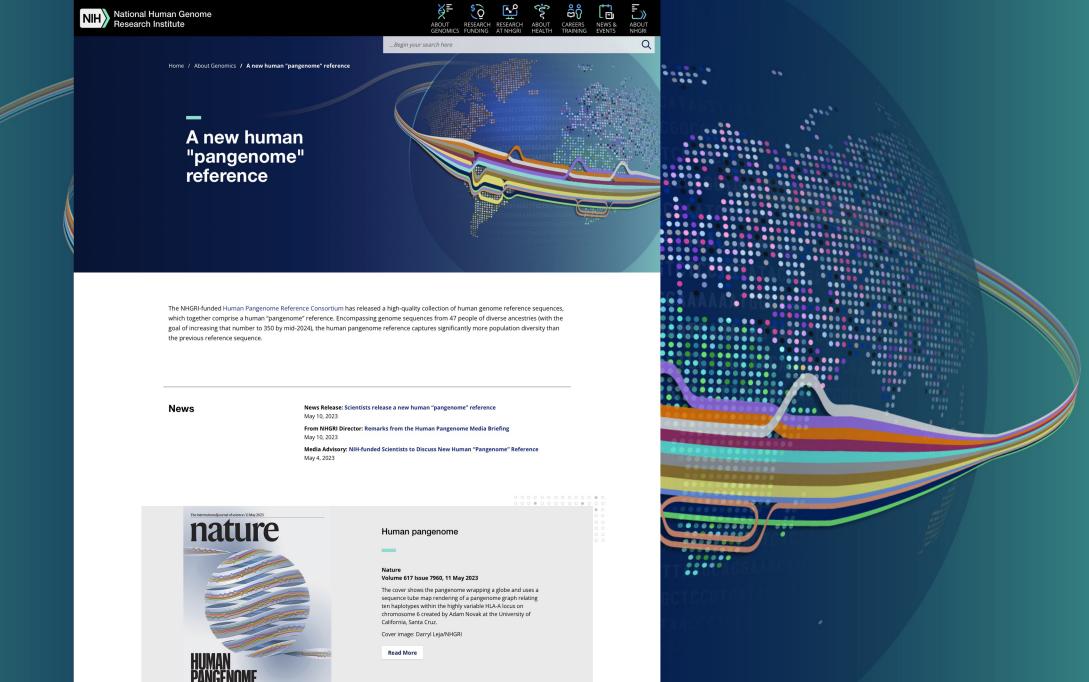
History of Eugenics Symposium Team

For extraordinary contributions to understanding the history of eugenics and scientific racism and their complex legacies in the modern health sciences.

- Sarah Bates, NHGRI
- Ernesto Del Aguila III., NHGRI
- · Christopher Donohue, NHGRI
- · Alvaro Encinas, NHGRI
- Prabarna Ganguly, NHGRI
- · Radwanullah Kakar, NHGRI
- Britny Kish, NHGRI
- · Jennifer Montooth, NHGRI

- Mukul Nerurkar, NHGRI
- Devona Perrineau, NHGRI
- Ellaha Sadat, NHGRI
- Jerryl Somani, NHGRI
- Jill Thomas, NHGRI
- · Zachary Utz, NHGRI
- Kris Wetterstrand, NHGRI

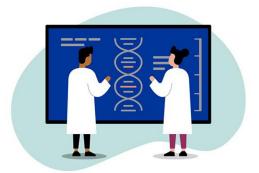




What is a reference genome sequence?



Why do we need a new human pangenome reference?

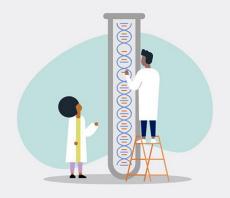


The original human genome reference sequence is outdated.

The original human genome reference sequence was generated by the Human Genome Project in 2003. While this reference sequence has been regularly updated as researchers fixed errors and filled in missing regions of the genome, it only reflected data generated from about 20 people. Most of that first human genome reference sequence was just from one person.

The previous human genome reference sequence has missing pieces (i.e., gaps).

The previous human genome reference sequence is only 92% complete, with an estimated 8% of the human genome missing because of gaps in the sequence. Recently, new types of DNA sequencing technologies have helped researchers read longer stretches of DNA at a time, allowing them to fill in missing sequences within those gaps, especially in areas that were repetitive and harder to read. The new human pangenome reference is more comprehensive and incorporates the missing 8% of the human genome sequence, adding over 100 million new bases.

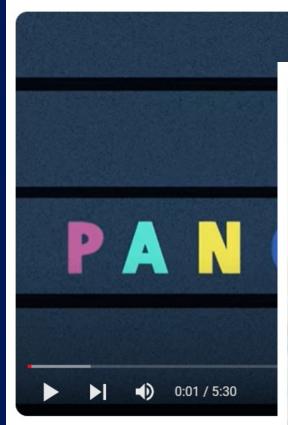




A human pangenome reference better reflects human diversity.

The new human pangenome reference includes genomic data from 47 people who are collectively more globally diverse. Researchers expect that number to reach 350 people by 2024. A human pangenome reference that better reflects genomic variation across all human populations will help ensure that it is beneficial for





The Human Pangenome



National Huma...

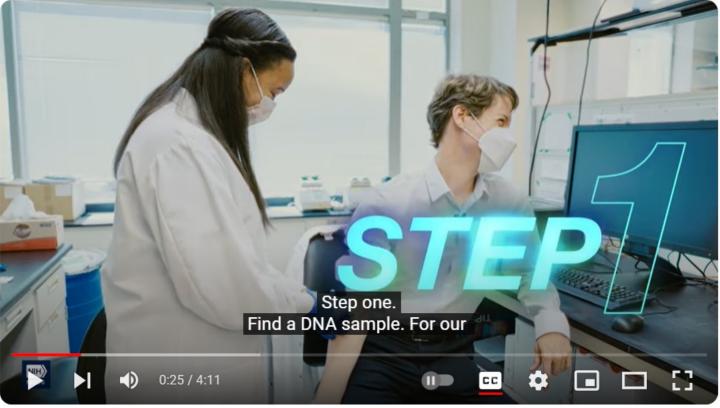
40.7K subscribers



Washaribasa

25K views 2 years ago

In 2003, biologists created the first ever l reference genome, was mostly made up



How to Sequence a Human Genome in 7 'Easy' Steps!



National Huma... 40.7K subscribers







Share





Join NHGRI researchers at the NIH Intramural Sequencing Center (NISC) as they show you step-by-step how to extract human DNA, sequence it, and interpret the data -- with some fun DNA high jinks along the way.





National Human Genome Research Institute

@genome_gov

Researchers from the @genome_gov-funded Human Pangenome Reference Consortium (@HumanPangenome) have completed a collection of new human reference genome sequences that much more accurately reflect global diversity! genome.gov/pangenome



11:08 AM · May 10, 2023 · 114K Views

III View Tweet analytics

194 Retweets 26 Quotes 417 Likes 41 Bookmarks





Uh oh. Our opossum is back and he looks very upset. Luckily, researchers are working to create a "pangenome," a collection of complete genomes in which everyone's differences are represented! go.usa.gov/xz5N2.

11:03 AM · Mar 16, 2022





NIH) Nati

National Human Genome Research Institute @genome gov

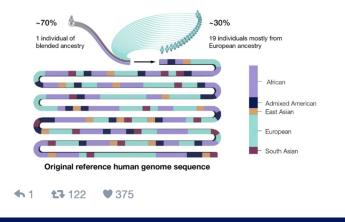
You don't need spidey sense to know that one reference genome cannot represent every population! That's why researchers are working to create a "pangenome," a collection of complete genomes in which everyone's differences are represented. go.usa.gov/xeMzw

11:20 AM · May 11, 2022



Top Tweet earned 54.1K impressions

Why did we need to update the human genome reference sequence? When it was created during the Human Genome Project, around 70% of it came from only one person with blended ancestry, which includes African, European, Admixed American, East Asian and South Asian ancestry. pic.twitter.com/xkx9jXwXAW



Using one reference genome to study all humans isn't fetch at all. It cannot possibly represent everyone! That's why researchers are working to create a "pangenome," a collection of complete genomes in which everyone's differences are represented. go.usa.gov/xeMzw



III View Tweet analytics

130 Retweets 17 Quotes 542 Likes 14 Bookmarks

Top media Tweet earned 31.7K impressions

There's no wrong time or place to remind people that it's time to stop seeing ourselves as having one complete human genome reference! One genome sequence can't possibly represent everyone's diversity. pic.twitter.com/EQHgoB3zIP





pangenome dramatically expands upon the original human genome reference.

Science

4 minute read · May 10, 2023 11:26 AM EDT · Last Updated 4 days ago

Human genome reboot better reflects global population

By Will Dunham v



Researchers say the new genetic map of humanity is more representatives of variety

By Pallab Ghosh

Science correspondent

The New Hork Times

Scientists Unveil a More Diverse Human Genome

The "pangenome," which collated genetic sequences from 47 people of diverse ethnic backgrounds, could greatly expand the reach of personalized medicine.



Genetics Breakthrough: Promising new era of ethnic diversity-informed tests and treatments



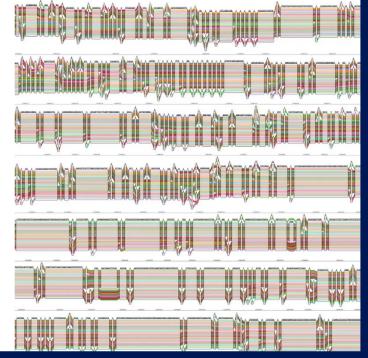














How we measure impact

- Monitoring tools: web, social, news
- Quantitative + qualitative measures



Top Articles

н	EΑ	DL	IN	ES

DNA project gives scientists diverse genome for comparison

Human genome reboot better reflects global population

A new, more diverse human genome offers hope for rare genetic diseases

A diverse human genome: "pangenoma"

DNA \"reference guide\" expanded to reflect human diversity

DNA \"reference guide\" expanded to reflect human diversity

World's first human PANGENOME is released

Scientists have updated the human genome to make it more equitable and inclusive

Ground-Breaking Genetics Library Finally Represents the Whole of Humanity

Scientists Just Made a Massive Change to the Human Genome: The 'Pangenome'

DNA project gives scientists diverse genome for comparison

This Updated Human Genome Map Will Change Medicine Forever

Collection of genome sequences hails new era in scientific research

Pangenome: DNA breakthrough could transform healthcare for people from diverse ethnic backgrounds

Scientists Unveil a More Diverse Human Genome

Scientists release a new human "pangenome" reference

Scientists have updated the human genome to make it more equitable and inclusive | CNN

Scientists have updated the human genome to make it more equitable and inclusive

Updated human DNA map captures diversity of life | CNN

Updated human DNA map captures diversity of life

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MSN Salud US (es)	67,151,557
MSN News Canada	67,151,557
MSN Health & Fitness	64,480,000
MSN News	59,740,000
MSN News	59,740,000
MSN News	59,740,000
MSN UK	59,520,000
MSN UK	59,520,000
New York Times Online, The	38,168,535
National Institutes of Health	35,266,063
CNN Online	33,909,950

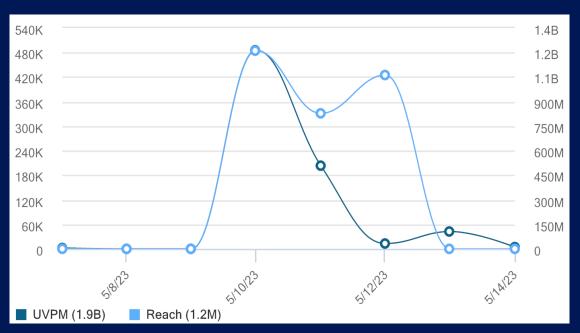


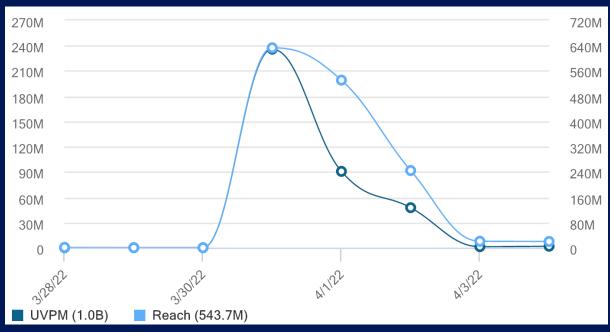


Reach (1.2M)



Measuring "reach"





Pangenome

T2T



National Human Genome Research Institute (NHGRI)

Y chromosome being annoyingly proud of the many, many repetitive regions in i DNA sequence.

All chromosomes have repetitive regions, but the Y chromosome has an unusual high percentage of repetitive DNA sequence (over 60% of the sequence!). This made it particularly difficult for scientists to study. Learn more about the Y chromosome: https://lnkd.in/e6k5FCwG







View video on YouTube. Credit: Ernesto Del Aguila III, NHGRI

The Y chromosome, along with the X chromosome, is often discussed for its role in sexual development. While these chromosomes play a central role, the factors involved in human sexual development are spread across the genome and very complex, giving rise to the array of human sex characteristics found among male, female and intersex individuals. These categories are not equivalent to gender, which is a social category. Additionally, recent work demonstrates that genes on the Y chromosome contribute to other aspects of human biology, such as cancer risk and severity.



History of Genomics Program

NHGRI Historian Christopher Donohue



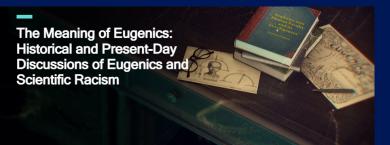
The story of the creation of the program









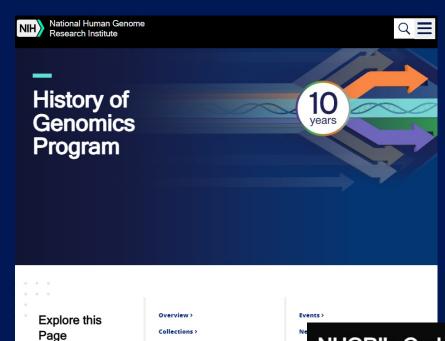


Event Details

Eugenics and scientific racism are widely misunderstood despite their long histories. Studying and sequencing the human genome were supposed to help eliminate common misconceptions about the biological differences between humans. After all, we are 99.9% the same according to our DNA.

And yet, why do these misconceptions continue to persist, resulting in modern day discrimination and bias? We look to the history of science and medicine to help explain.

Since its inception, the National Human Genome Research Institute (NHGRI) has funded forward-thinking research on the historical study of eugenics and other misuses of genetics and genetic information. This includes the broader social, ethical and legal implications (ELSI) of genomics through NHGRI'S ELSI Research Program.



Archive >
Educational Resources



Event Details

The National Human Genome Research Institute (NHGRI) of the National Institutes of Health will host a virtual roundtable to discuss social and behavioral genetics and genomics, including their benefits, limitations and potential for misuse. Social genomics is a field of emerging research that suggests scientists can use genomic variation to understand complex social behavior. Panelists will discuss genetics and genomics studies that may be stigmatizing as well as strategies

Educational Resources



TIMELIN

Eugenics: Its Origin and Development (1883 - Present) >



FACT SHEE

Eugenics and Scientific Racism >

NHGRI's Oral History Collection

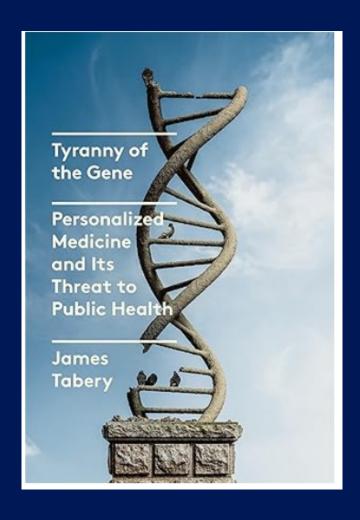


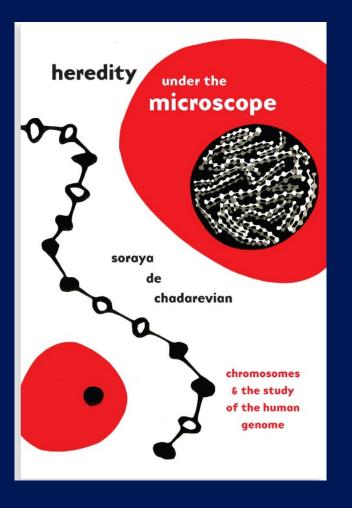
Erich Jarvis

Erich Jarvis, Ph.D., is a professor and head of the Laboratory of Neurogenetics of Language at the Rockefeller University. Dr. Jarvis' lab, which is part of the Howard Hughes Medical Institute, investigates the neurogenomics of complex traits such as vocal learning in animals, specifically in



Examples of publications







Archival Development and Analysis Guiding Principles

- Development and Implementation guided by FAIR (Findable, Accessible, Interoperable, and Reusable) Principles
- Further development of Core Collection and future datasets for scholarly community and other stakeholders
- Making more files and datasets available to public, scholarly community through ArchviesSpace
- Committed to asking (and answering) the big, complex questions about the HGP, the historical development of genomics, and how "team science" works



Archival initiative

ArchivesSpace



About this site

This archival repository contains over 1 million pages of scanned and digitized items pertaining to the history of both the field of genomics and the crucial role that the National Human Genome Research Institute has played in the fields development. It contains the largest single repository of items from the milestone scientific endeavor, the publicly-funded Human Genome Project (1990 - 2003), including the personal collections of key former NHGRI leadership and staff.

An important note for users navigating this site: Although we have captured and preserved digitally all the items contained within this archive, we are only able to make a small portion of those items publicly viewable. Many of the items within this archive contain sensitive information about grant funding processes, as well as patient information and

Research & analysis through SharePoint

Computational enrichment of the NHGRI archive for institutional insight and public access

Spencer Hong, Luís Amaral, Thomas Stoeger

100th session of the National Advisory Council for Human Genome Research



