



Guns Germs & Alleles

Gold Lab
Symposium

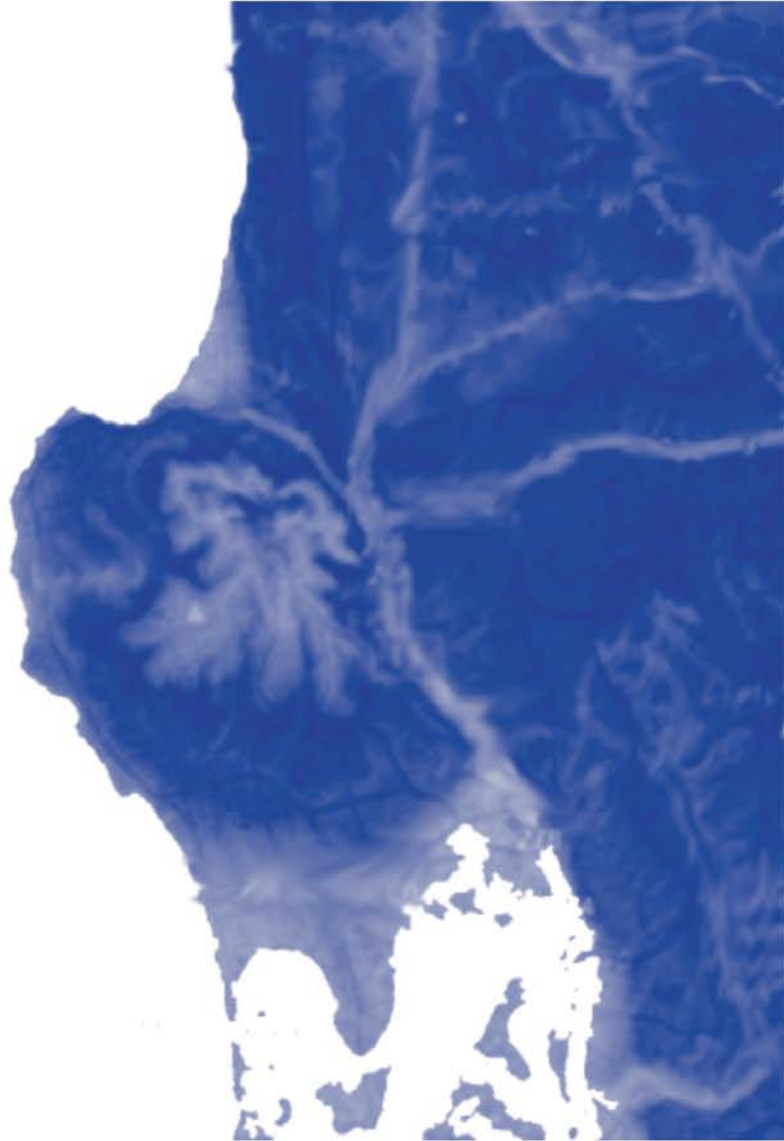
Keolu Fox, PhD



University of California, San Diego



SURFER

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INDIGENOUS FUTURES INSTITUTE

The IFI is a project concerned, principally, with the transformative power of the future. From its inception, the Western academy has excluded Black, Indigenous, and other minority communities from research. Relationships that existed, hinge on the violent history of experimentation, exploitation, and extraction within Black and Indigenous communities by scientists, anthropologists, and other researchers; fostering a legacy of harm and distrust.

Unchallenged, such histories catalyze futures that continue to foreclose the possibility of Black and Indigenous knowledge production, innovation, and, ultimately, life. In other words, unless we actively challenge harmful narratives, practices, and theories that haunt the halls of the academy, harm and violence will continue to shape Black and Indigenous futures. A focus on the future is not merely a utopian project; it requires the recognition of past harms and a commitment to addressing them on Black and Indigenous people's terms.

Rather than take "futurity" as an abstract concept focused uncritically on potentiality, the IFI takes to task the practice of futurity as an act of relational accountability and transformation. In pursuit of this goal, the IFI aims to put the power of scientific and academic knowledge back into the hands of communities that have been framed by dominant academic and scientific discourse as objects of study rather than producers of knowledge.



Kumeyaay Water Craft
(Tule Boats Grant)
Action Lab

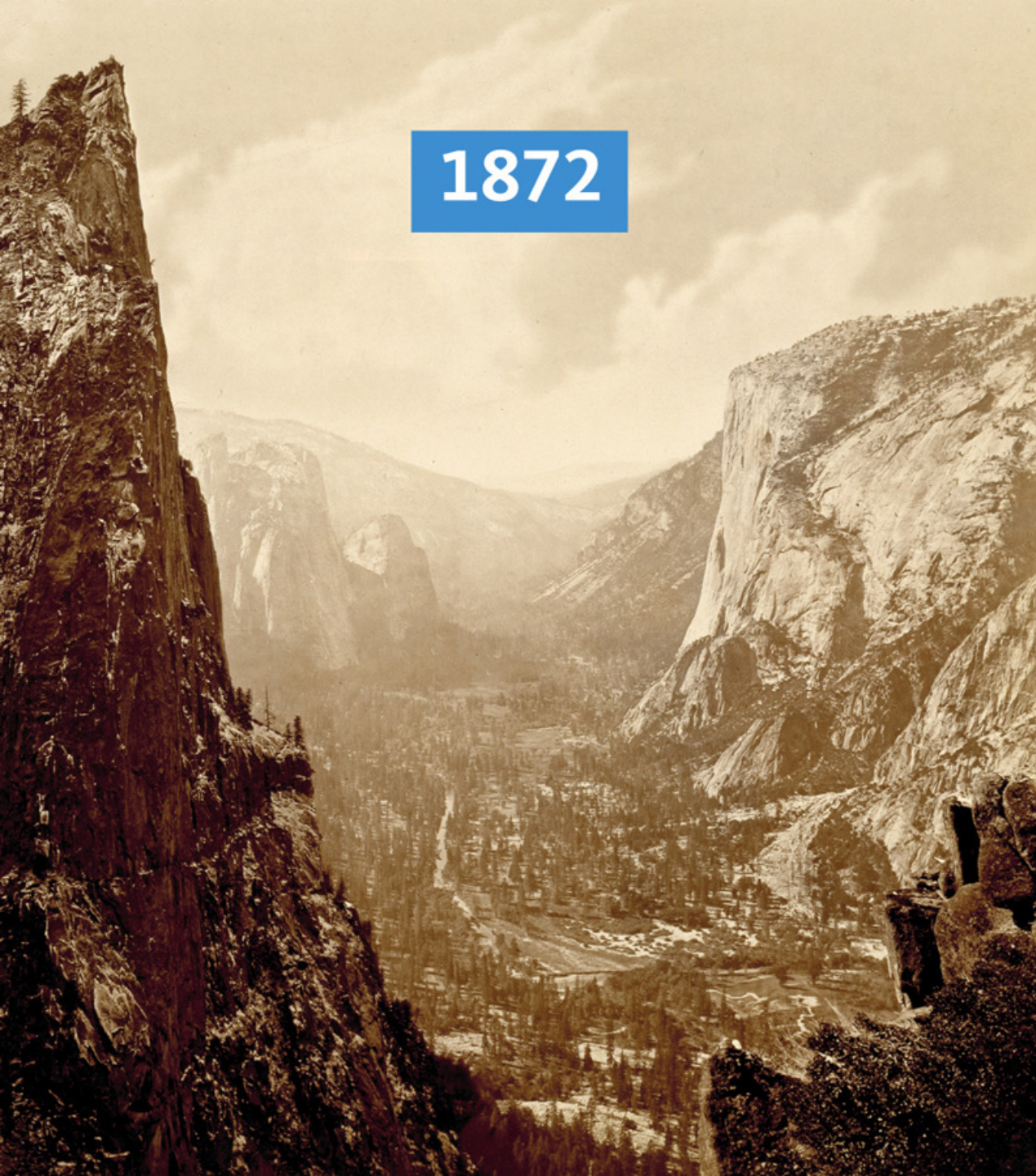
Quisque elit velit, efficitur eu erat non, suscipit consectetur neque. Sed a dignissim ex. Donec nec eleifend ipsum. Curabitur ligula dui.



Pasifika futurism
Action Lab

Aenean ut bibendum lacus. Nam vitae felis diam. Aenean ligula ligula, malesuada at volutpat ullamcorper, convallis quis dolor.

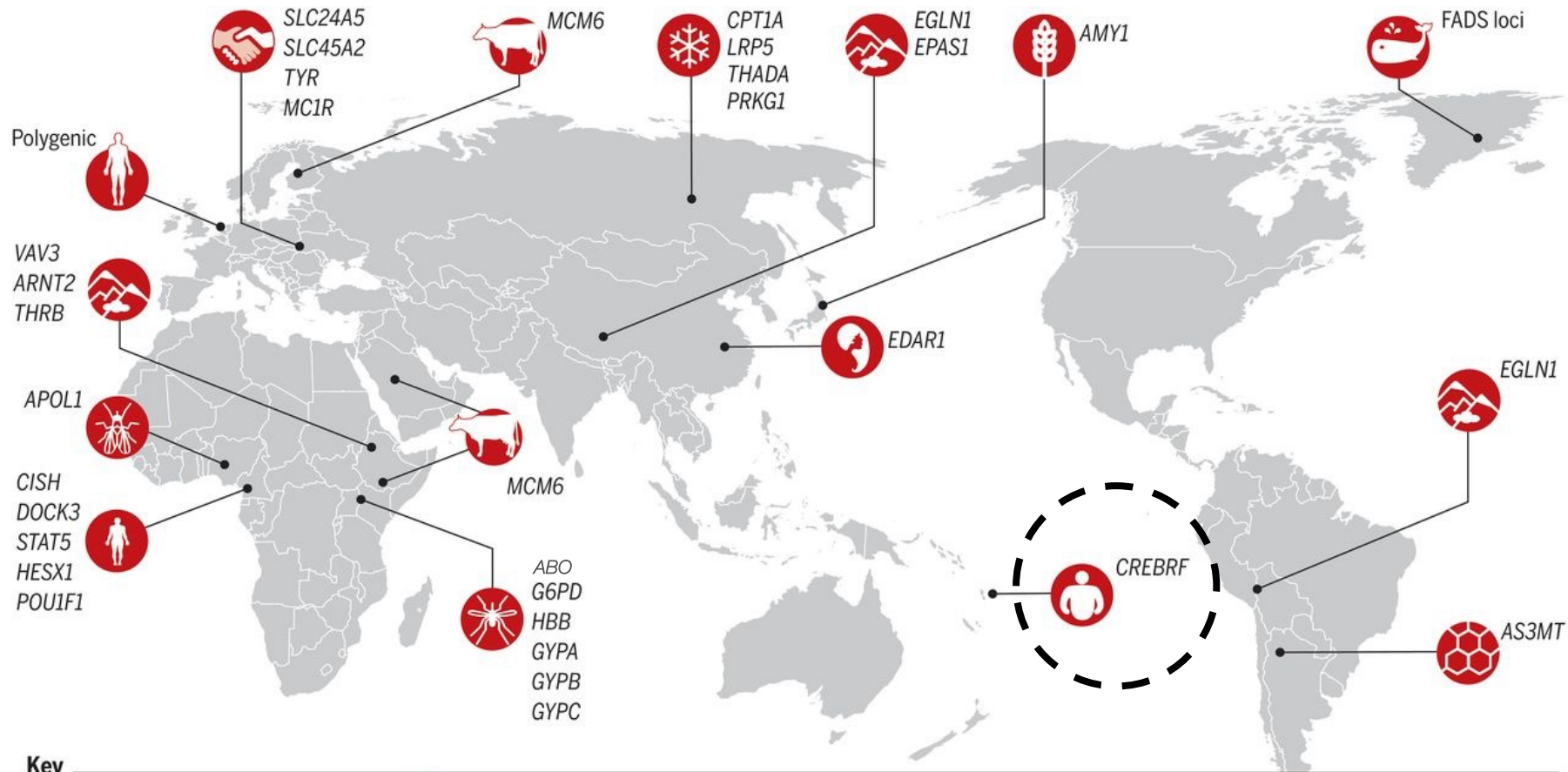
1872



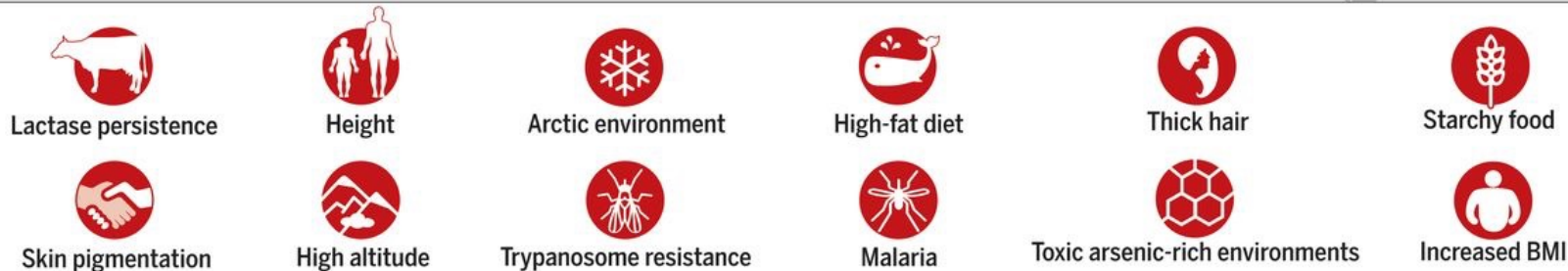
2020



Global distribution of locally adaptive traits

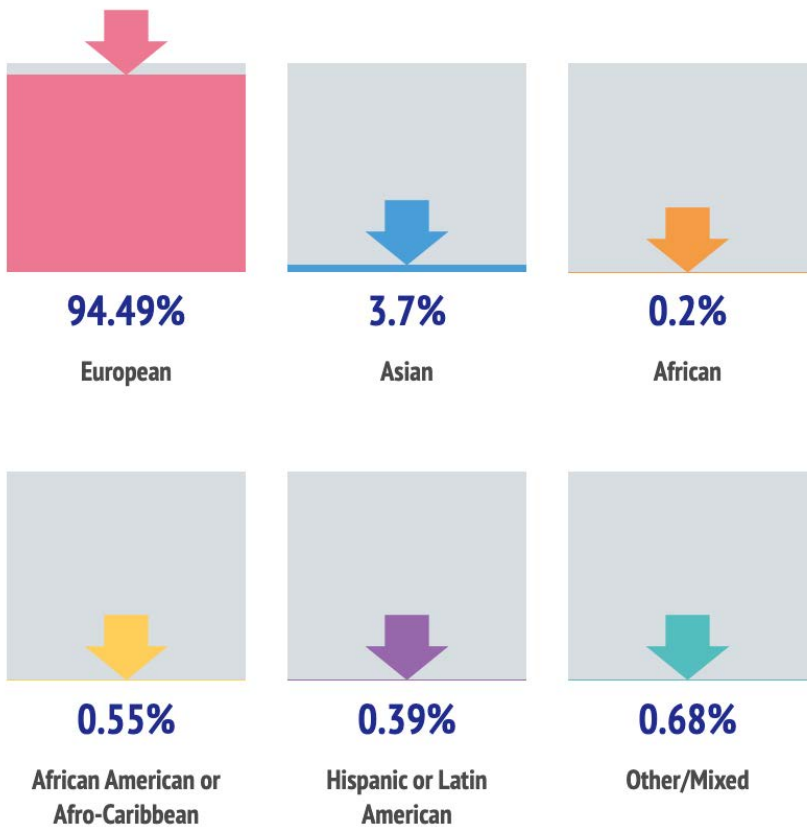


Key



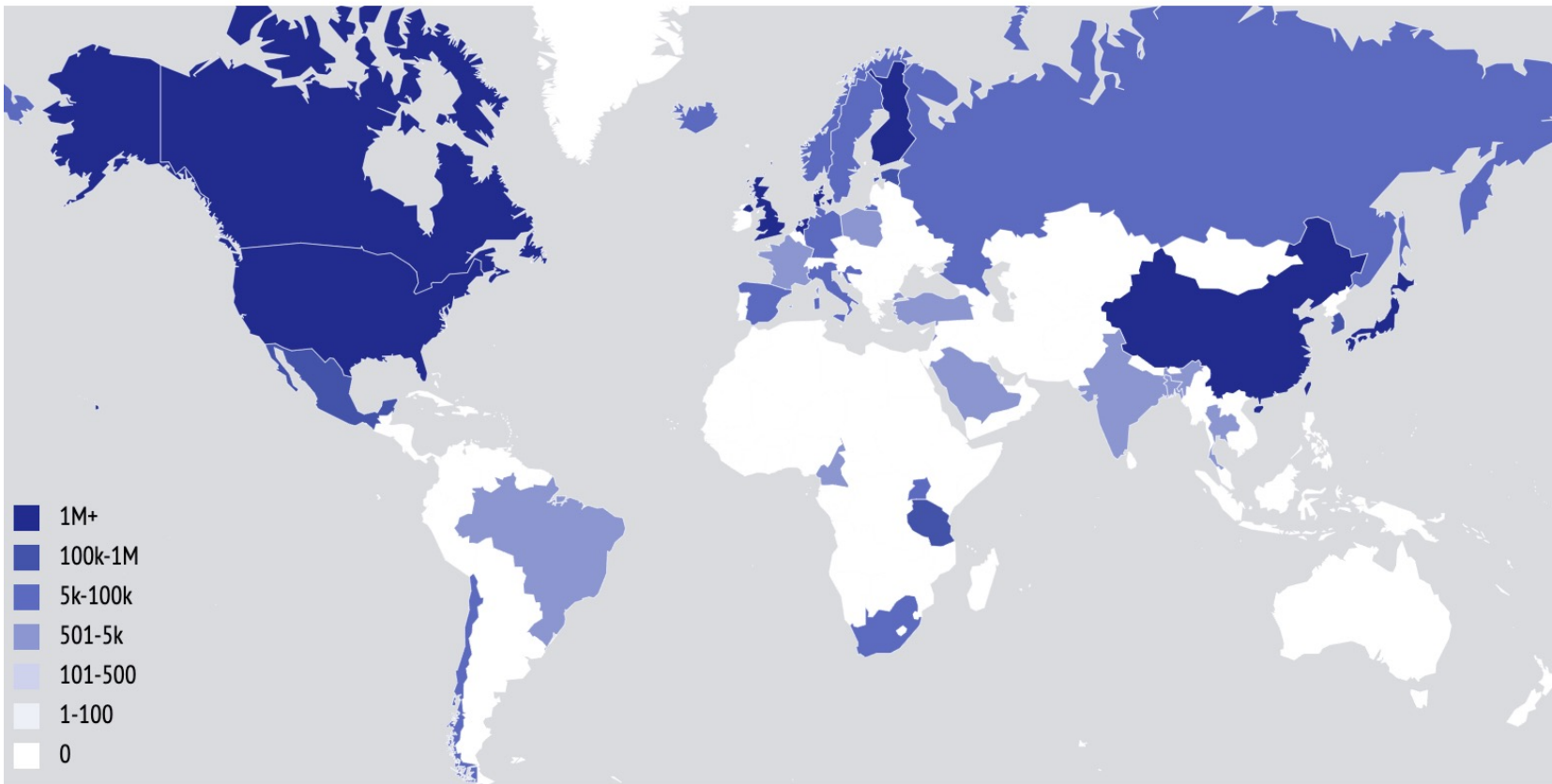
Total GWAS participants diversity

Version 1.0.0. Last check for data: 2024-03-18 00:20:16 .



Participants by country (all parent terms)

Both Stages



<< < 2023 > >>



<https://gwasdiversitymonitor.com/>

***72%** of genetic discoveries have taken places in three countries



Illumina HQ, La Jolla, CA 2023

There were approximately **45,000** patents filed worldwide that mention **DNA sequencing** or analysis as a significant application or method

*Liddicoat & Leachman
Nature (2018)*



The Native BioData Consortium is led by Indigenous scientists and tribal community members

RESEARCH FOR NATIVES, BY NATIVES

The **Native BioData Consortium (NBDC)** is the first 501(c)(3) nonprofit research institute led by Indigenous scientists and tribal members in the United States. As a biorepository (or “biobank”), we ensure that advances in genetics and health research benefit all Indigenous people.





Diversity



Soil



Extinction



Invasion

Four of Hawaii's counties ranked among the top 15 most diverse counties in the Nation

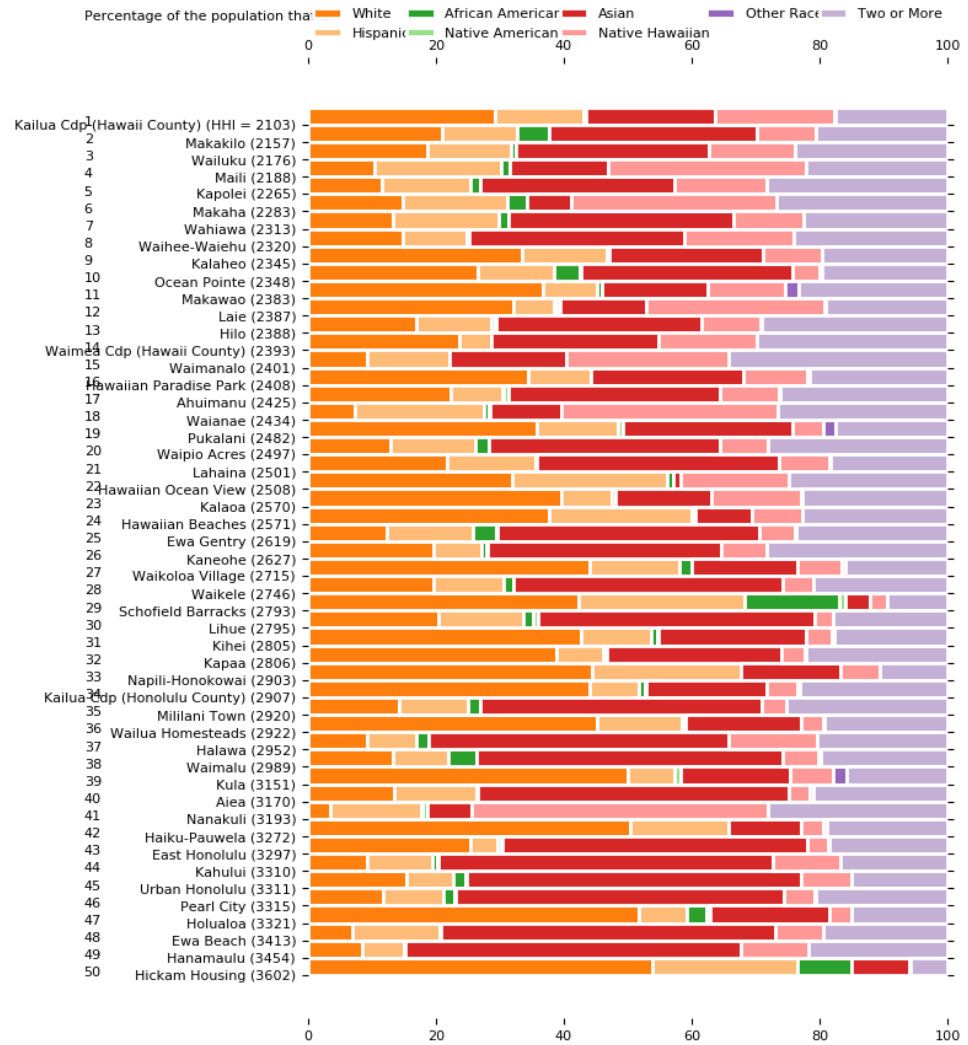
Hawaii County, Hawaii
(#1)

Maui County, Hawaii
(#2)

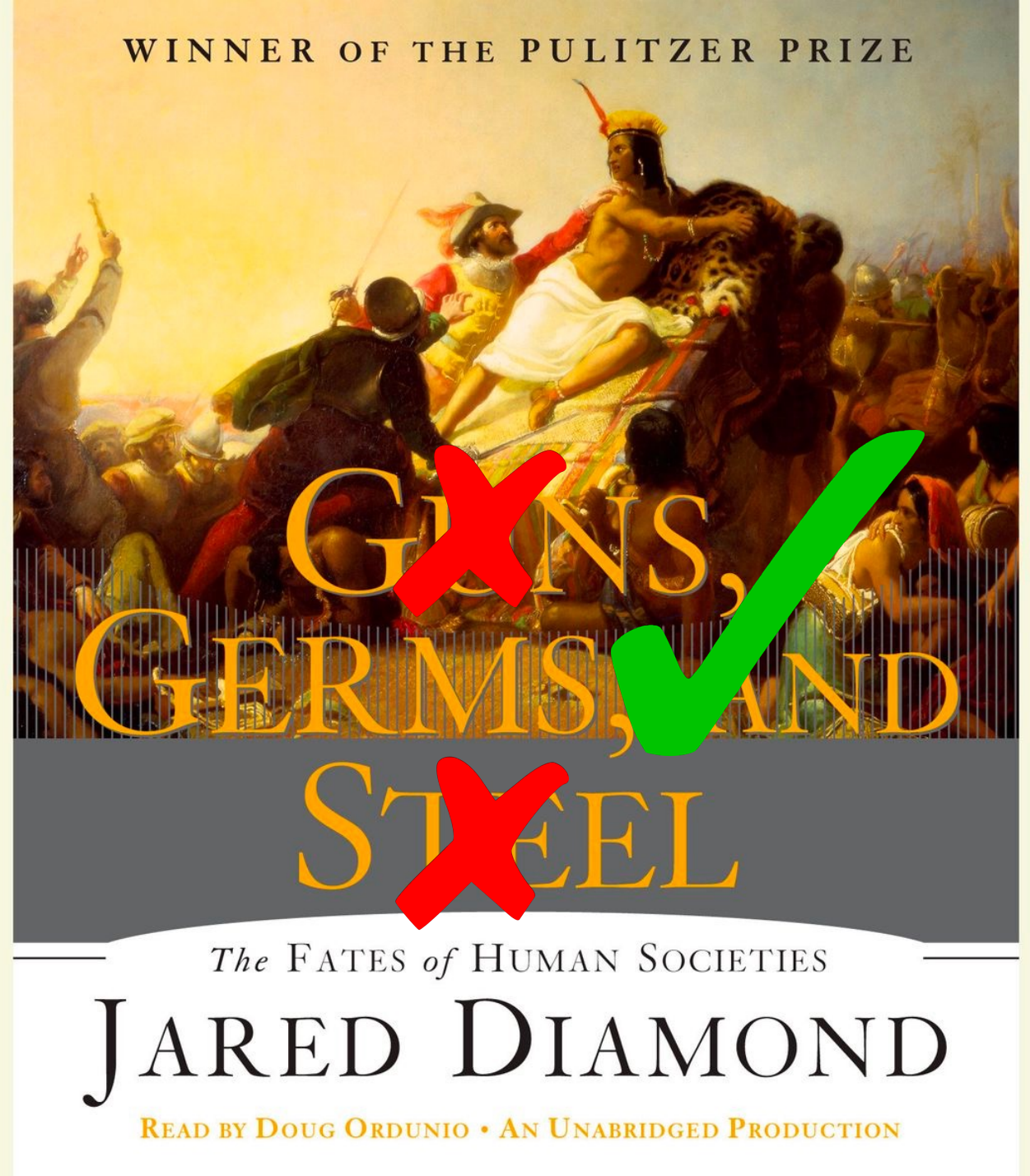
Kauai County, Hawaii
(#4)

Honolulu County, Hawaii
(#11)

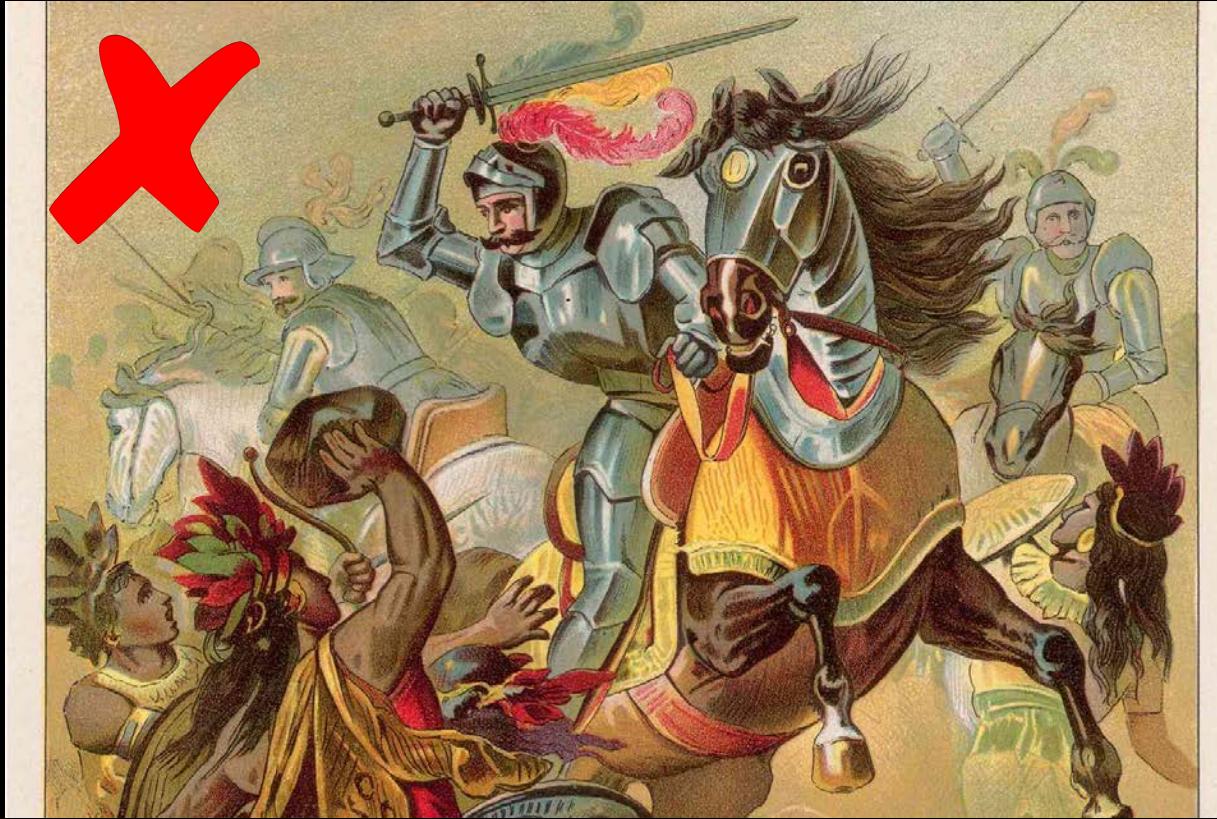
Most Diverse Cities In Hawaii



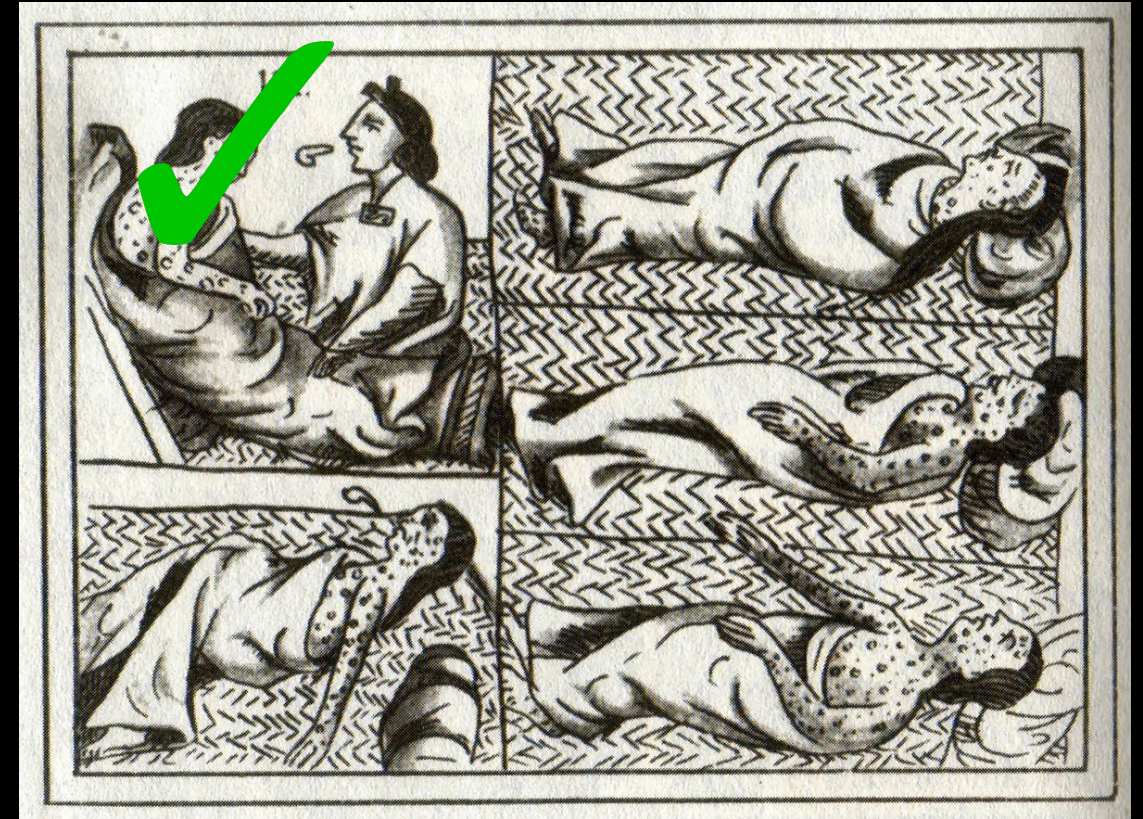
From
Cook
→
Cortes



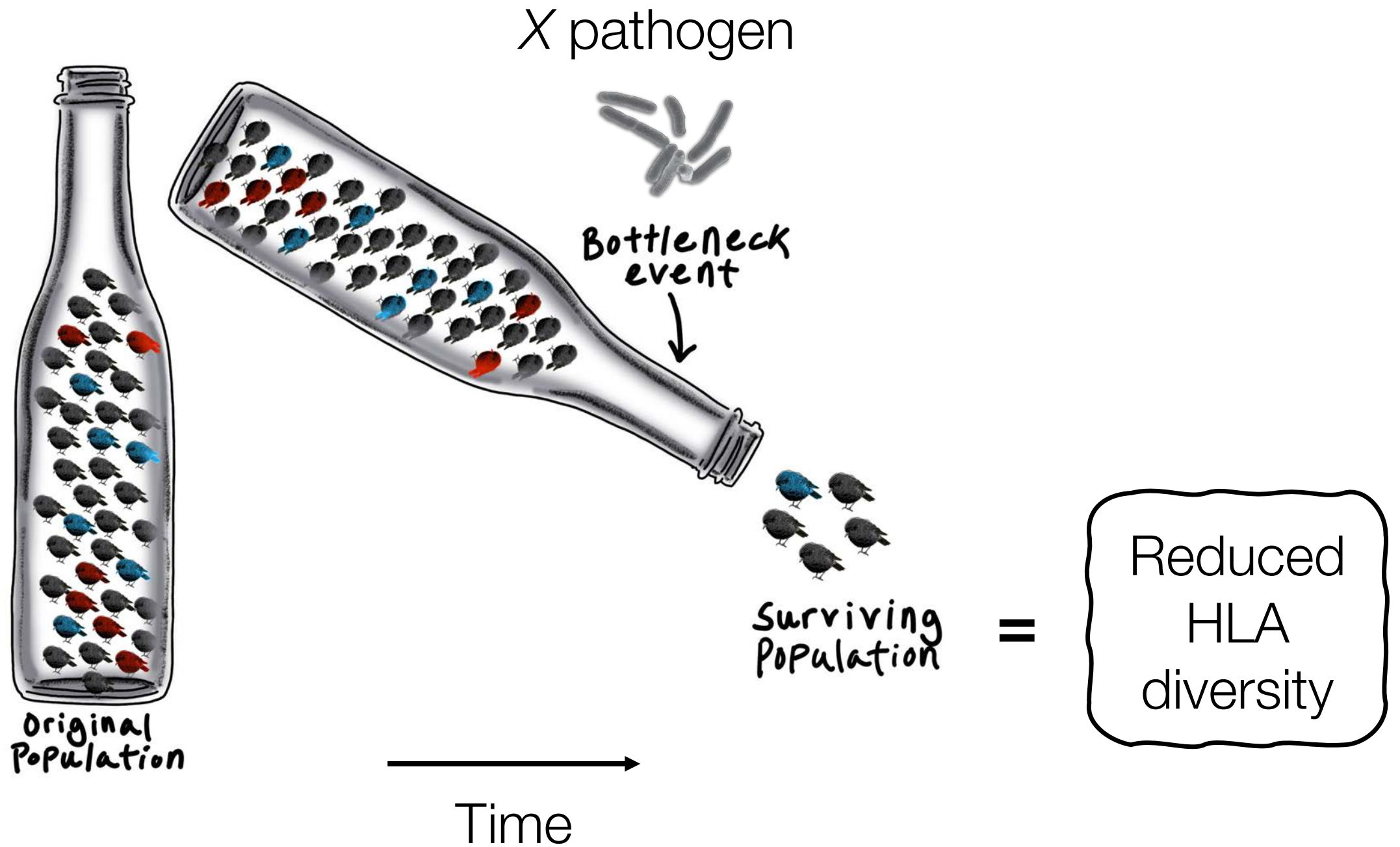
💀 = 200,000



💀 = 20,000,000



“It will never be definitively determined how many Aztecs were killed by Cortes, but it is estimated that Cortes and his army killed as many 200,000 people during the Battle of Tenochtitlan alone. If European borne diseases are included, the death count could go as high as 20 million people.”





outline

Paths and timing of the Peopling of Polynesia:

Inferred from genomic networks

The Origins of Leprosy Bacterium in Oceania:

A Genomic History

The Gout Epidemic in French Polynesia:

A modelling study of data from the Ma'i u'u epi-survey



outline

Paths and timing of the Peopling of Polynesia:
Inferred from genomic networks



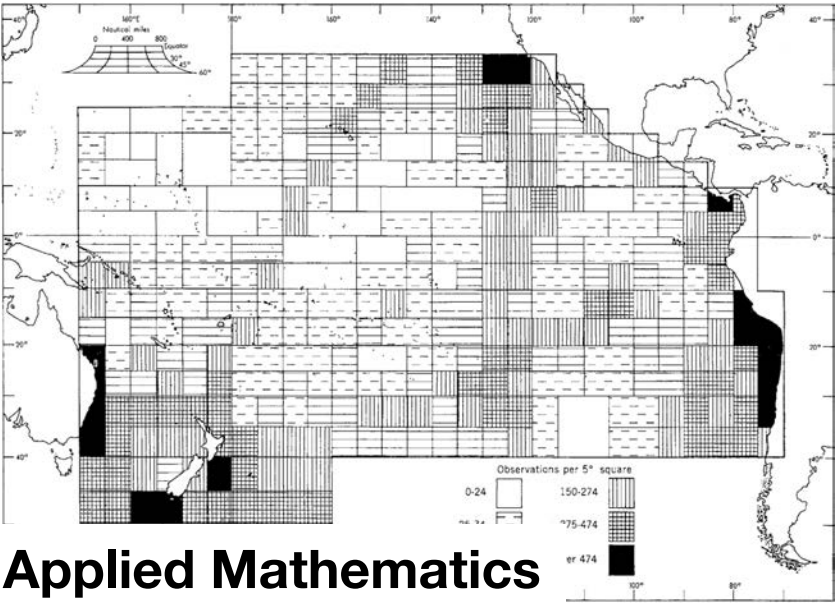
The Origins of Leprosy Bacterium in Oceania:
A Genomic History

The Gout Epidemic in French Polynesia:
A modelling study of data from the Ma'i u'u epi-survey

Where did
these
time
estimates
come
from?

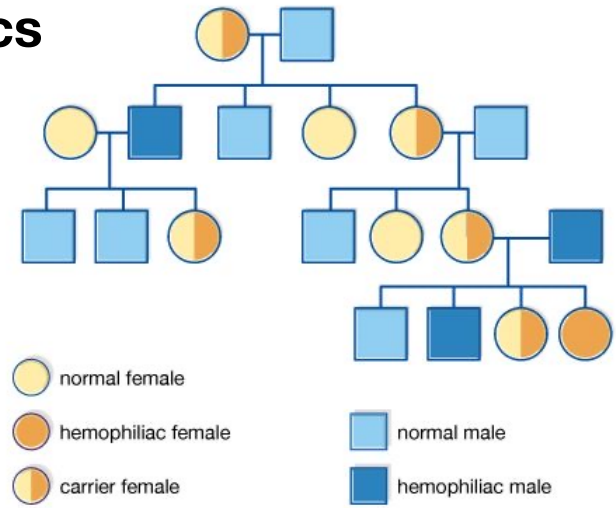


Archeology

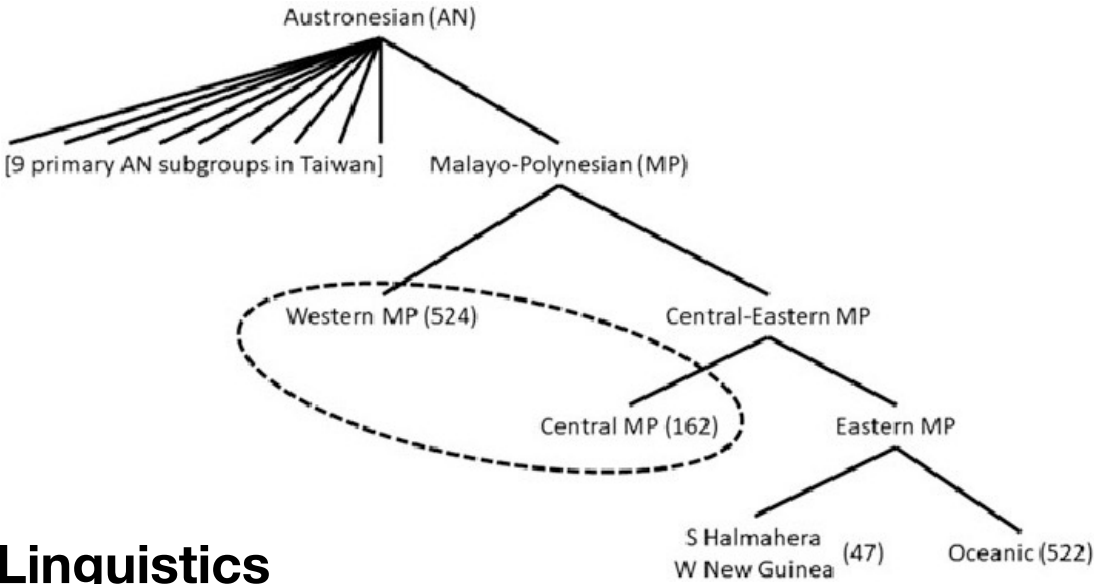


Applied Mathematics

Genetics



© Merriam-Webster, Inc.



Linguistics

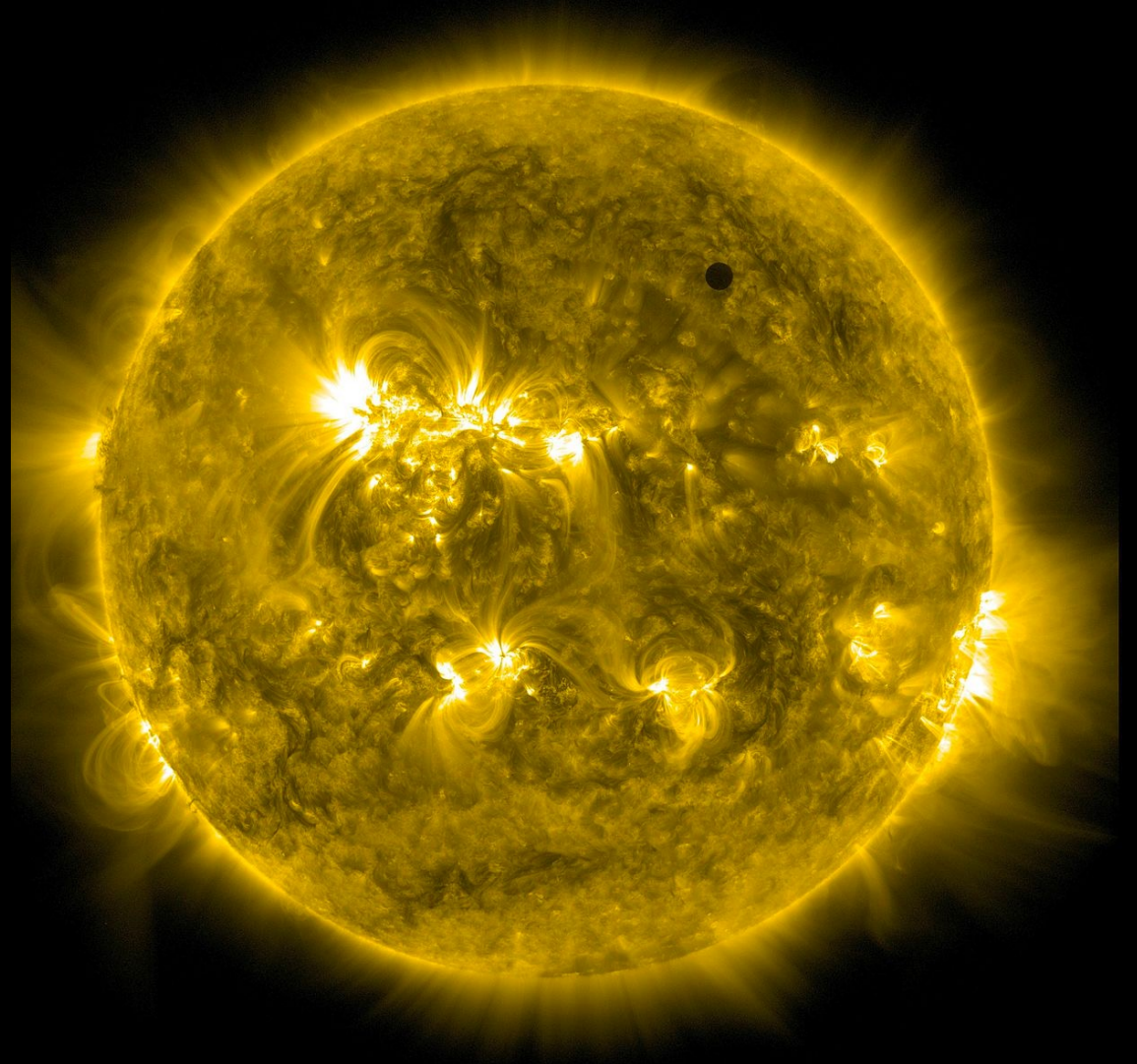
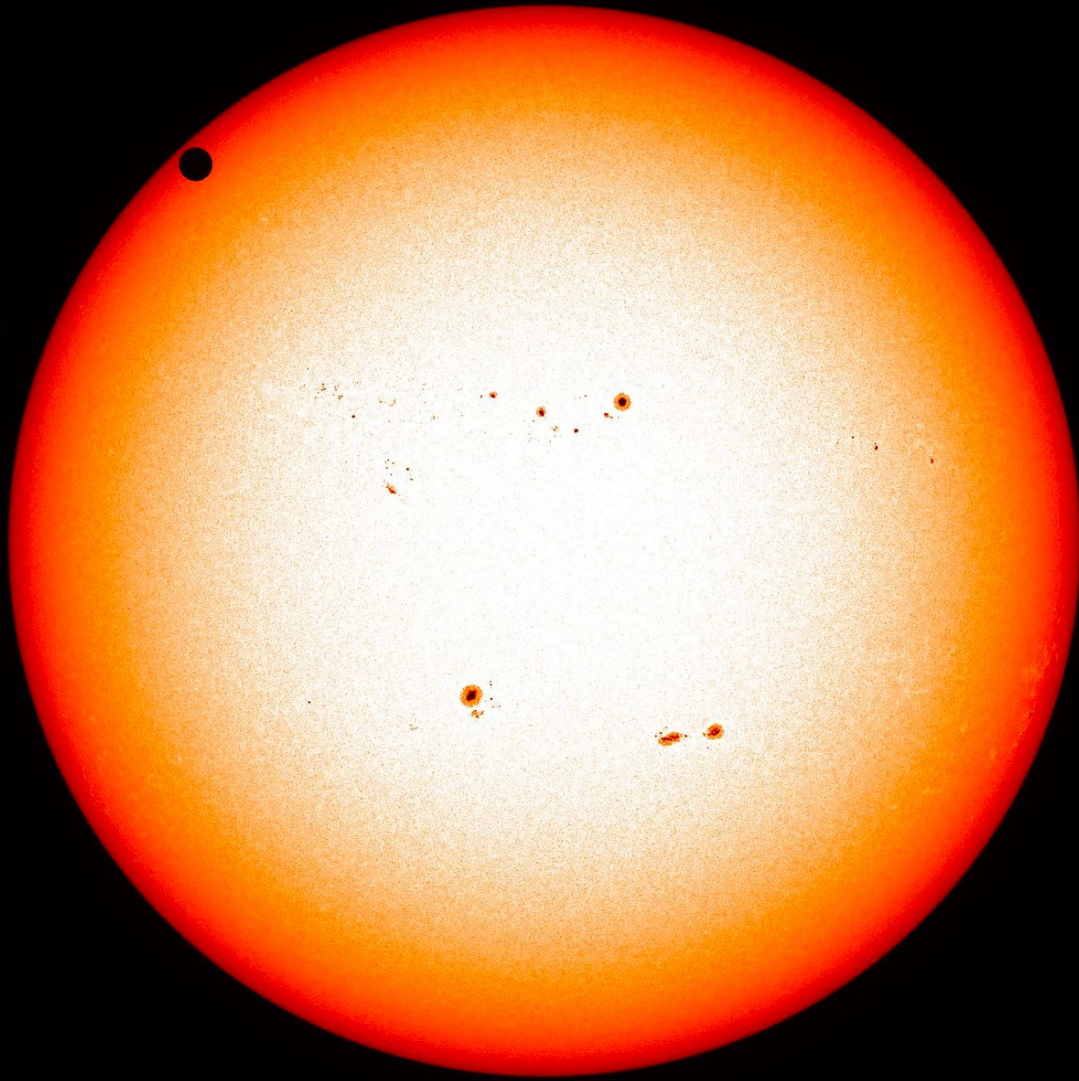


How it started...

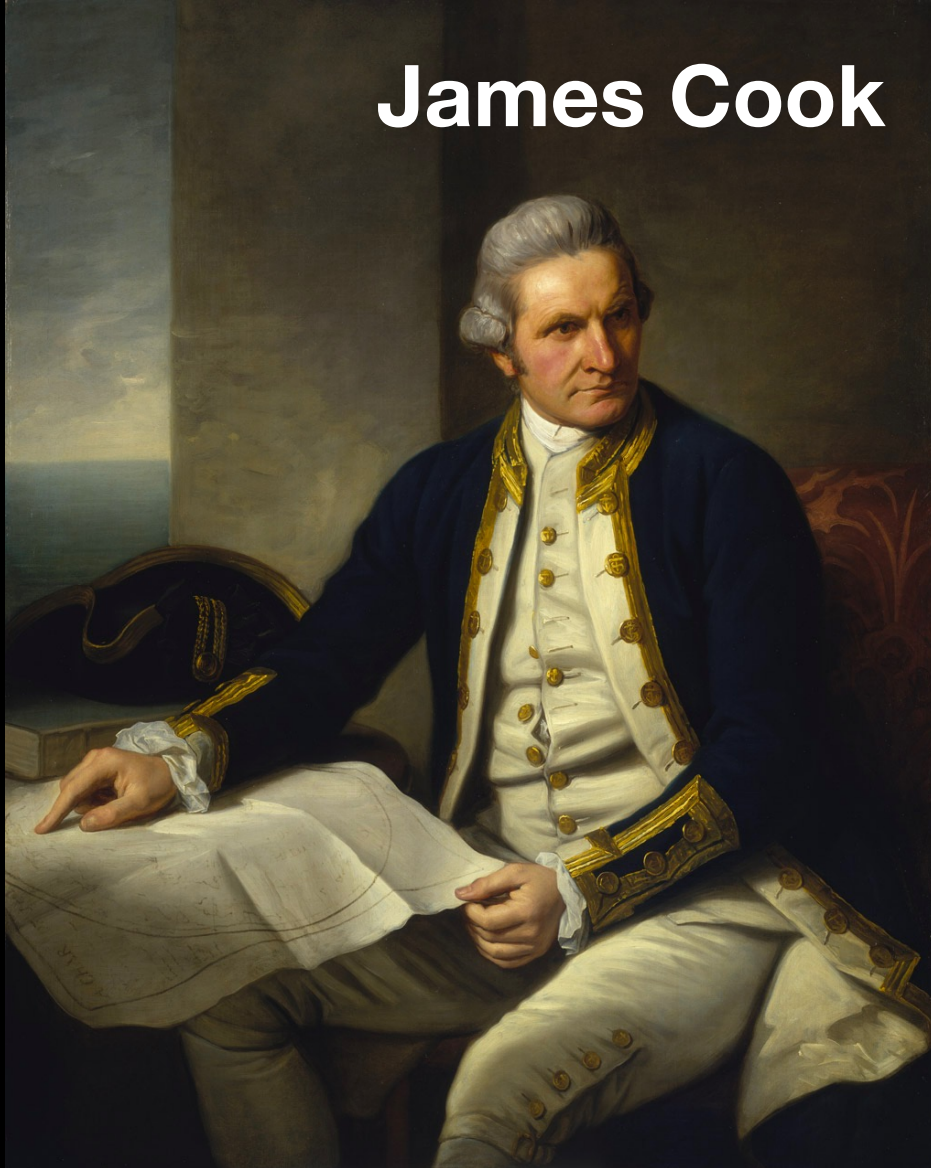


How it ended...

Transit of Venus



James Cook



Tupaia









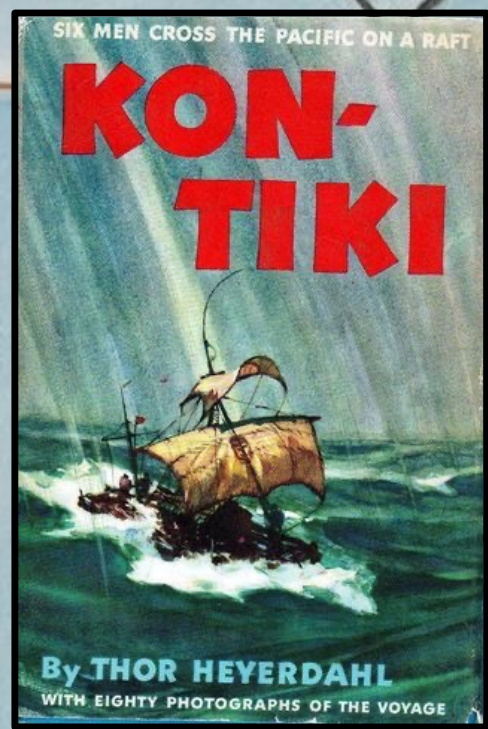
1. Who's in control of the narrative?

2. Who's biasing the data?

3. Who's hypothesis are we testing?

4. Is it even your question to ask?

1947



Tahiti

Tuamotu Islands

Easter Island

101 days
4,300 nautical miles

Key

- Kon-Tiki voyage
- ← ← ← currents





1976

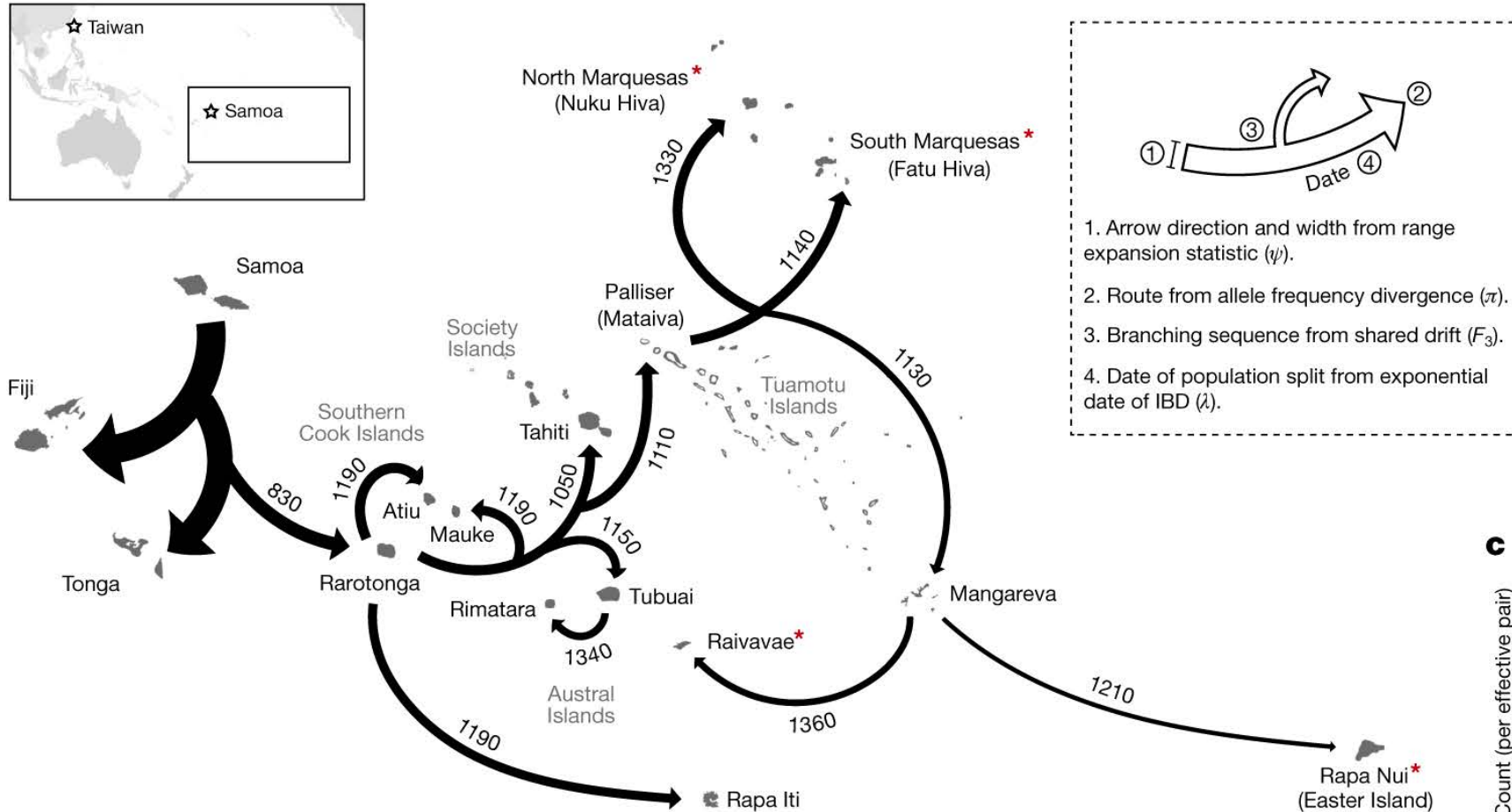
***Ka Wā Ma Mua, Ka
Wā Ma Hope –***
**“Walking backwards
into the future.”**



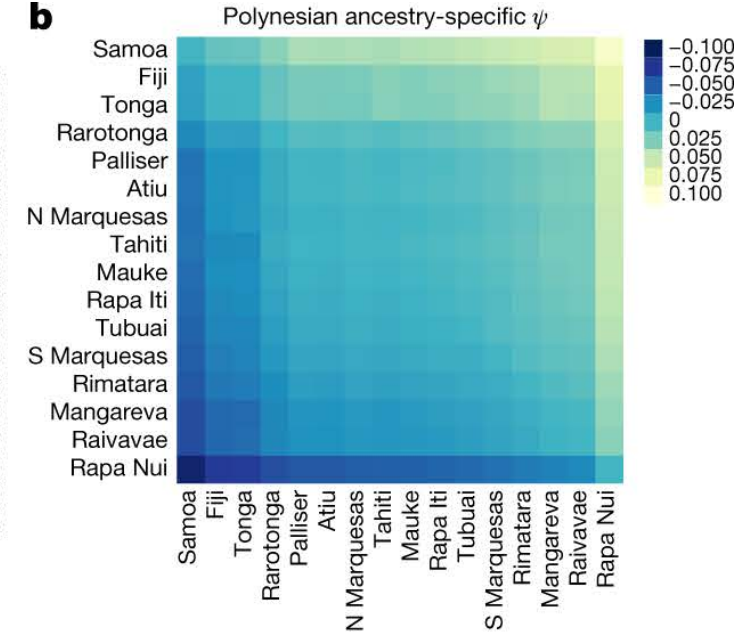
Paths and timings of the peopling of Polynesia inferred from genomic networks

nature

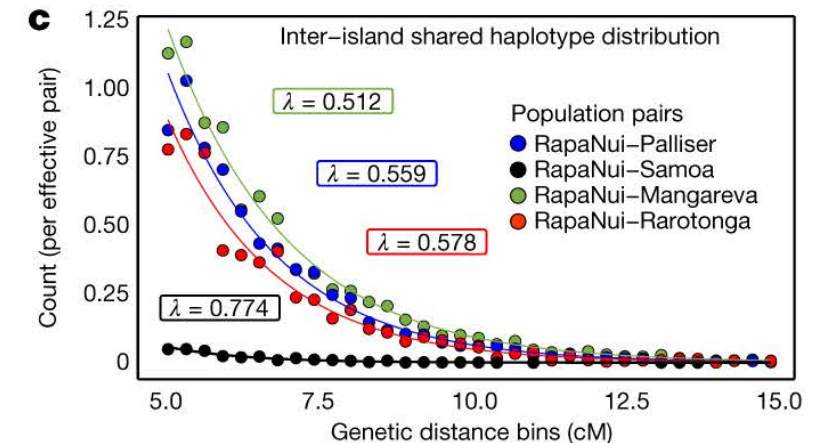
a



b



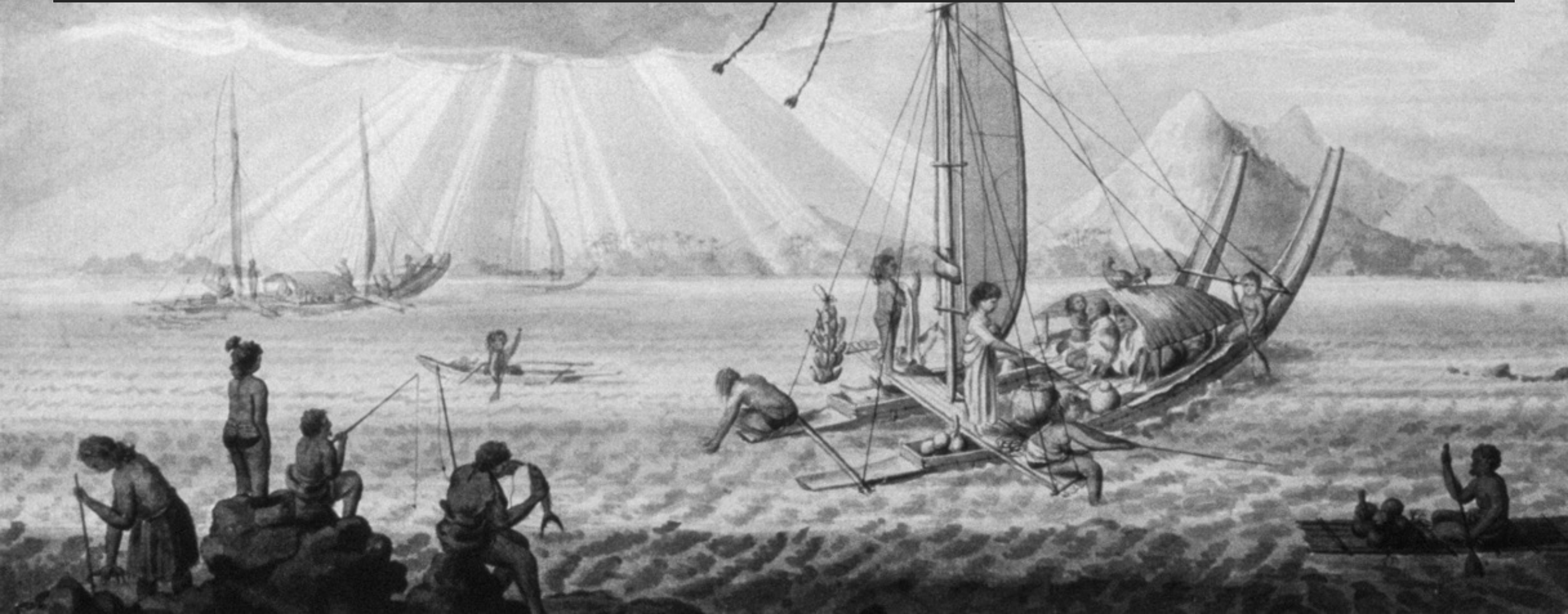
c



'No one could have predicted.' DNA offers surprises on how Polynesia was settled

Science

Early explorers island hopped to discover islands thousands of kilometers apart



Genomes Show the History and Travels of Indigenous Peoples

A new study demonstrates “*I ka wā mamua, ka wā ma hope*,” or “the future is in the past”

AUTHOR

Keolu Fox is an assistant professor at the University of California, San Diego, where he is affiliated with the department of anthropology, the Global Health Program, the Halicioğlu Data Science Institute, the Climate Action Lab, the Design Lab and the [Indigenous Futures Institute](#). His work focuses on designing and engineering genome sequencing and editing technologies to advance precision medicine for Indigenous communities.



Wa'a Kiakahi in Keaukaha, Hawaii. Credit: Keolu Fox



outline

Paths and timing of the Peopling of Polynesia:

Inferred from genomic networks

The Origins of Leprosy Bacterium in Oceania:

A Genomic History

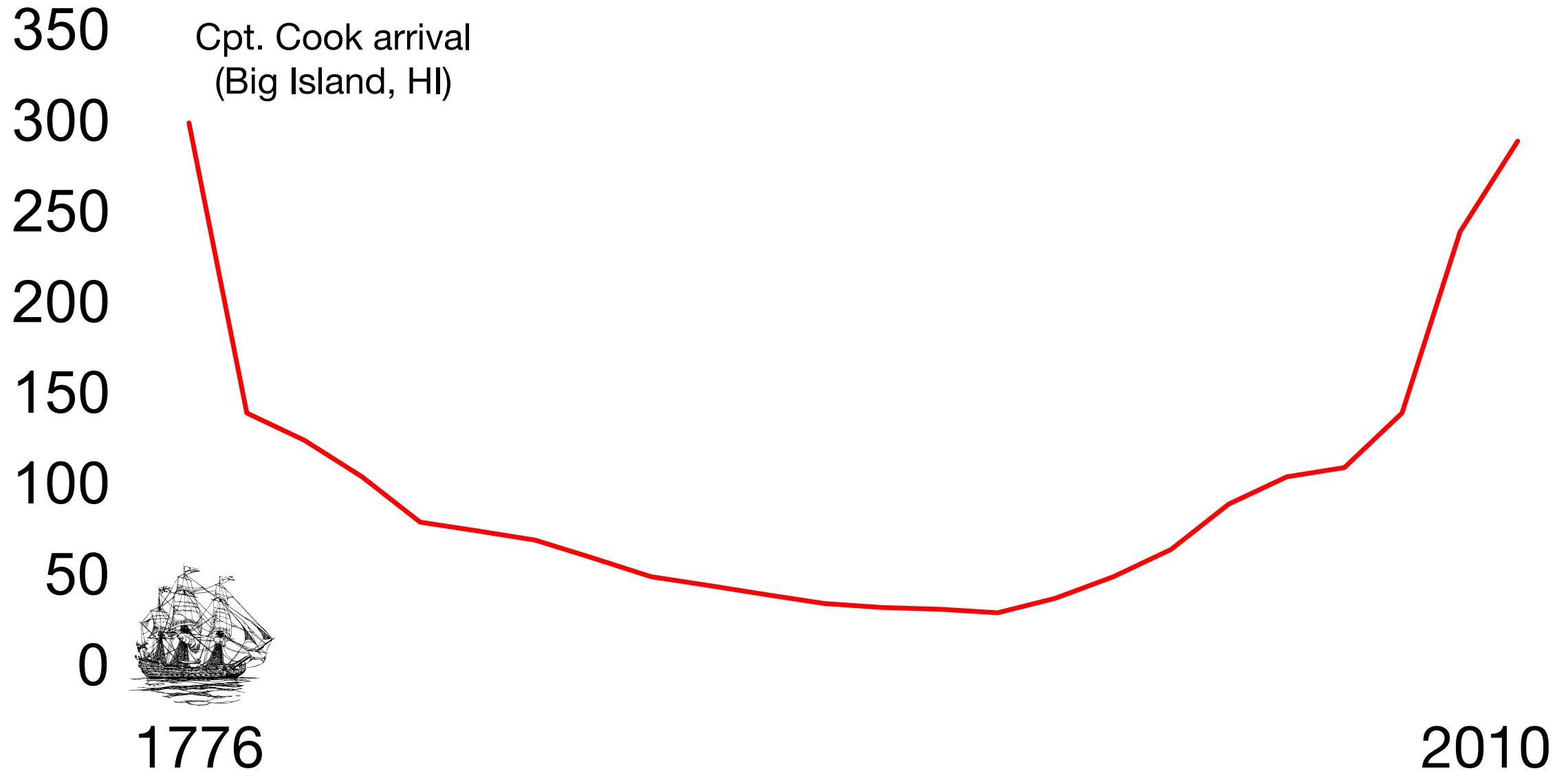


The Gout Epidemic in French Polynesia:

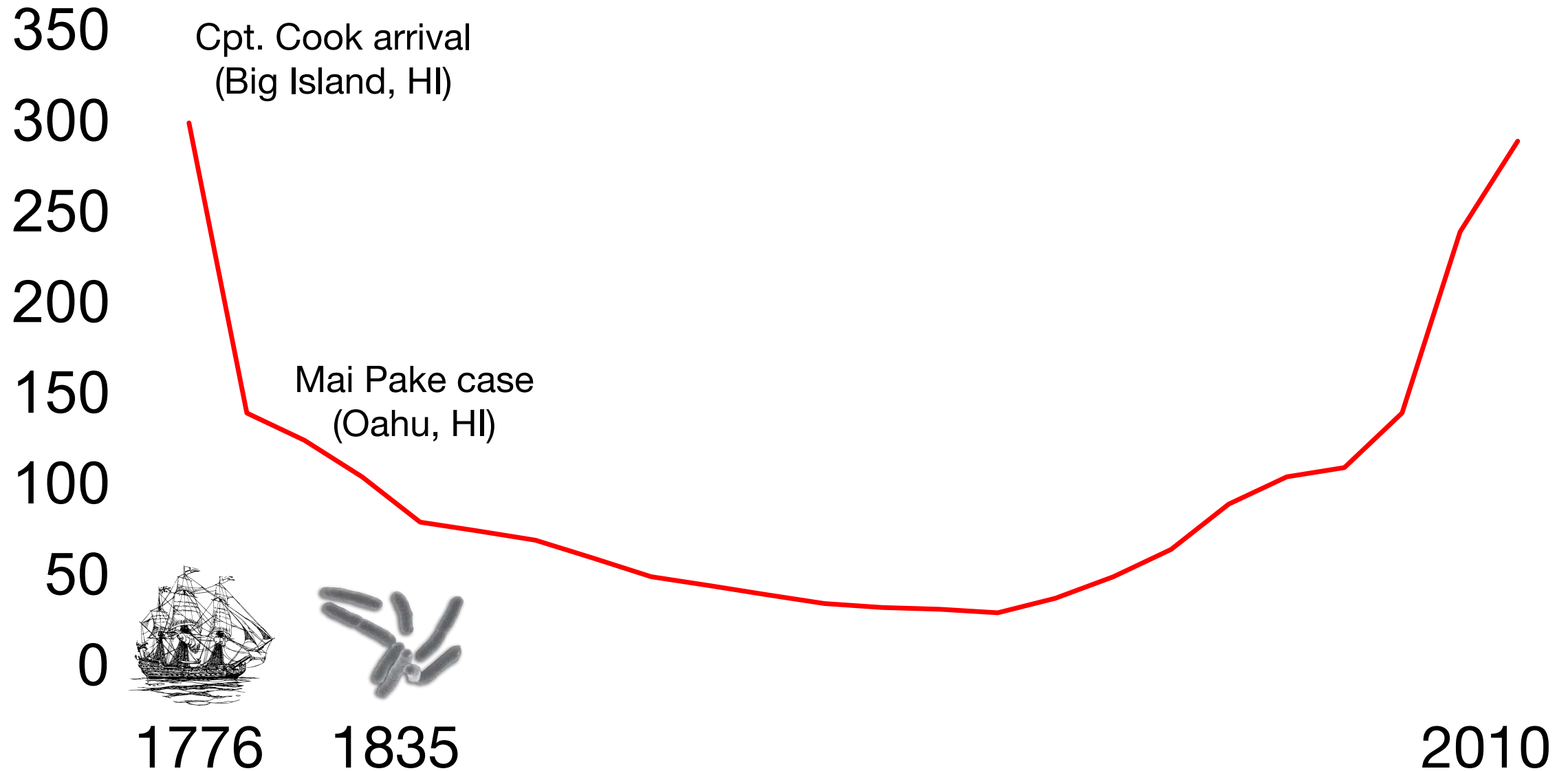
A modelling study of data from the Ma'i u'u epi-survey



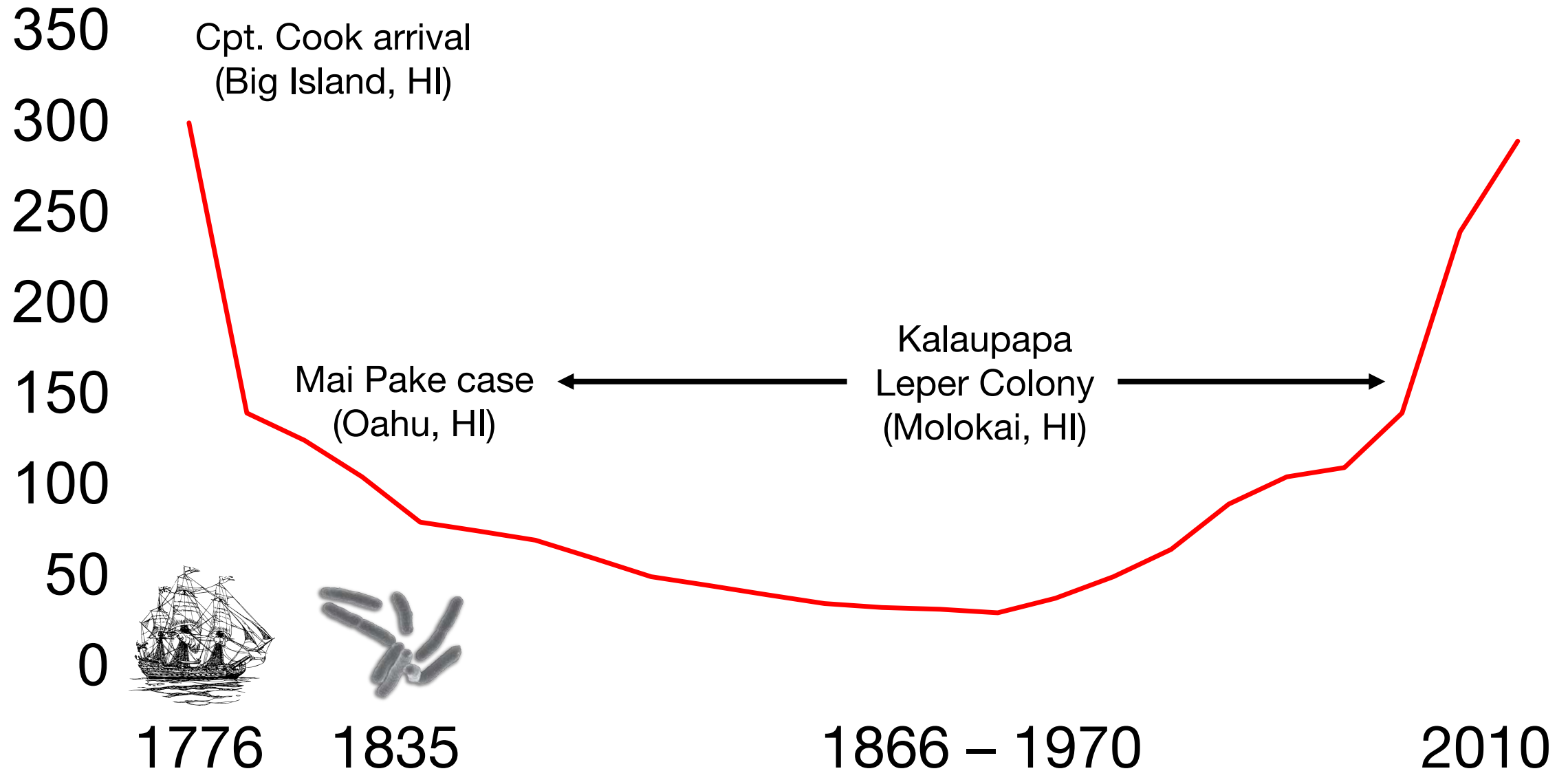
Native Hawaiian Population (in thousands)



Native Hawaiian Population (in thousands)



Native Hawaiian Population (in thousands)



Kalaupapa

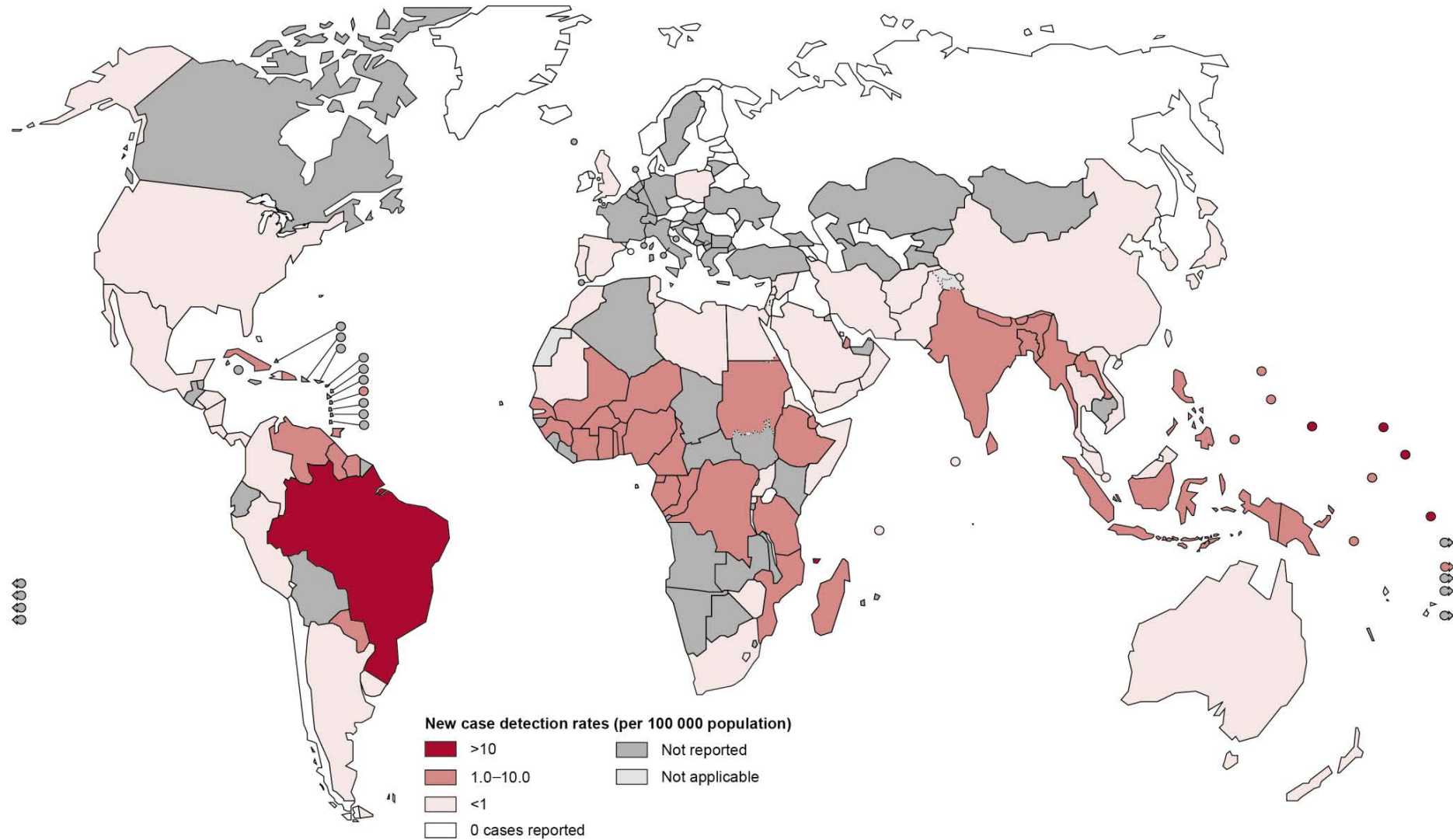






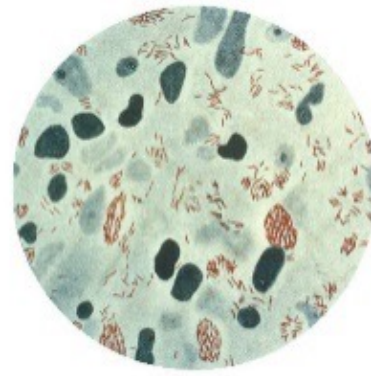


Leprosy: A Neglected Tropical Disease



215,000 new leprosy cases each year

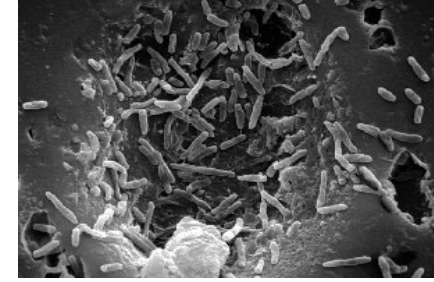
Hansen's Disease or Leprosy



- No vaccine
- Multi-drug therapy - rifampicin, clofazimine, and dapson
- Completely curable with timely MDT
- Since 1980s, 16 million leprosy patients have been cured
- Prevalence and incidence < 1 in 10,000 individuals

****So, why are there nearly 215,000 new cases each year?
Why have we not been able to eradicate leprosy?***

Causative Agent



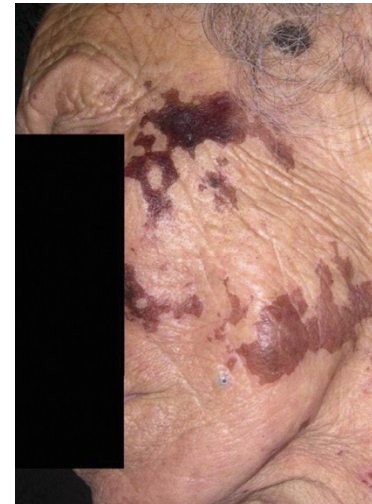
~13.9 MYA

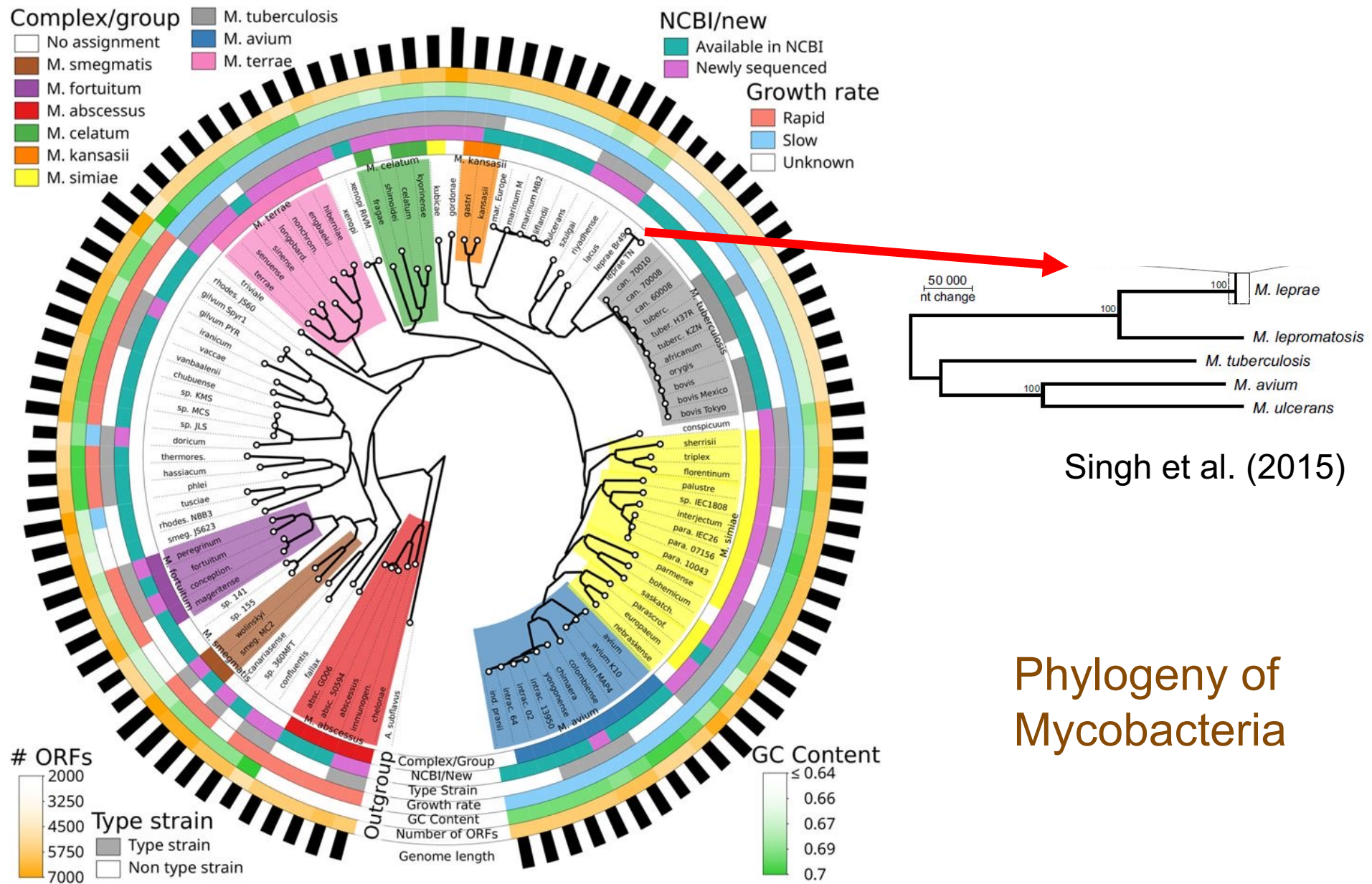
Mycobacterium leprae

Mycobacterium lepromatosis

Majority of leprosy cases

Diffuse lepromatous leprosy





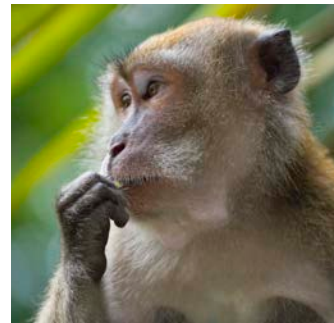
Fedrizzi et al. (2017)

Phylogeny of Mycobacteria

Confirmed natural animal reservoir of *M. leprae*: the nine-banded armadillo

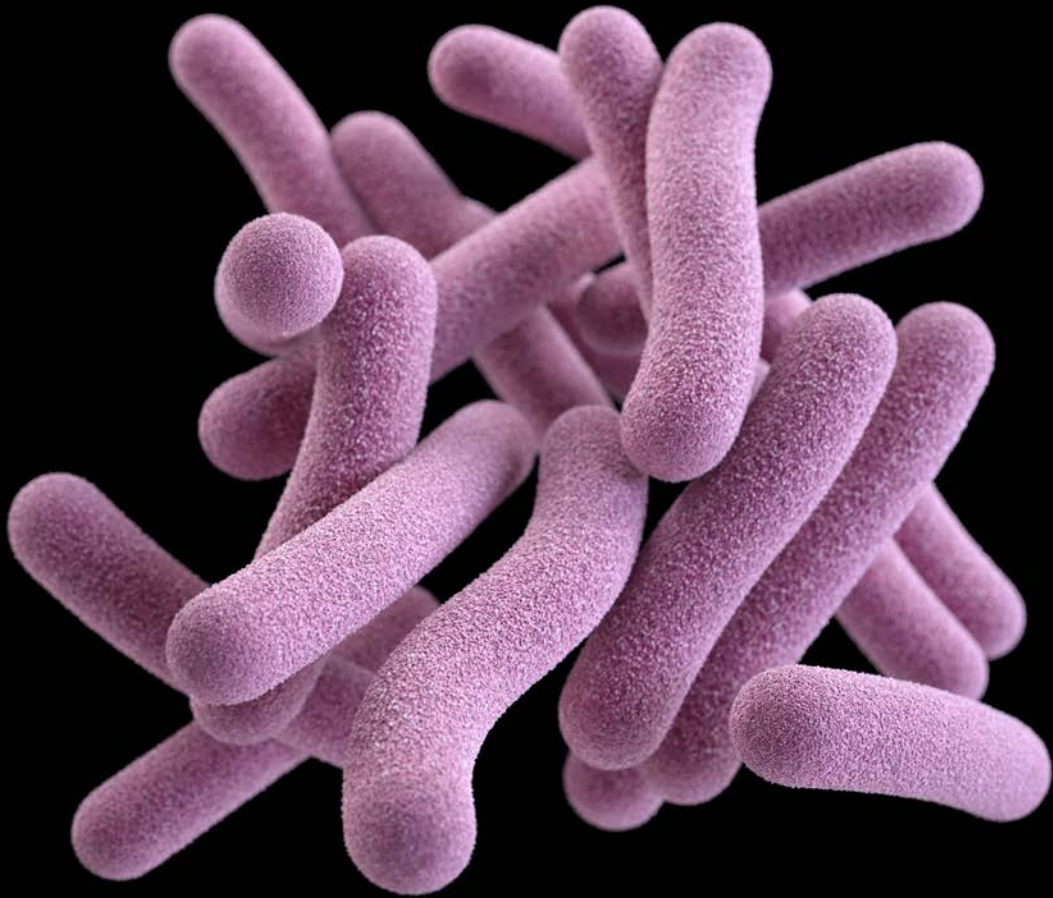


Both *M. lepromatosis* and *M. leprae* isolated from red squirrel populations in UK

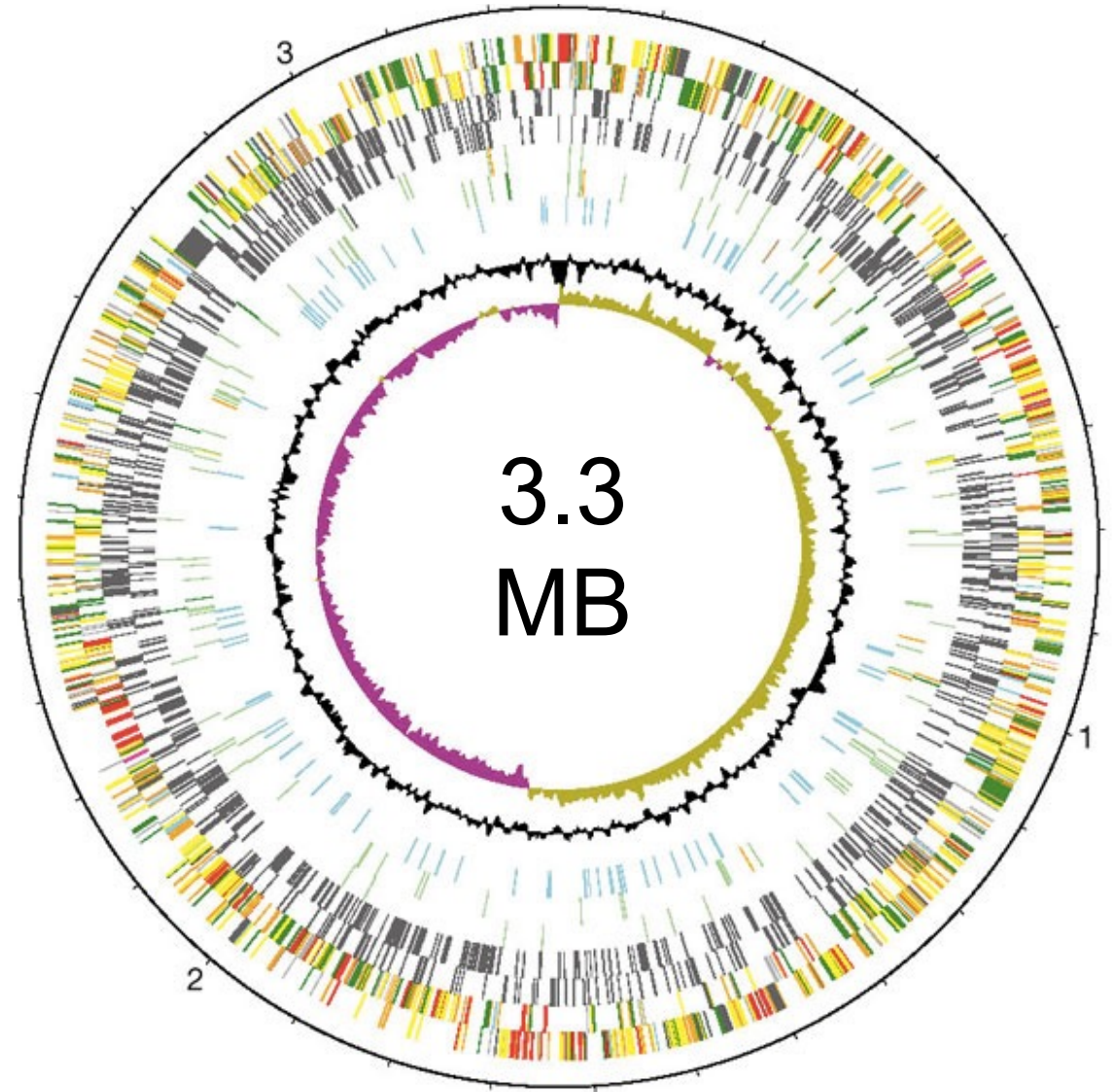


M. leprae has been isolated from several species of primates





Mycobacterium leprae

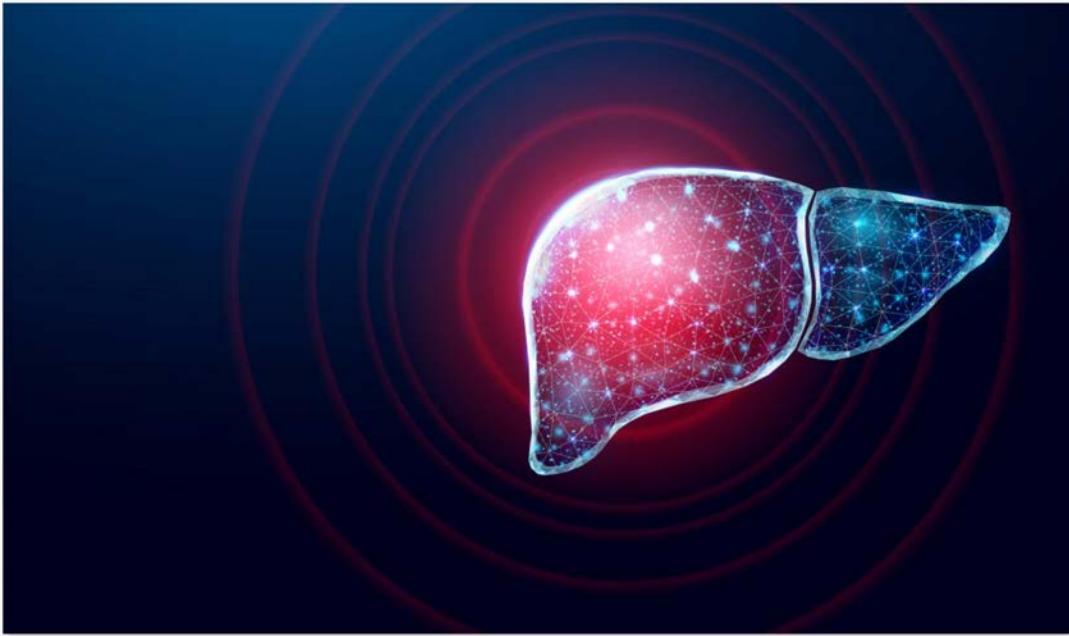


M. leprae genome

Could Hansen's disease be the cure to cancer?

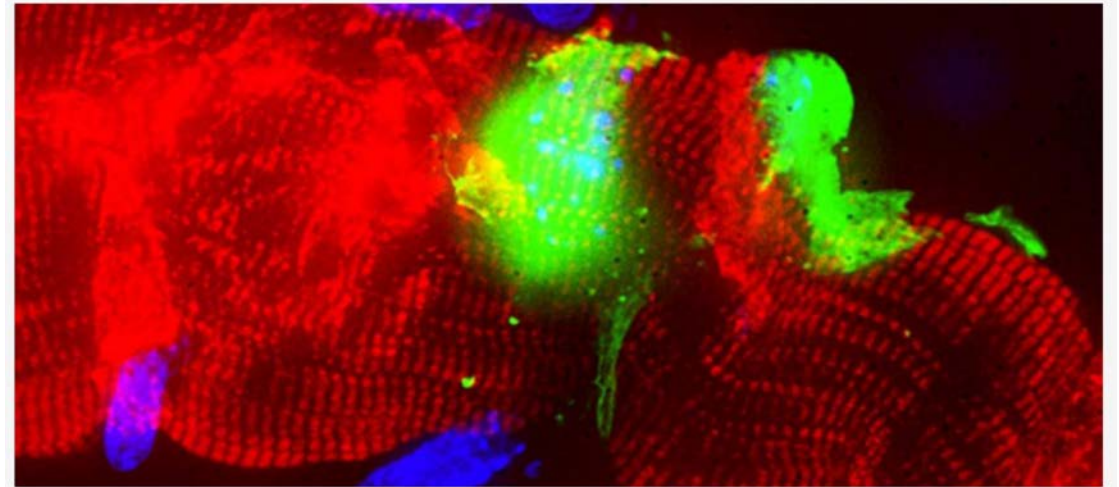
Ancient disease has potential to regenerate livers

Leprosy is one of the world's oldest and most persistent diseases but the bacteria that cause it may also have the surprising ability to grow and regenerate a vital organ.



New study from Edinburgh researchers shows that leprosy bacteria can promote host cell reprogramming

A discovery about the way in which bugs spread throughout the body could help to develop stem cell treatments.



Masaki T. et al., Cell (2022)

Sequencing Ma'i Pa'ke: *Kanaka* 'Oiwī *serving institutions*



The Queens Hospital, Honolulu, HI (1859)



The Queens Medical Center, Honolulu, HI (2017)



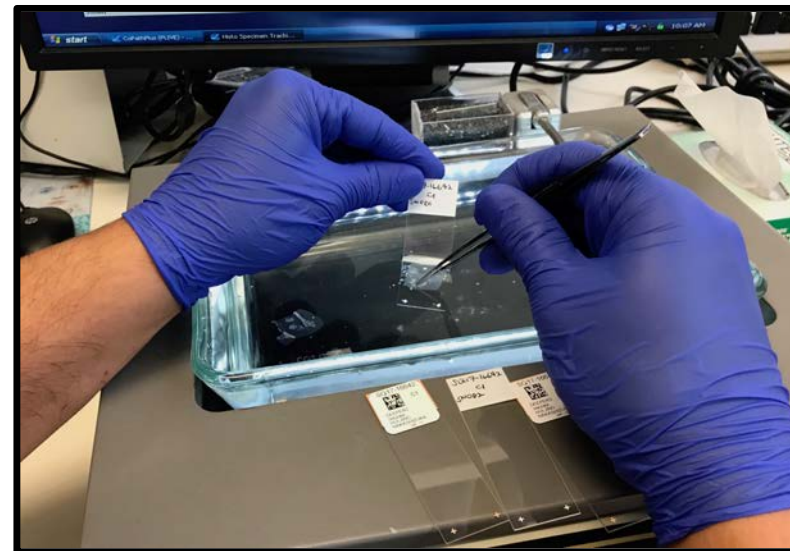
Dermatopathology & Molecular Diagnostics, The Queens Medical Center, Honolulu HI

A.



Biopsy wax block

B.



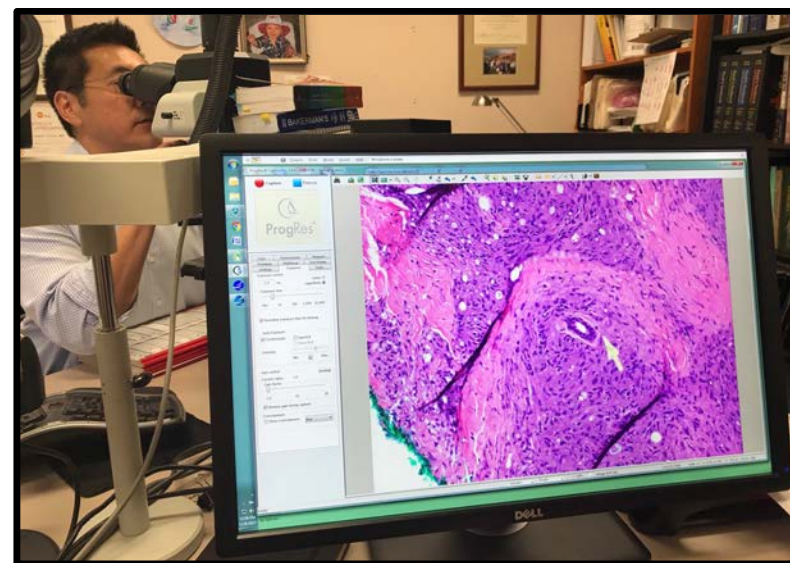
Create pathology slide

C.



Create pathology slide

D.

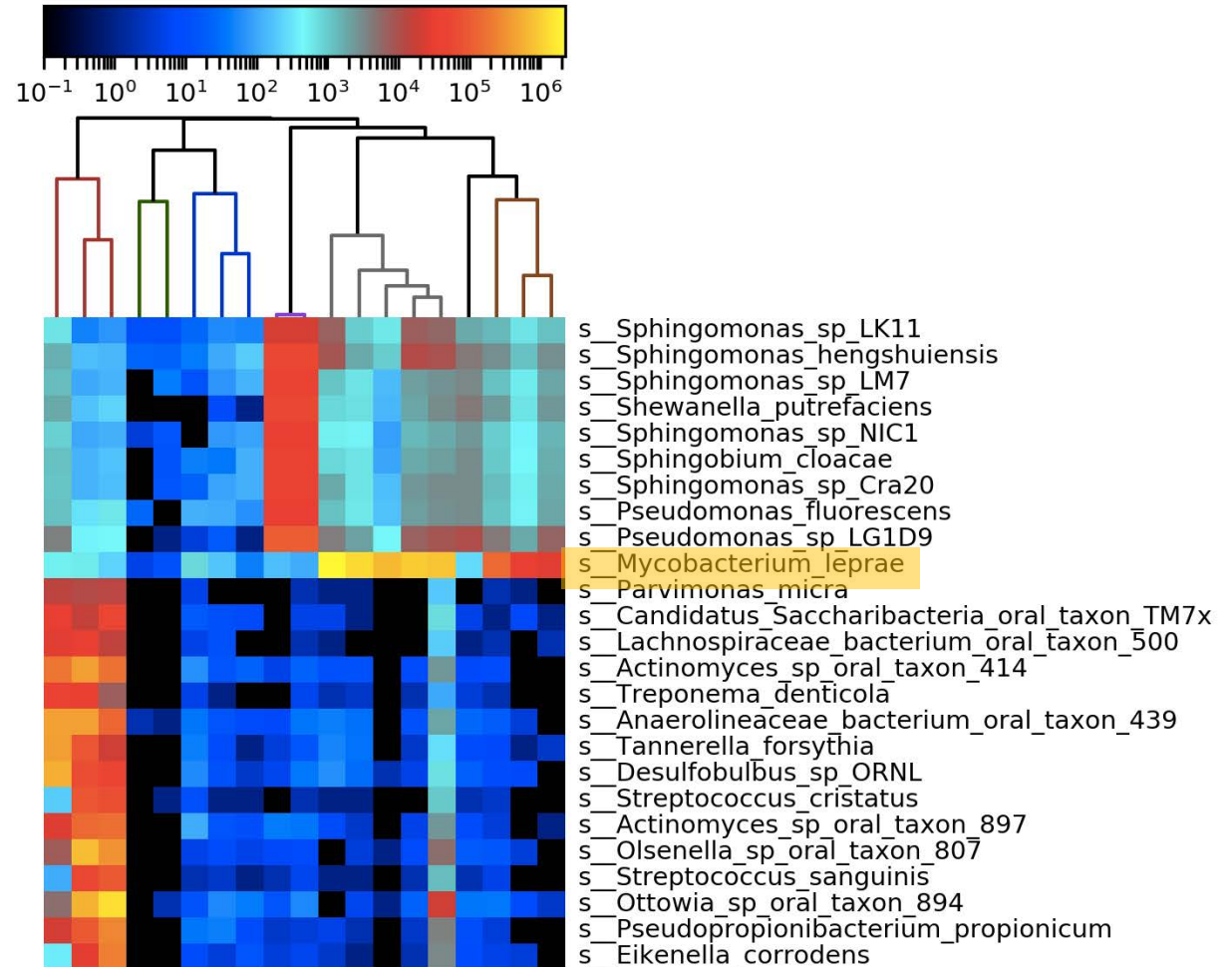


Confirming the presence of Leprosy

Sequencing ancient *ma'i pa'ke* bacteria from Polynesia



Processing ancient leprosy samples
(Stone aDNA Lab, Arizona State University)



A person wearing a white protective suit, hood, and face mask is shown in a laboratory setting. A gloved hand is pointing upwards. The background includes laboratory equipment and papers.

Fox et al., in prep (2019)

Research



Cite this article: Blevins KE, Crane A, Lum C, Furuta K, Fox K, Stone AC. 2020 Evolutionary history of *Mycobacterium leprae* in the Pacific Islands. *Phil. Trans. R. Soc. B* 20190582. <http://dx.doi.org/10.1098/rstb.2019.0582>

Accepted: 16 May 2020

One contribution of 14 to a theme issue 'Insights into health and disease from ancient biomolecules'.

Subject Areas:
evolution, health and disease and
epidemiology, genomics

Keywords:
Mycobacterium leprae, whole genome, leprosy,
Hansen's disease, Pacific Islands, FFPE

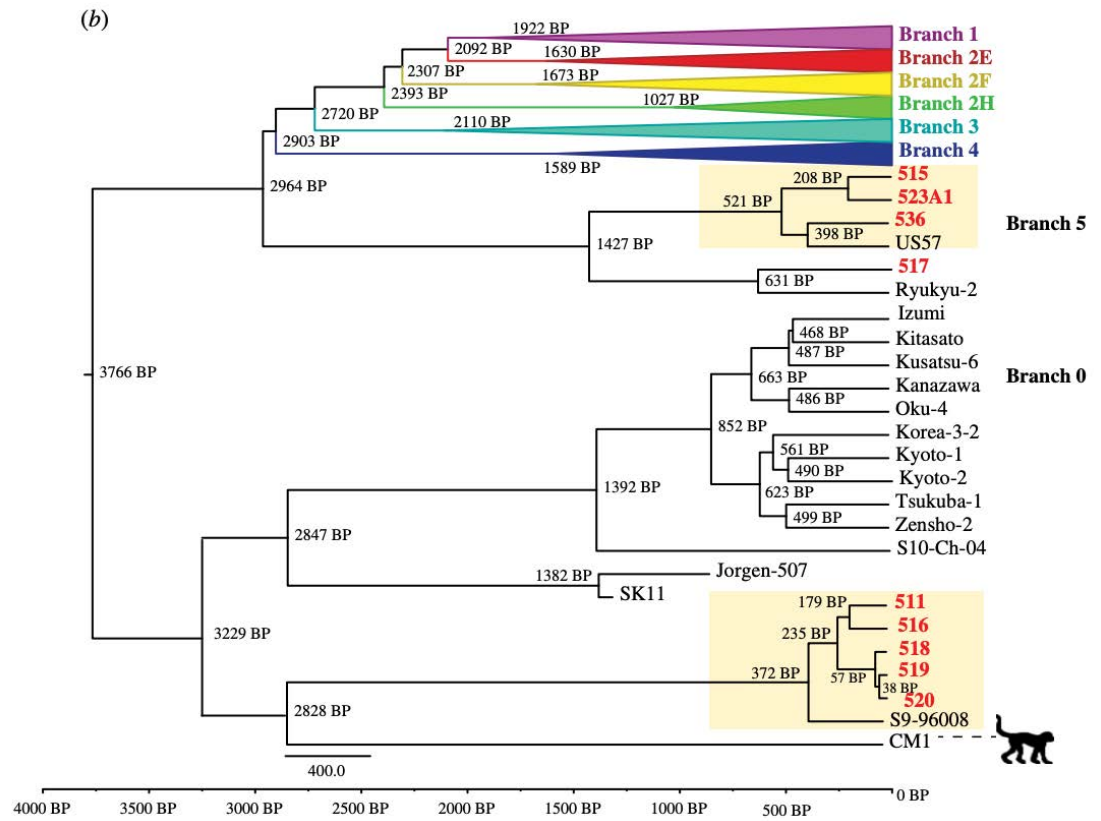
Evolutionary history of *Mycobacterium leprae* in the Pacific Islands

Kelly E. Blevins^{1,2,†}, Adele Crane^{3,4,†}, Christopher Lum⁵, Kanako Furuta⁶, Keolu Fox^{7,‡} and Anne C. Stone^{1,3,4,‡}

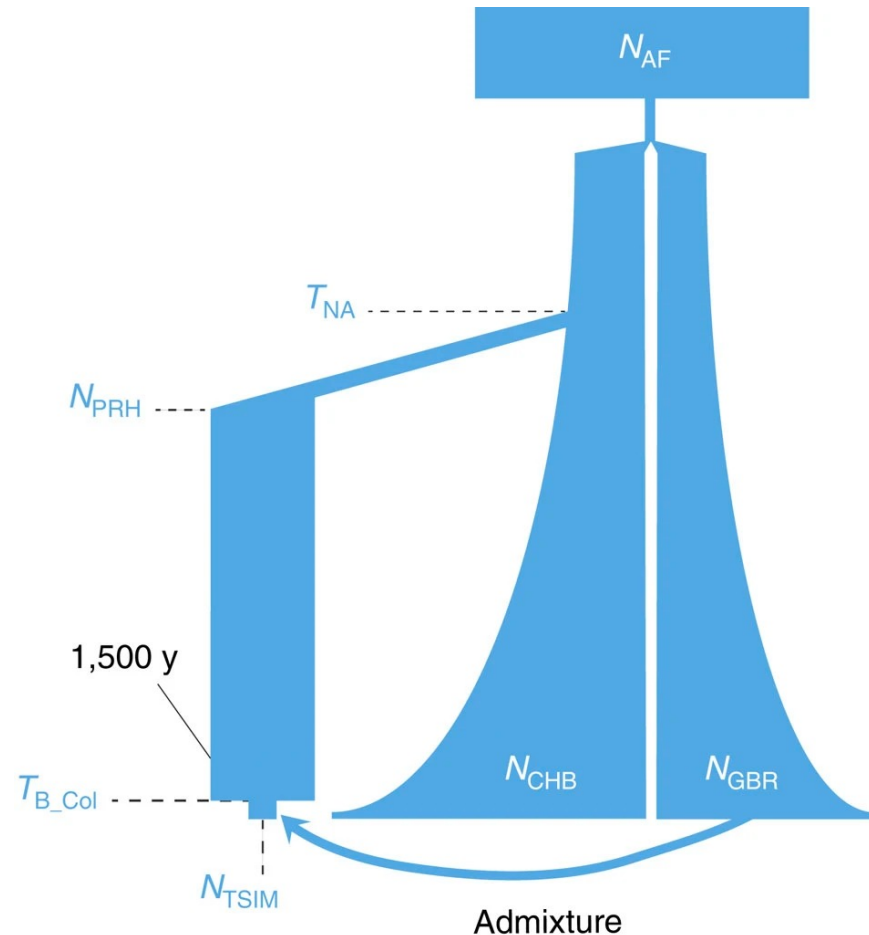
¹School of Human Evolution and Social Change, ²Center for Bioarchaeological Research, ³School of Life Sciences, and ⁴Center for Evolution and Medicine, Arizona State University, Tempe, AZ, USA
⁵Department of Pathology, John A Burns School of Medicine, University of Hawaii, Honolulu, HI, USA
⁶Hawaii Pathologists Laboratory, Honolulu, HI 96813, USA
⁷Departments of Anthropology & Global Health, University of California, San Diego, CA, USA
 KEB, 0000-0002-5740-639X; AC, 0000-0001-5761-4271; ACS, 0000-0001-8021-8314

As one of the oldest known human diseases, leprosy or Hansen's disease remains a public health concern around the world with over 200 000 new cases in 2018. Most human leprosy cases are caused by *Mycobacterium leprae*, but a small number of cases are now known to be caused by *M. lepromatosis*, a sister taxon of *M. leprae*. The global pattern of genomic variation in *M. leprae* is not well defined. Particularly, in the Pacific Islands, the origins of leprosy are disputed. Historically, it has been argued that leprosy arrived on the islands during nineteenth century colonialism, but some oral traditions and palaeopathological evidence suggest an older introduction. To address this, as well as investigate patterns of pathogen exchange across the Pacific Islands, we extracted DNA from 39 formalin-fixed paraffin-embedded biopsy blocks dating to 1992–2016. Using whole-genome enrichment and next-generation sequencing, we produced nine *M. leprae* genomes dating to 1998–2015 and ranging from 4–63× depth of coverage. Phylogenetic analyses indicate that these strains belong to basal lineages within the *M. leprae* phylogeny, specifically falling in branches 0 and 5. The phylogeographic patterning and evolutionary dating analysis of these strains support a pre-modern introduction of *M. leprae* into the Pacific Islands.

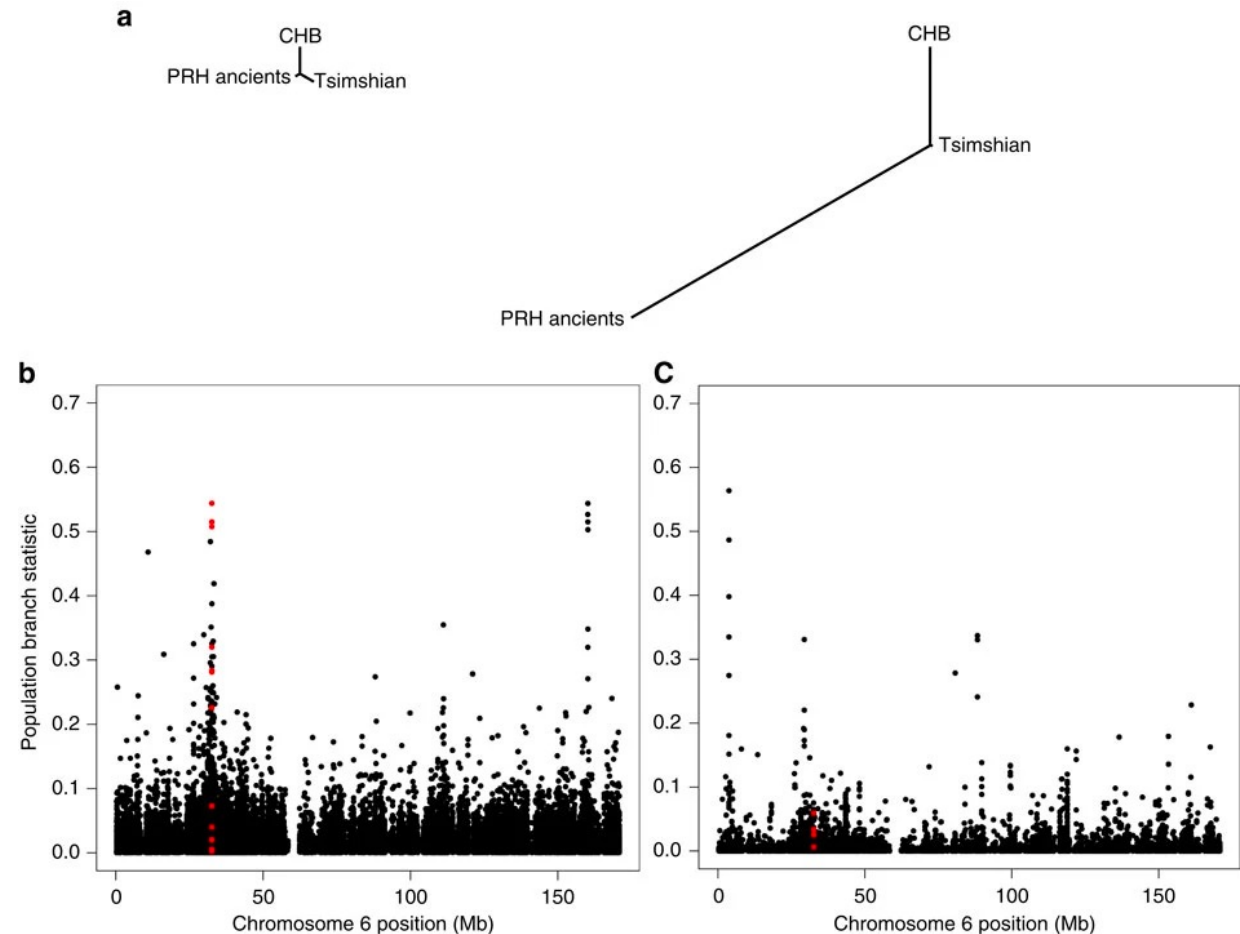
This article is part of the theme issue 'Insights into health and disease from ancient biomolecules'.



Population Collapse: Identifying bottlenecks after European contact

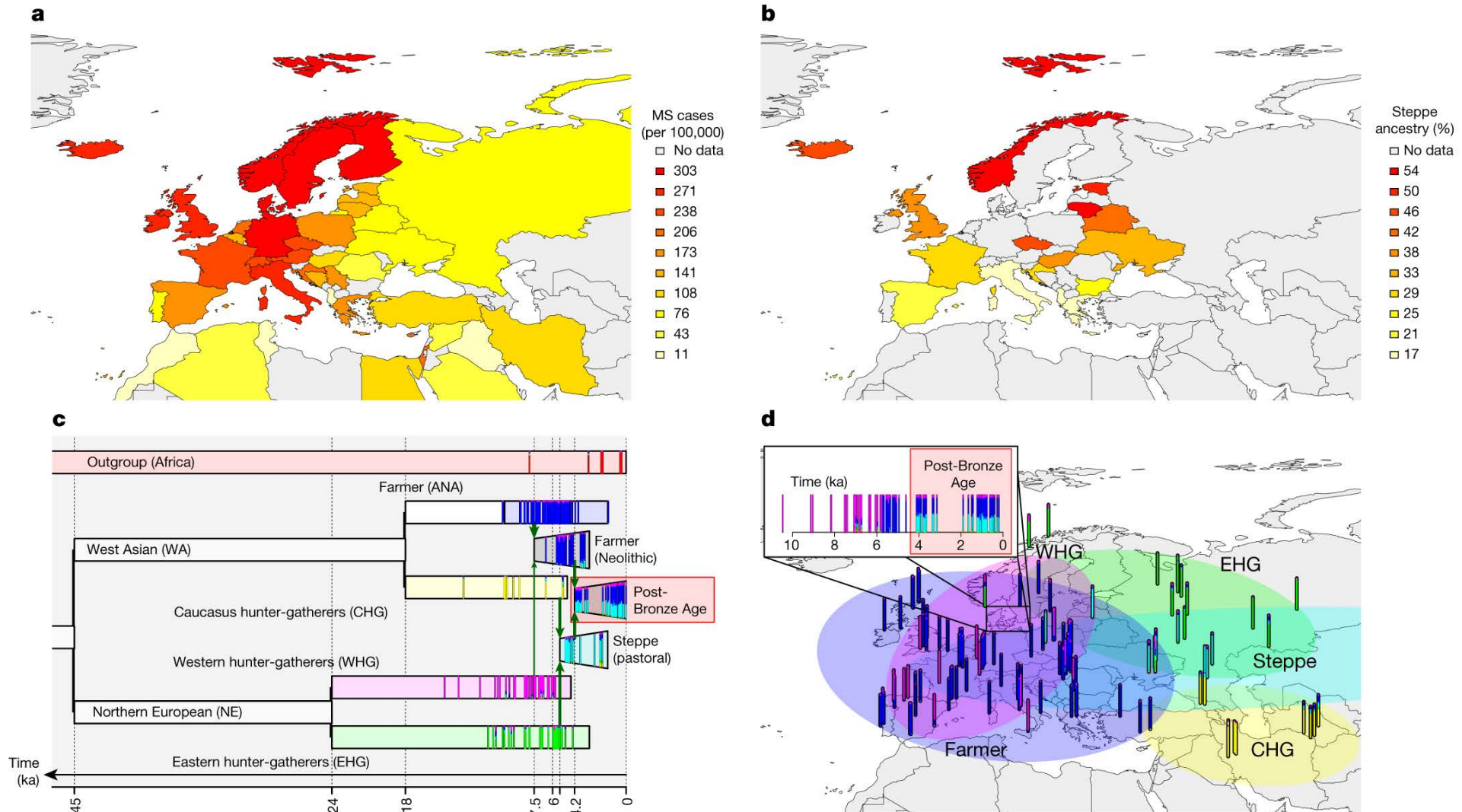


Lindo et al., (2016)



Population branch statistic (PBS) of the *HLA-DQA1* gene

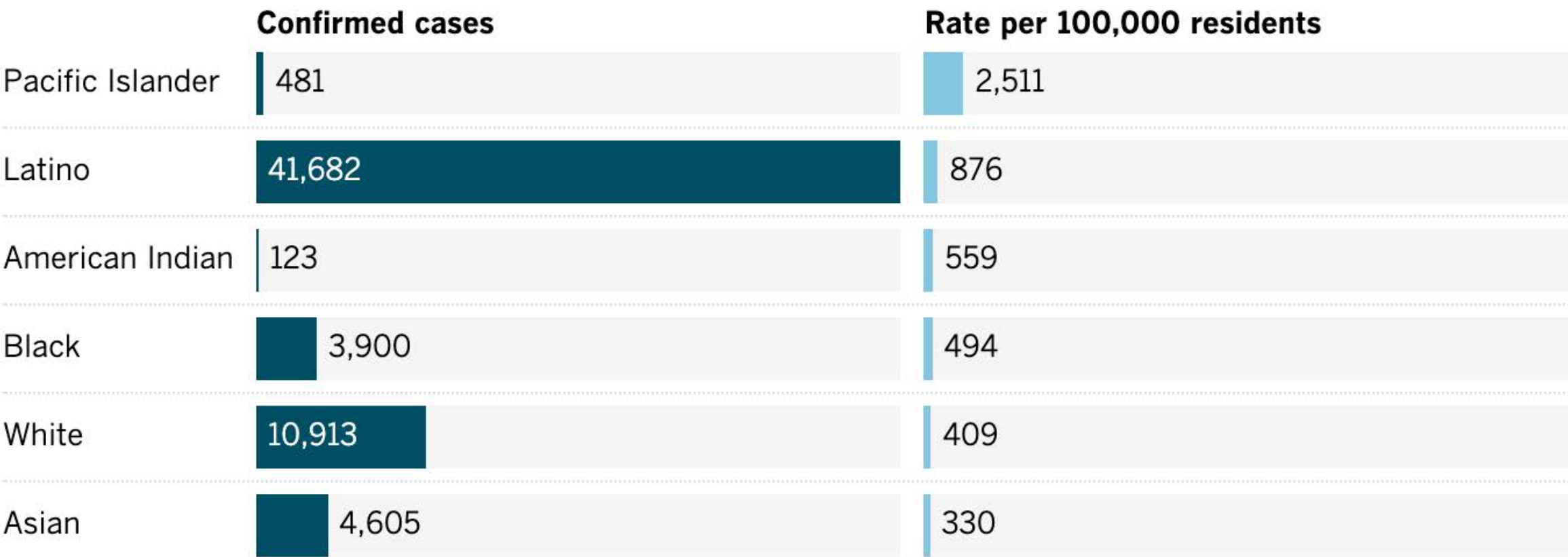
The population history of Europe is associated with the modern-day distribution of MS





Pacific Islanders see highest COVID-19 rate in L.A. County

Coronavirus infection rates among Pacific Islander residents of Los Angeles County are six times higher than white residents and three times higher than Latino residents.

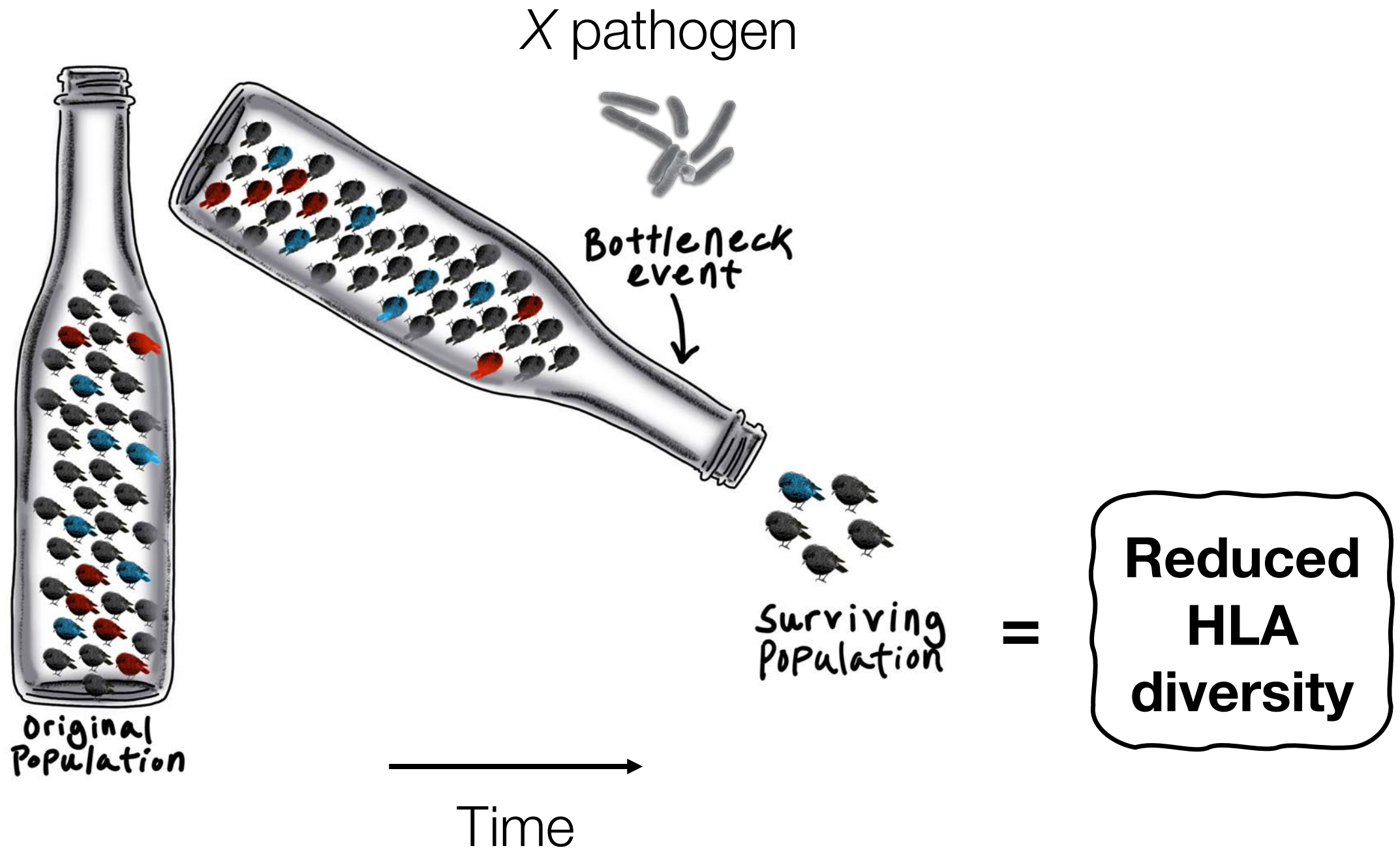


NOTE: Figures as of July 15 and do not include Long Beach or Pasadena
Los Angeles County Department of Public Health

Los Angeles Times

By TONY BARBOZA, BEN POSTON

JULY 19, 2020 | 7 AM





outline

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Tahiti





Pascart et al., Lancet Global Health (2024)

Perspective

Why community consultation matters in genomic research benefit-sharing models

Sarah LeBaron von Baeyer,¹ Rebecca Crocker,² Rindra Rakotoarivony,³ Jean Freddy Ranaivoarisoa,³ Germain Jules Spiral,³ Stephane Castel,¹ Andrew Farnum,¹ Holly Vance,¹ Noah Collins,⁴ Keolu Fox,^{5,6} and Kaja Wasik^{1,6}

¹Variant Bio, Seattle, Washington 98109, USA; ²Cancer Center, University of Arizona, Tucson, Arizona 85721, USA; ³Department of Anthropobiology and Sustainable Development, University of Antananarivo, Antananarivo 101 Madagascar; ⁴Department of Anthropology, Princeton University, Princeton, New Jersey 08540, USA; ⁵Indigenous Futures Institute, University of California, San Diego, La Jolla, California 92093, USA ⁶J. Craig Venter Research Institute, La Jolla, California 92037, USA

The gout epidemic in French Polynesia: a modelling study of data from the Ma'i u'u epidemiological survey

Tristan Pascart, Kaja A Wasik, Cristian Preda, Valérie Chune, Jérémie Torterat, Nicolas Prud'homme, Maryline Nassih, Agathe Martin, Julien Le Masson, Vahinetua Rodière, Sylvain Frogier, Georges Canova, Jean-Paul Pescheux, Charles Shan Sei Fan, Charlotte Jauffret, Patrick Claeys, Sarah LeBaron von Baeyer, Stéphane E Castel, Anne-Katrin Emde, Laura Verges-Armstrong, Keolu Fox, Megan Leask, Jean-Jacques Vitagliano, Sahara Graf, Laurene Norberciak, Jacques Raynal, Nicola Dalbeth, Tony Merriman, Thomas Bardin, Erwan Oehler

Summary

Background Gout is the most common cause of inflammatory arthritis worldwide, particularly in Pacific regions. We aimed to establish the prevalence of gout and hyperuricaemia in French Polynesia, their associations with dietary habits, their comorbidities, the prevalence of the *HLA-B*58:01* allele, and current management of the disease.

Methods The Ma'i u'u survey was epidemiological, prospective, cross-sectional, and gout-focused and included a random sample of adults from the general adult population of French Polynesia. It was conducted and data were collected between April 13 and Aug 16, 2021. Participants were randomly selected to represent the general adult population of French Polynesia on the basis of housing data collected during the 2017 territorial census. Each selected household was visited by a research nurse from the Ma'i u'u survey who collected data via guided, 1-h interviews with participants. In each household, the participant was the individual older than 18 years with the closest upcoming birthday. To estimate the frequency of *HLA-B*58:01*, we estimated *HLA-B* haplotypes on individuals who had whole-genome sequencing to approximately 5x average coverage (mid-pass sequencing). A subset of individuals who self-reported Polynesian ancestry and not European, Chinese, or other ancestry were used to estimate Polynesian-ancestry specific allele frequencies. Bivariate associations were reported for weighted participants; effect sizes were estimated through the odds ratio (OR) of the association calculated on the basis of a logistic model fitted with weighted observations.

Findings Among the random sample of 2000 households, 896 participants were included, 140 individuals declined, and 964 households could not be contacted. 22 participants could not be weighted due to missing data, so the final weighted analysis included 874 participants (449 [51.4%] were female and 425 [48.6%] were male) representing the 196 630 adults living in French Polynesia. The estimated prevalence of gout was 14.5% (95% CI 9.9–19.2), representing 28 561 French Polynesian adults, that is 25.5% (18.2–32.8) of male individuals and 3.5% (1.0–6.0) of female individuals. The prevalence of hyperuricaemia was estimated at 71.6% (66.7–76.6), representing 128 687 French Polynesian adults. In multivariable analysis, age (OR 1.5, 95% CI 1.2–1.8 per year), male sex (10.3, 1.8–60.7), serum urate (1.6, 1.3–2.0 per 1 mg/dL), uraturia (0.8, 0.8–0.8 per 100 mg/L), type 2 diabetes (2.1, 1.4–3.1), BMI more than 30 kg/m² (1.1, 1.0–1.2 per unit), and percentage of visceral fat (1.7, 1.1–2.7 per 1% increase) were associated with gout. There were seven heterozygous *HLA-B*58:01* carriers in the full cohort of 833 individuals (seven [0.4%] of 1666 total alleles) and two heterozygous carriers in a subset of 696 individuals of Polynesian ancestry (two [0.1%]).

Interpretation French Polynesia has an estimated high prevalence of gout and hyperuricaemia, with gout affecting almost 15% of adults. Territorial measures that focus on increasing access to effective urate-lowering therapies are warranted to control this major public health problem.

Funding Variant Bio, the French Polynesian Health Administration, Lille Catholic University Hospitals, French Society of Rheumatology, and Novartis.



Lancet Glob Health 2024; 12: e685–96

See Comment page e550

Service de Rhumatologie

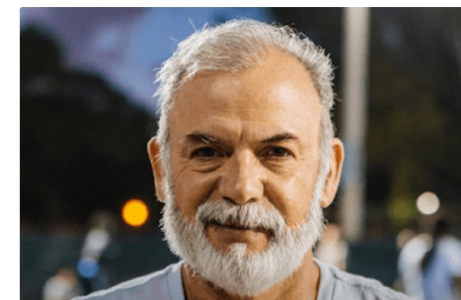
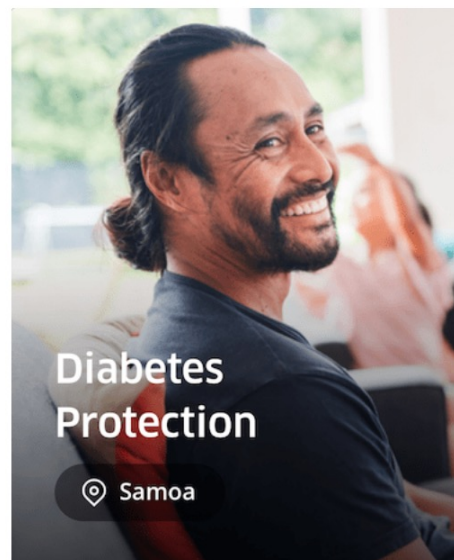
(Prof T Pascart MD, C Jauffret MD) and Department of Methodology and Biostatistics (Prof C Preda PhD, S Graf BSc, L Norberciak BSc), Lille Catholic University and Research Department (M Nassih BSN, A Martin BSN, J Le Masson BSN, V Rodière BSN, S Frogier BSN, G Canova BSN, J-P Pescheux BSN, J-J Vitagliano PhD), Hôpital Saint-Philibert, Lille, France; Variant Bio, Seattle, WA, USA (K A Wasik PhD, S L von Baeyer PhD, S E Castel PhD, A-K Emde PhD, L Verges-Armstrong PhD); Department of Biology (V Chune MD, P Claeys BSN) and Department of Internal Medicine and Infectious Diseases (E Oehler MD), Centre Hospitalier de Polynésie Française, Pape'ete, Tahiti, French Polynesia; Institut de la Statistique de Polynésie Française, Papeete, Tahiti, French Polynesia (J Torterat BSc, N Prud'homme BSc); Direction de la Santé de Polynésie Française, Papeete, Tahiti, French Polynesia (V Rodière, S Frogier, G Canova, J-P Pescheux); Rheumatology Private Practice, Papeete, Tahiti, French Polynesia (C Shan Sei Fan MD); Global Health Program, Department

PEOPLE-DRIVEN THERAPEUTICS

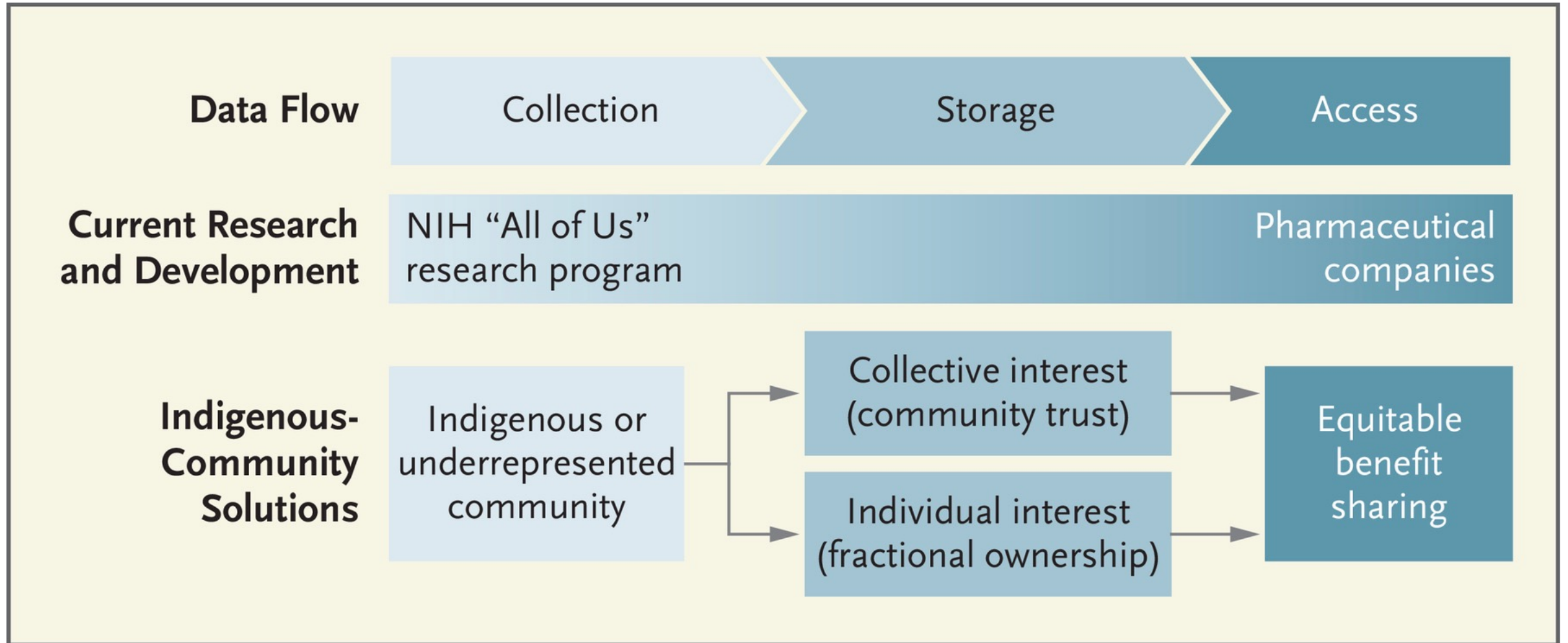
Exceptional Traits Among Us

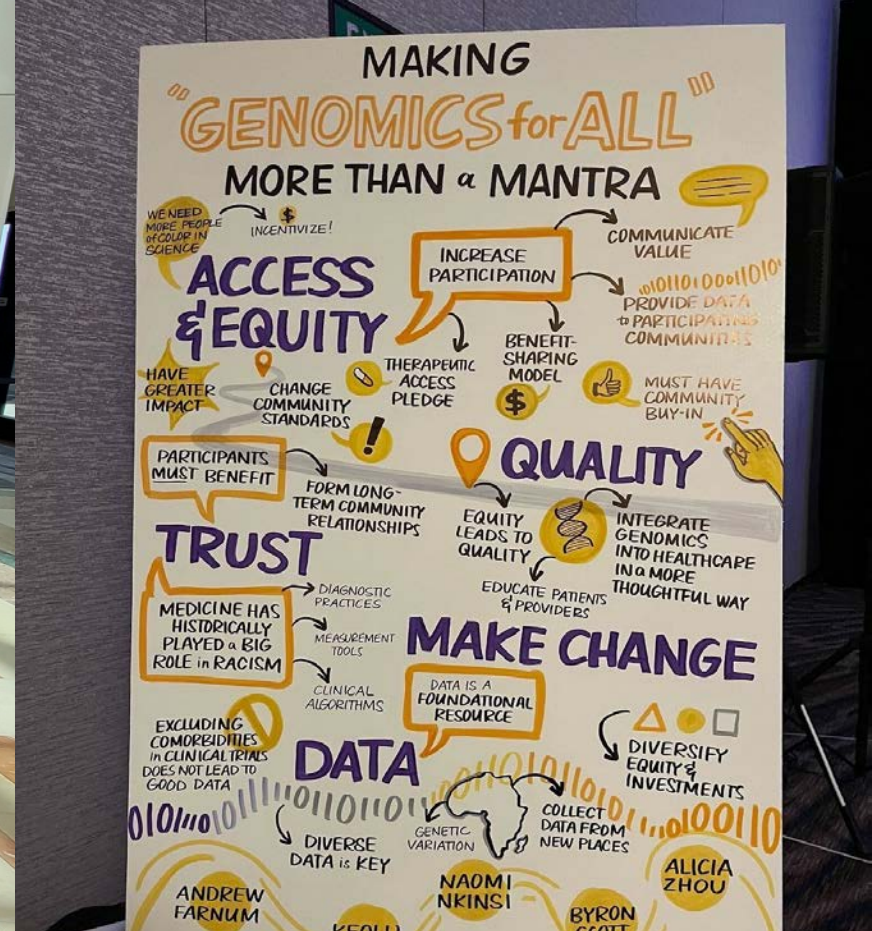
Variant Bio is developing therapies that will improve global health by studying the genes of people with exceptional health-related traits. These examples are just some of the studies that have inspired us.

[Our Approach →](#)



Approaches to Equitable Benefit Sharing

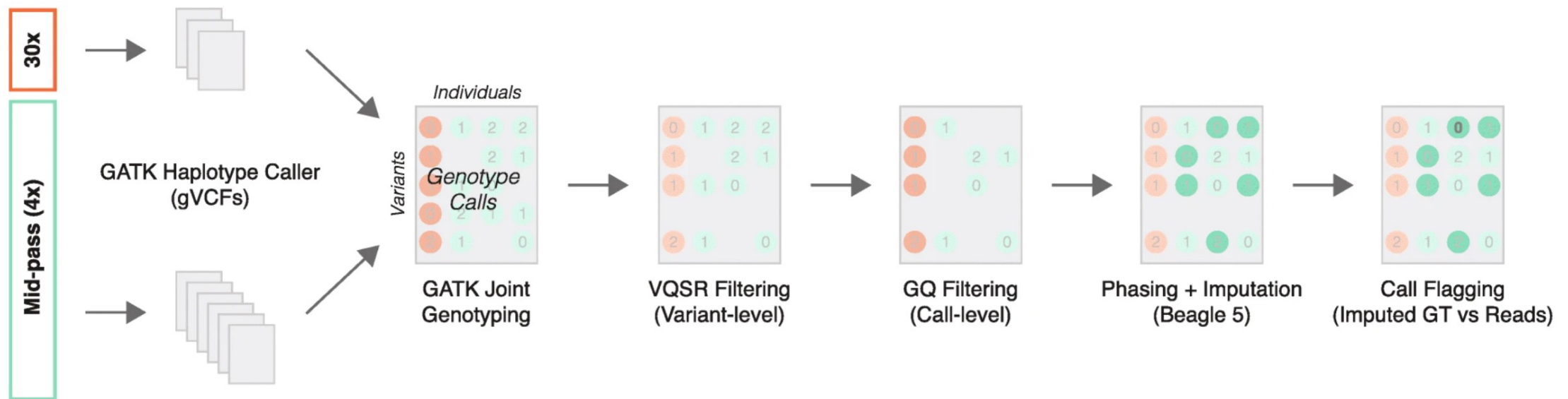




Announcing Variant Bio's Affordable Medicines Pledge



Mid-pass whole genome sequencing enables biomedical genetic studies of diverse populations

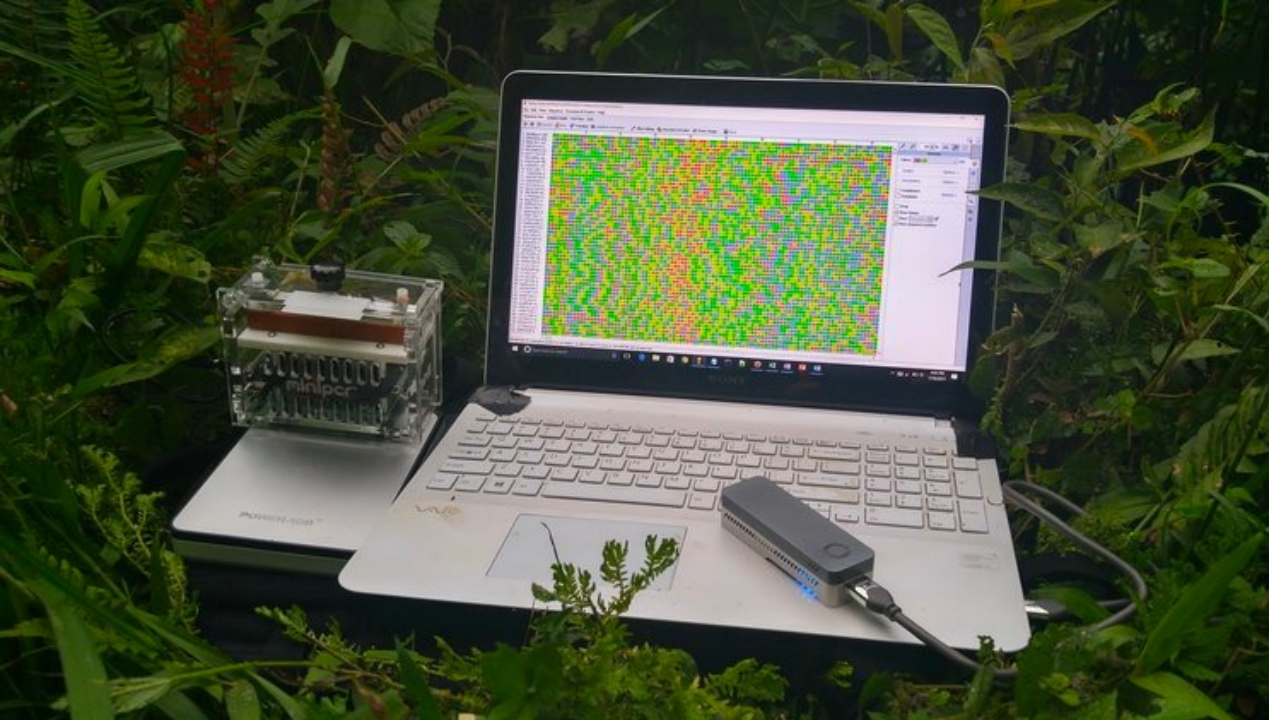


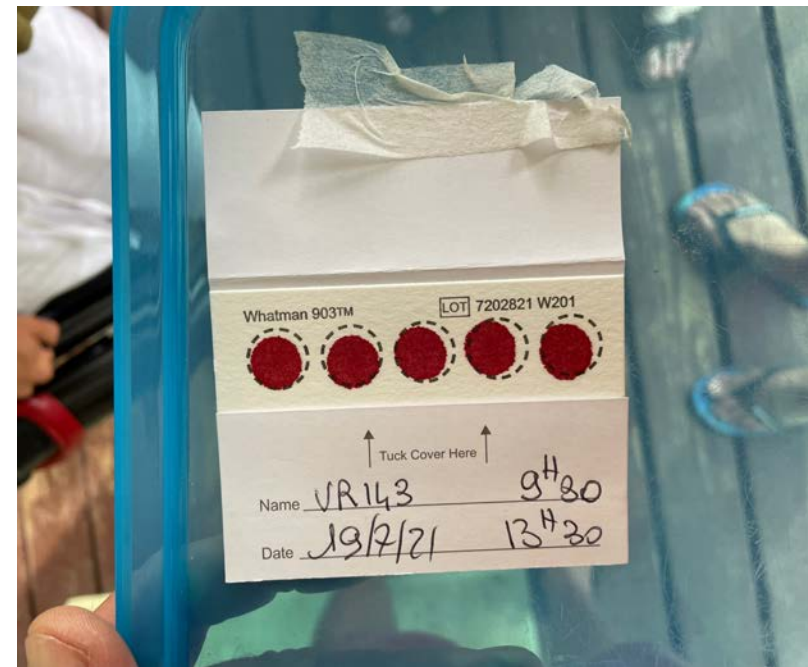
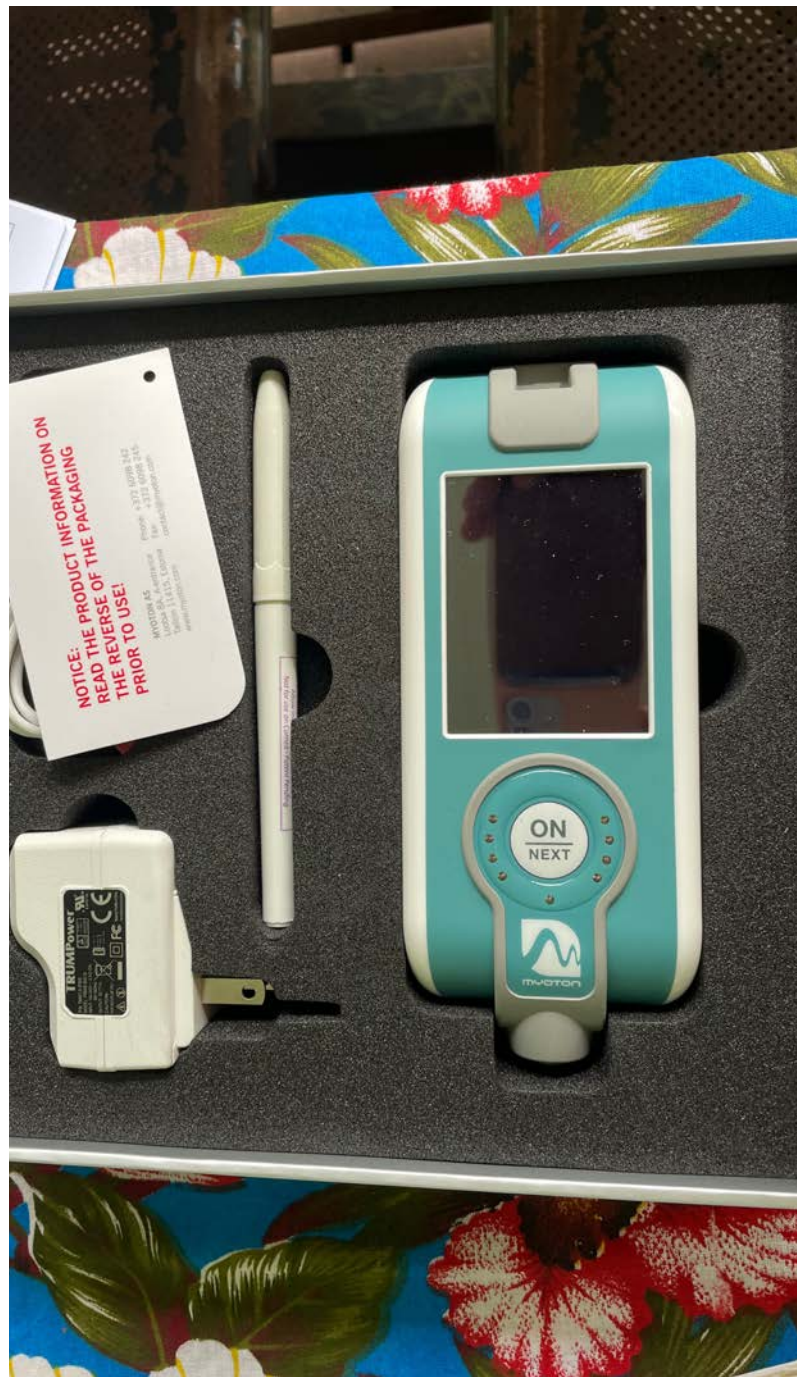


Grassroots Research



Democratizing Technology



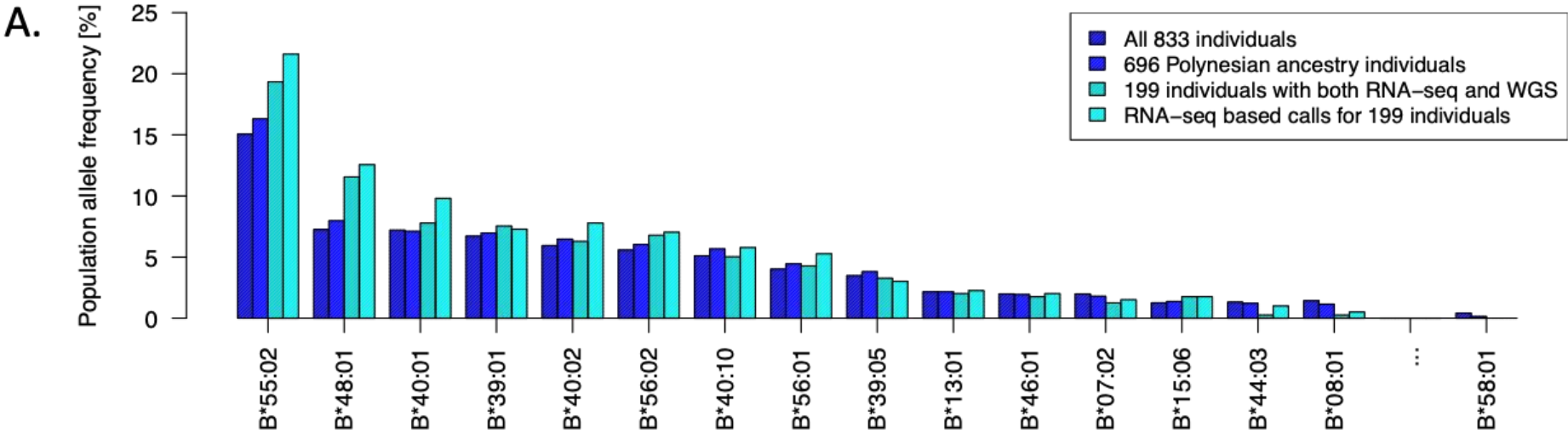




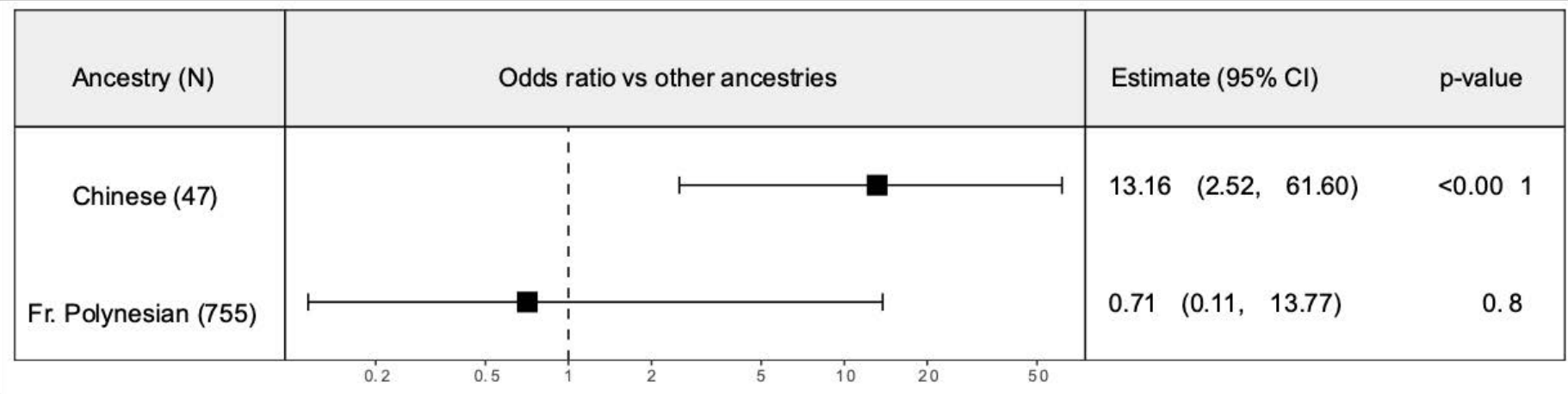
***Gout is estimated to affect
one in seven individuals in
French Polynesia***

The gout epidemic in French Polynesia: Results from the *Ma'i u'u* Territorial Survey

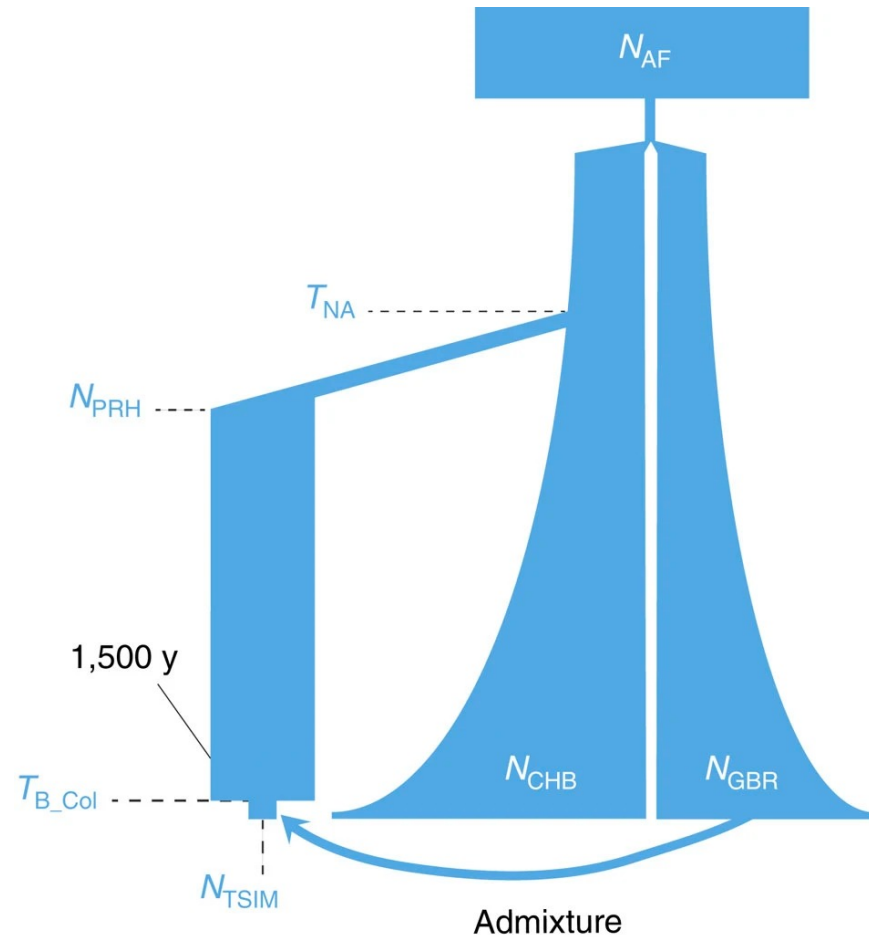
HLA-B allele frequencies in
Polynesian ancestry individuals



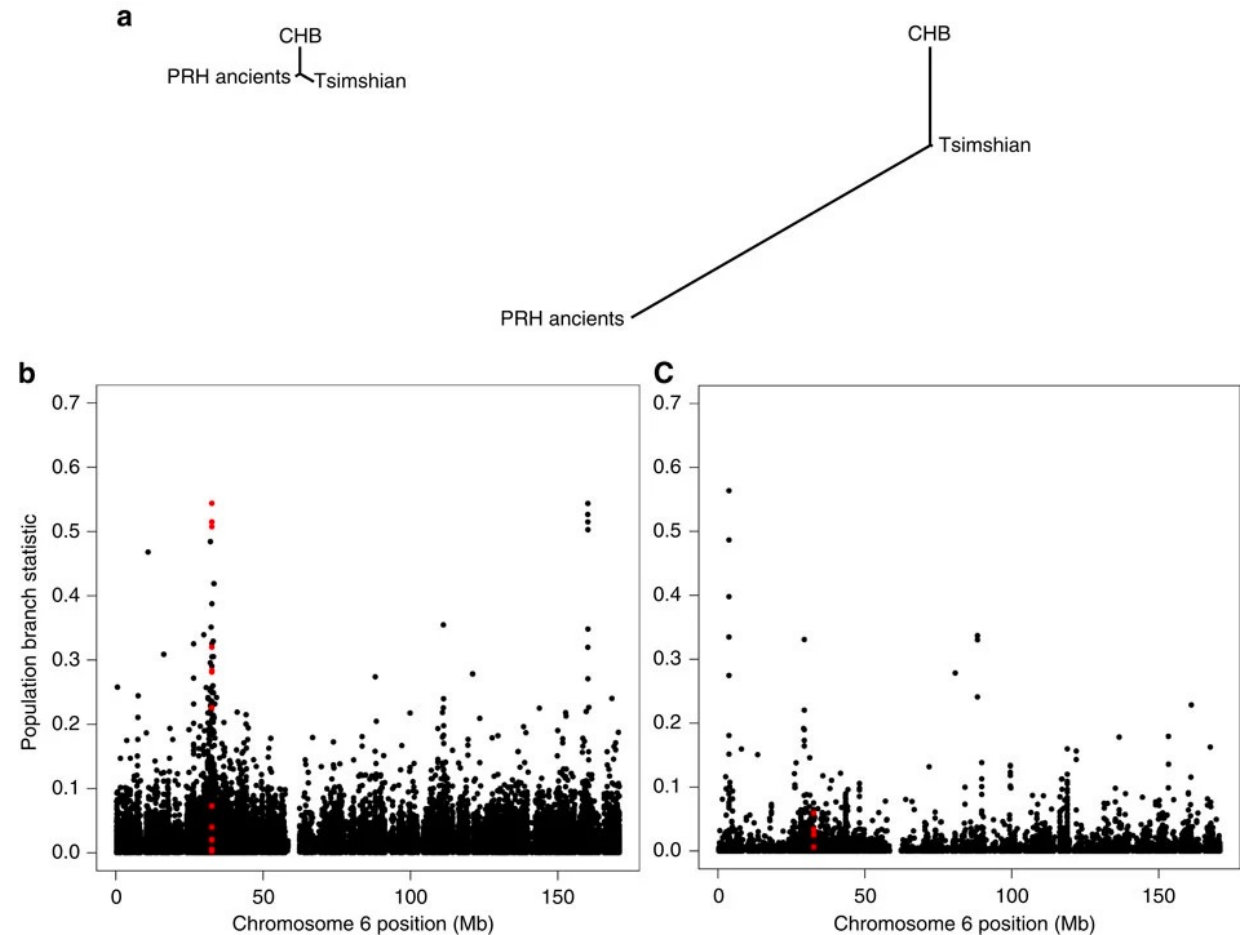
B.



Population Collapse: Identifying bottlenecks after European contact

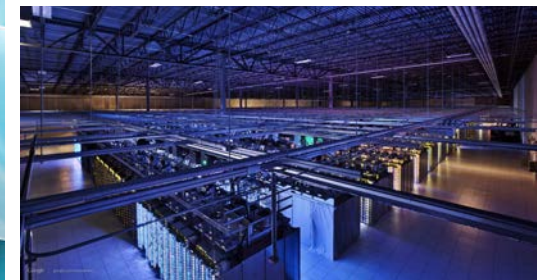
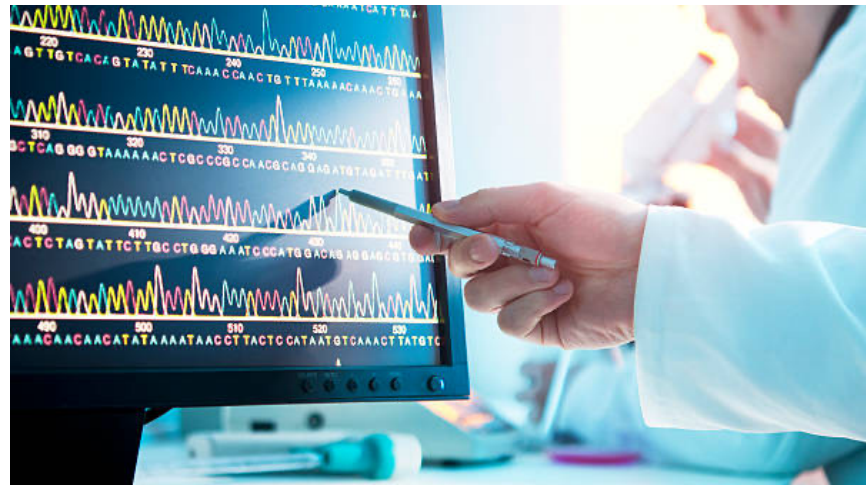
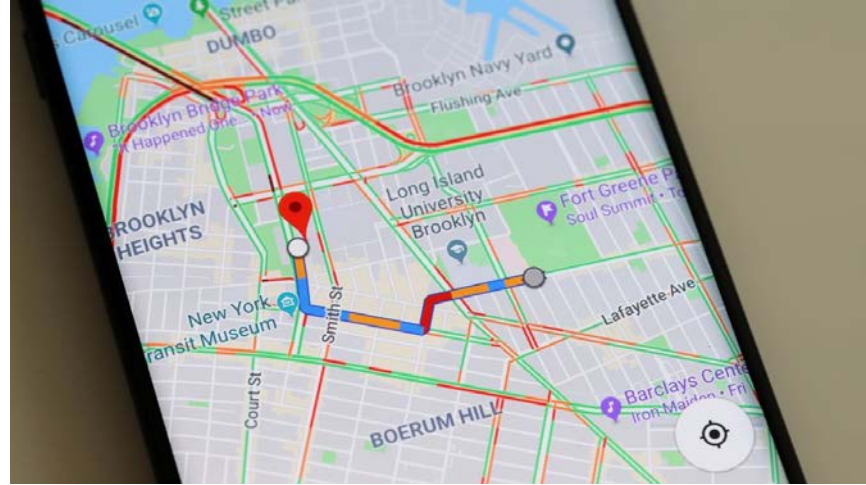
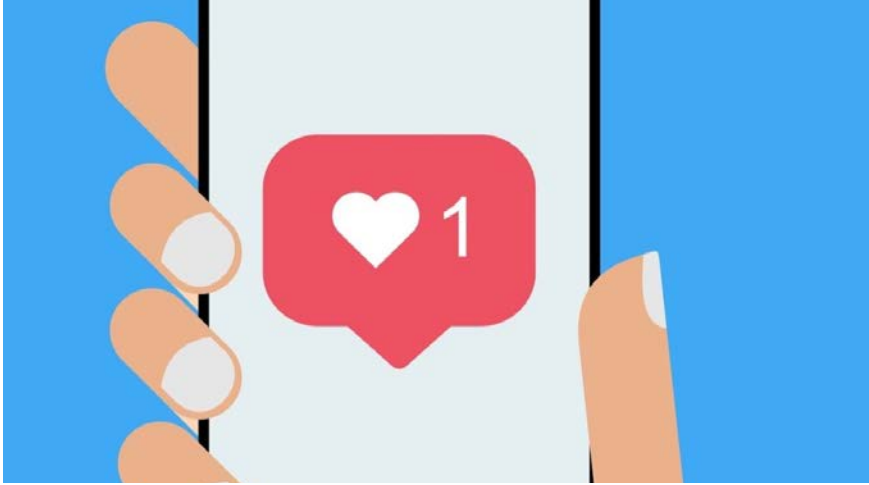


Lindo et al., (2016)



Population branch statistic (PBS) of the *HLA-DQA1* gene

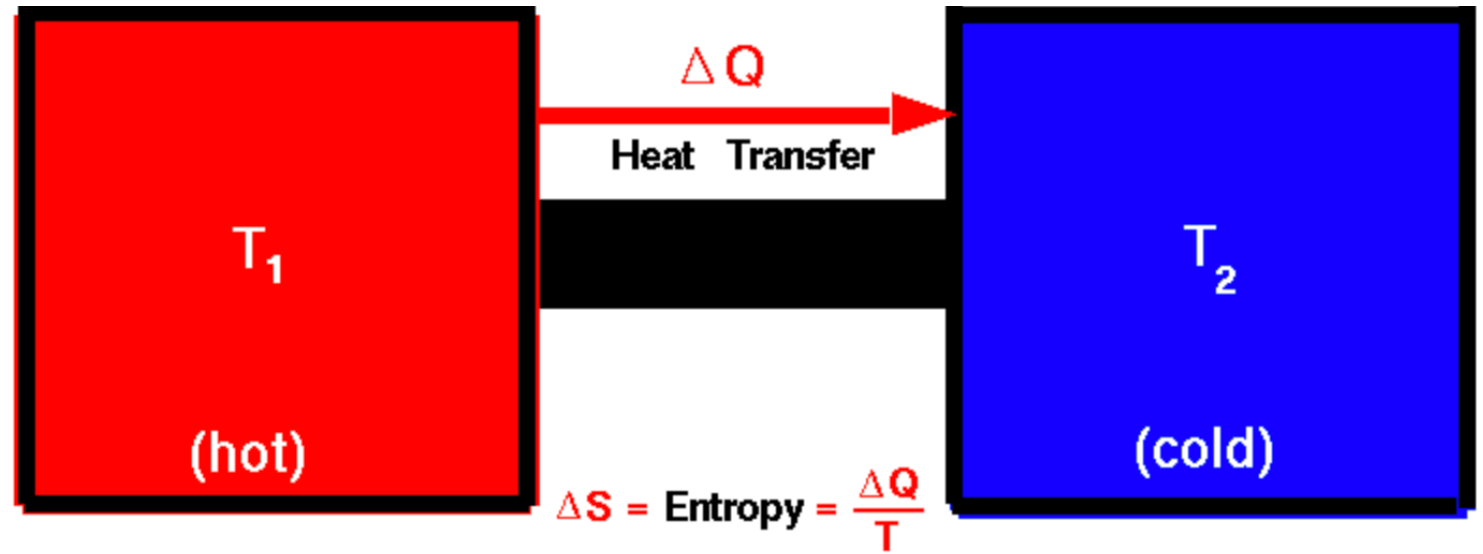
- In 2020, the world generated approximately **59 zettabytes (ZB) of data**



- This is expected to grow to **175 ZB by 2025** driven by the increasing use of IoT devices, social media, and other digital technologies
- To put this into perspective, **one zettabyte = one billion terabytes**

The second law of thermodynamics is a physical law based on universal experience concerning heat and energy interconversions.

One simple statement of the law is that heat always moves from hotter objects to colder objects (or "downhill"), unless energy in some form is supplied to reverse the direction of heat flow.

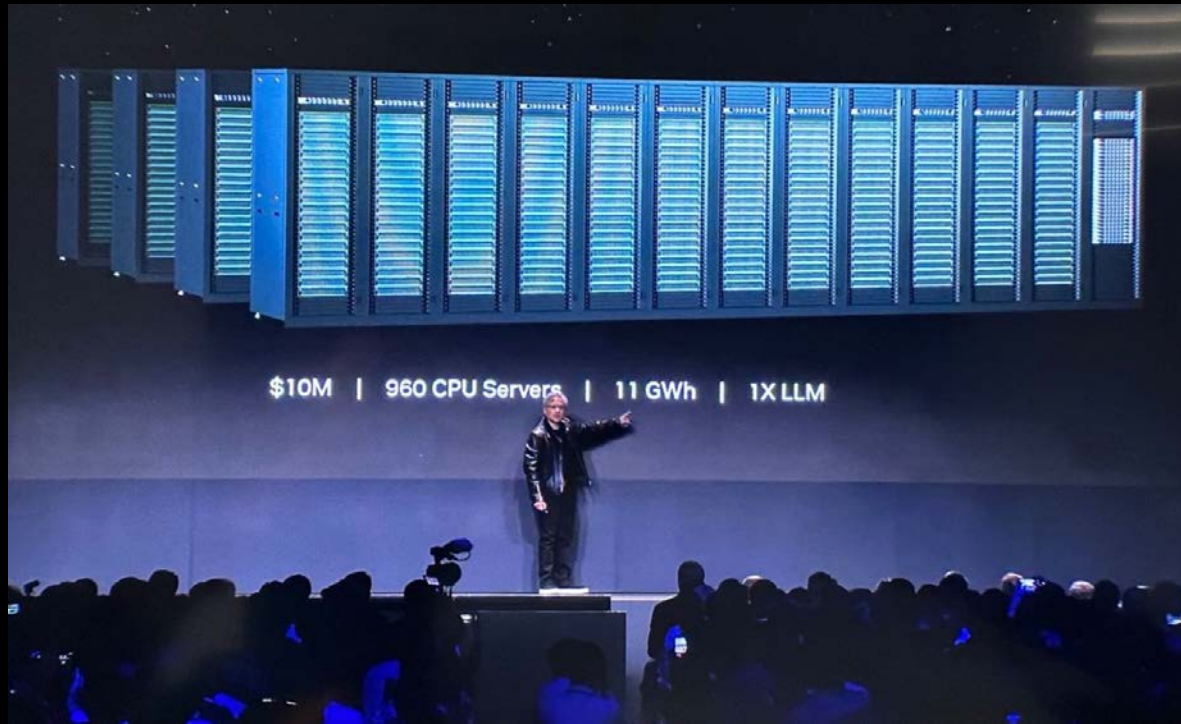


There exists a useful thermodynamic variable called entropy (S). A natural process that starts in one equilibrium state and ends in another will go in the direction that causes the entropy of the system plus the environment to increase for an irreversible process and to remain constant for a reversible process.

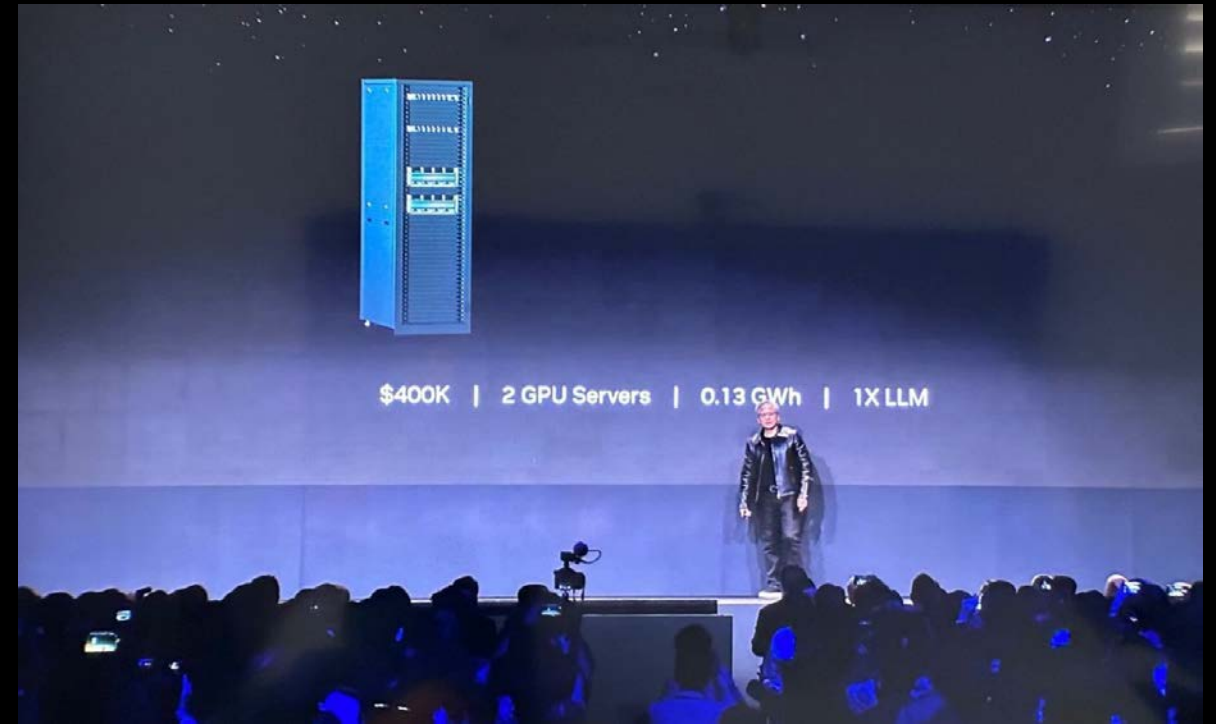
$$S_f = S_i \text{ (reversible)}$$

$$S_f > S_i \text{ (irreversible)}$$

How it started



How it's going



That power consumption though 🔥😓

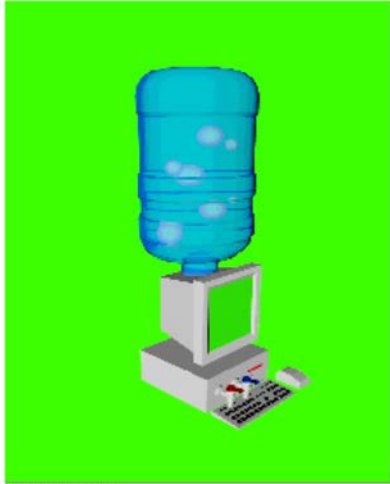


Illustration by Erik Carter

TECHNOLOGY

AI IS TAKING WATER FROM THE DESERT

New data centers are springing up every week. Can the Earth sustain them?

By Karen Hao

DAILY COMMENT

THE OBSCENE ENERGY DEMANDS OF A.I.

How can the world reach net zero if it keeps inventing new ways to consume energy?



By Elizabeth Kolbert

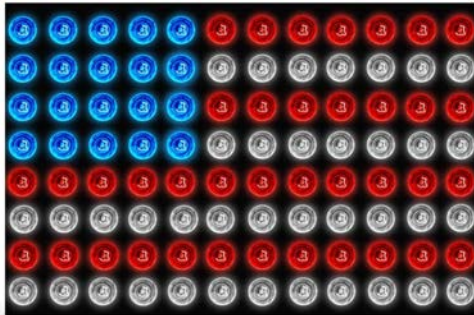
March 9, 2024

Amid explosive demand, America is running out of power

AI and the boom in clean-tech manufacturing are pushing America's power grid to the brink. Utilities can't keep up.



By ExactHabitat
March 7, 2024 at 6:05 a.m. EST



electrek

Amazon just bought a 100% nuclear-powered data center

Michelle Lewis | Mar 5 2024 - 8:06 am PT | 48 Comments



Photo: Telen Energy



It's been estimated that ChatGPT is consuming more than half a million kilowatt-hours of electricity per day. Photograph by Mark Felix / AFP / Getty

welcome

key dates

call for session proposals

call for workshop proposals

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Pacific Symposium on Biocomputing (PSB) 2025

*January 4-8, 2025
The Big Island of Hawaii*

@PacSymBio #psb25

Our hearts go out to our Lahaina ohana.

<https://psb.stanford.edu/>

Mahalo nui ☺ – Questions?

