

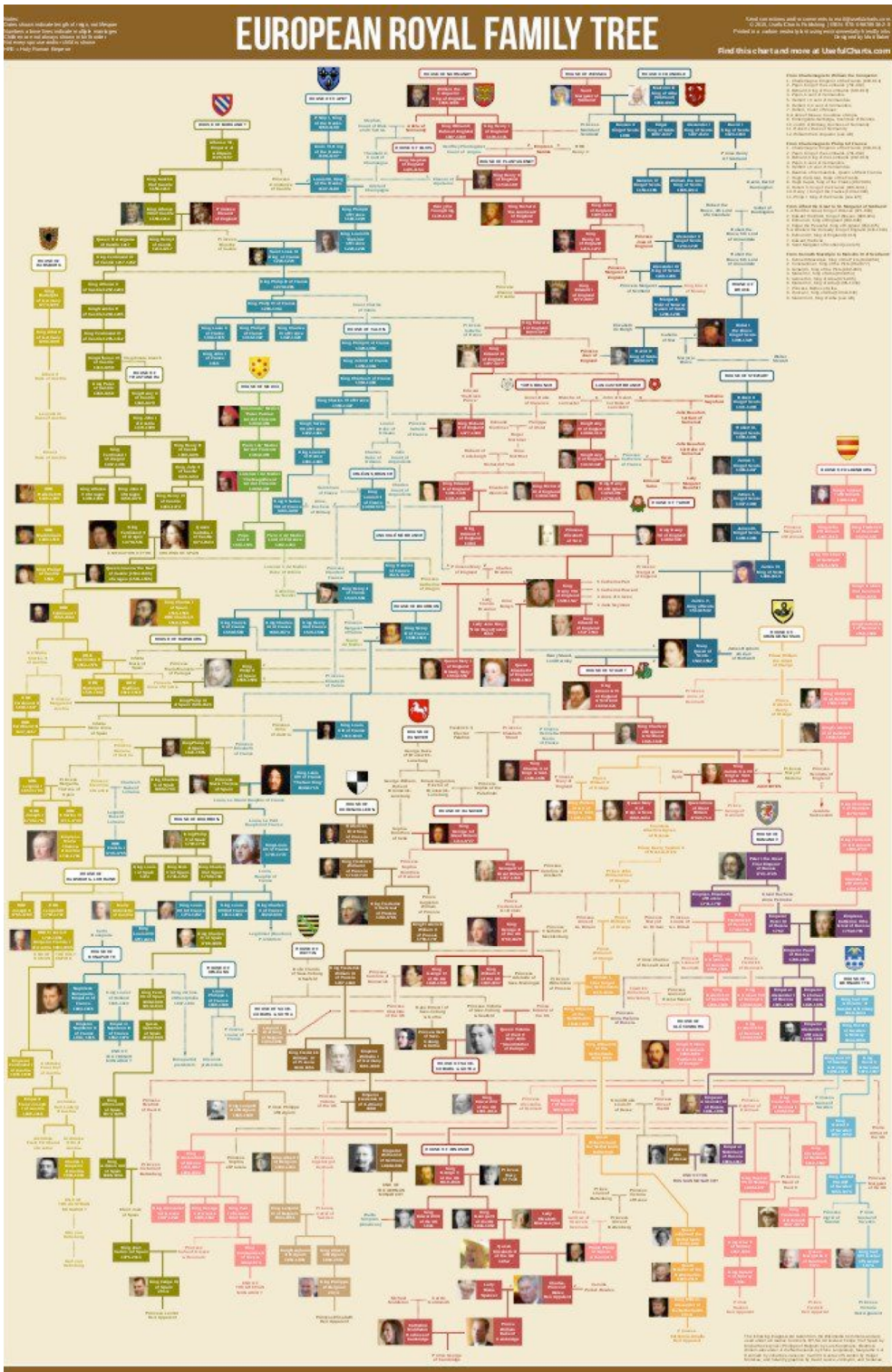
# Genetics, genealogy, and our vast family tree

Graham Coop  
Evolution and Ecology, UC Davis

<http://gcbias.org/category/genetic-genealogy/>

@graham\_coop





Born 742  
 Charlemagne  
 Holy Roman Emperor



Graham Coop  
 Evolution and Ecology, UC Davis

<http://gcbias.org/category/genetic-genealogy/>

@graham\_coop



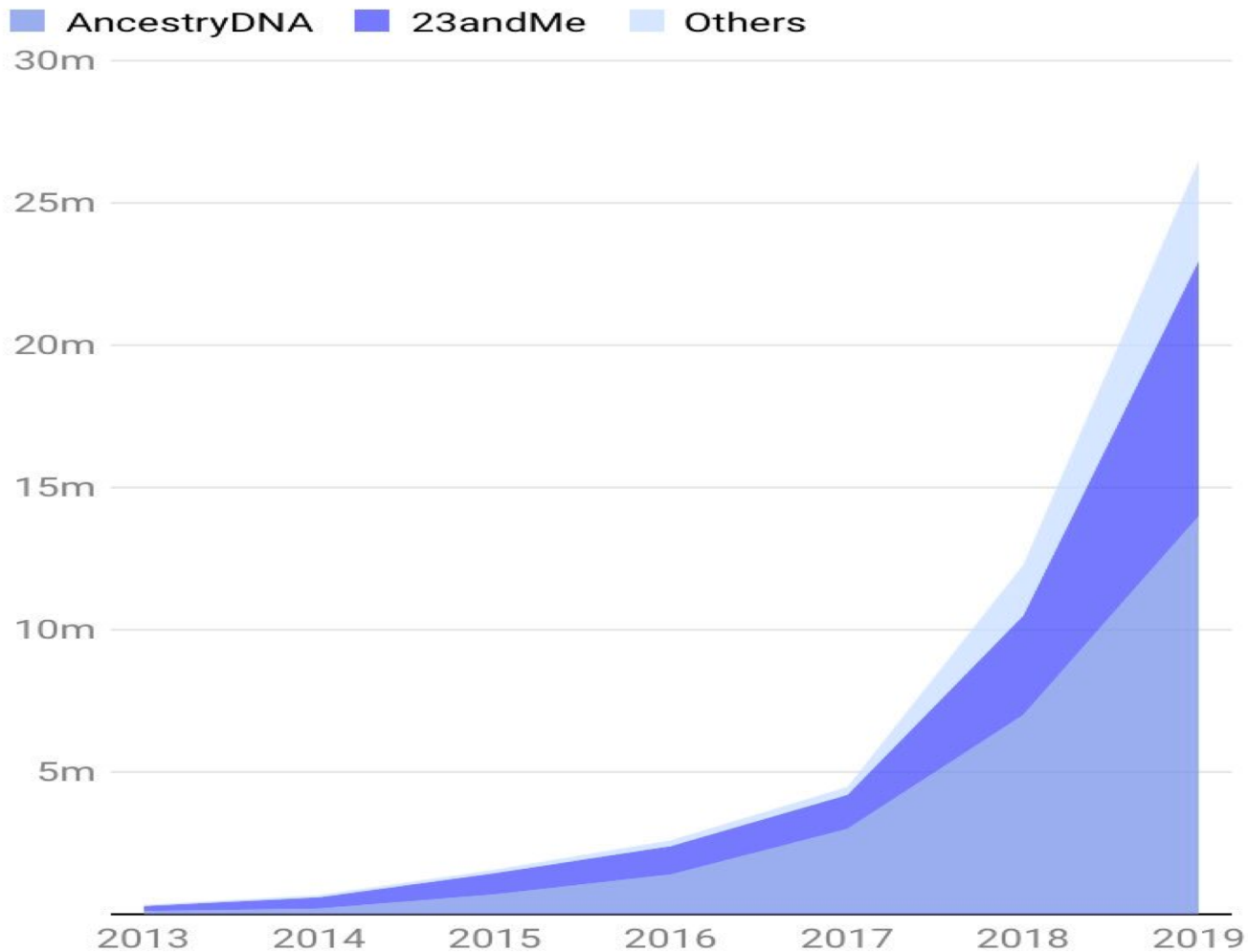


Chart: MIT Technology Review  
• Source: Company reports, Leah Larkin, ISOGG



# Connecting the chromosomes: Adoptees find, reunite with birth mothers through online DNA services



By **Brittany Britto** · **Contact Reporter**  
The Baltimore Sun

## To find alleged Golden State Killer, investigators first found his great-great-great-grandparents

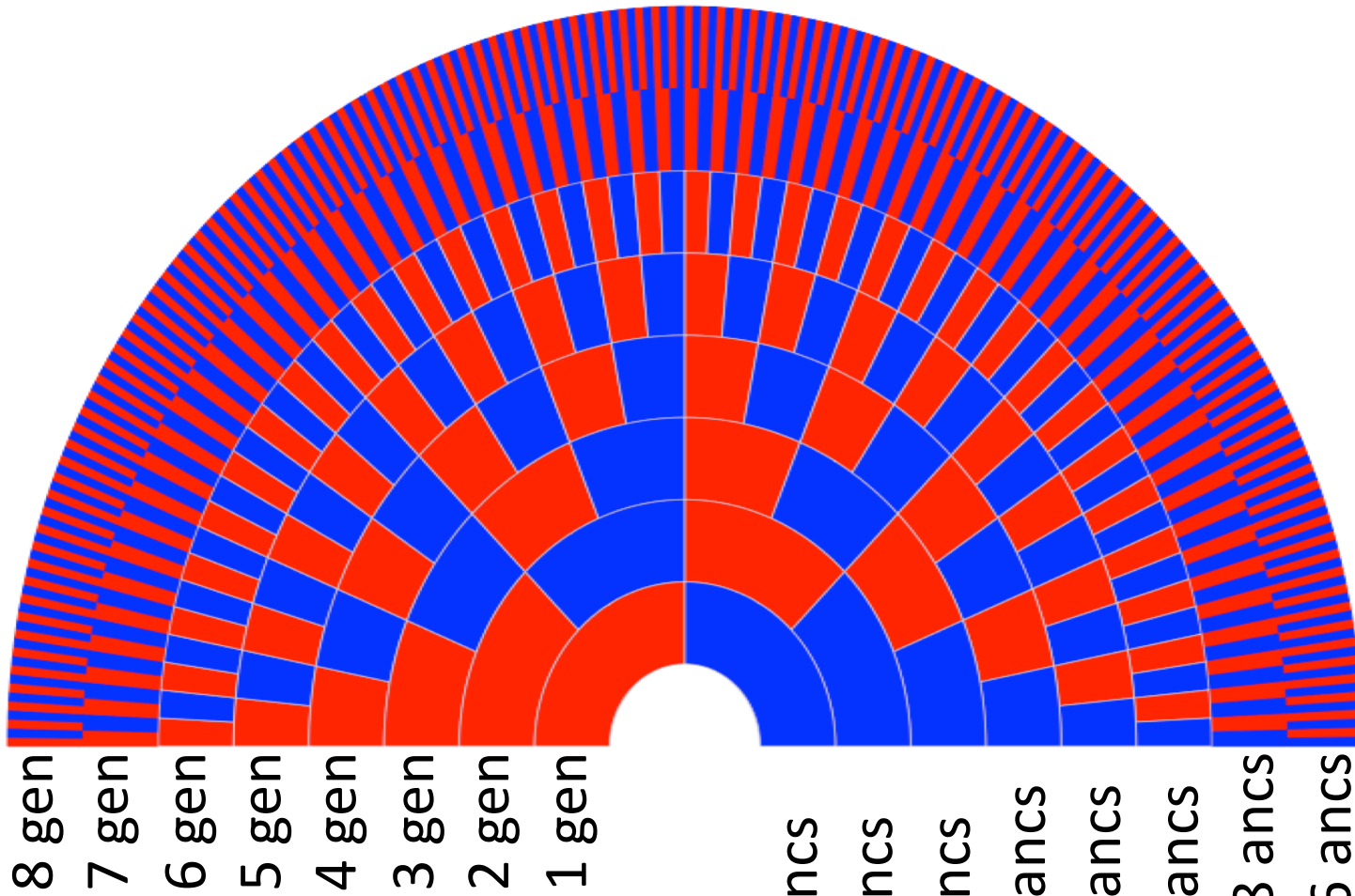
STAT [Sections](#) [Topics](#) [Multimedia](#)

By **Justin Jouvenal** April 30 [✉ Email the author](#)

[HEALTH](#)

**White nationalists are flocking to genetic ancestry tests. Some don't like what they find**

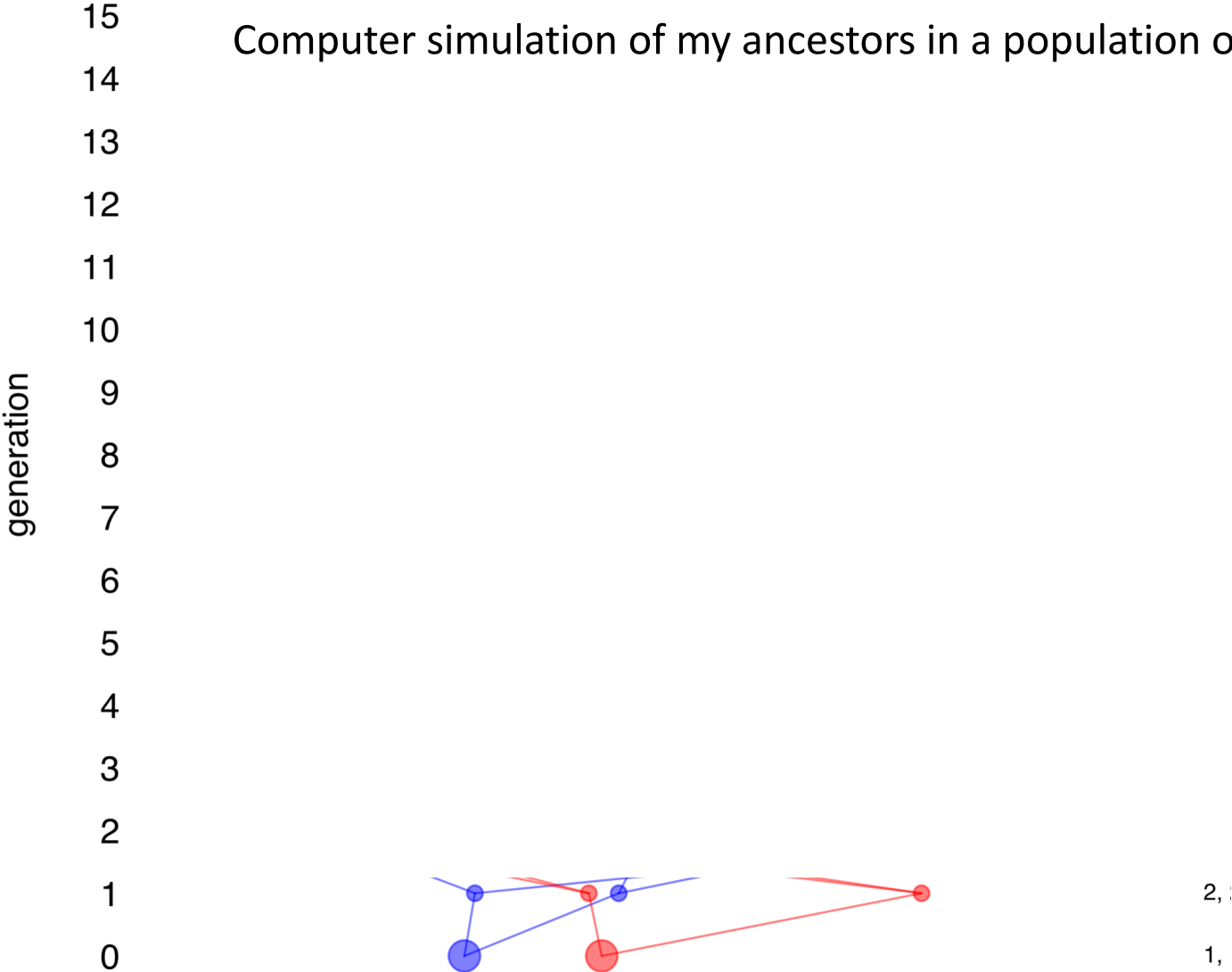




Gens	Years	# Ancs
1	30	2
2	60	4
3	90	8
4	120	16
5	150	32
6	180	64
7	210	128
8	240	256
9	270	512
10	300	1024
11	330	2048
12	360	4096
13	390	8192
14	420	16384
15	450	32768
16	480	65536
17	510	131072
18	540	262144
19	570	524288
20	600	1M
21	630	2.1M
22	660	4.2M
23	690	8.4M
24	720	16.8M
25	750	33.6M



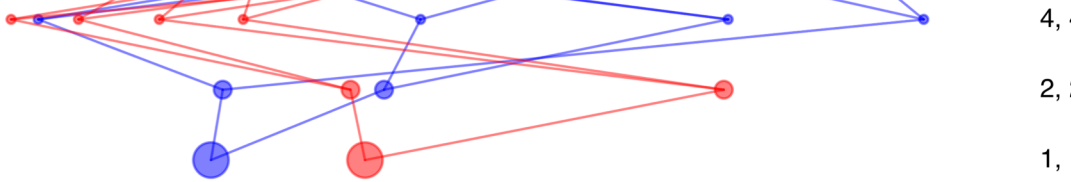
# Computer simulation of my ancestors in a population of 100,000 people



# Computer simulation of my ancestors in a population of 100,000 people

generation

16  
15  
14  
13  
12  
11  
10  
9  
8  
7  
6  
5  
4  
3  
2  
1  
0



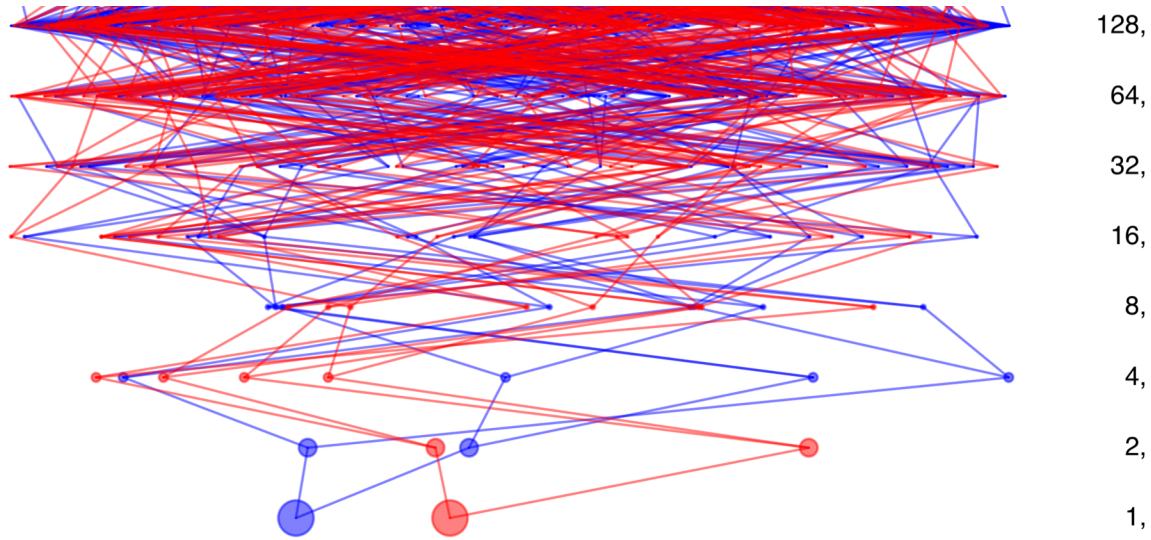
4,  
2,  
1,



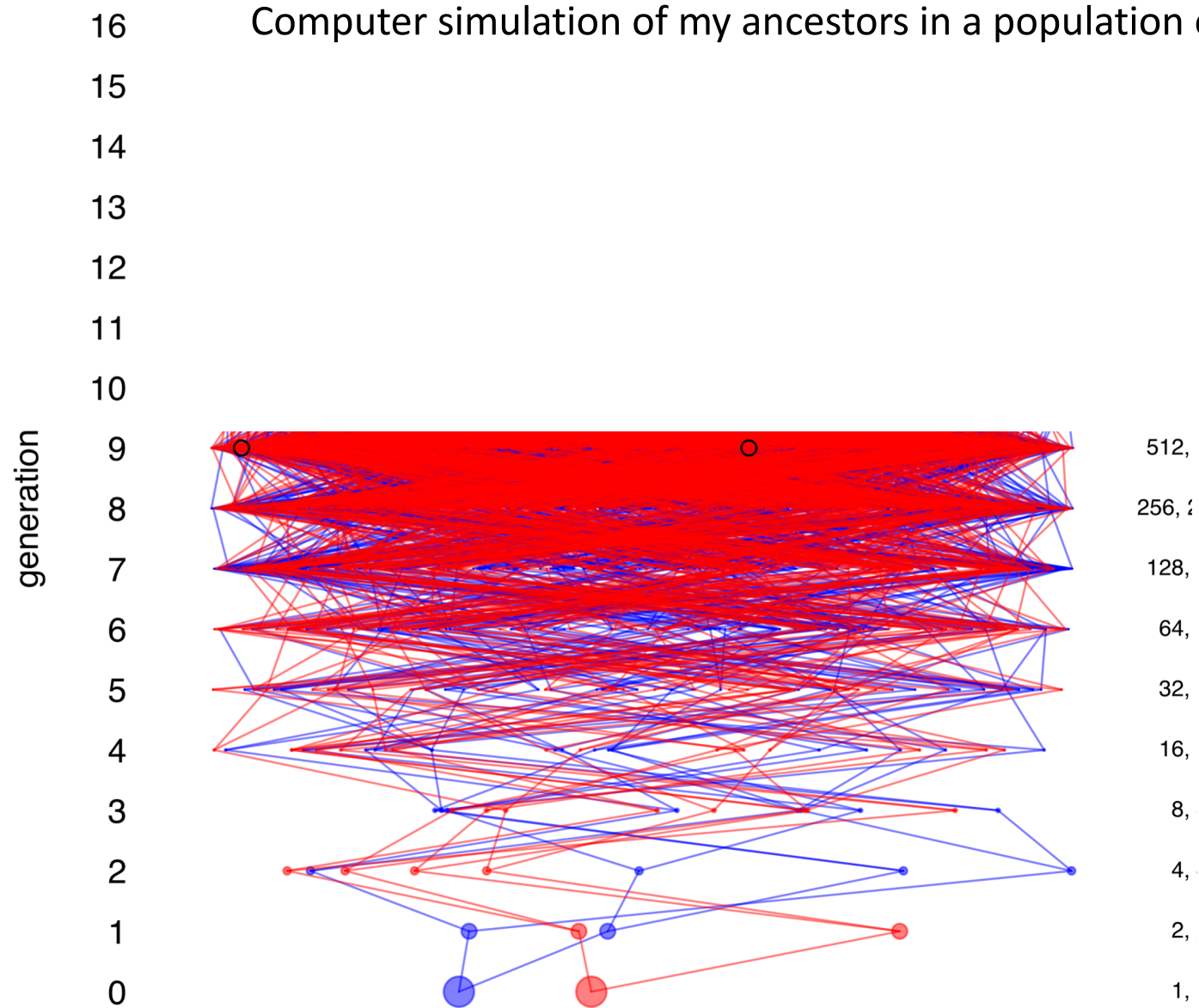
# Computer simulation of my ancestors in a population of 100,000 people

generation

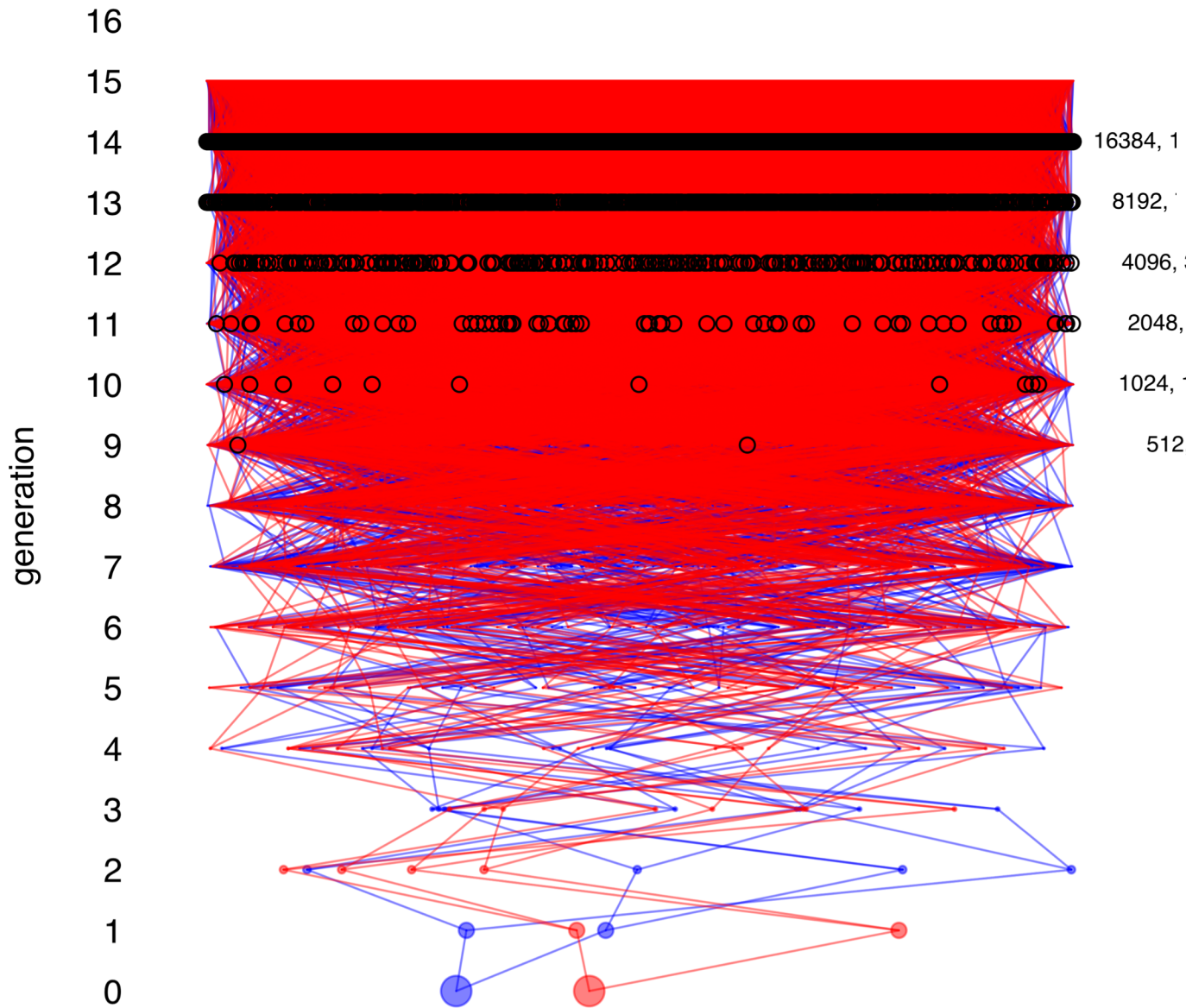
16  
15  
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13  
12  
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10  
9  
8  
7  
6  
5  
4  
3  
2  
1  
0



# Computer simulation of my ancestors in a population of 100,000 people







In a well-mixed population of 10 million we find the C. Anc of all individuals ~23 generations ago (~600 years)  
 ~1000 years ago all inds. will share all of their ancestors

*Adv. Appl. Prob. 31, 1002-1026 (1999)*  
 Printed in Northern Ireland  
 © Applied Probability Trust 1999

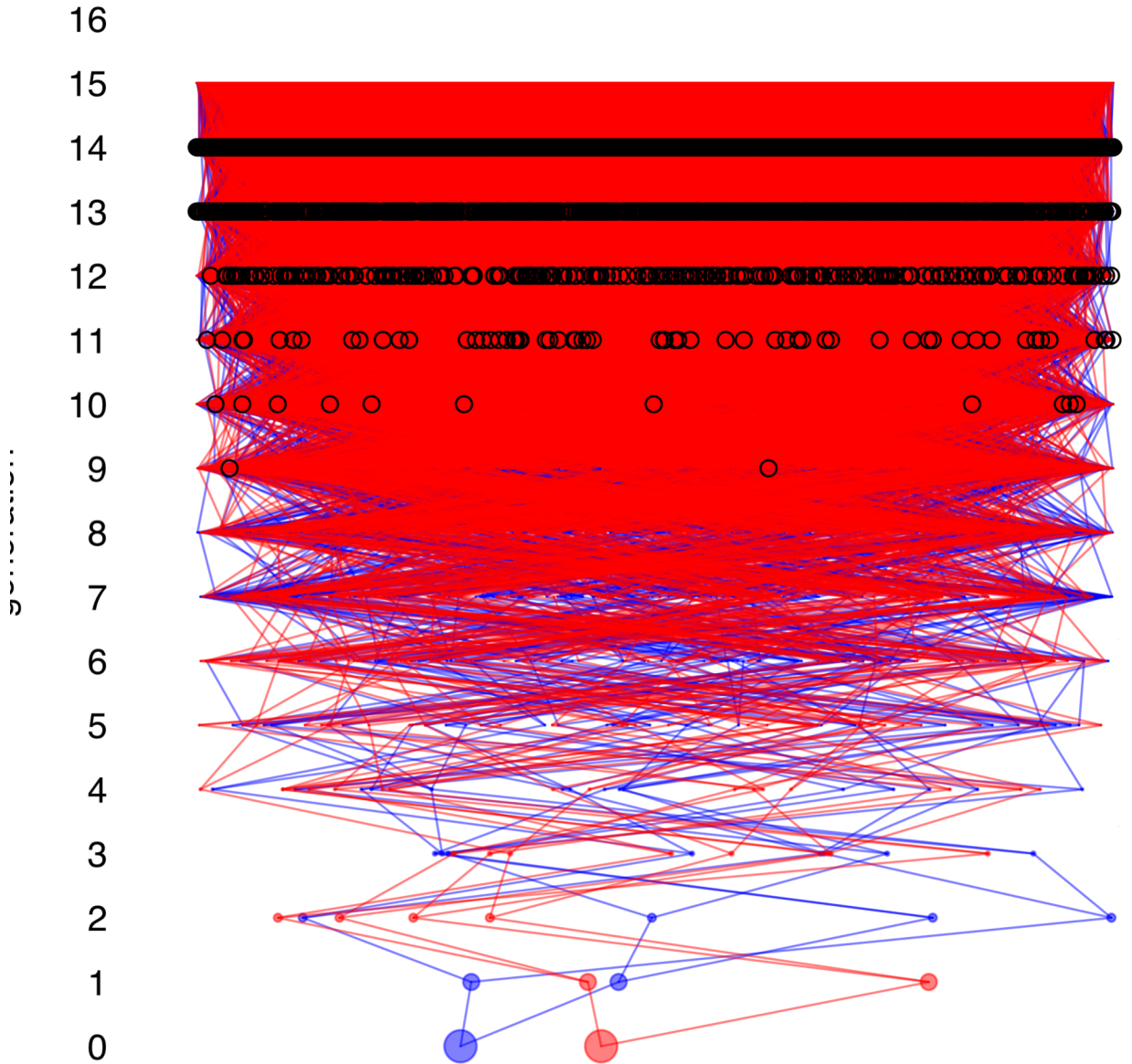
**RECENT COMMON ANCESTORS OF ALL PRESENT-DAY INDIVIDUALS**

JOSEPH T. CHANG,\* *Yale University*

In a well-mixed population of 10 million we find the  
C. Anc of all individuals ~23 generations ago (~600 years)  
~1000 years ago all inds. will share all of their ancestors

### RECENT COMMON ANCESTORS OF ALL PRESENT-DAY INDIVIDUALS

JOSEPH T. CHANG,\* Yale University



THE LOOM

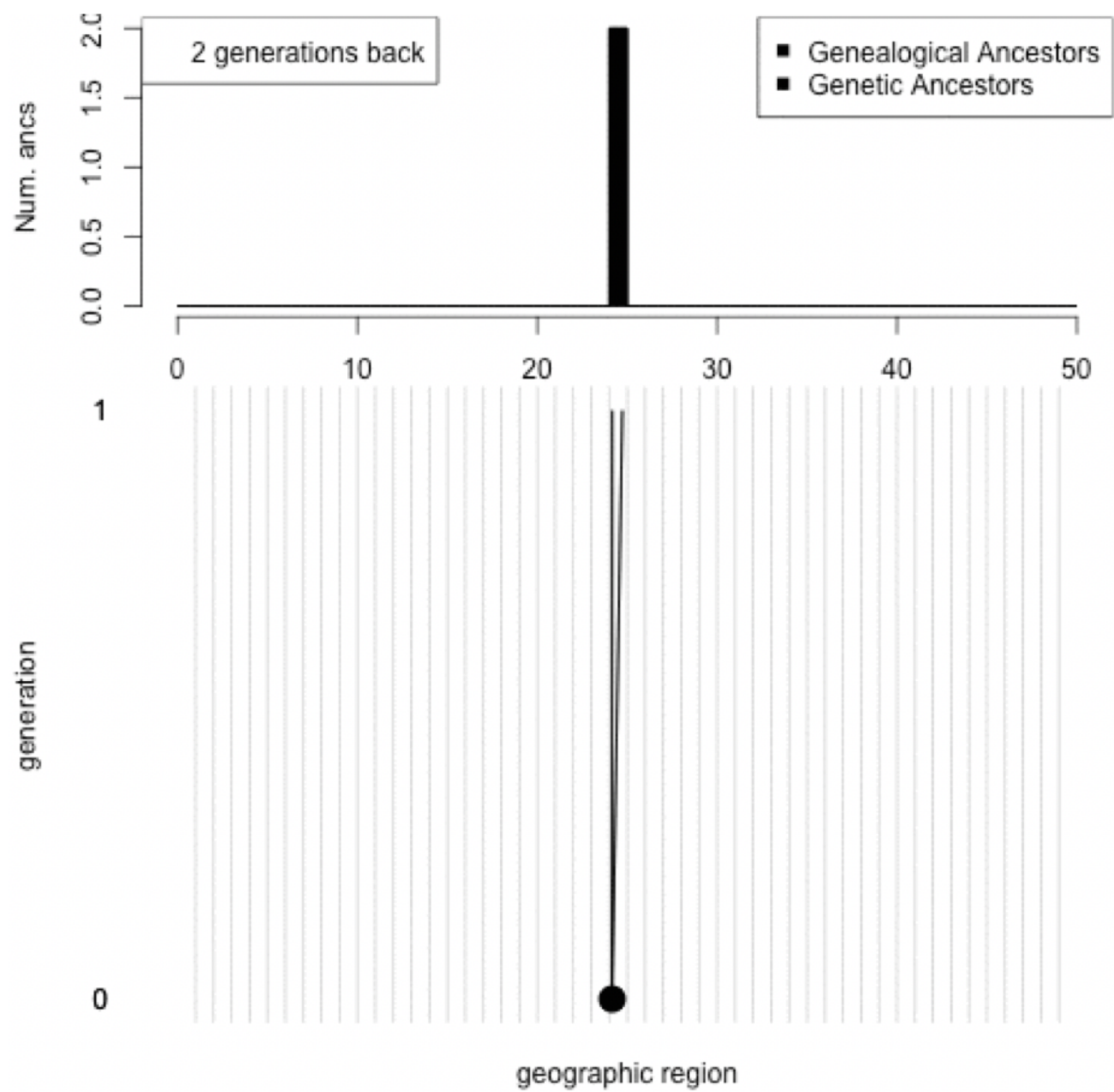
## Charlemagne's DNA and Our Universal Royalty

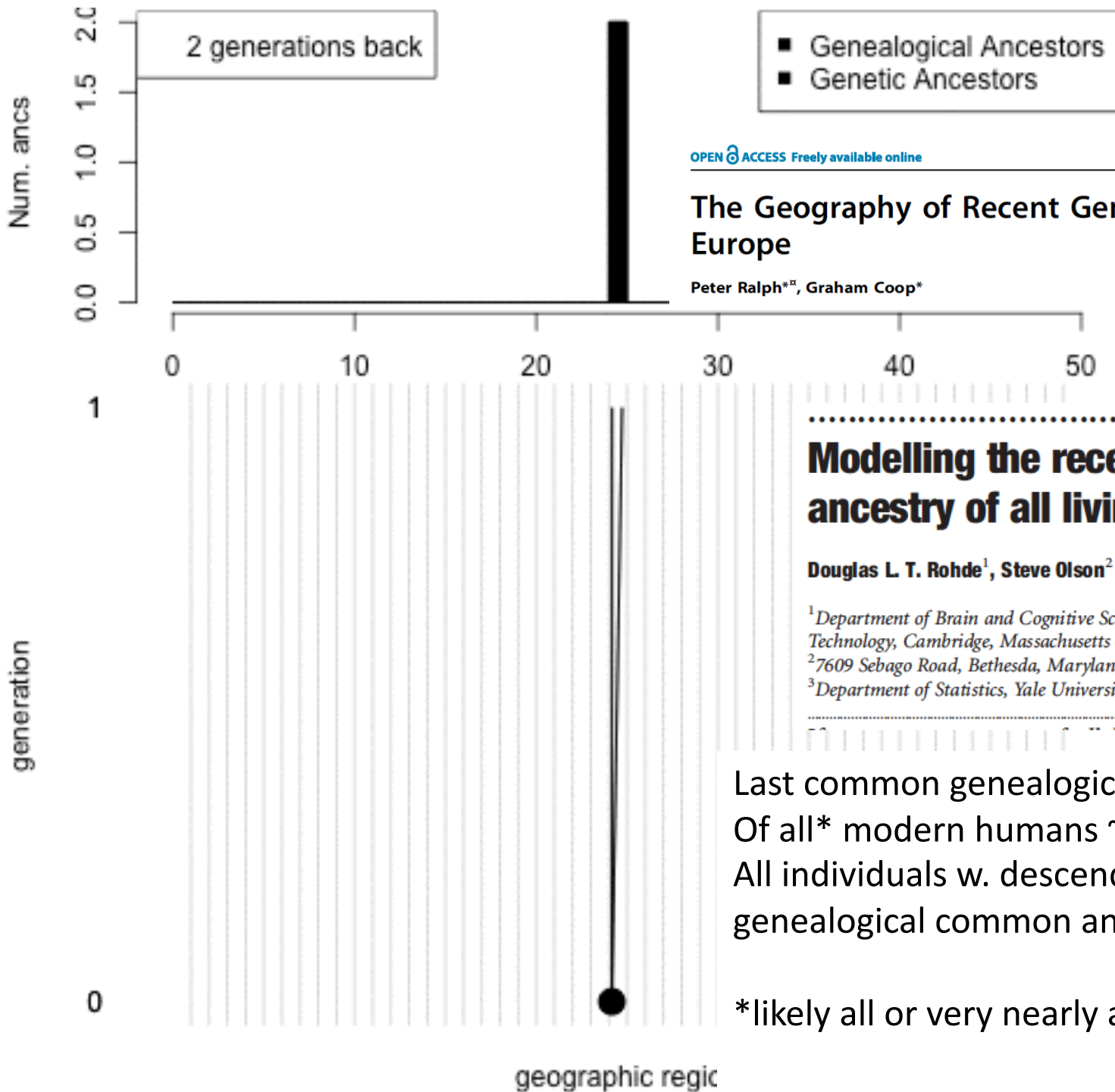
POSTED TUE, 05/7/2013

Carl Zimmer

<http://phenomena.nationalgeographic.com/2013/05/07/charlemagnes-dna-and-our-universal-royalty/>







OPEN ACCESS Freely available online

## The Geography of Recent Genetic Ancestry across Europe

Peter Ralph<sup>1\*</sup>, Graham Coop<sup>\*</sup>

### Modelling the recent common ancestry of all living humans

Douglas L. T. Rohde<sup>1</sup>, Steve Olson<sup>2</sup> & Joseph T. Chang<sup>3</sup>

<sup>1</sup>Department of Brain and Cognitive Sciences, Massachusetts Institute of Technology, Cambridge, Massachusetts 02139, USA

<sup>2</sup>7609 Sebago Road, Bethesda, Maryland 20817, USA

<sup>3</sup>Department of Statistics, Yale University, New Haven, Connecticut 06520, USA

Last common genealogical ancestor  
Of all\* modern humans ~3000 years ago  
All individuals w. descendants ~7000BCE are  
genealogical common ancestors to all of us.

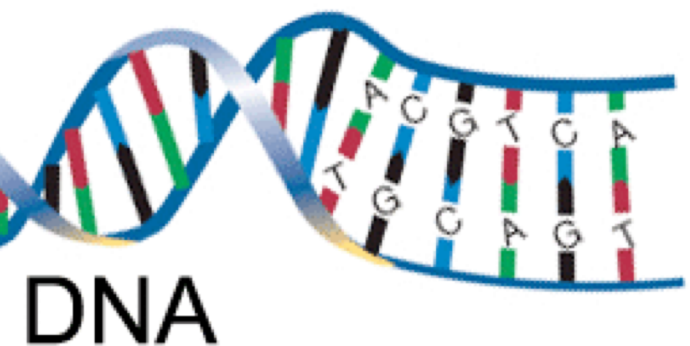
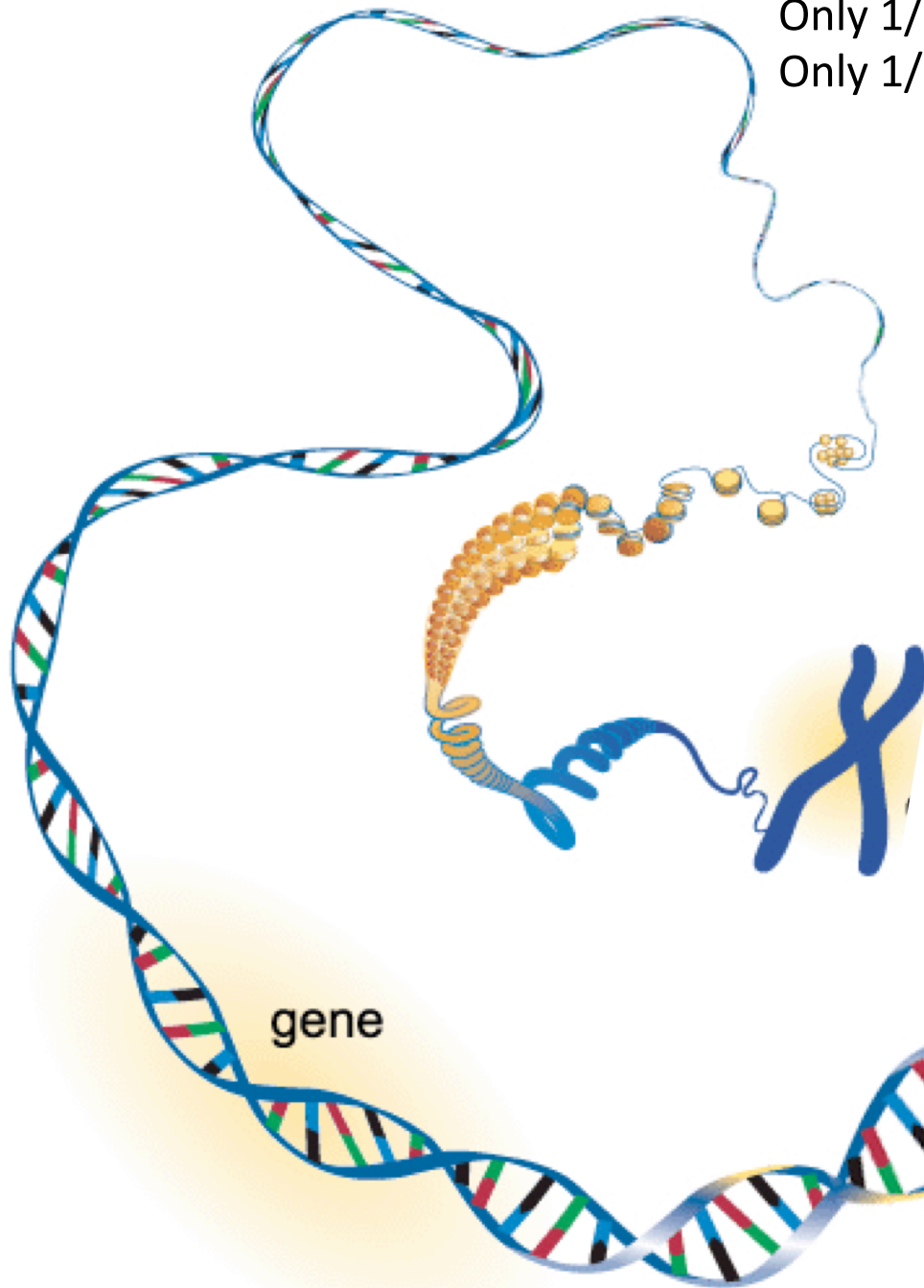
\*likely all or very nearly all.



What did I inherit from all those  
people?

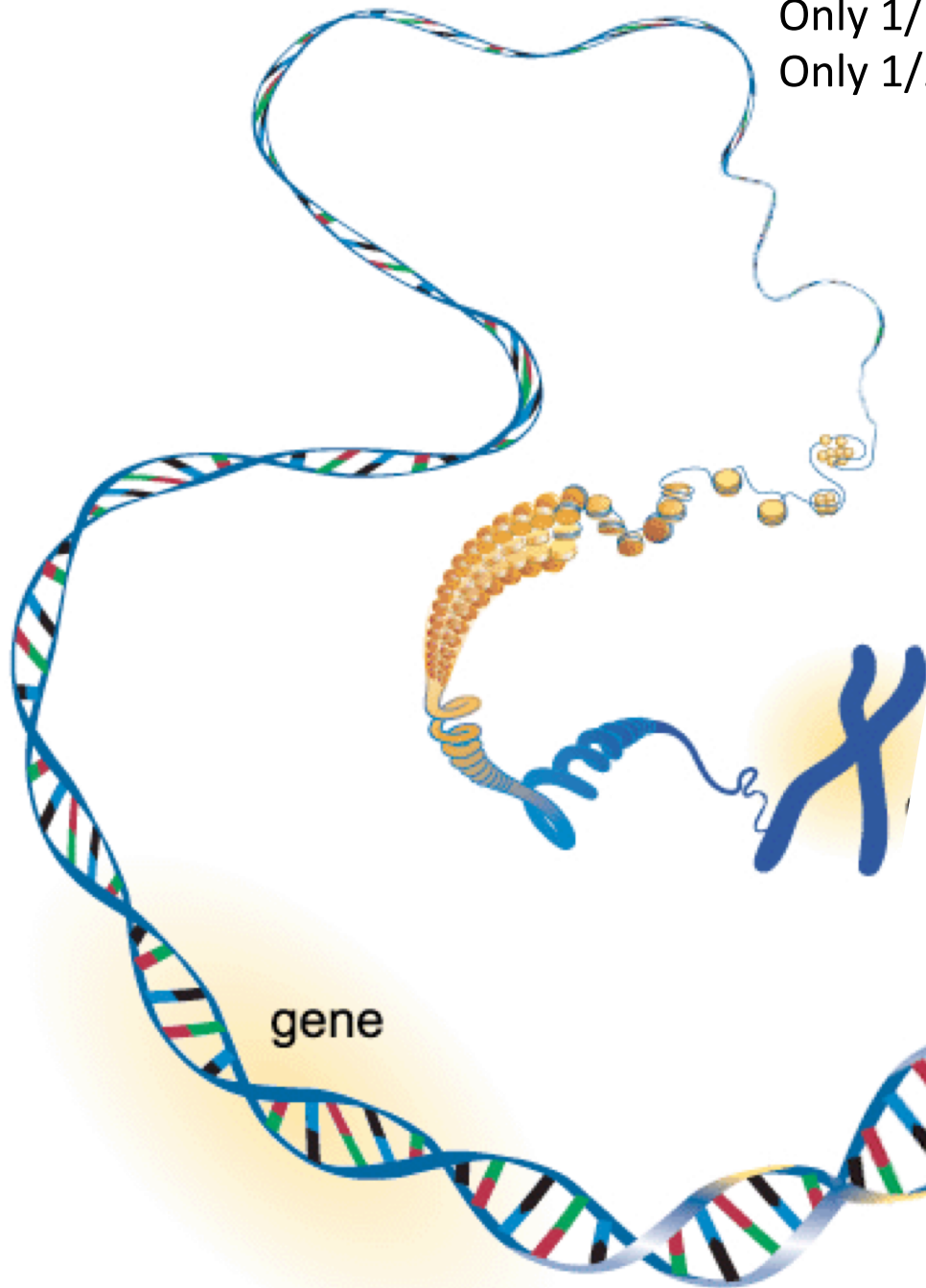
What do I share with all those distant  
cousins?

Your genome 3 billion bases (base: A, T, C, or G)  
Only 1/1000 bases differ between 2 humans  
Only 1/2000 bases differ between me & sister

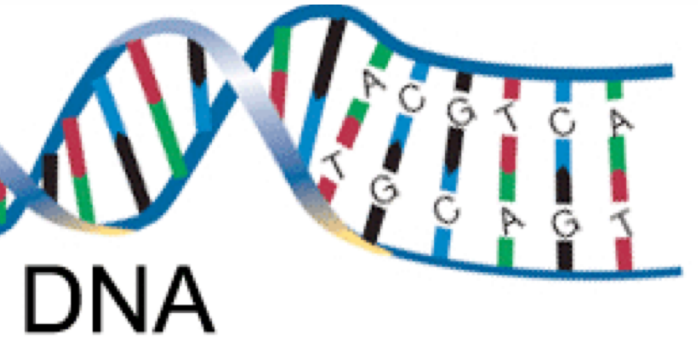


Adapted from National Human Genome Research Institute

Your genome 3 billion bases (base: A, T, C, or G)  
Only 1/1000 bases differ between 2 humans  
Only 1/2000 bases differ between me & sister



 **ancestryDNA™**



Adapted from National Human Genome Research Institute

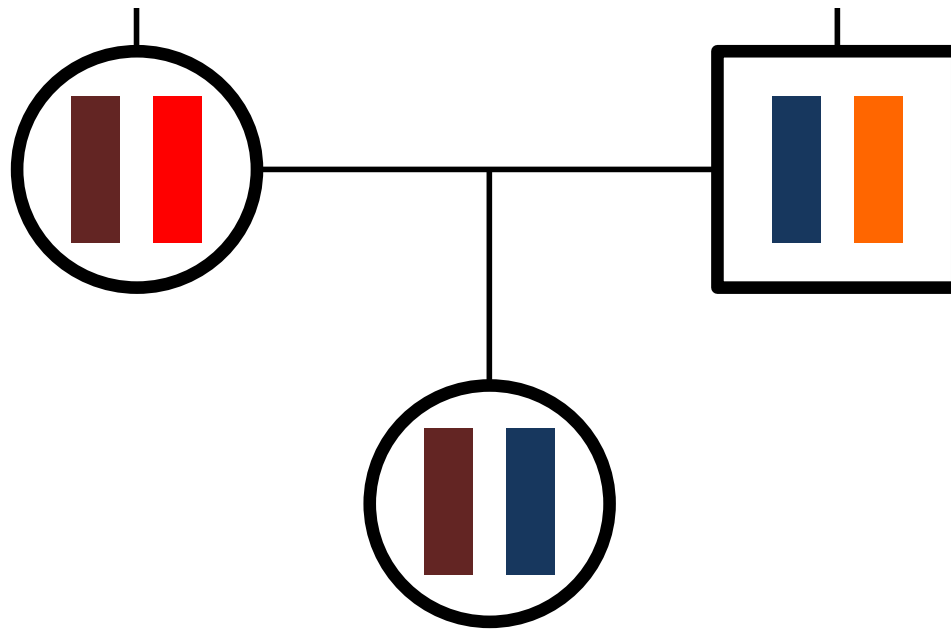


# Your genome

3 billion bases (base: A, T, C, or G)

Divided up into: 22 autosomal chromosomes, X chromosome, Y chromosome (for males), and mitochondria

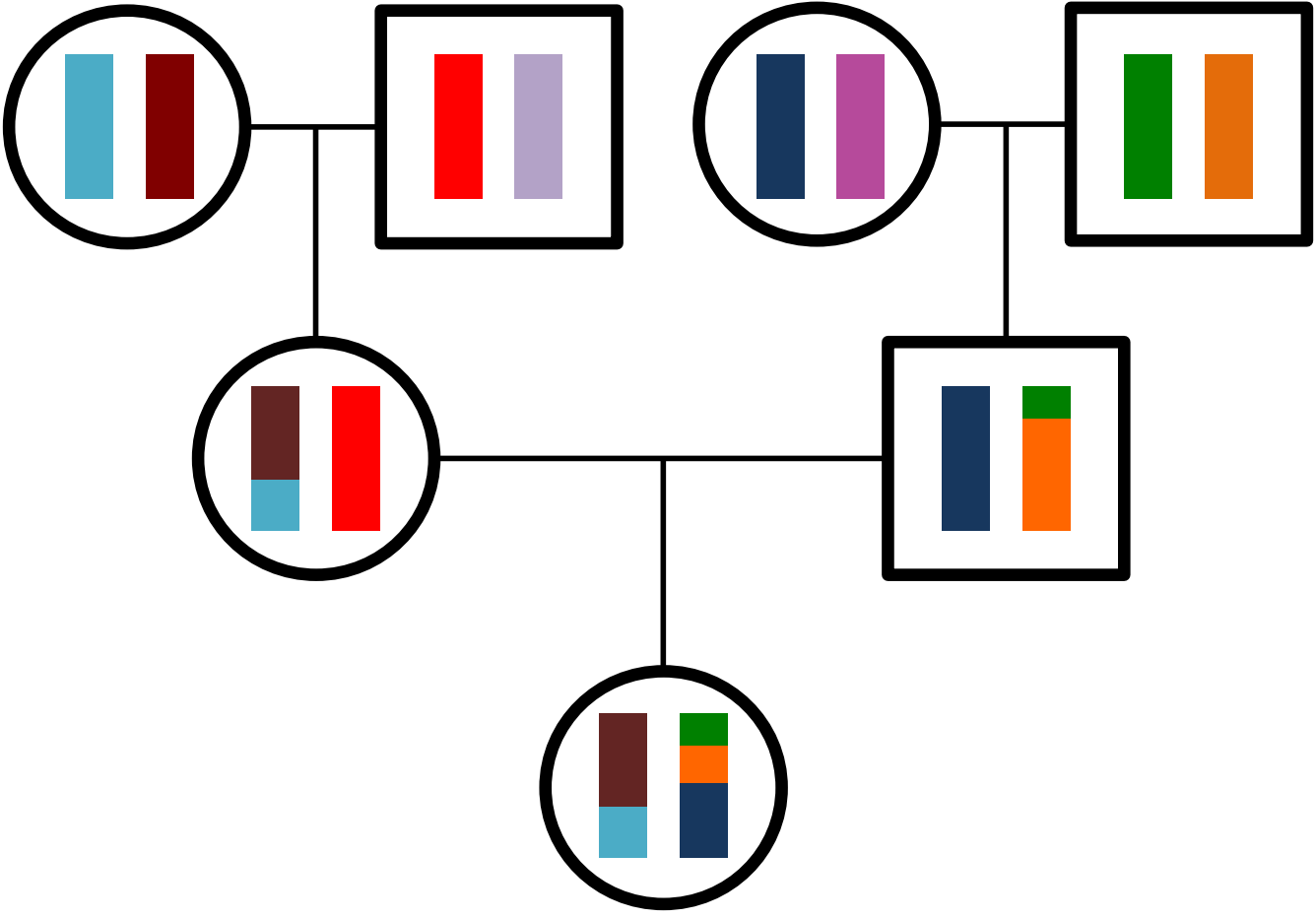


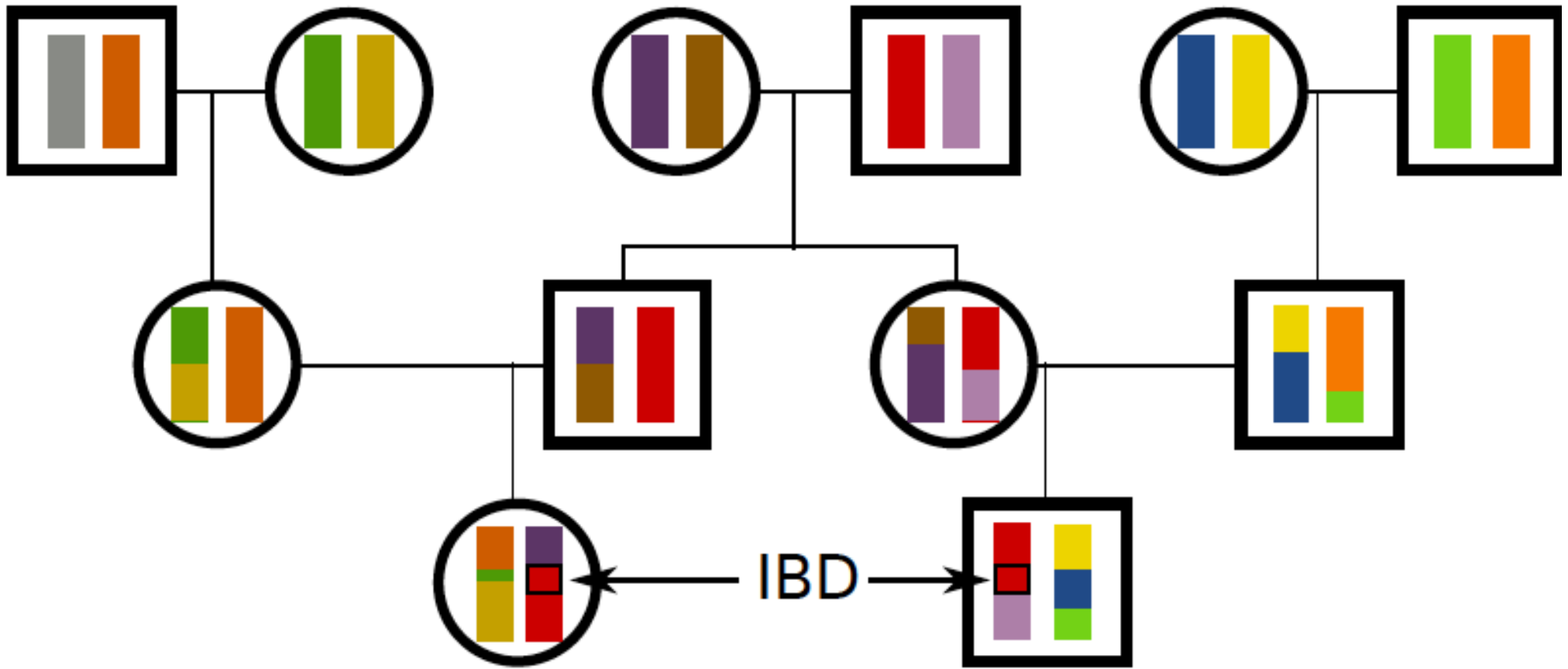


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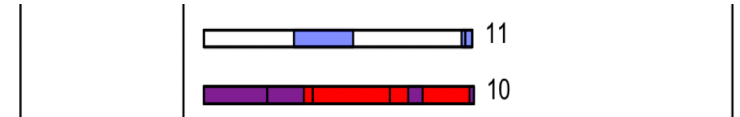
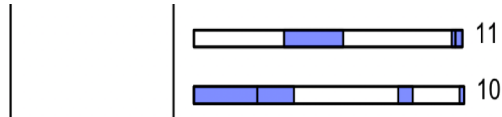
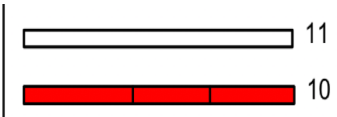
Sharing of chromosome regions between individuals due to inheritance from a ancestor (identity by descent, IBD)



Your maternal  
Grandmother's  
Contribution to you

Your maternal  
Grandmother's  
Contribution to  
your cousin

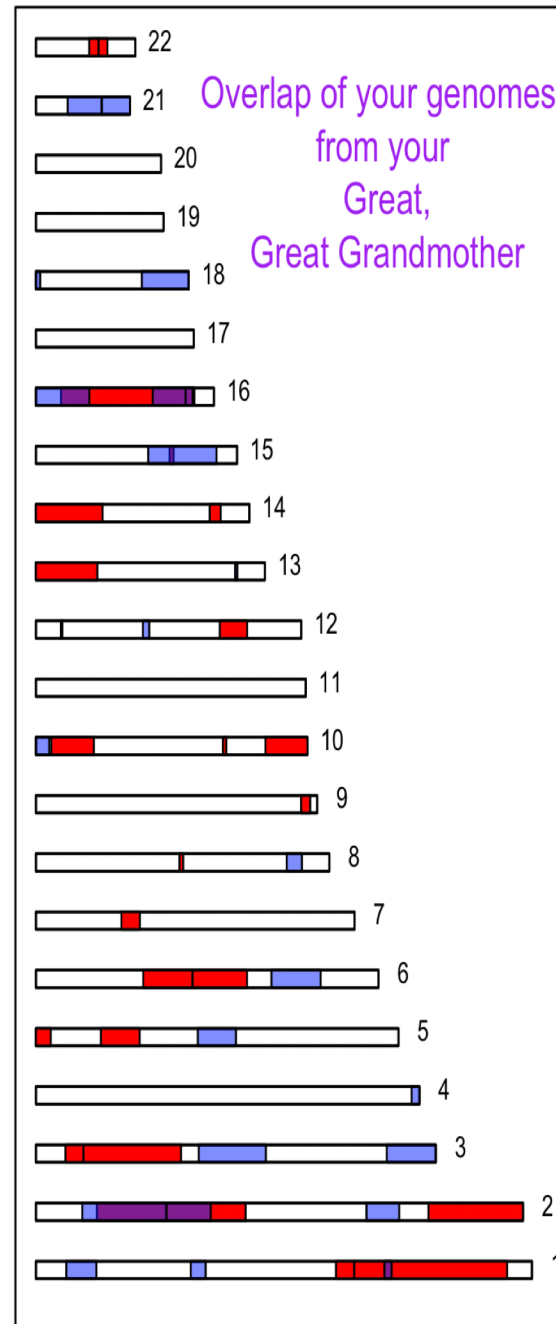
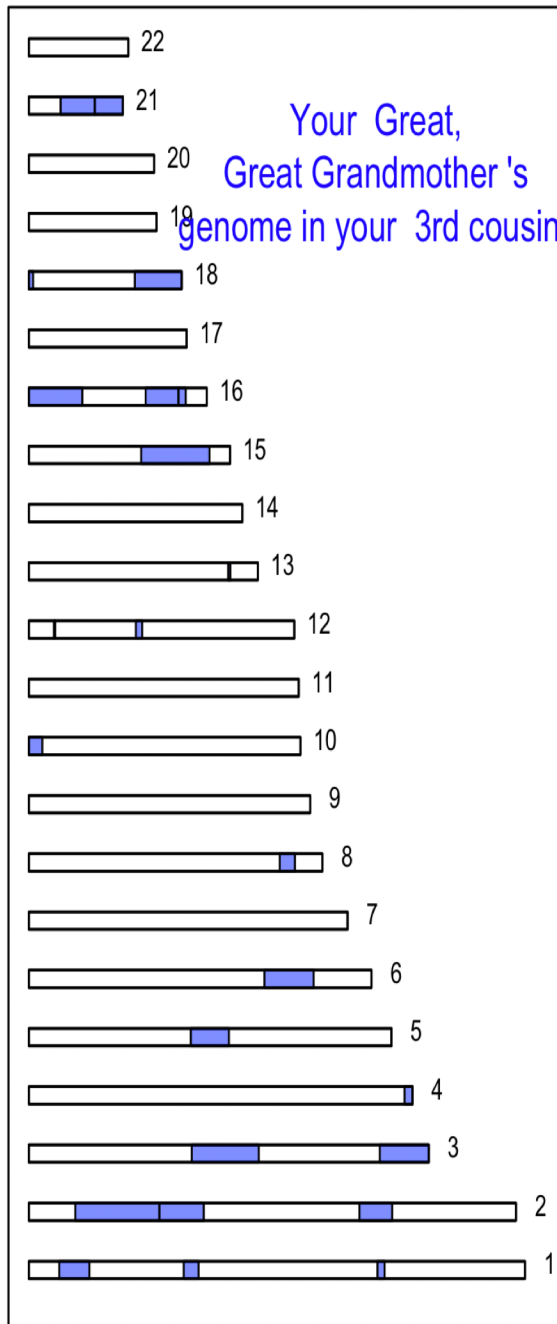
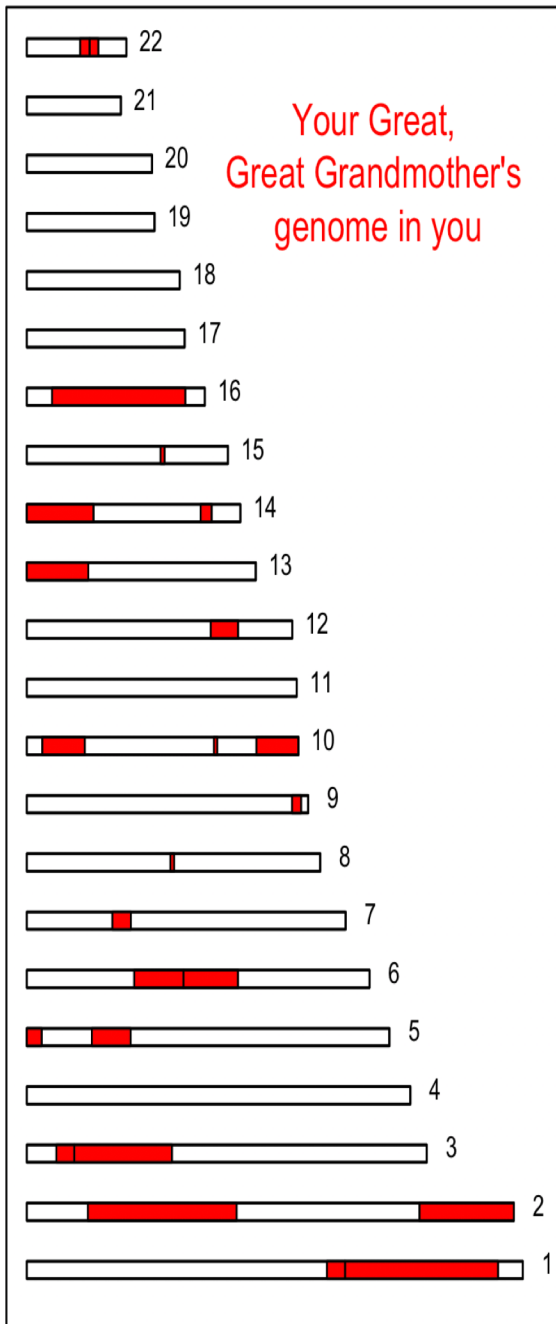
Overlap of  
Grandmother's  
Contribution to  
you & cousin



# A person and their 1<sup>st</sup> cousin On 23&me

Half identical  
1039 cM  
38 segments





3<sup>rd</sup> cousins

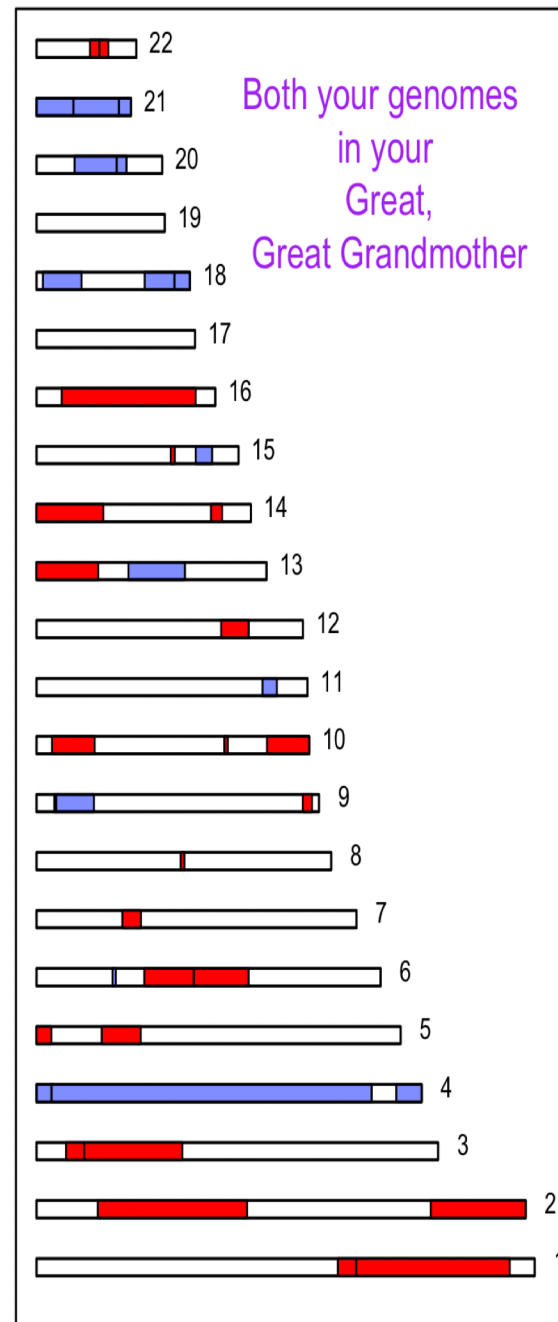
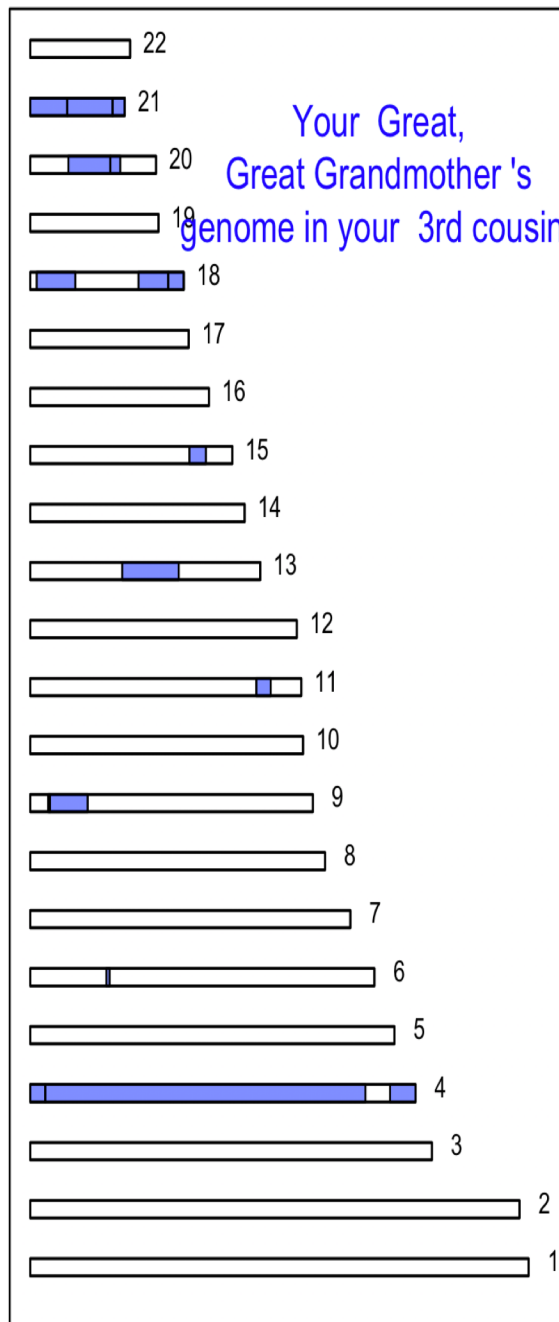
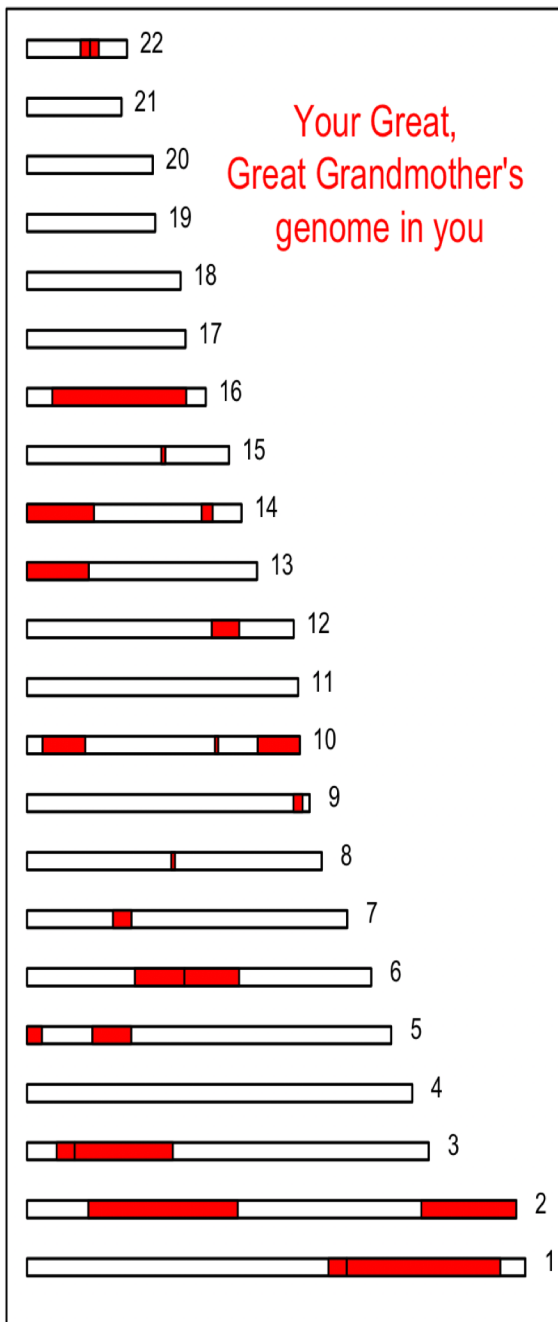
# Me and my 3<sup>rd</sup> cousin (?) On 23&me

Half identical  
66 cM  
3 segments



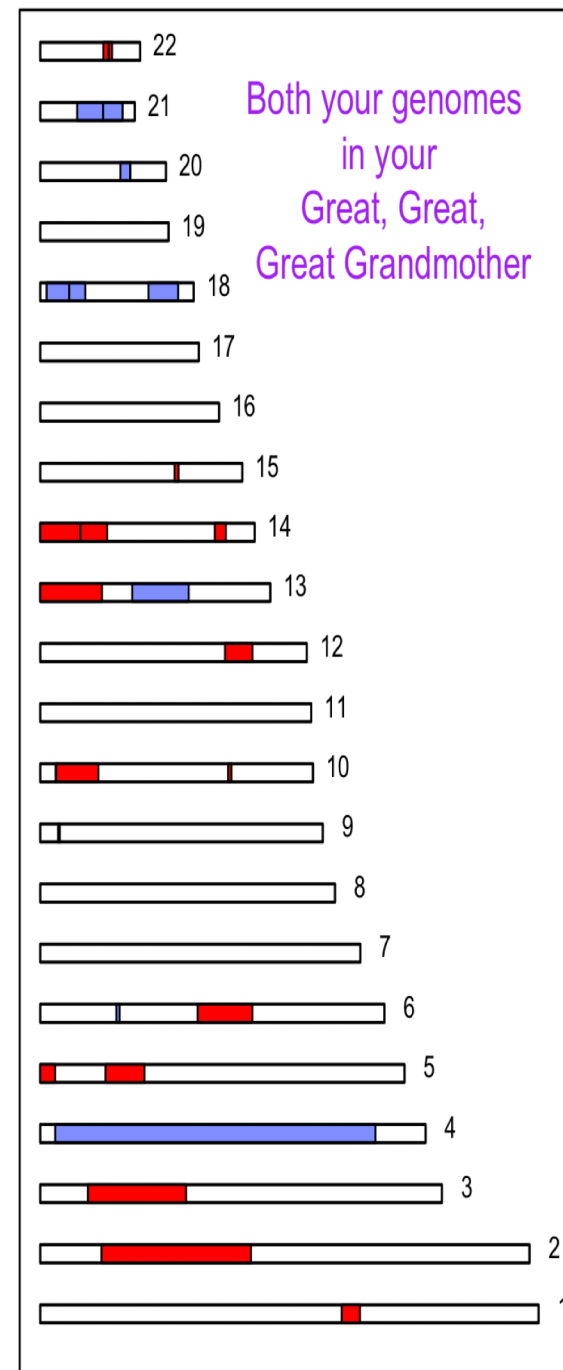
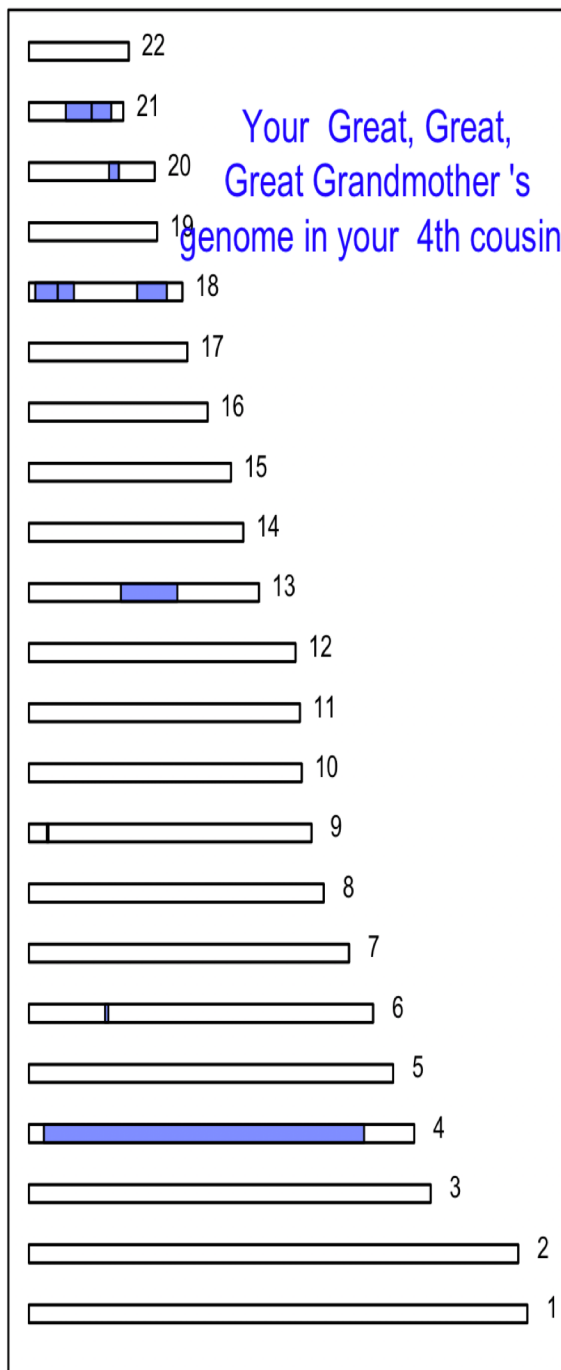
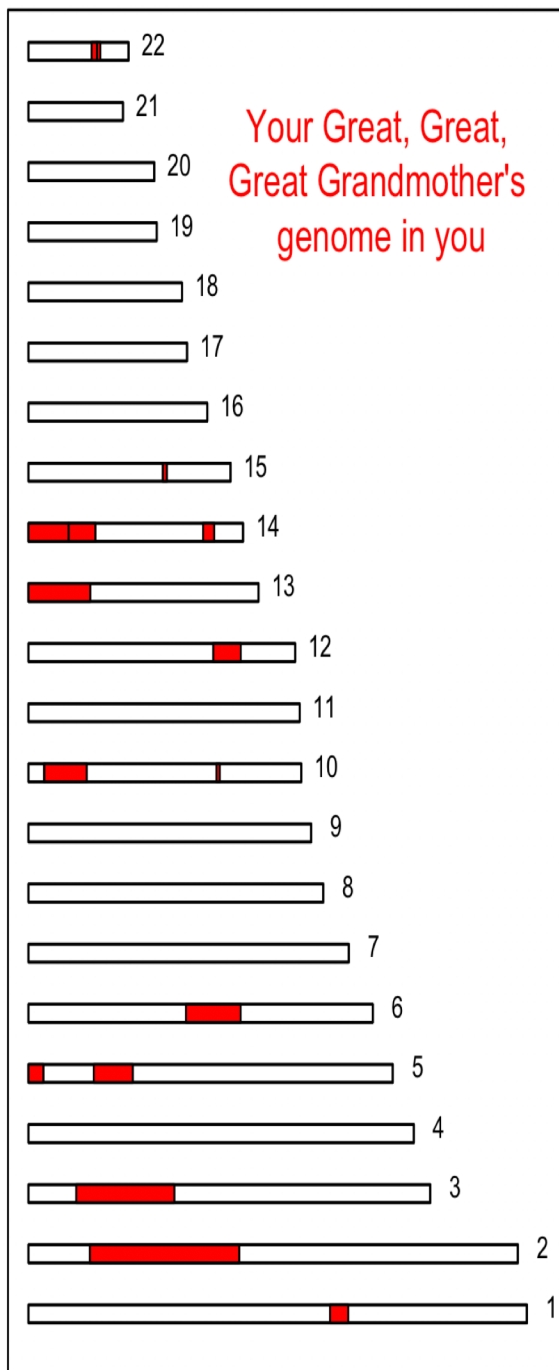


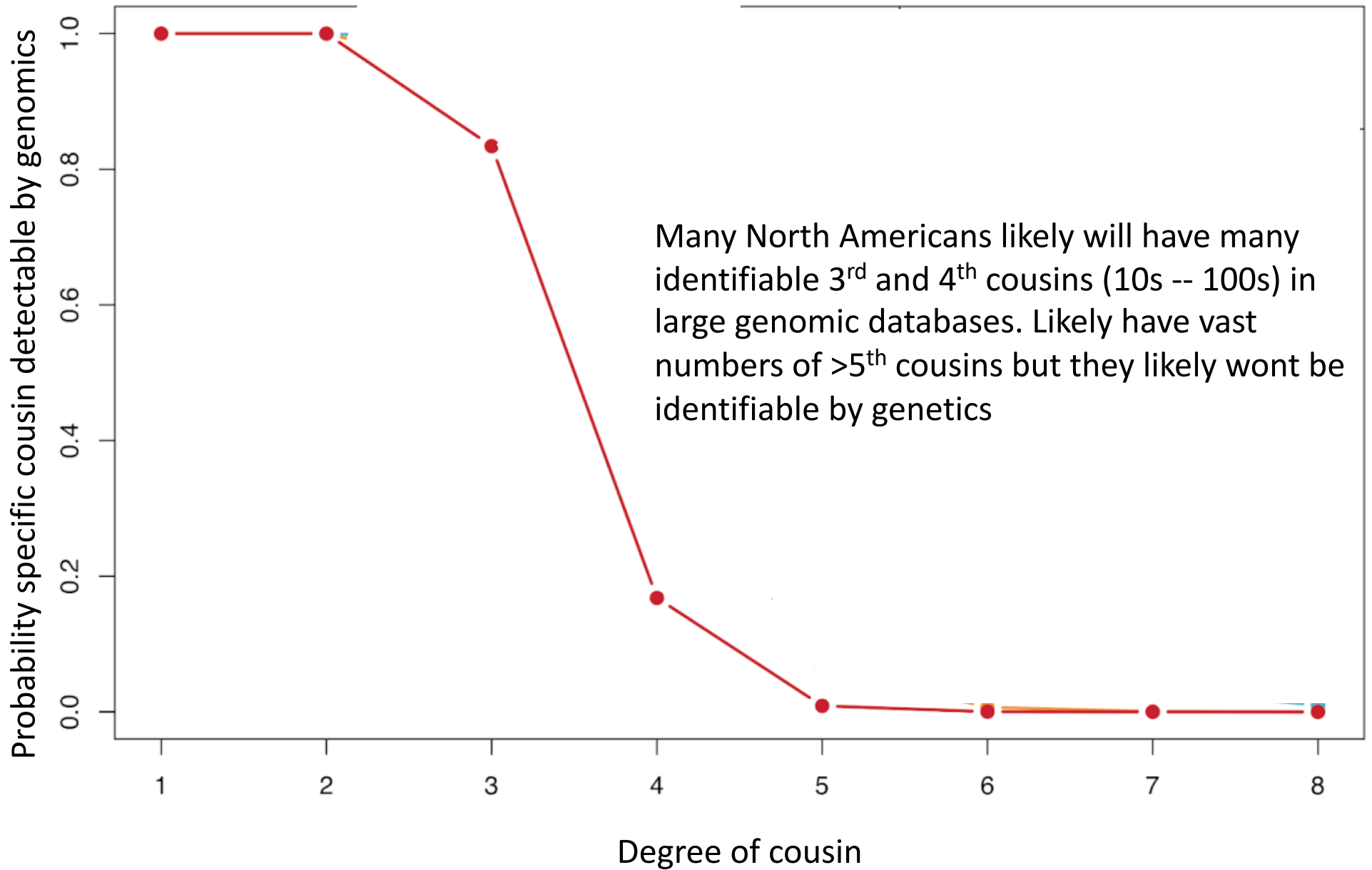
# A rare case where 3<sup>rd</sup> cousins don't share any of their genomes due to a recent ancestor



3<sup>rd</sup> cousins

# 4<sup>th</sup> cousins likely share zero of their genome from their great, great, great Grandparents





## Joseph DeAngelo, suspected Golden State Killer



# To find alleged Golden State Killer, investigators first found his great-great-great-grandparents

By **Justin Jouvenal** April 30 [✉ Email the author](#)

## Work with Doc Edge



Many people in US likely will have many identifiable 3<sup>rd</sup> and 4<sup>th</sup> cousins (10s -- 100s) in large genomic databases. Likely have vast numbers of >5<sup>th</sup> cousins but they likely wont be identifiable by genetics

<https://gcbias.org/2018/05/07/how-lucky-was-the-genetic-investigation-in-the-golden-state-killer-case/>



Joseph DeAngelo, suspected Golden State Killer



# Easy DNA Identifications With Genealogy Databases Raise Privacy Concerns

STAT Topics Opinion Podcast Video Newsletters Events Q

October 11, 2018 · 3:58 PM ET  
Heard on [All Things Considered](#)

BUSINESS

## 'We are increasingly exposed': New studies show how easy it is to identify people using genetic databases

By REBECCA ROBBINS @rebeccarobbins / OCTOBER 11, 2018



Health » Food | Fitness | Wellness | Parenting | Live Longer

Live TV U.S. Edition +

## You might not be anonymous, thanks to genealogy databases

By Susan Scutti. CNN

HEALTH | HEALTH & WELLNESS

### Researchers Identify Relatives From DNA Data Online

'In principle, anybody can do this,' replicating the techniques to pinpoint people using their relatives' genetic-test results, researcher says

## Supercharged crime-scene DNA analysis sparks privacy concerns



Consumer genetics poised to enable comparison of DNA evidence to genetic profiles of almost any American of European descent.

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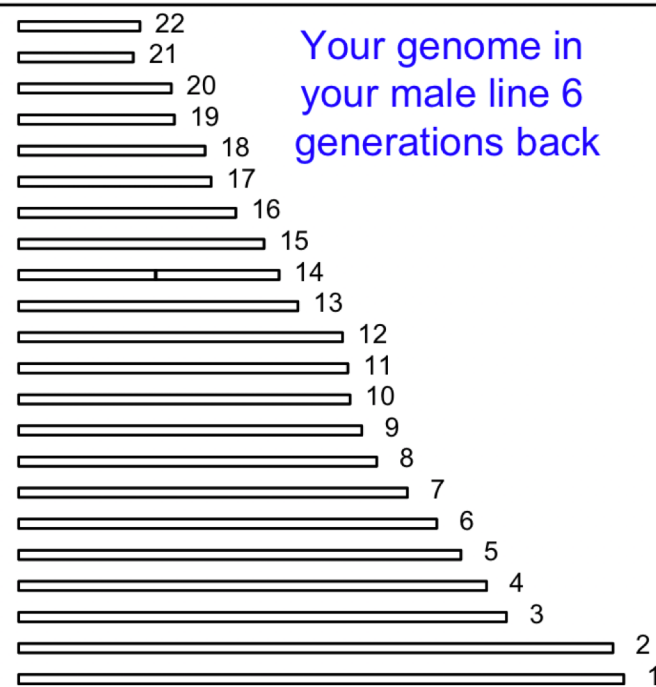
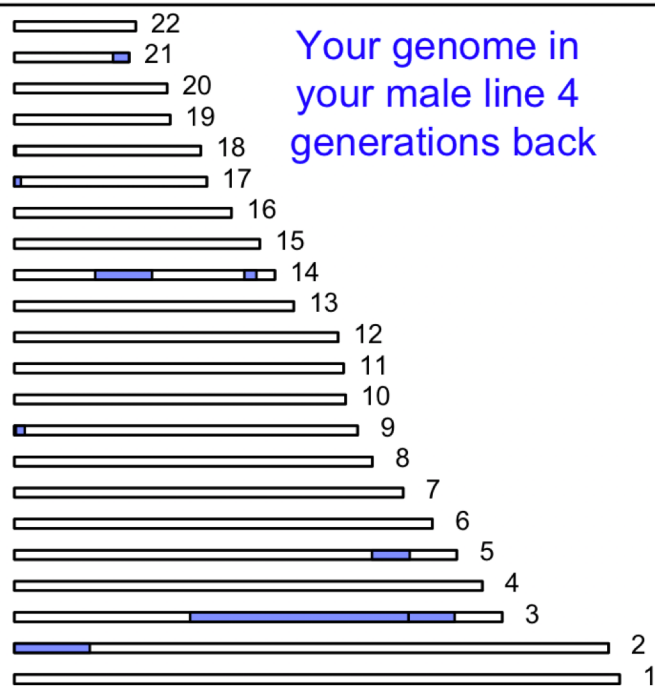
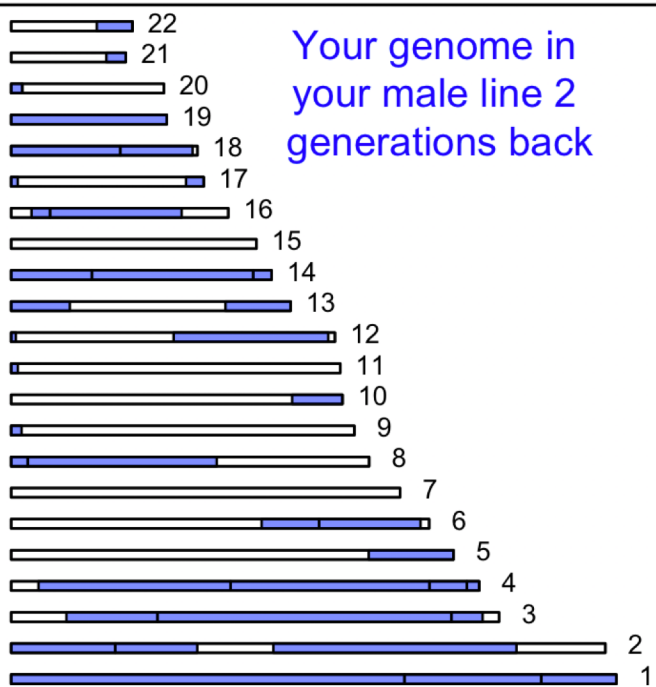
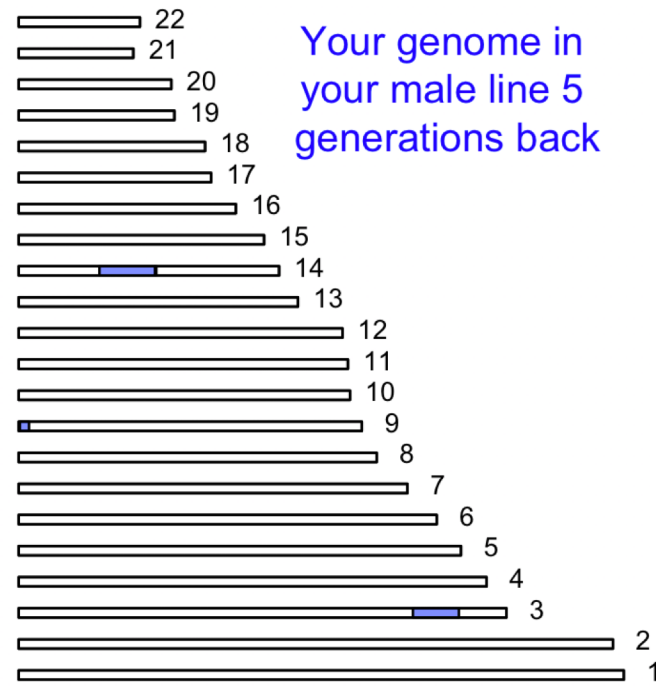
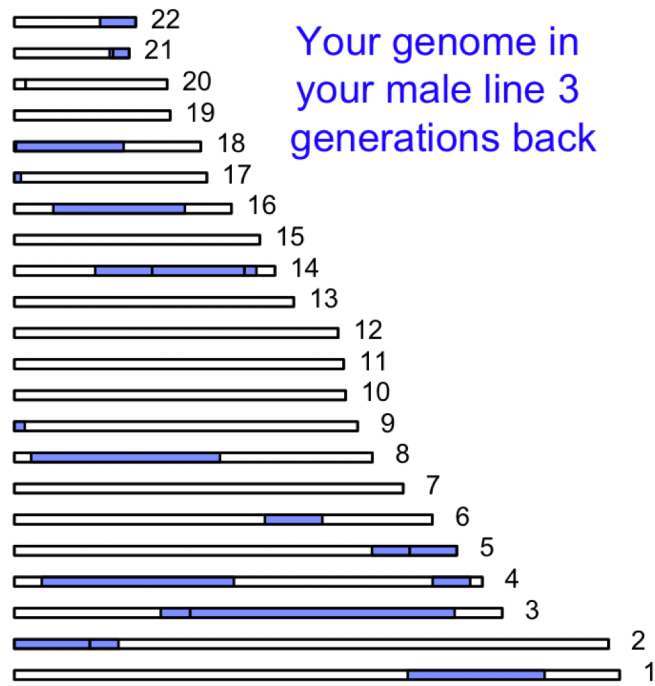
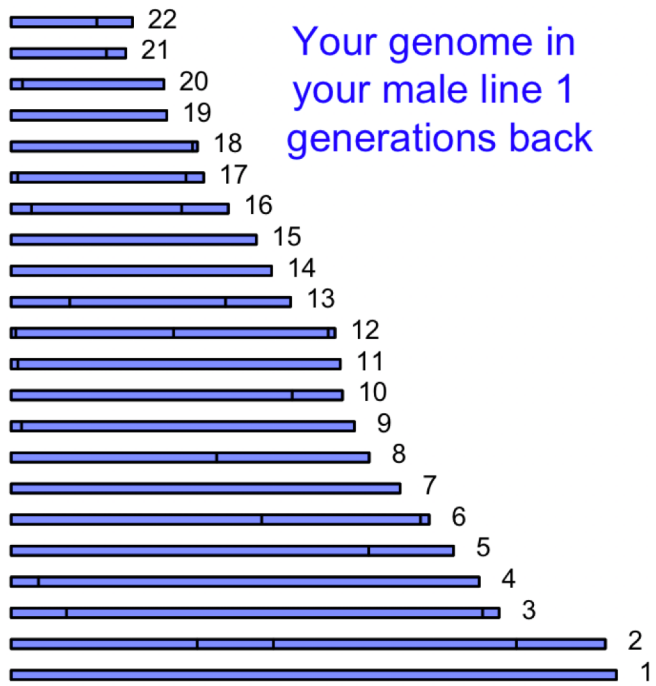
Report this ad Why this ad? ↗

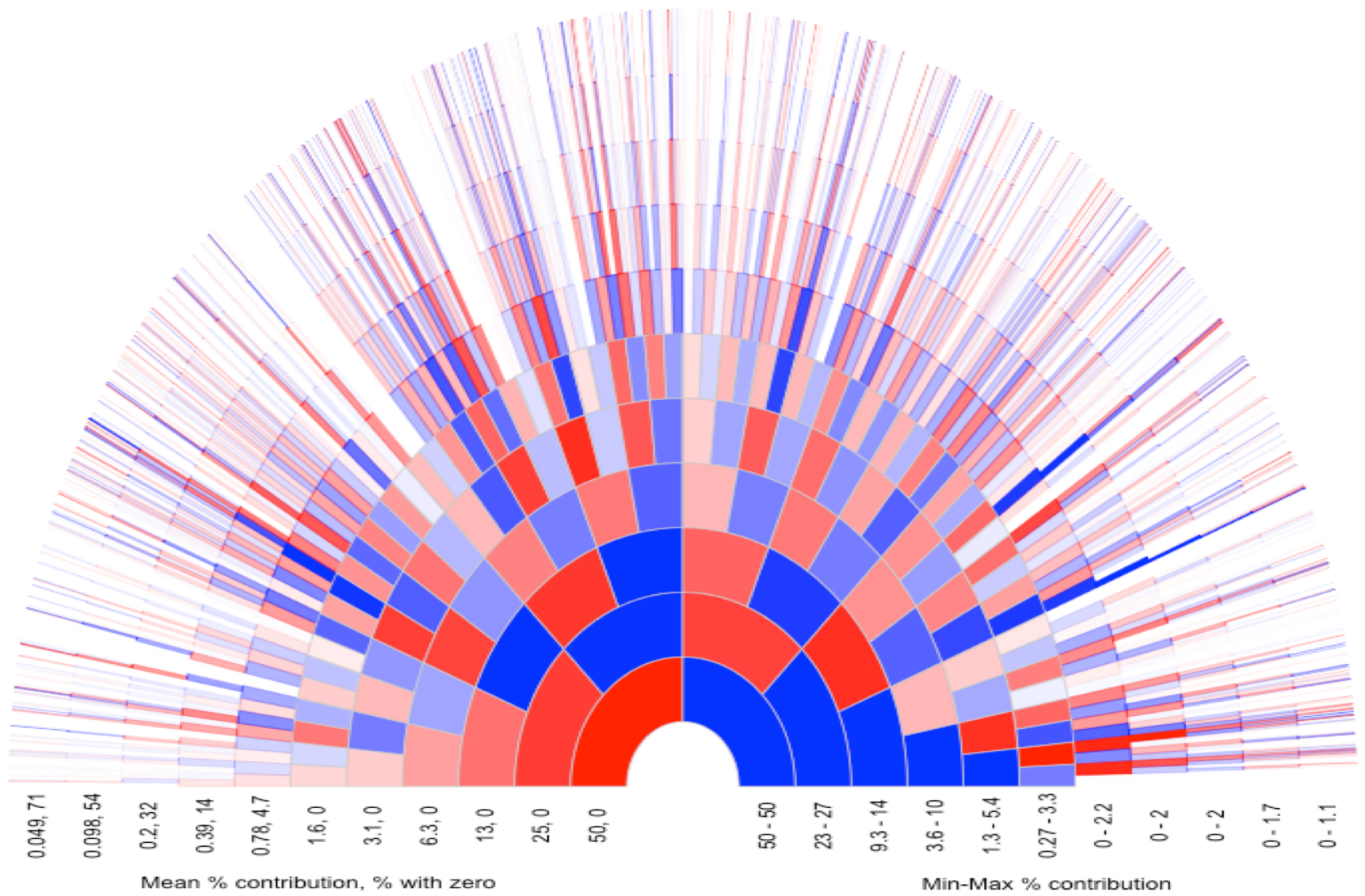
### The 'Wild West' of genetic privacy: New technology enables law enforcement to use DNA from sites like Ancestry.com to track down criminals by finding their relatives

## How to Identify Almost Anyone in a Consumer Gene Database

MEGAN MOLTENI SCIENCE 10.11.18 02:04 PM

# GENOME HACKERS SHOW NO ONE'S DNA IS ANONYMOUS ANYMORE

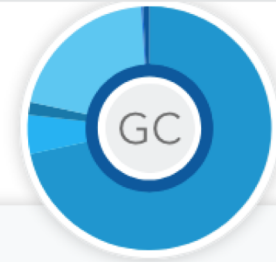
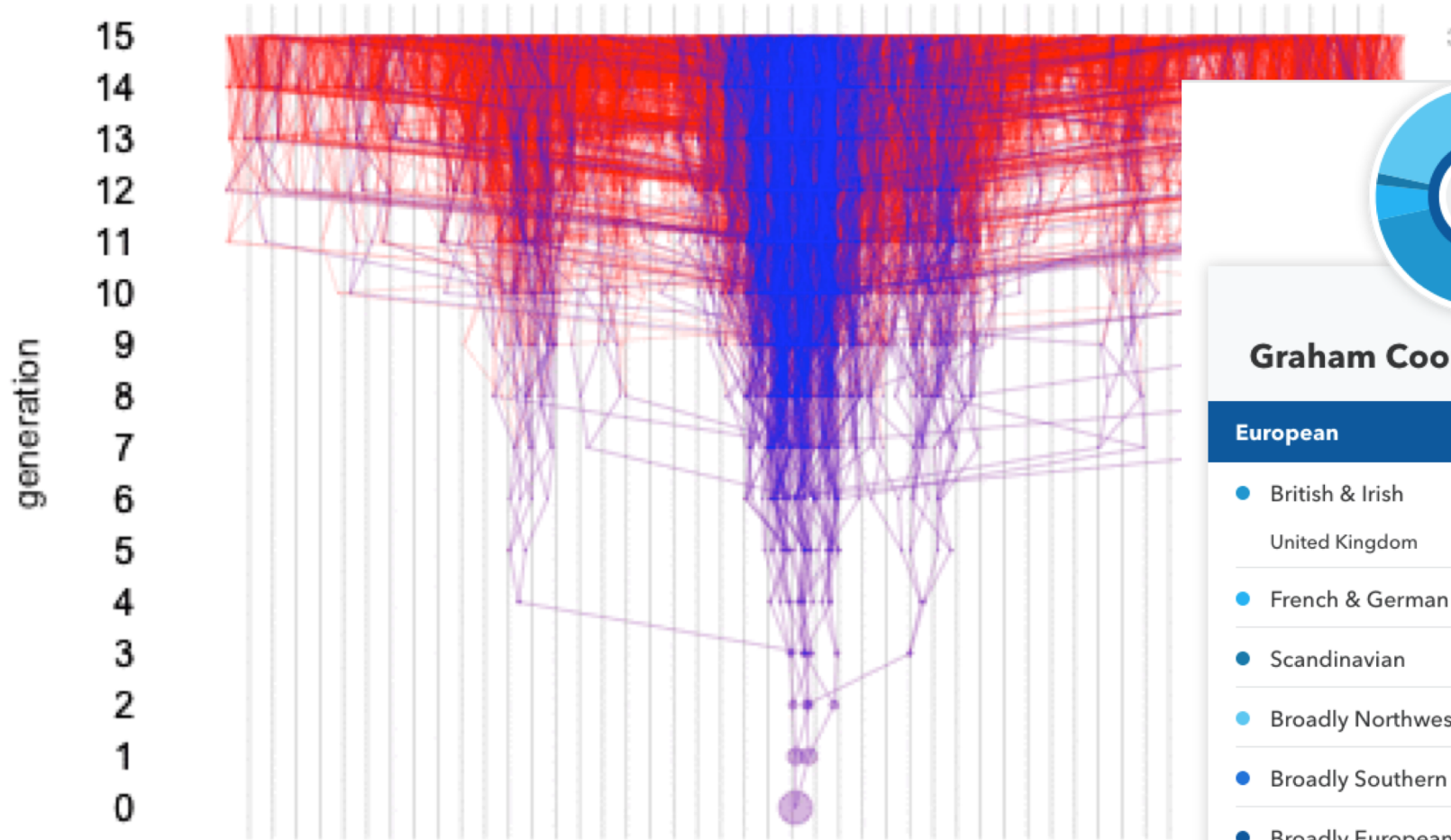
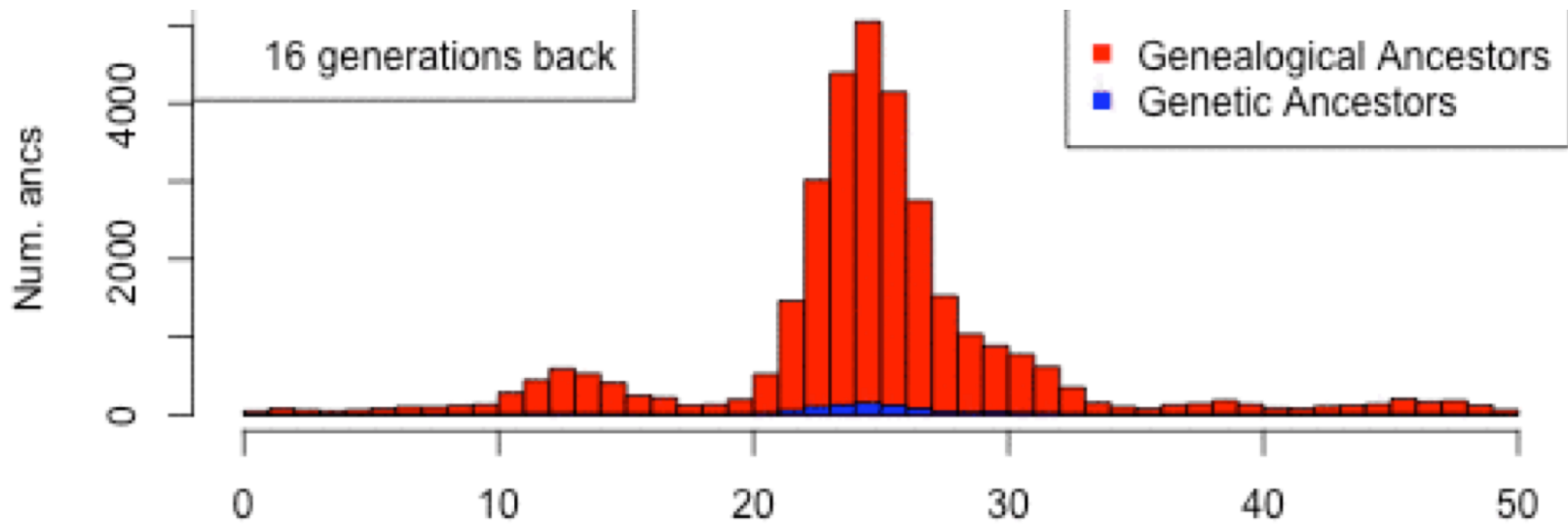




You're descended from most people  
most places, but few of them are  
genetic ancestors





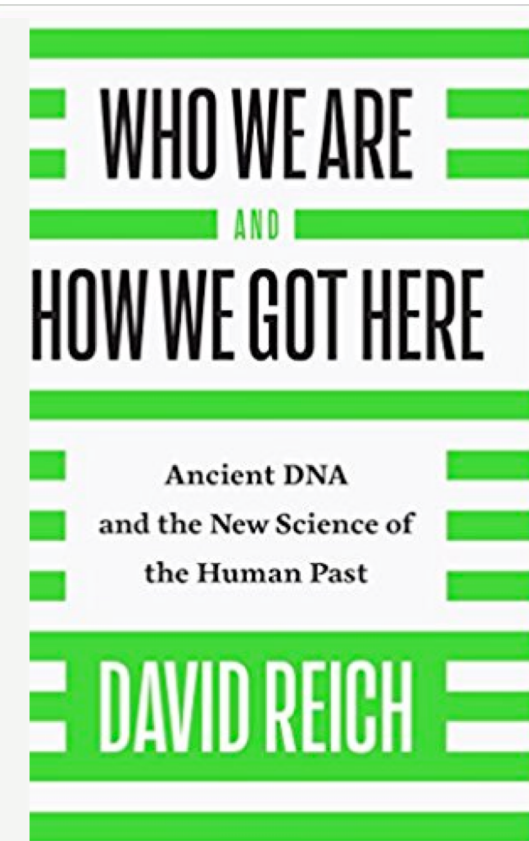
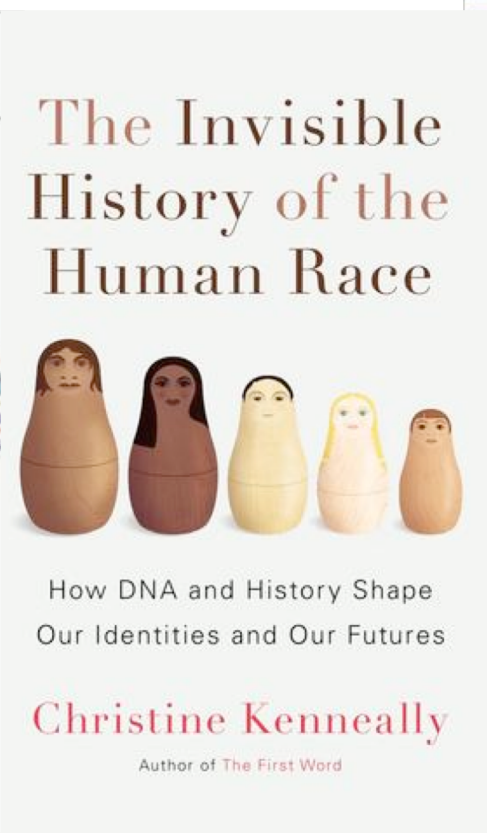
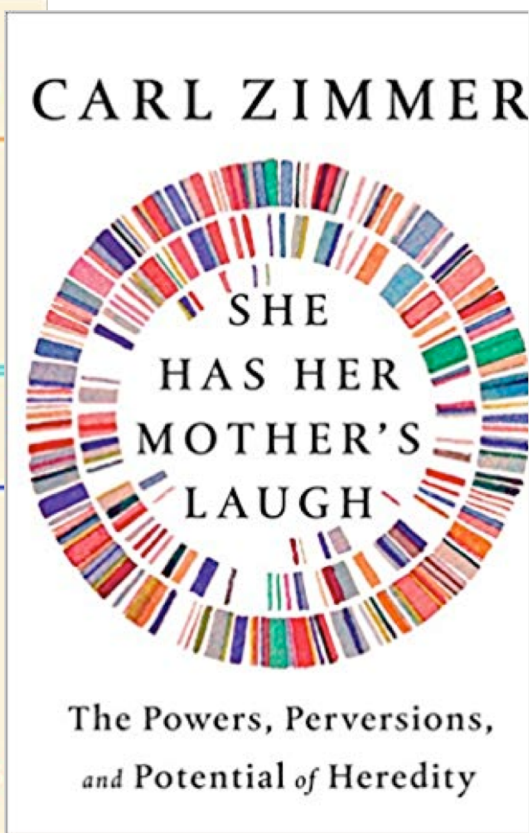
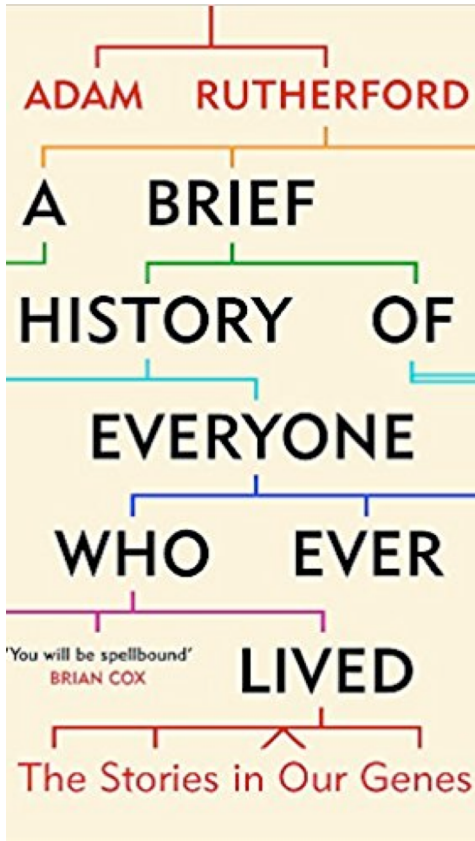


<b>Graham Coop</b>		<b>100%</b>
<b>European</b>		<b>100%</b>
● British & Irish	United Kingdom	71.6%
● French & German		5.2%
● Scandinavian		1.7%
● Broadly Northwestern European		20.4%
● Broadly Southern European		0.3%
● Broadly European		0.8%



# Our Human family tree is more like a bramble thicket

- We're all very closely related genealogically.
- We're all descended from nearly everyone who has descendants ~6000 years ago.
- Many of these individuals are not your genetic ancestors, but you do have vast numbers of genetic ancestors.
- Some of them were likely Neanderthals!

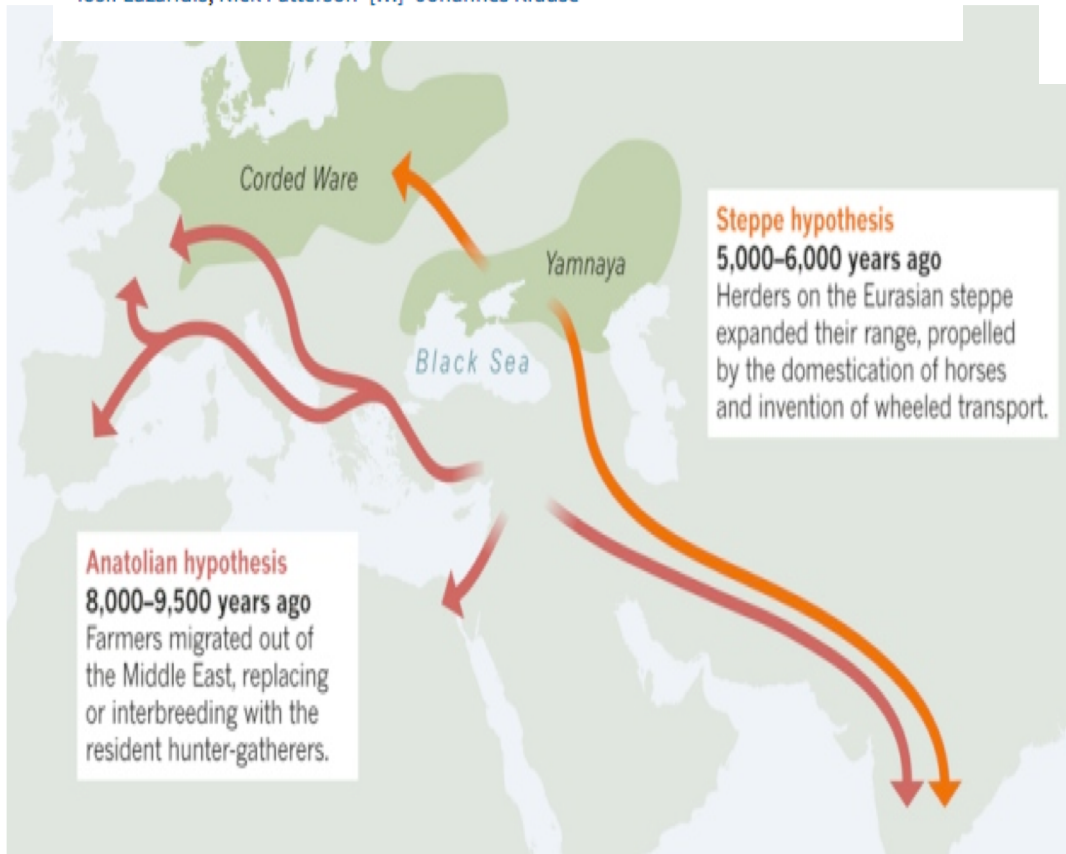


- <http://gcbias.org/category/genetic-genealogy/>
- @graham\_coop

We are starting to learn about a very dynamic history of humans from ancient genetic data

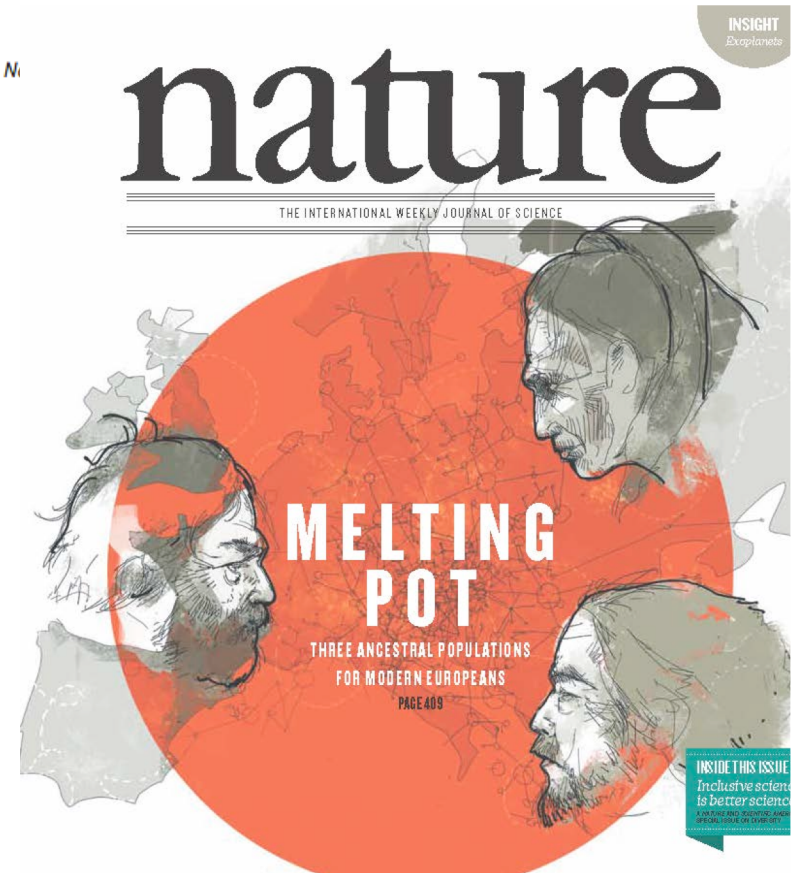
## Ancient human genomes suggest three ancestral populations for present-day Europeans

Iosif Lazaridis, Nick Patterson [...] Johannes Krause



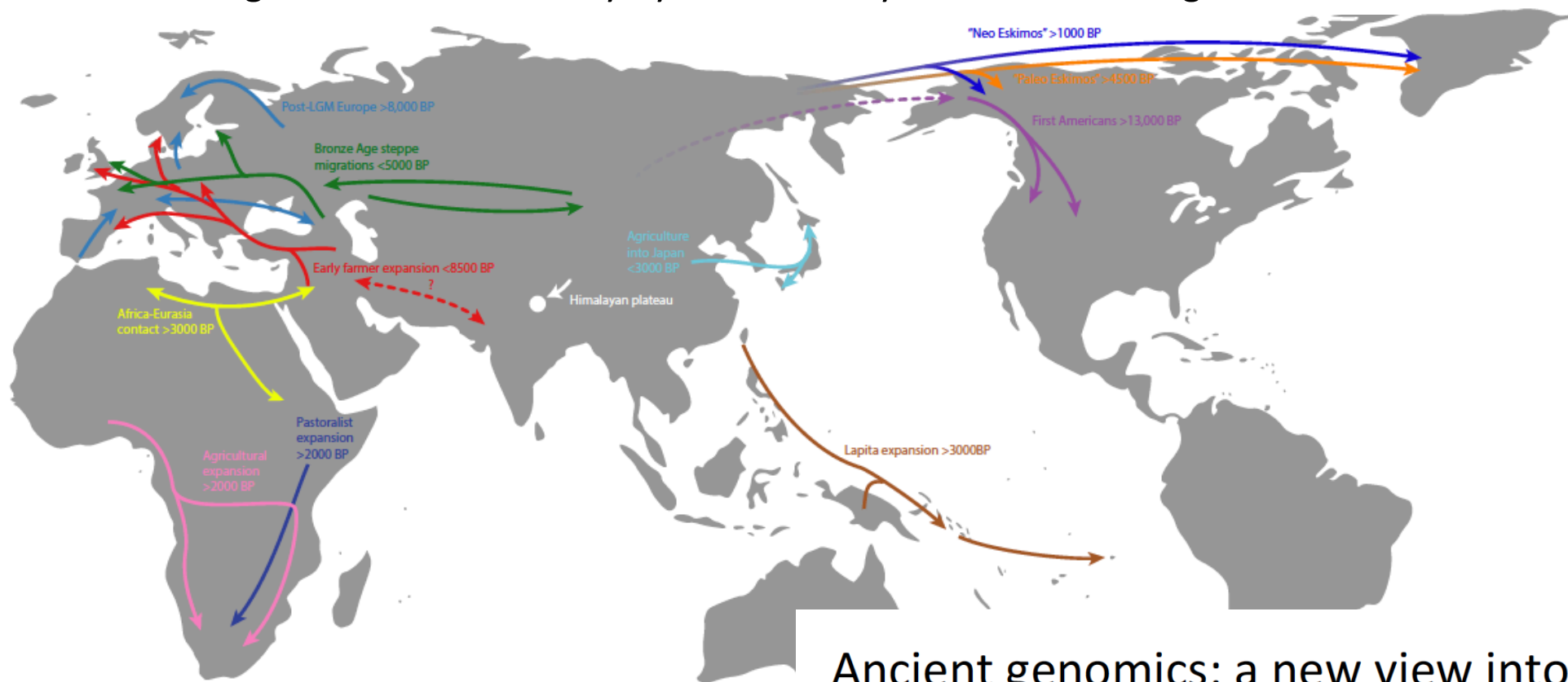
## Massive migration from the steppe was a source for Indo-European languages in Europe

Wolfgang Haak, Iosif Lazaridis [...] David Reich



Up to 10,000 years ago Europe was dominated by Western Hunter Gathers  
Expansions of Early farmers (Neolithic) 8000 years ago  
Followed by expansion of bronze-age Yamnaya from Russian Steppe

We are starting to learn about a very dynamic history of humans from genetic data



Major Holocene (<11kya) population movements and expansions that have been demonstrated using ancient DNA.

## Ancient genomics: a new view into human prehistory and evolution

Pontus Skoglund<sup>1</sup> & Iain Mathieson<sup>2</sup>

## Reconstructing Prehistoric African Population Structure

Pontus Skoglund,<sup>1,\*</sup> Jessica C. Thompson,<sup>2</sup> Mary E. Prendergast,<sup>3</sup> Alissa Mitnik,<sup>4,5,33</sup> Kendra Sirak,<sup>2,6,33</sup>

## The genome of a Late Pleistocene human from a Clovis burial site in western Montana

Morten Rasmussen<sup>1\*</sup>, Sarah L. Anzick<sup>2\*</sup>, Michael R. Waters<sup>3</sup>, Pontus Skoglund<sup>4</sup>, Michael DeGiorgio<sup>5†</sup>, Thomas W. Stafford Jr<sup>1,6</sup>, Simon Rasmussen<sup>7</sup>, Ida Moltke<sup>8,9</sup>, Anders Albrechtsen<sup>8</sup>, Shane M. Doyle<sup>10</sup>, G. David Poznik<sup>11</sup>, Valborg Gudmundsdottir<sup>7</sup>, Rachita Yadav<sup>7</sup>, Anna-Sapfo Malaspinas<sup>1</sup>, Samuel Stockton White V<sup>12</sup>, Morten E. Allentoft<sup>1</sup>, Omar E. Cornejo<sup>13</sup>, Kristiina Tambets<sup>14</sup>, Anders Eriksson<sup>15,16</sup>, Peter D. Heintzman<sup>17</sup>, Monika Karmin<sup>14</sup>, Thorfinn Sand Korneliusen<sup>1</sup>, David J. Meltzer<sup>18</sup>, Tracey L. Pierre<sup>1</sup>, Jesper Stenderup<sup>1</sup>, Lauri Saag<sup>14</sup>, Vera M. Warmuth<sup>15,19</sup>, Margarida C. Lopes<sup>19</sup>, Ripan S. Malhi<sup>20</sup>, Søren Brunak<sup>7</sup>, Thomas Sicheritz-Ponten<sup>7</sup>, Ian Barnes<sup>17†</sup>, Matthew Collins<sup>21</sup>, Ludovic Orlando<sup>1</sup>, Francois Balloux<sup>22</sup>, Andrea Manica<sup>15</sup>, Ramneek Gupta<sup>7</sup>, Mait Metspalu<sup>14</sup>, Carlos D. Bustamante<sup>23,24</sup>, Mattias Jakobsson<sup>4,25</sup>, Rasmus Nielsen<sup>5</sup> & Eske Willerslev<sup>1</sup>



## Human family tree



Source: Nature

## Sequencing and Analysis of Neanderthal Genomic DNA

James P. Noonan,<sup>1,2</sup> Graham Coop,<sup>3</sup> Sridhar Kudaravalli,<sup>3</sup> Doug Smith,<sup>1</sup> Johannes Krause,<sup>4</sup> Joe Alessi,<sup>1</sup> Feng Chen,<sup>1</sup> Darren Platt,<sup>1</sup> Svante Pääbo,<sup>4</sup> Jonathan K. Pritchard,<sup>3</sup> Edward M. Rubin<sup>1,2\*</sup>

## A Draft Sequence of the Neanderthal Genome

Richard E. Green<sup>1,†,††</sup>, Johannes Krause<sup>1,†§</sup>, Adrian W. Briggs<sup>1,†§</sup>, Tomislav Maricic<sup>1,†§</sup>, Udo Stenzel<sup>1,†§</sup>, Martin Kircher<sup>1,†§</sup>, ...



<https://www.flickr.com/photos/hmnh/3033749380/>