

THE BUSHES OF LIFE
MODEL AND HUMAN
ANCESTRY IN LIGHT OF
GENETICS DATA

Ola Hössjer

ELF

May 27 2024

STH
ACADEMIC

EDITED BY

OLA HÖSSJER & SAMUEL LAMPA

BIBLICAL CREATION ON SOLID GROUND

ARGUMENTS FROM SCIENCE,
PHILOSOPHY AND THEOLOGY

FOREWORDS BY

JONATHAN SARFATI
& FRANK KARLSEN

BIBLICAL CREATION ON SOLID GROUND

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ACADEMIC

A creationist perspective on the origin of diversity in biological life



Thursday 17 - Friday 18 October
Immanuel Church, Malmö

The First Nordic Creation Research Conference is a collaboration between the Genesis Society and Scandinavian School of Theology in Uppsala. We are planning this conference as the first of its kind, where creation organizations from different Nordic countries will take turns hosting. This year's conference will primarily focus on the advancements in modern genetics regarding species boundaries and mechanisms of speciation.

Pre-registration is required; payment of the conference fee is necessary.
Conference fee: by 30/6 SEK 450, from 1/7 SEK 500, from 1/8 SEK 550, from 1/9 SEK 600.
More information will be continuously updated on the Genesis Society website genesis.nu/konferens.
All presentations will be in English.

PRESENTATION OF OUR GUEST SPEAKERS



Tomi Aalto holds a master's degree in education and currently works as an elementary school teacher. With previous roles in the industry as an ICT educator, programmer, and robotics specialist, Aalto transitioned to genetics, epigenetics, molecular biology, and cell biology since 2017. His work culminated in the book "Epigenetic Information and the Lost Evolution," exploring how epigenetic mechanisms adapt organisms to environmental changes. Aalto is a technology enthusiast who also engages in music, photography, and various physical activities during his free time.



Peter Borger, a molecular biologist with an MSc in biology and a PhD in medical sciences, has held positions at universities in the Netherlands, Australia, and Switzerland. Specializing in molecular processes of signal transmission and gene activity, Borger has authored 70 articles in international scientific journals. Actively involved in creation issues for many years, he serves as a speaker and writer, focusing on non-coding DNA and epigenetics. Since 2019, he has been a board member of the German creation organization "Wort und Wissen" and he authored the book "Darwin Revisited or How to Understand Biology in the 21st Century."



Nigel Crompton, a biology professor at Cornerstone University in Michigan, USA, holds BSc and MSc degrees from Manchester University (UK), a PhD from Justus Liebig University in Giessen (Germany), and a DSc from Zurich University in Switzerland. Crompton teaches biology, genetics, molecular cell biology, bioethics, evolution, and origin issues, along with neuroscience at Cornerstone University. On top of 100 scientific publications, half in peer-reviewed journals, he has developed a biomedical test predicting patient responses to cancer therapy. Crompton has been associated with the German creation organization "Wort und Wissen" for many years, contributing articles on Mendelian mechanisms in biblical speciation.



Frank Karlsen, a professor in micro- and nanotechnology at the University of Southeast Norway since 2006, has a background in clinical microbiology, virology, molecular pathology, molecular oncology, environmental effects, microbiology, and molecular biology. On top of 120 publications, 3 books, 28 patents, and 50 international clinical studies, Karlsen's mRNA-based method for detecting uterine cancer has received awards. Actively involved in creation issues, he is a member of the Norwegian creation organization "Skaper."



Andy McIntosh, emeritus professor of thermodynamics at the University of Leeds (UK) with an adjunct professorship at Mississippi State University, holds a DSc in applied mathematics from the University of Wales and a PhD in combustion engineering from Cranfield University. With over 200 research articles, McIntosh's work spans combustion engineering, the relationship between thermodynamics and information, and biomimetics. Contributing to Answers Genesis UK, he lectures globally on origin issues and has authored several books, including "Genesis for Today" and "Wonders of Creation - Design in a Fallen World" (with Stuart Burgess). Engaging in public debates with atheists and evolutionary biologists, McIntosh has been active in creation issues for many years.



Boris Schmidtgall, with a background in chemistry and a PhD from the University of Göttingen (Germany), focused his doctoral research on modified DNA molecules. During a postdoctoral fellowship in Strasbourg, France, he researched the chemical properties of certain flexible proteins. Since 2018, Schmidtgall has been a member, and he is the current chairman, of the German creation organization "Wort und Wissen." Actively giving lectures and publishing articles on topics related to faith, science, and creation-evolution, his primary scientific interest lies in biomolecular chemistry and models for the origin of life.

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6. Case study: Humans – a kind of its own?

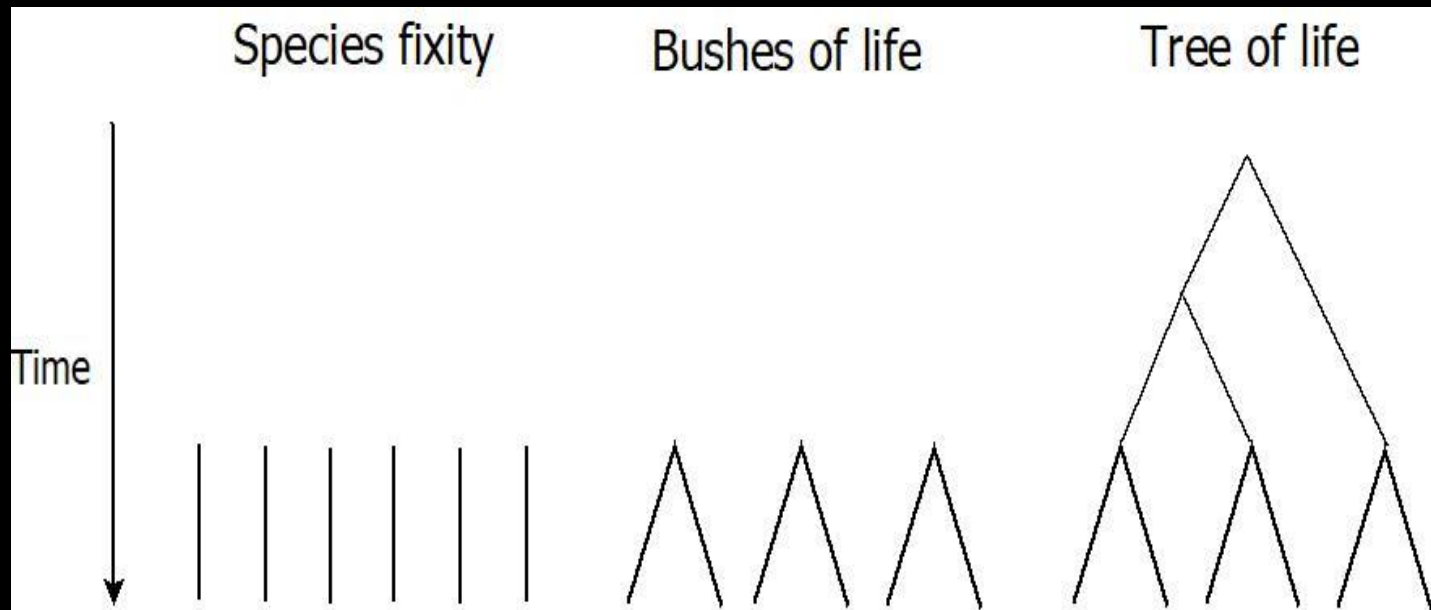
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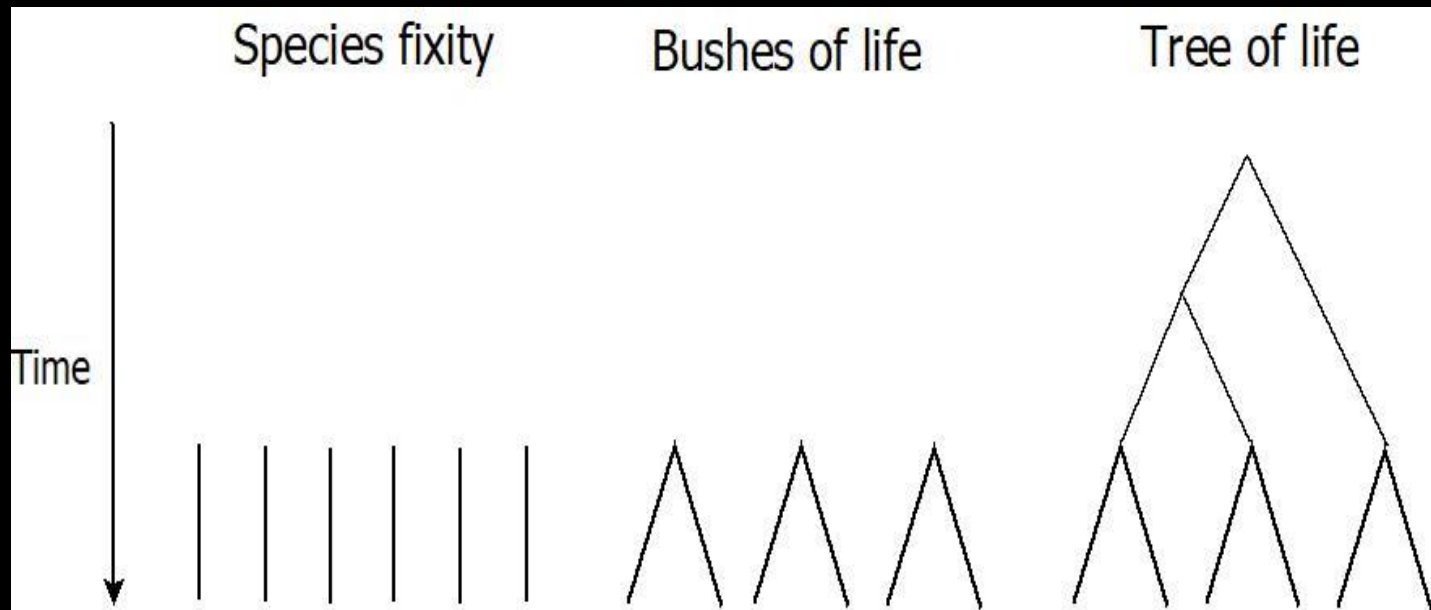
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 - Species fixity (creationist)
 - Bushes of life model (BLM; creationist)
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- The bushes of life model is between the species fixity and tree of life models
- Let us give some examples of kinds/bushes

1.1 EXAMPLES OF SUGGESTED CREATED KINDS/BUSHES

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- Great apes (*Pongidae*)
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- Is there a biblical motivation for kinds in general?

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- Limiting factor
 - Land animals experienced severe bottleneck with two or fourteen individuals/kind surviving (Flood of Noah, Gen 6:18–7:9)

1.3 BUSHES OF LIFE AND BARAMINOLOGY

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- Baramin is a Hebrew word for created kind
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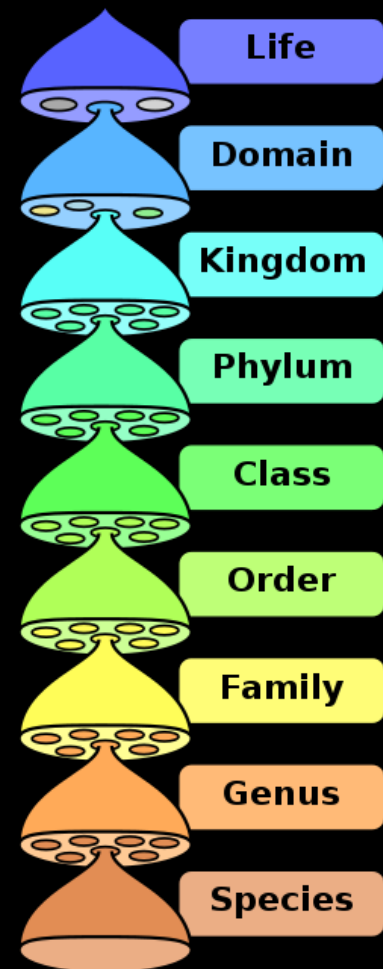
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- Baramin is a Hebrew word for created kind
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- **Three main goals of baraminology (Lightner et al., 2011):**
 - I. Identify all created kinds
 - II. Find mechanisms of divergence and speciation within each created kind
 - III. Find the ancestral history of each created kind

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- **Chicken like birds (*Galliformes*, order level)**

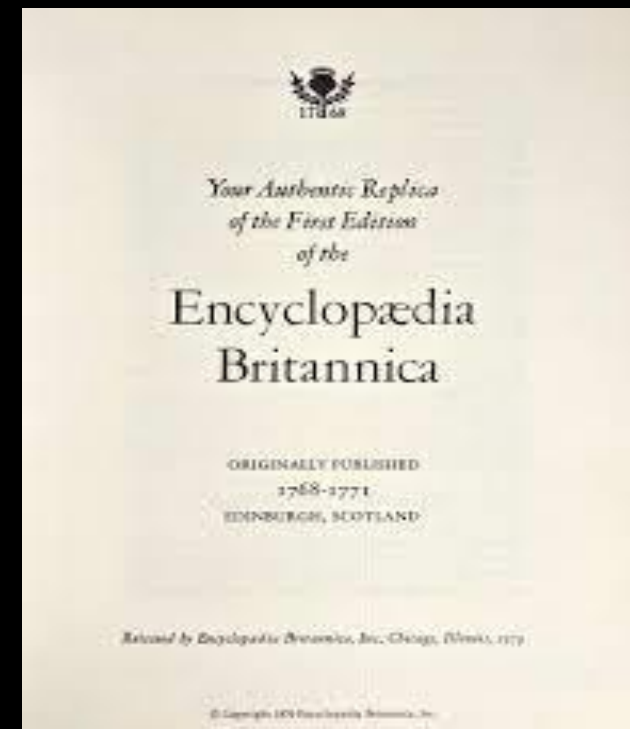


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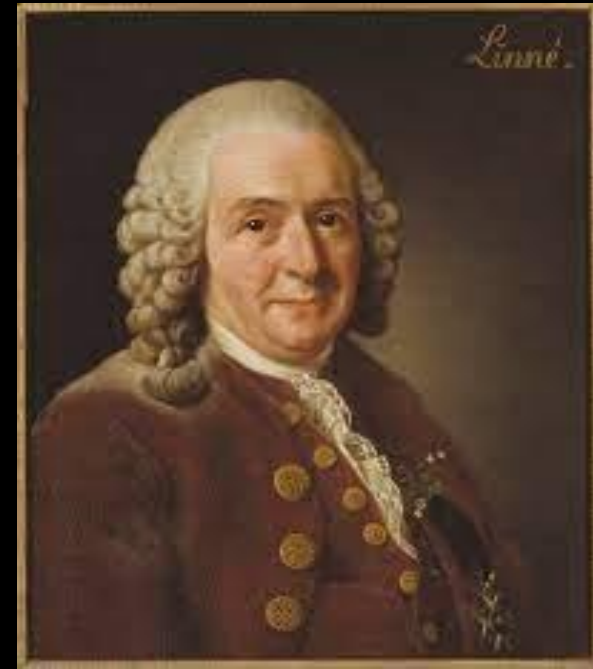
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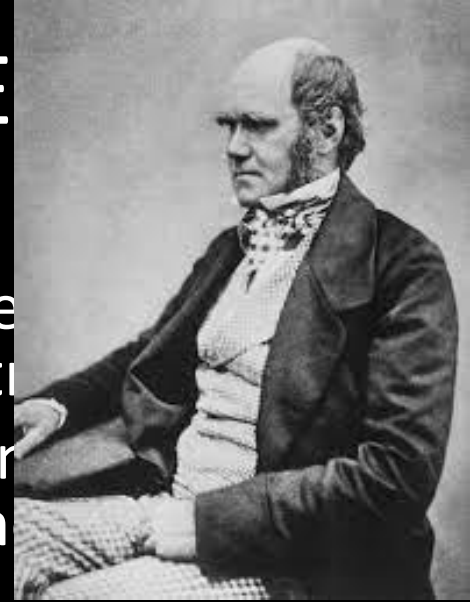


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 - **In spite of this, Darwin equated creationism with species fixity in the Origin of Species (1859)**

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 - **Creationist models**
 - **1900–1940: Increasingly many creationists favored the bushes of life model (Erich Wasmann, Harold C. Morton, George McCready Price, Dudley Joseph Whitney, Harold W. Clark, Byron C. Nelson)**



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 - 1940s: Frank Marsh defined baraminology as the systematic study of created kinds
 - From 1950s: Species fixity became a minority position among creationists, in favor of the bushes of life model

GOALS OF BARAMINOLOGY

Let us now return to the three main goals of baraminology:

- I. Identify all created kinds
- II. Find mechanisms of divergence and speciation within each created kind
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3. GOAL I: IDENTIFY CREATED KINDS

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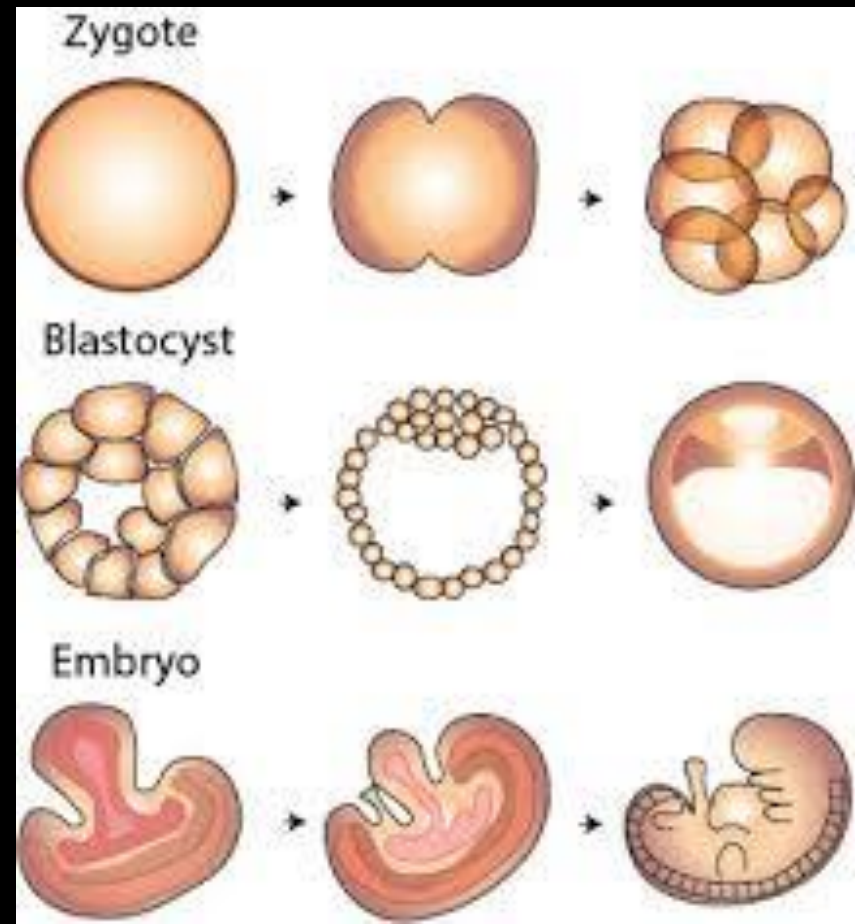
3. GOAL I: IDENTIFY CREATED KINDS

- There are three main methods for identifying biblical kinds
 - 3.1 Hybridization observations/experiments
 - 3.2 The cognitum method
 - 3.3 Statistical baraminology

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 - Reproduction is an extremely complicated process → the two organisms must be related to have viable offspring



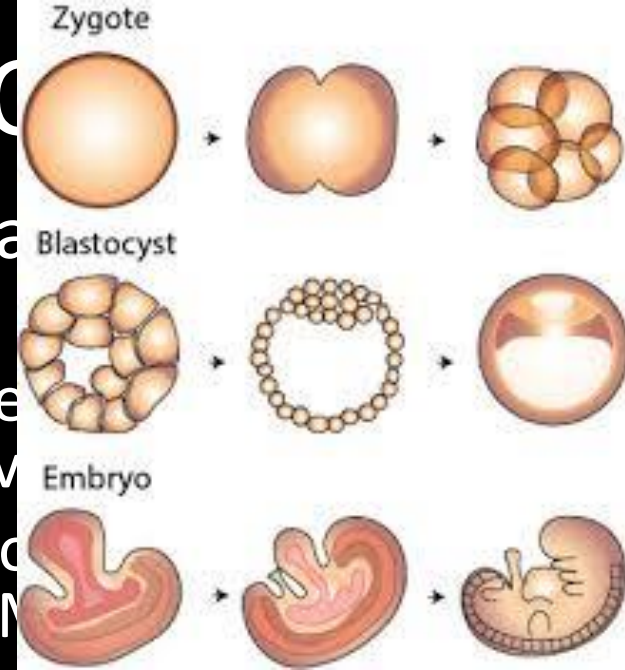
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- **Hybridization data**
 - See for instance Gray (1972) and Lightner (2012)

HYBRIDIZATION WITHIN THE CAT FAMILY

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- Cat family (*Felidae*) has 40 species and 14 genera

3.2 THE COGNITUM METHOD

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- Idea
 - It is possible to use human senses and sort species into groups (Sanders and Wise, 2003)
 - Each such group could include several kinds (e.g. mammals) or be part of a kind (e.g. foxes)
 - Still a useful tool (among others) to identify kinds

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 - Still a useful tool (among others) to identify kinds
- **Biblical motivation**
 - Adam was able to name all animals (Gen 2:19–20), that is, to identify kinds
 - Noah was able to get land animals of each kind into the Ark (Gen 6:19 – 20, 7:8)

COGNITUM METHOD CAT FAMILY

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- Strong visual resemblance between species of the cat family *Felidae*

Cat



Jungle cat



Bobcat



Cougar



Leopard



Tiger



COGNITUM METHOD CAT FAMILY

- Strong visual resemblance between species of the cat family *Felidae*
- Supports conclusion of hybridizations: *Felidae* a kind

Cat



Jungle cat



Bobcat



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3.3 STATISTICAL BARAMINOLOGY

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- Used for large morphological/molecular datasets, which cannot be analyzed by humans senses alone

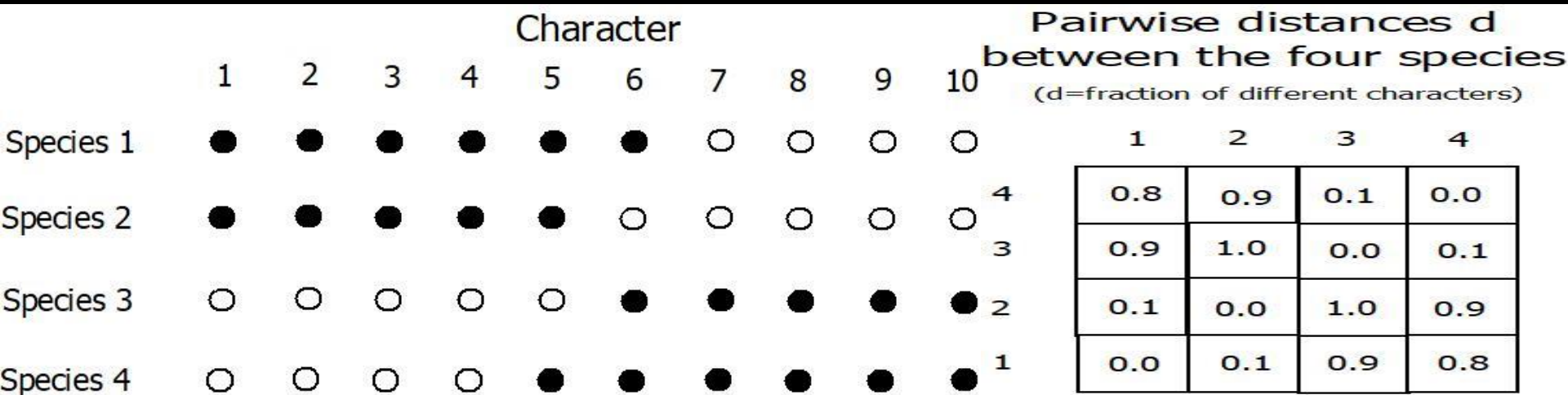
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- Used for large morphological/molecular datasets, which cannot be analyzed by humans senses alone
- **Three major steps:**
 - i. Find a list of characters (morphological or genetic) and list for each species which characters are present

	Character									
	1	2	3	4	5	6	7	8	9	10
Species 1	●	●	●	●	●	●	○	○	○	○
Species 2	●	●	●	●	●	○	○	○	○	○
Species 3	○	○	○	○	○	●	●	●	●	●
Species 4	○	○	○	○	●	●	●	●	●	●

3.3 STATISTICAL BARAMINOLOGY

- Used for large morphological/molecular datasets, which cannot be analyzed by humans senses alone
- Three major steps:
 - Find a list of characters (morphological or genetic) and list for each species which characters are present
 - Compute a distance between each pair of species, based on fraction of characters that differ

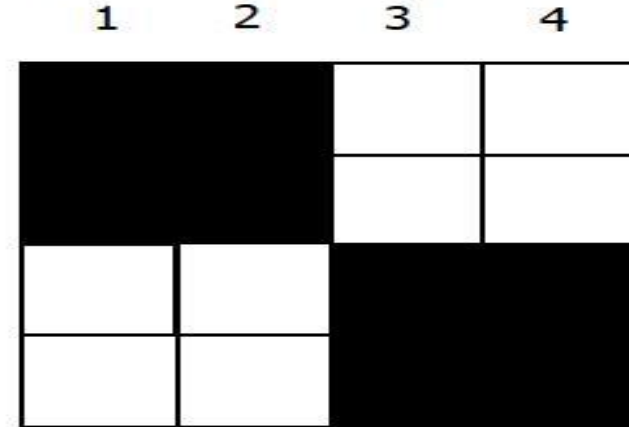


3.3 ST

Pairwise distances d
between the four species
(d =fraction of different characters)

	1	2	3	4
4	0.8	0.9	0.1	0.0
3	0.9	1.0	0.0	0.1
2	0.1	0.0	1.0	0.9
1	0.0	0.1	0.9	0.8

Heat map for
the four species
(white if $d < 0.2$, black if $d > 0.2$
gives two clusters 1,2 and 3,4)

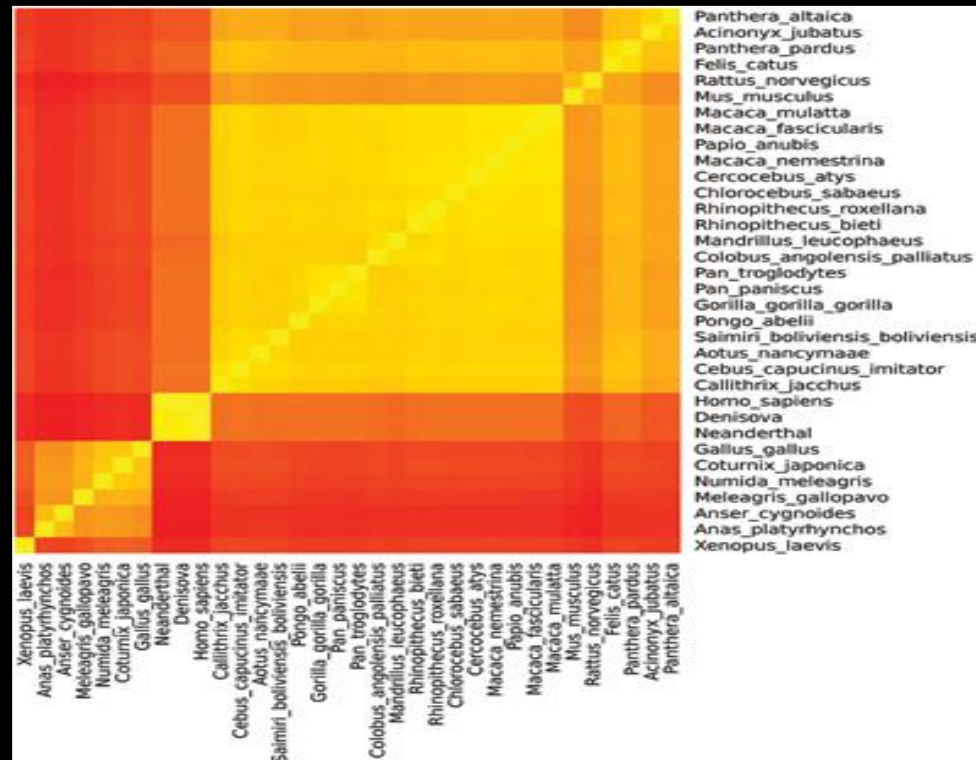


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- Three major
 - i. Find a list of characters (morphological or genetic) and list for each species which characters are present
 - ii. Compute a distance between each pair of species, based on fraction of characters that differ
 - iii. Cluster species into groups (presented as heat maps) so that distances are small (light) or large (dark) between species from the same or different groups

EXAMPLE OF A HEAT MAP

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- 34 animal groups/species
- 20 000 characters (proteins)



- We will return to this heat map later

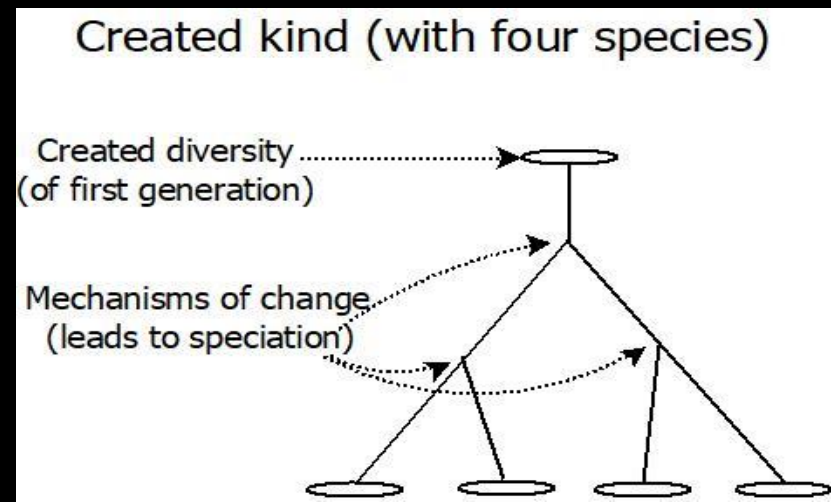
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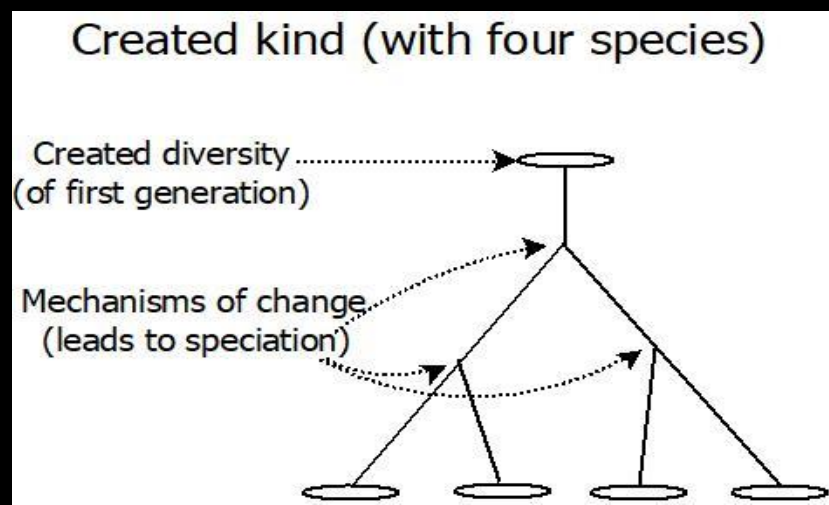
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- God created each kind to rapidly adjust to changed environmental conditions
 - This includes two main features
 - 4.1 Created diversity in the first generation of each kind
 - 4.2a) Designed mechanisms of change



4. GOAL II: MECHANISMS OF DIVERGENCE AND SPECIATION WITHIN KINDS

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 - **Implies that observed degree of speciation in each created kind is possible within a YEC timescale**



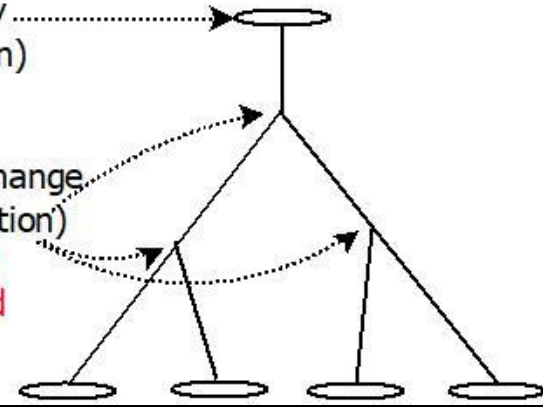
4. GOAL II: MECHANISM AND SPECIATION

Created kind (with four species)

Created diversity (of first generation)

Mechanisms of change (leads to speciation)

Designed or non-designed



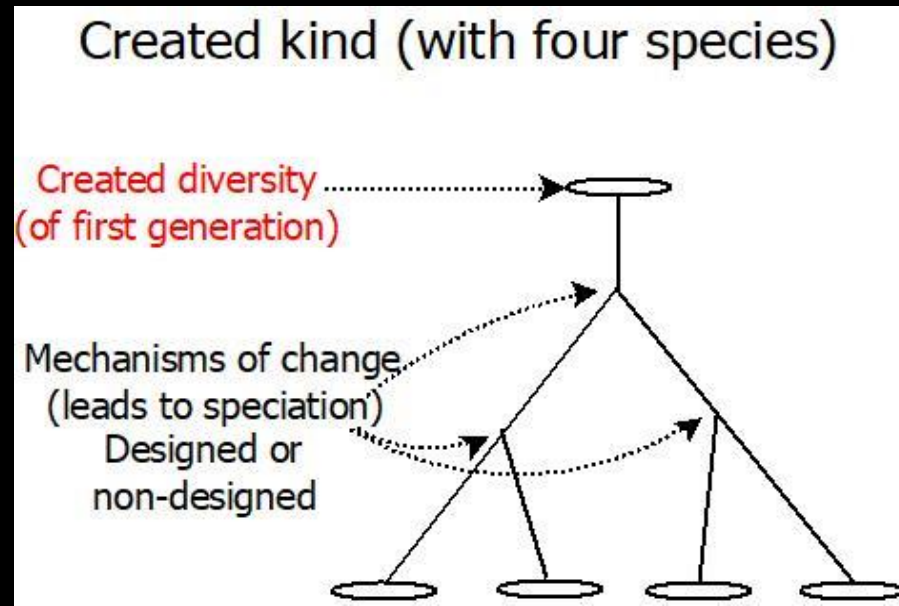
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 - Implies that observed degree of speciation in each created kind is possible within a YEC timescale
- **Additionally there are evolutionary non-designed mechanisms of change (4.2b)**
 - They are much less efficient
 - Mostly deleterious changes (devolution)
 - An effect of the Fall of Man

4. GOAL II: MECHANISMS OF DIVERGENCE AND SPECIATION WITHIN KINDS

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4.1 God created first gener of each kind with diversity (designed)

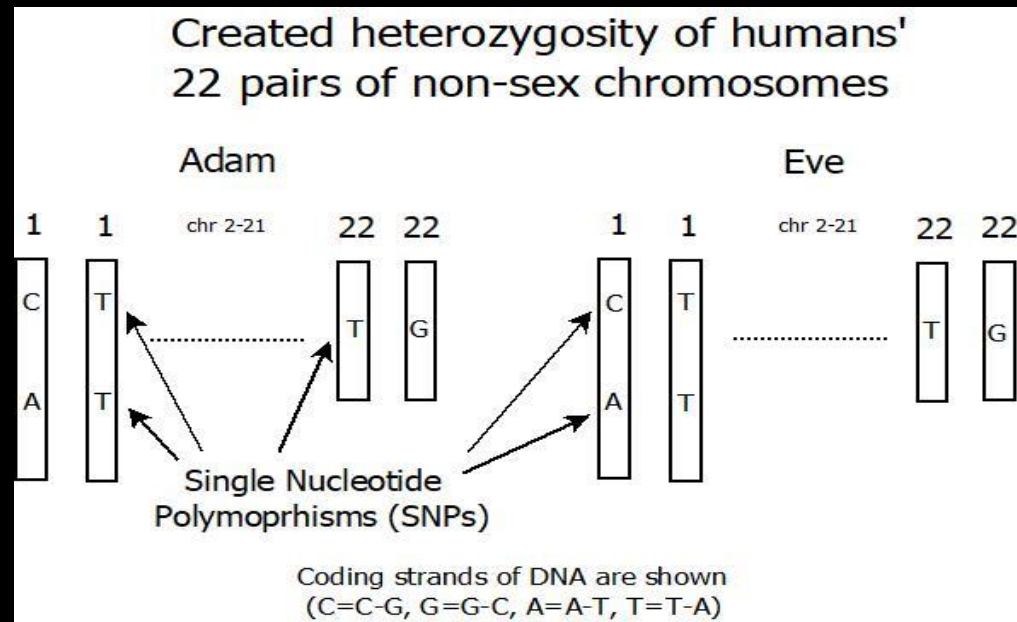
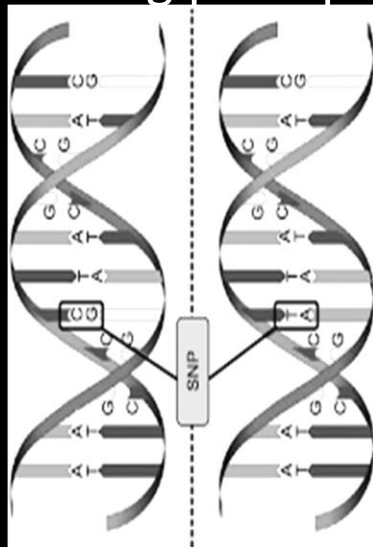
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- Epigenetic (non-genetic) structures
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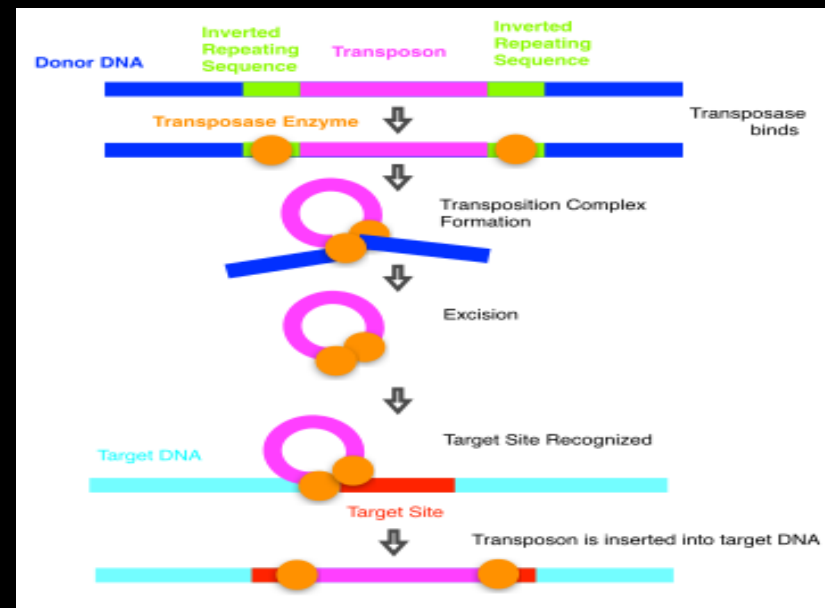
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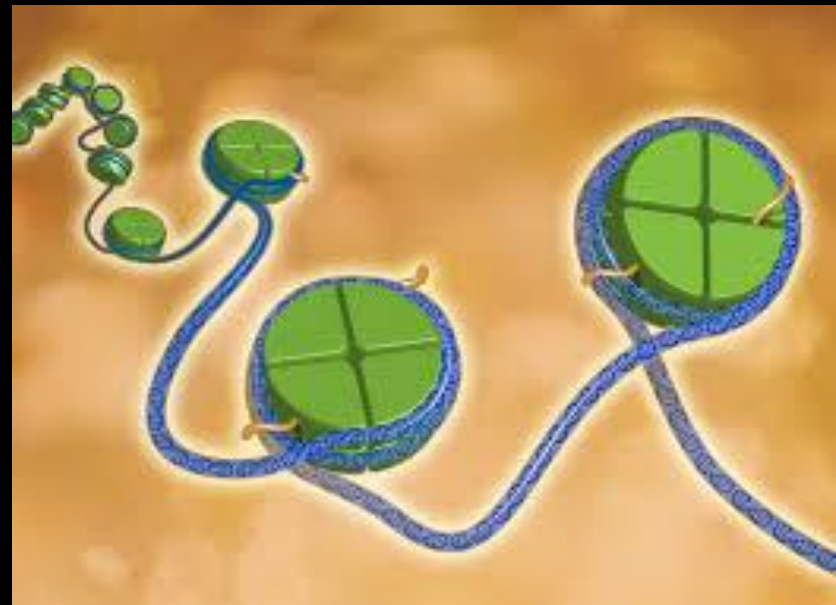
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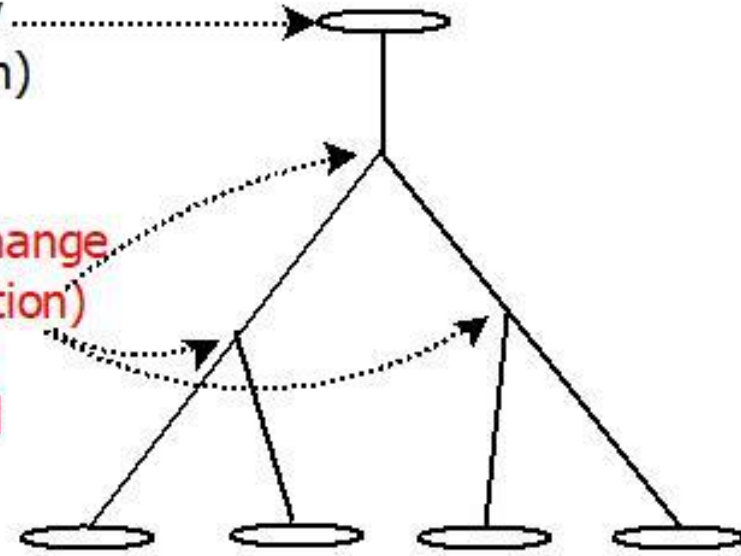
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4.2 Designed (a)/non-designed (b) mech of change after first generation

- Genetic drift and founder effects (non-designed or designed)
- Mutations (non-designed or designed)
- Crossovers/recombinations (designed)
- Natural selection (either nature or individuals doing the selection)
- The action of VIGEs (designed)
- Epigenetic mechanisms (designed)
- Developmental plasticity (designed)

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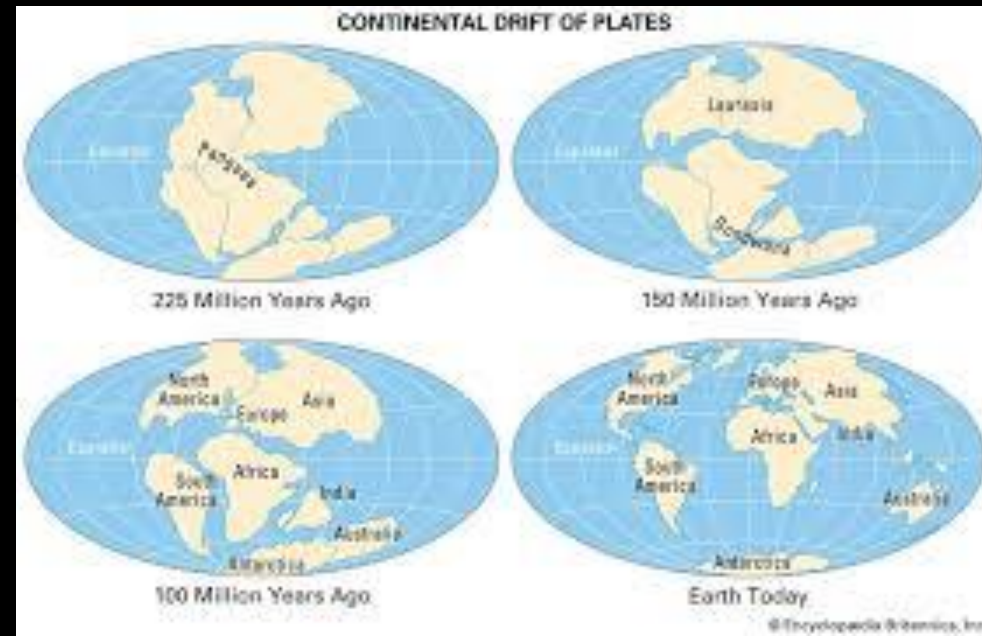
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- Plate tectonics and continental drift
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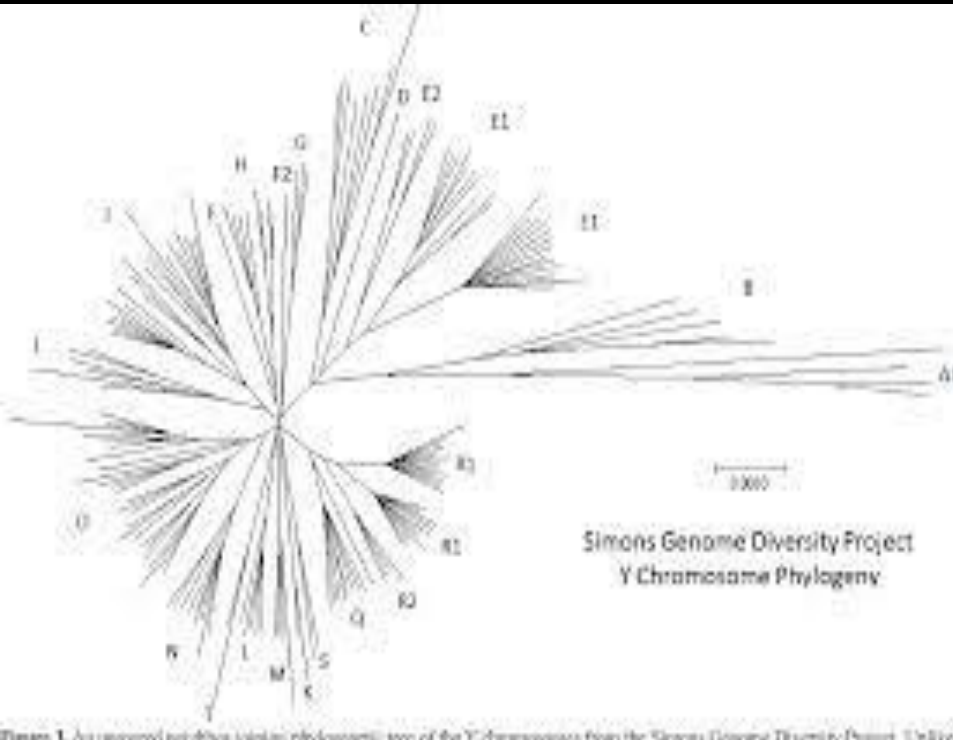
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ANCESTRAL HISTORY OF KIND

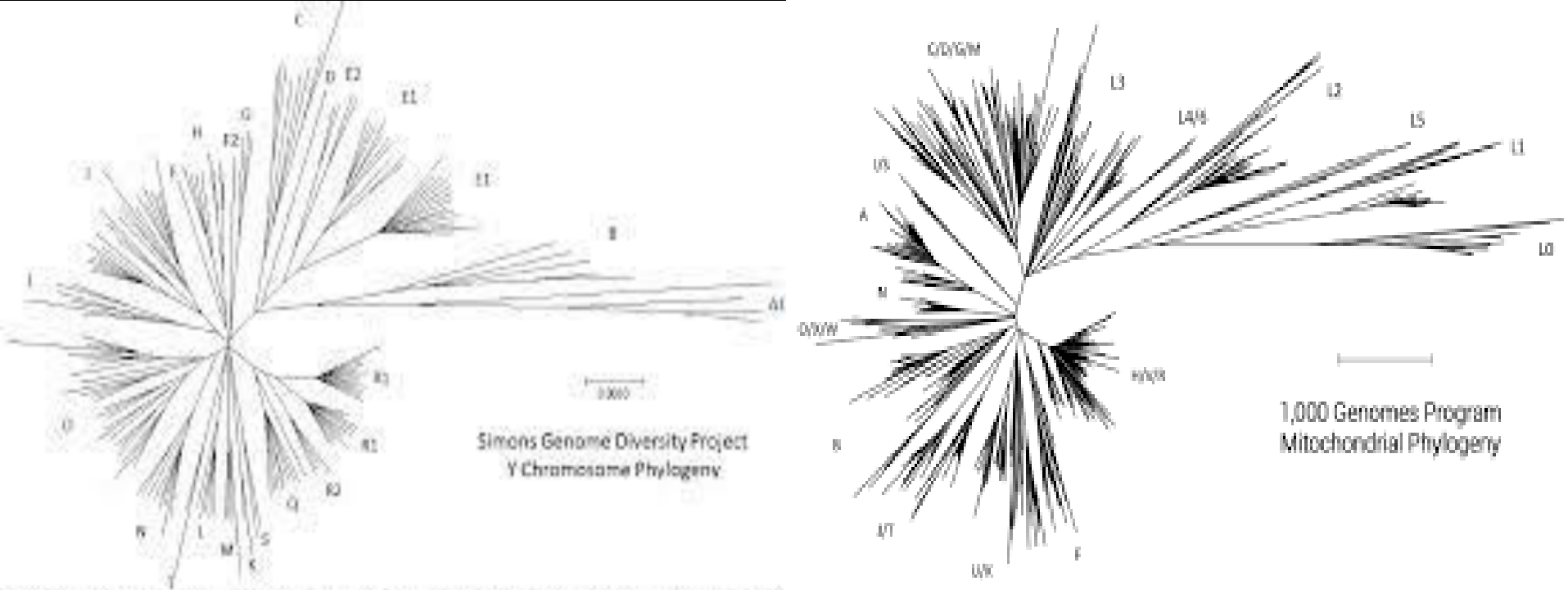
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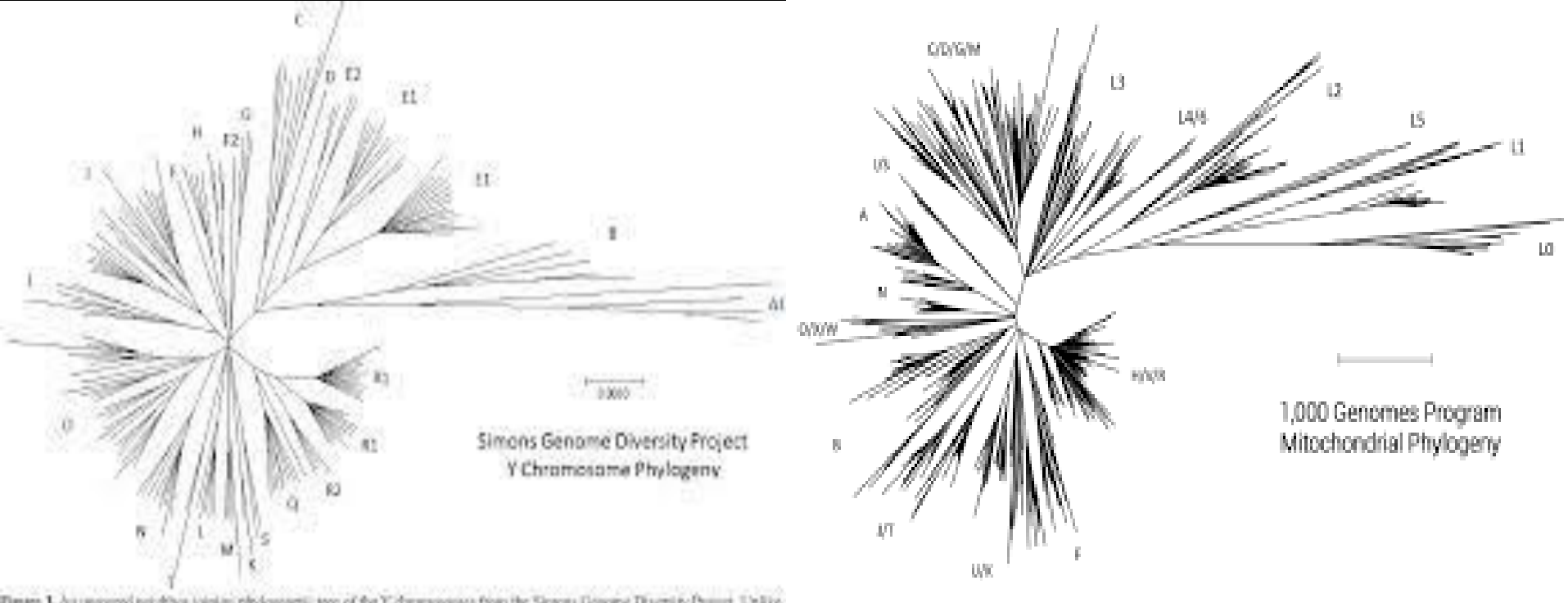
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- Use mitochondrial DNA data to build female ancestral trees

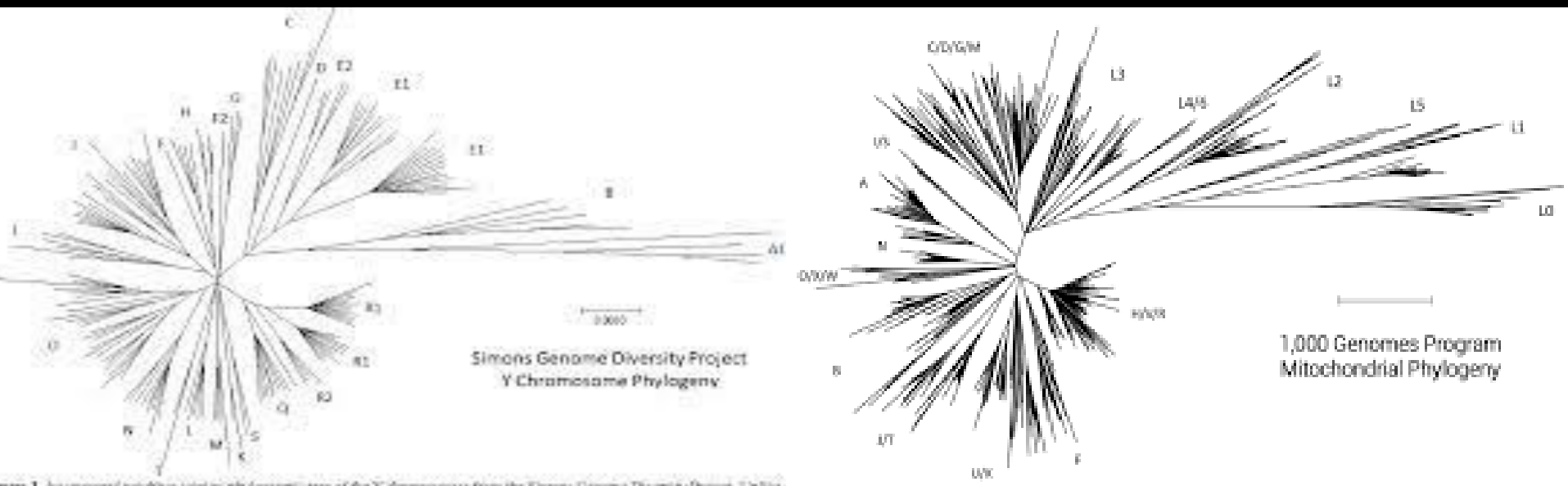


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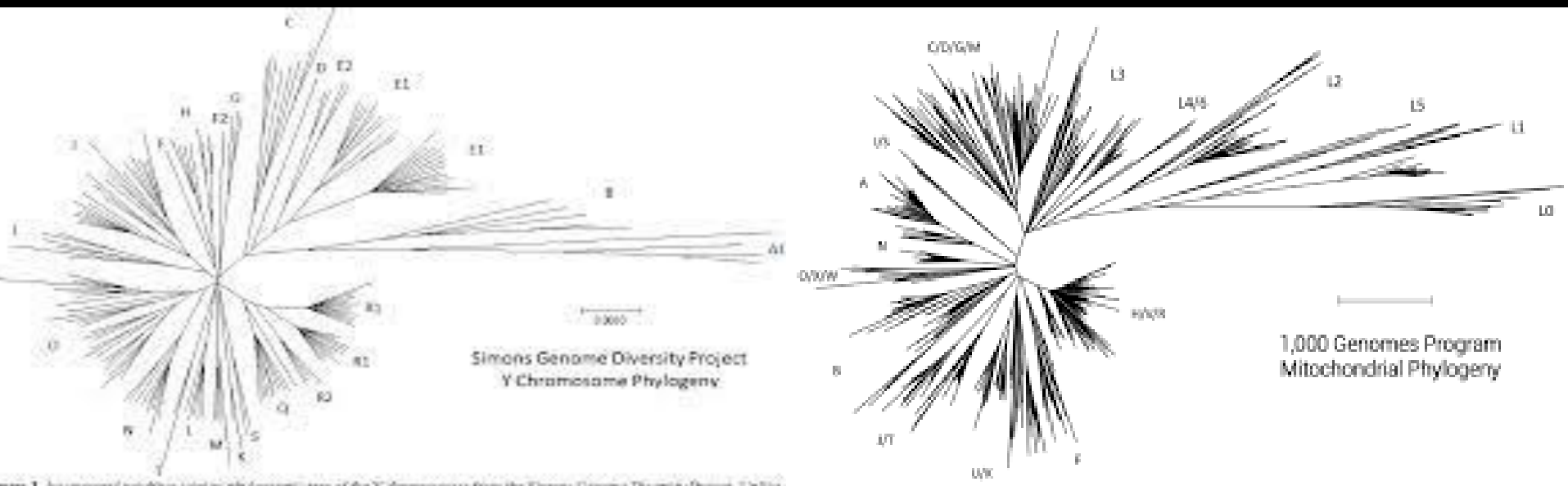
- Use Y chromosome data to build male ancestral trees
- Use mitochondrial DNA data to build female ancestral trees
- **These trees are consistent with a YEC timescale for a wide range of species (Jeanson, 2013, Jeanson & Lisle, 2016)**

HUMAN Y CHR (MTDNA) TREE



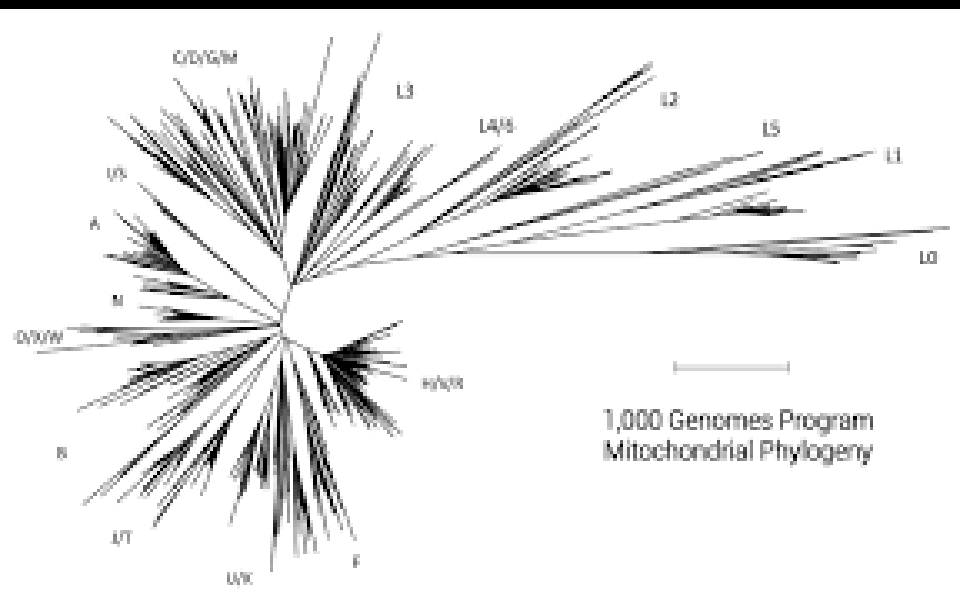
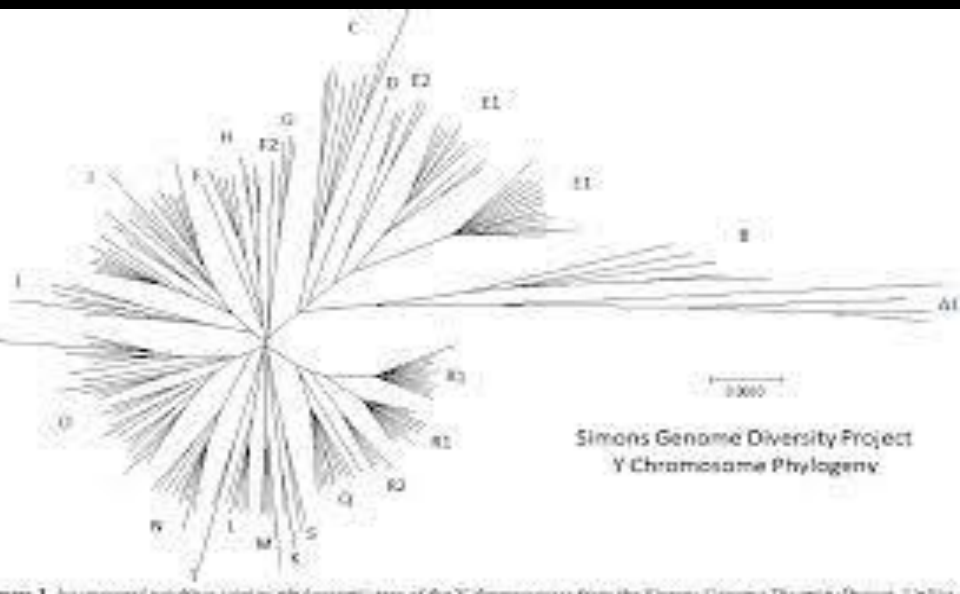
HUMAN Y CHR (MTDNA) TREE

- The tips are men (women) alive today



HUMAN Y CHR (MTDNA) TREE

- The tips are men (women) alive today
- Key questions
 - Data only gives unrooted tree. Where put the root (most recent common ancestor MRCA of all tips) of the tree?
 - How fast do the branches coalesce and when did the MRCA live?



AGE OF A TREE'S MRCA

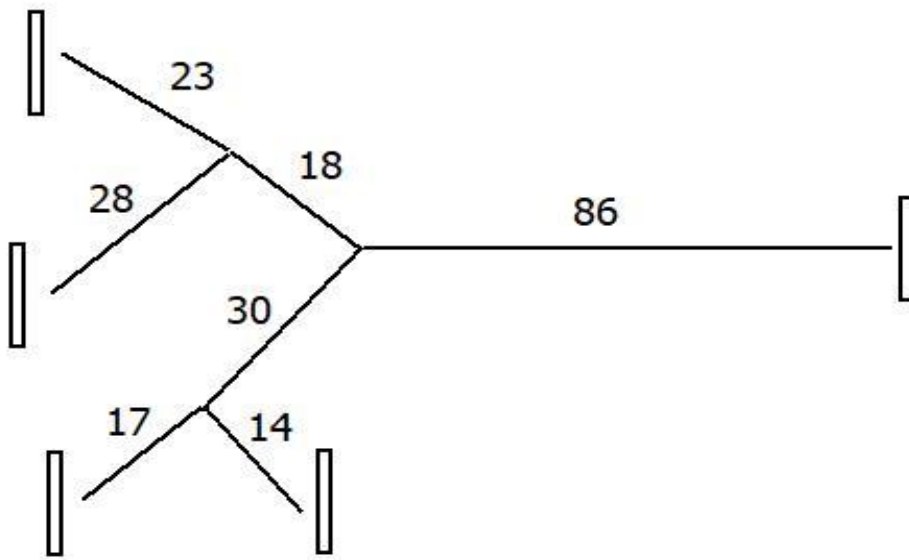
AGE OF A TREE'S MRCA

- Mutations

- Branches of a Y chr (mtDNA) tree differ because of mutations when a father (mother) passes on Y chr (mtDNA) to the offspring
- Branches that differ by fewer mutations merge more quickly (depending on mutation rate and generation time)

Unrooted Y chromosome tree of 5 men

(with number of mutations along each branch)

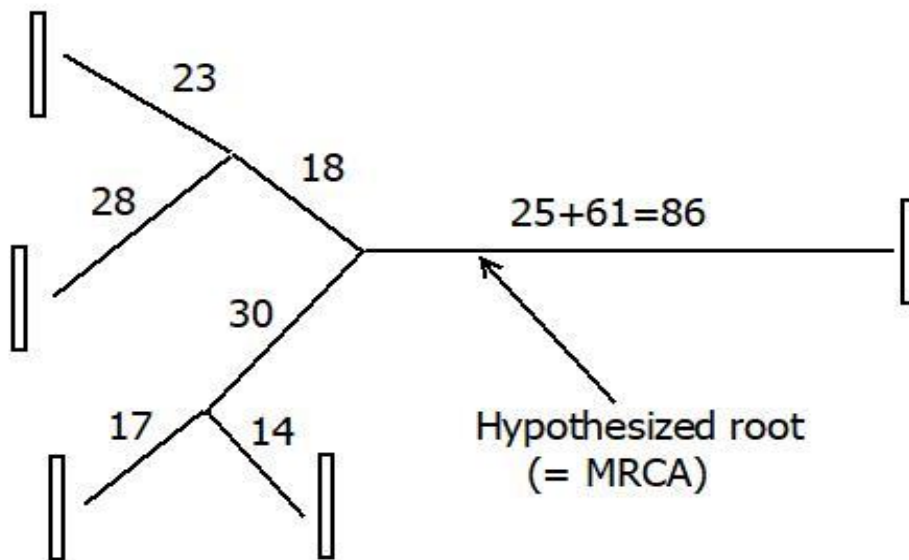


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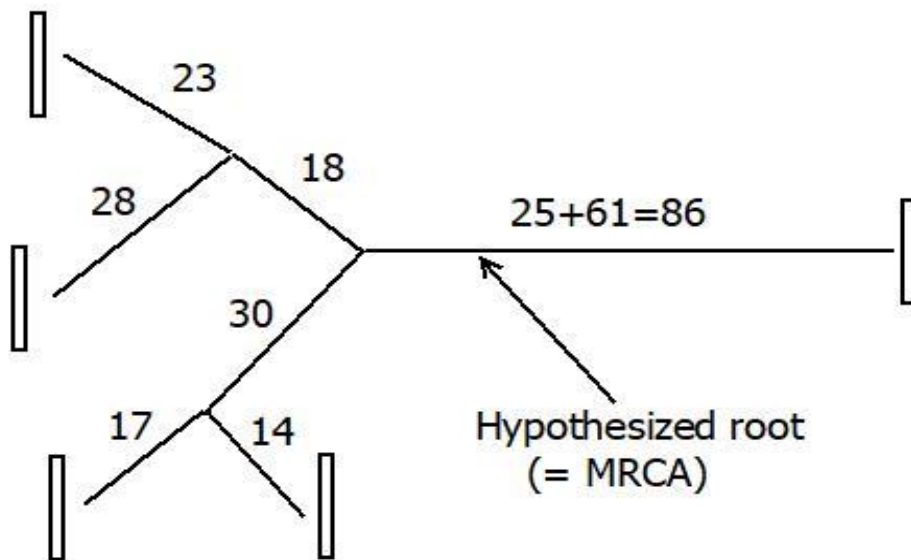
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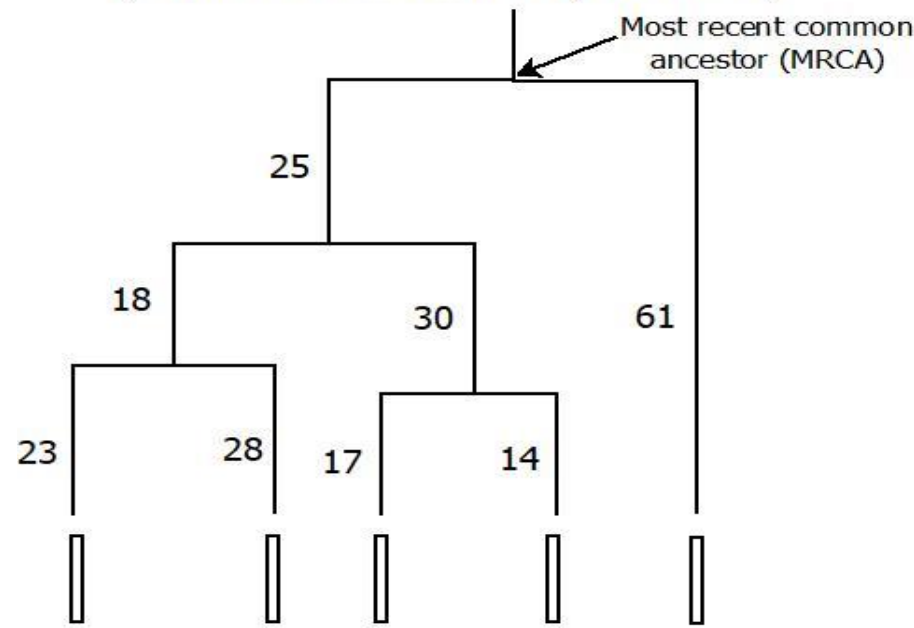
Unrooted Y chromosome tree of 5 men

(with number of mutations along each branch)



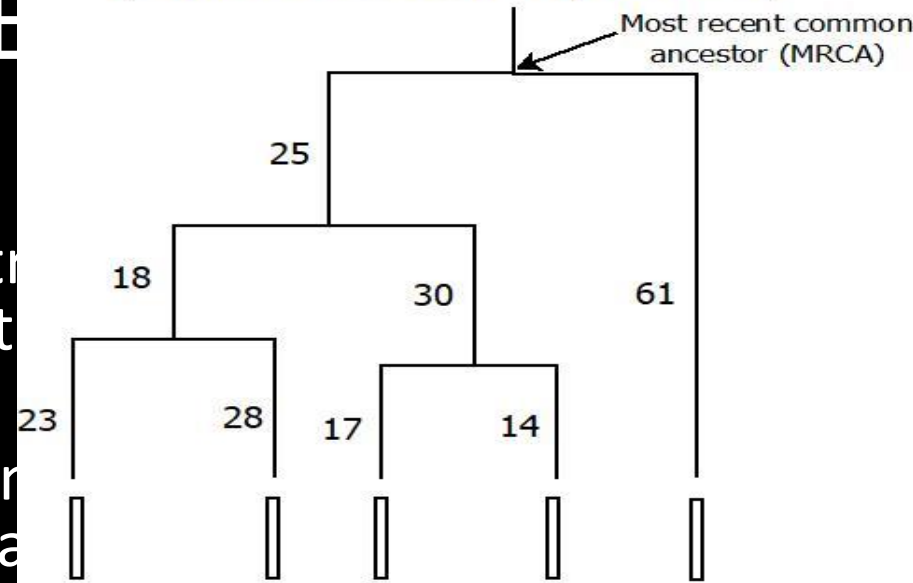
Rooted Y chromosome tree of 5 men

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AGE OF A TREE

Rooted Y chromosome tree of 5 men
(with number of mutations along each branch)



- Mutations

- Branches of a Y chr (mtDNA) track mutations when a father (mother) passes to the offspring
- Branches that differ by fewer mutations are more closely related (depending on mutation rate and time)

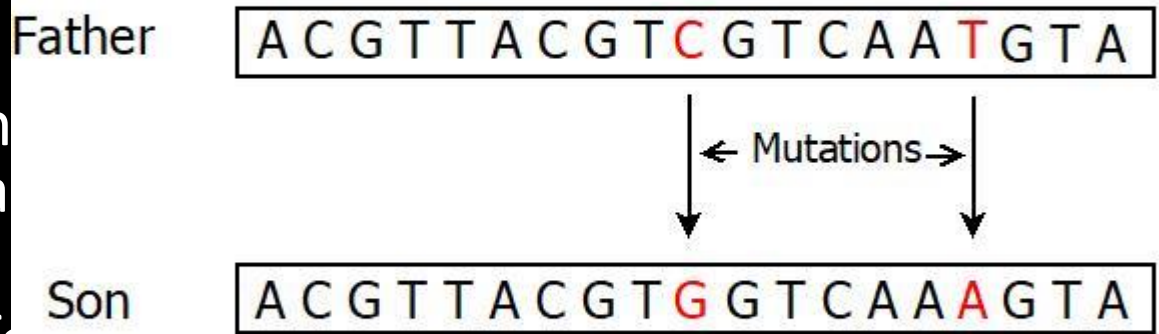
- Mutation rate (number of mutations/generation)

- The faster it is, the more recently the most recent common ancestor (MRCA) lived

AGE O

Pedigree method for Y chromosomes

Compare the coding strands of father's and son's Y chromosomes



Estimated mutation rate = average nr of mutations for
a large nr of father-son pairs

- Mutations
 - Branches of a Y chromosome are defined by mutations when a mutation is passed on to the offspring
 - Branches that differ by a single mutation (depending on mutation rate)
- Mutation rate (number of mutations per generation)
 - The faster it is, the more recently the most recent common ancestor (MRCA) lived
 - Has been estimated with accuracy only the last decades, using the pedigree method
 - It is much higher than previously believed for Y chr (mtDNA)

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- Age of the MRCA
 - Of the order 5,000-10,000 years for a wide variety of species

6. CASE STUDY - HUMANS

- We will argue that humans are unique (its own created kind) in three ways:

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6.2 Use non-sex chromosome data to argue that humans' genetic variation is consistent with ancestry from first couple (Goals I & III)

6.3 Use a) mitochondrial DNA and b) Y chromosome data to build humans' female and male ancestral trees (Goal III) with a YEC-consistent time frame

6.1 STATISTICAL BARMINOLOGY APPLIED TO HUMANS AND GREAT APES

- Statistical barminology study by Lightner and Cserathi (2019)

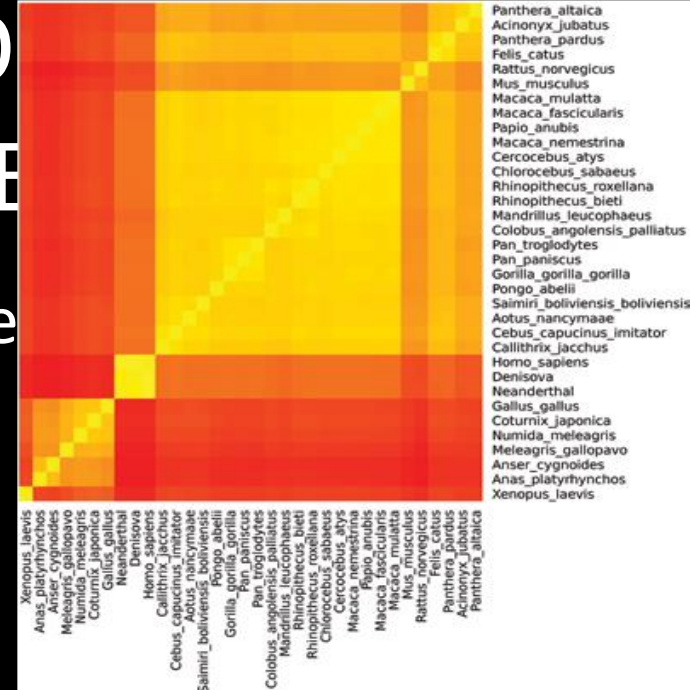
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- Statistical barminology study by Lightner and Cserathi (2019)
- A total of 34 species/groups
 - Cat animals (*Felidae*, 4)
 - Mice and rat animals (*Muridae*, 2)
 - Monkeys and apes (*Simian primates*, 18)
 - Humans (modern humans, Neanderthals and Denisovans, 3)
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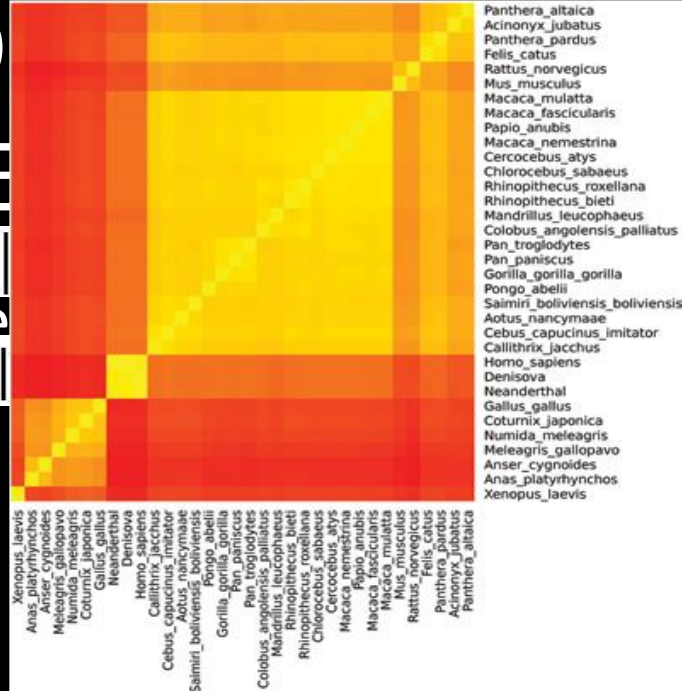
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 - 20 000 proteins
 - For each species/group, absence/presence of proteins were determined by sequence alignment methods

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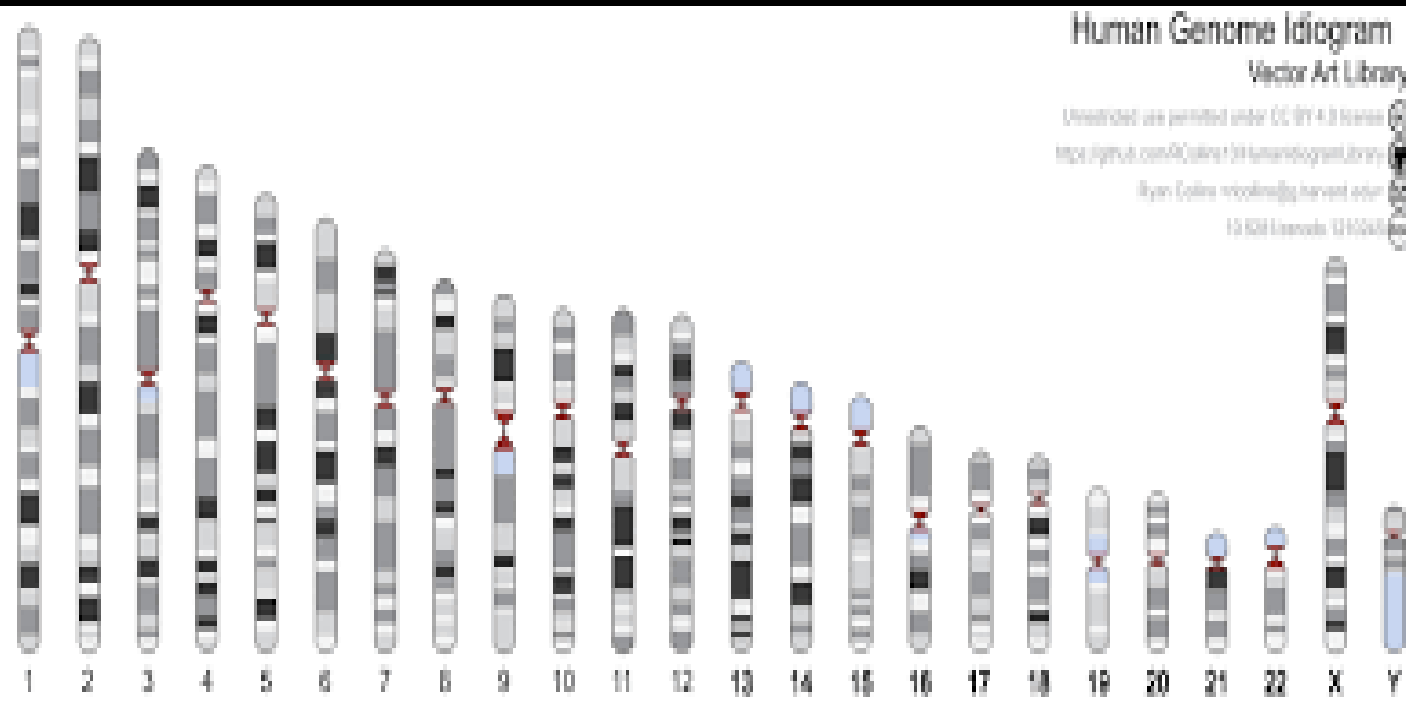
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6.2 NON SEX CHROMOSOME DATA SUPPORT HUMAN UNIQUENESS

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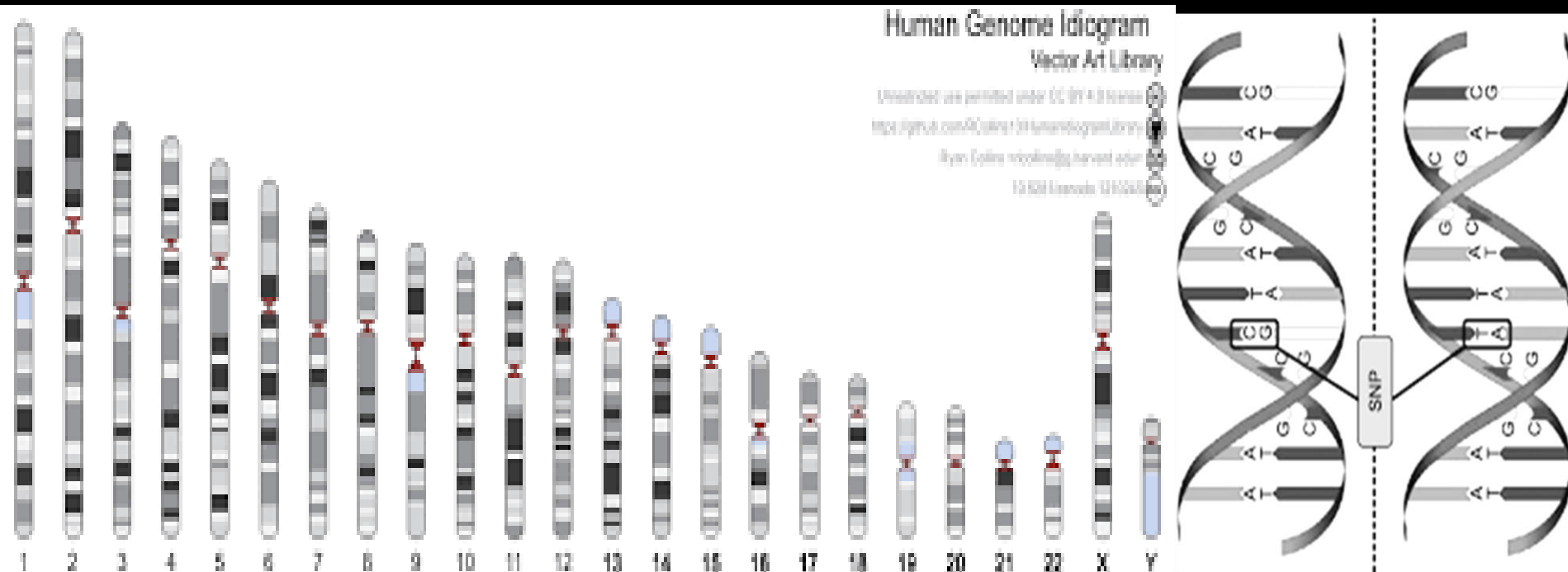
- Human DNA variaton
 - The total length of the 22 human non-sex chromosomes is about 3 billion nucleotides



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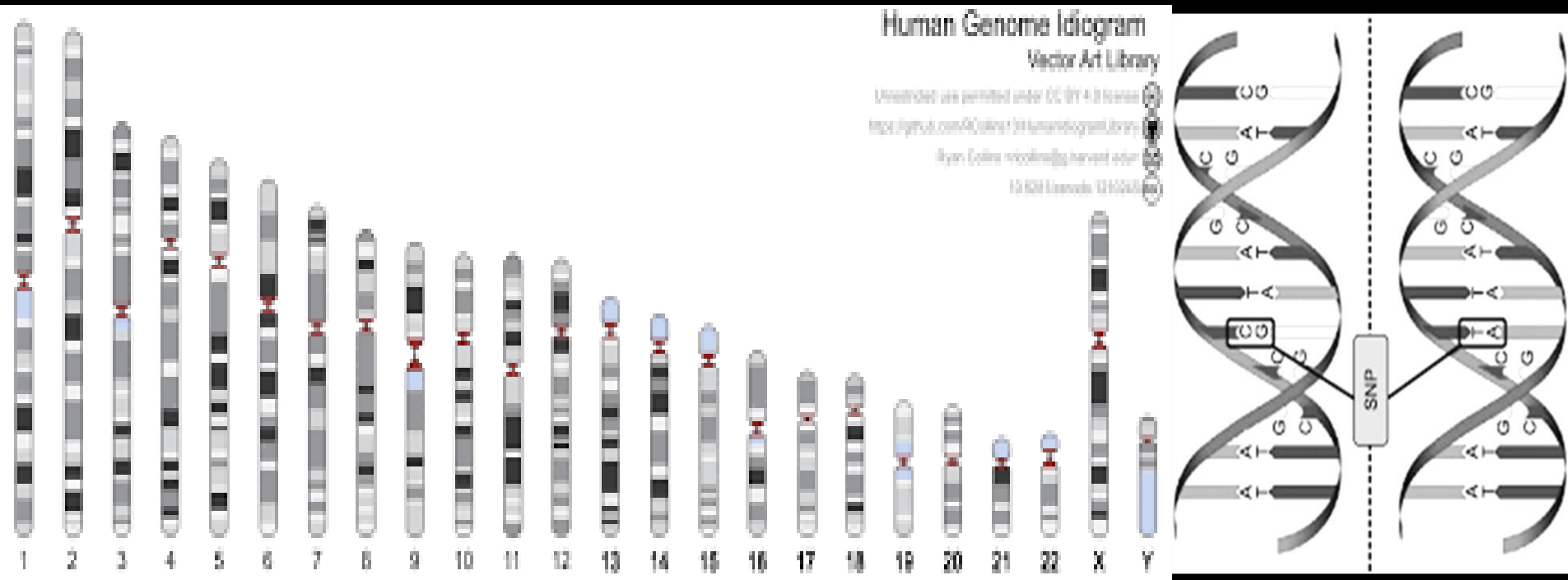
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6.2 NON SEX CHROMOSOME DATA

SUPPORT HUMAN UNIQUENESS

- Human DNA variation
 - The total length of the 22 human non-sex chromosomes is about 3 billion nucleotides
 - A biallelic SNP is a position with two possible nucleotides (alleles)
 - The minor allele frequency (MAF) of a biallelic SNP is the frequency of the less common allele (between 0% and 50%)
 - 10 million biallelic SNPs with a MAF of at least 1 % (0.3% of genome)



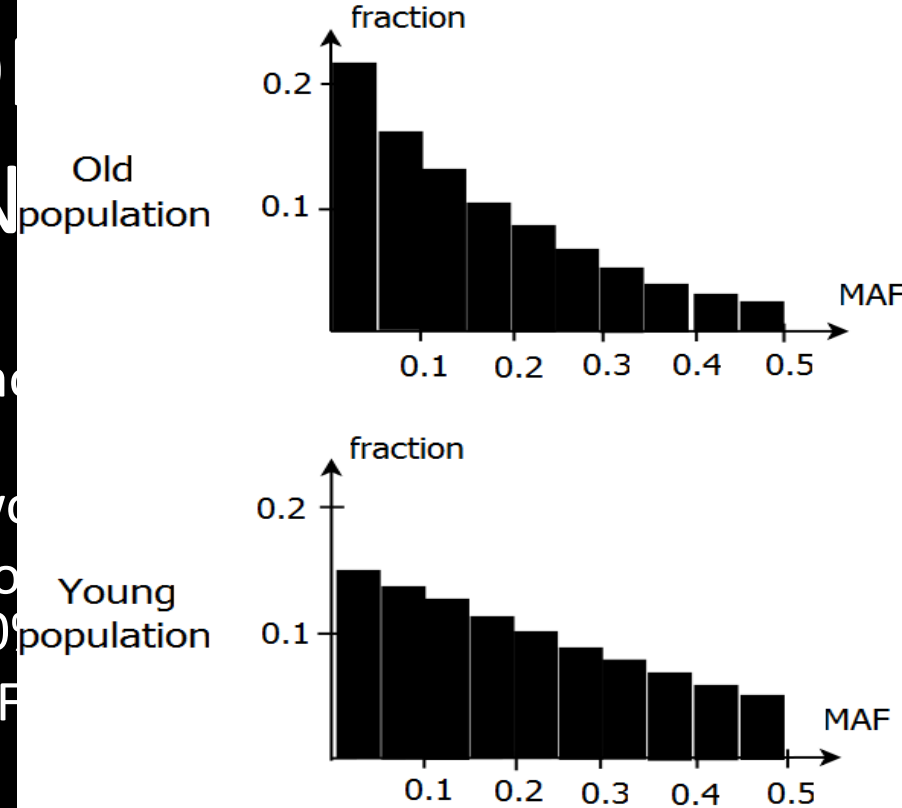
6.2 NON SEX CHROM

SUPPORT HUMAN

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 - 10 million biallelic SNPs with a MAF

- **Allele frequency spectrum (AFS)**

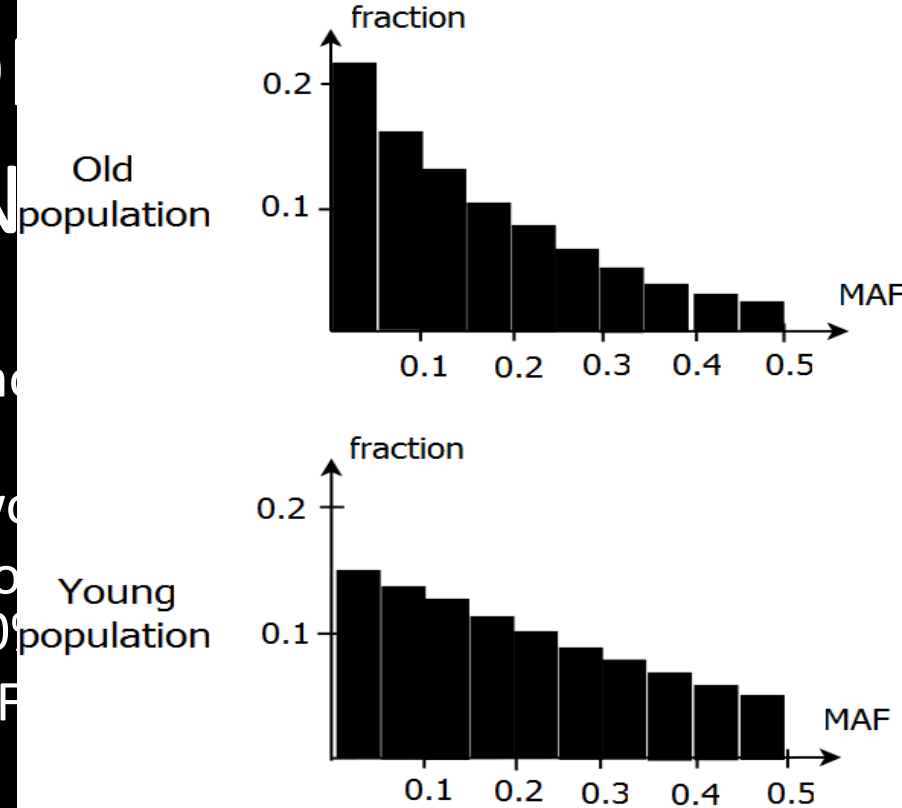
- A histogram of the MAF, at all 10 million SNPs, is referred to as the Allele Frequency Spectrum
- Its shape gives details about the history of humanity



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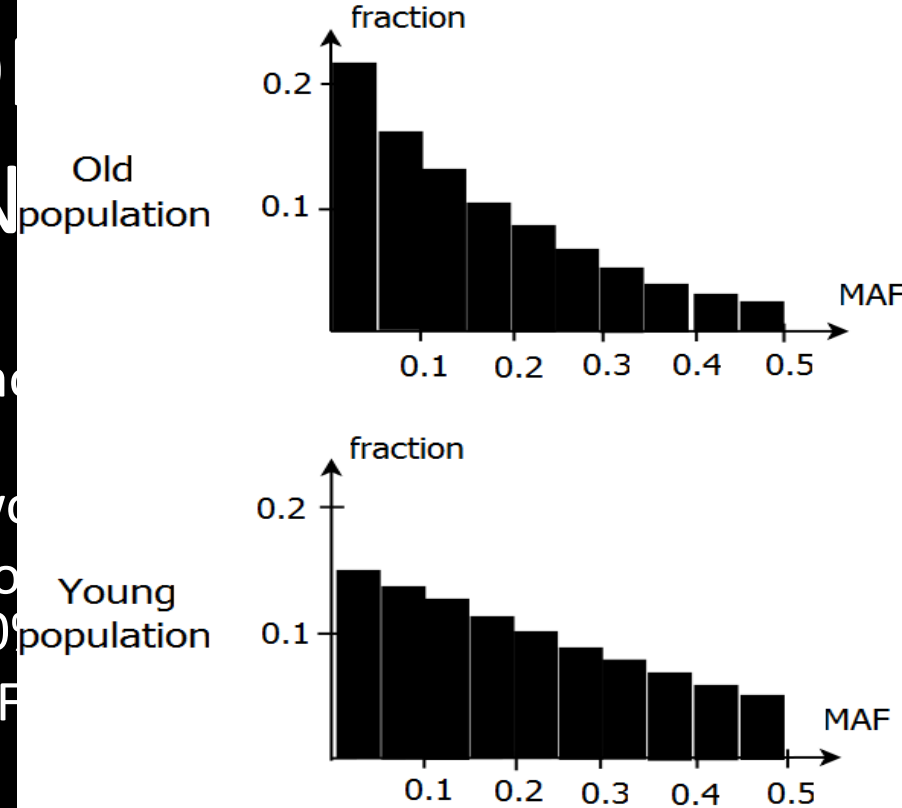
- Human DNA variaton
 - The total length of the 22 human non sex chromosomes is 3 billion nucleotides
 - A biallelic SNP is a position with two alleles
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 - 10 million biallelic SNPs with a MAF between 0.05 and 0.5
- Allele frequency spectrum (AFS)
 - A histogram of the MAF, at all 10 million SNPs, is referred to as the Allele Frequency Spectrum
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 - **Creationist model: An allele with large (small) MAF typically corresponds to created heterozygosity (a recent mutation)**



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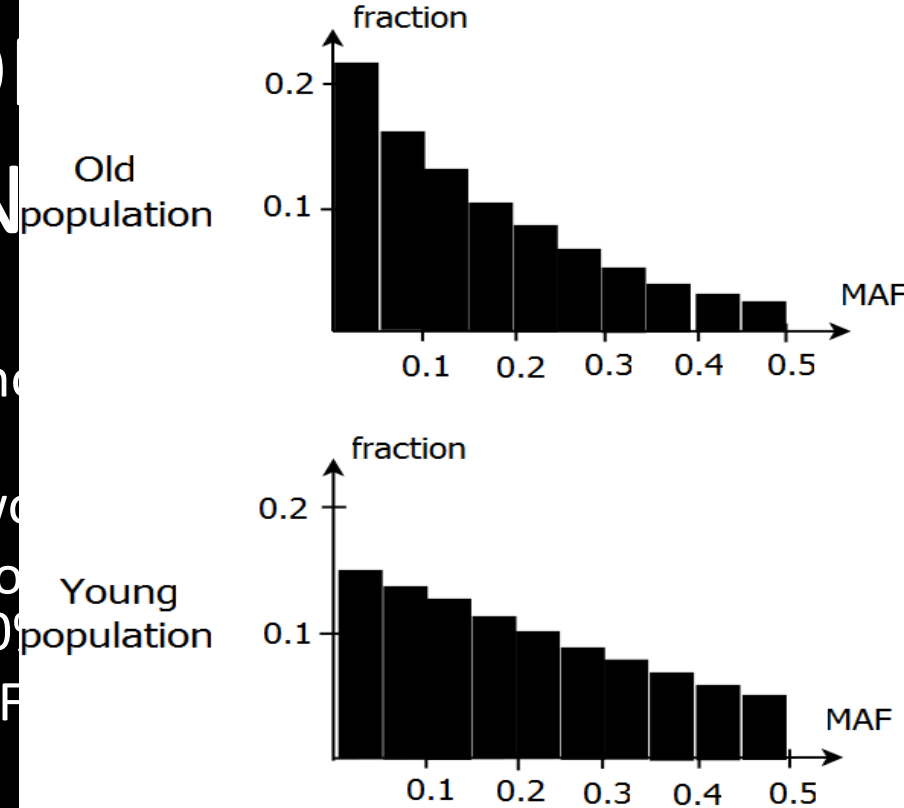
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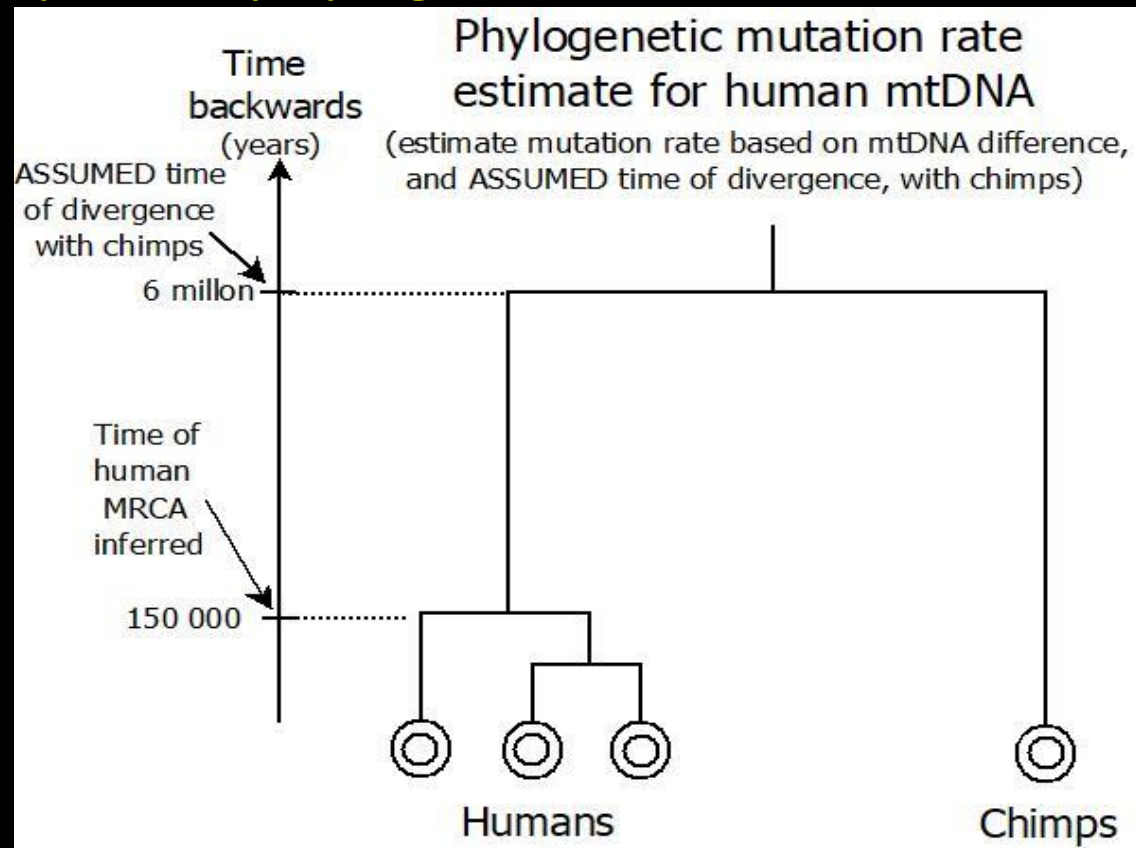
- Human DNA variaton
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 - Creationist model: An allele with large (small) MAF typically corresponds to created heterozygosity (a recent mutation)
 - Tree of life model: Large (small) MAF corresp to old (recent) mutation
- Human uniqueness
 - Hössjer and Gauger (2019) and Sanford et al (2018) fitted human AFS data with a unique origin (Adam and Eve) model of humanity



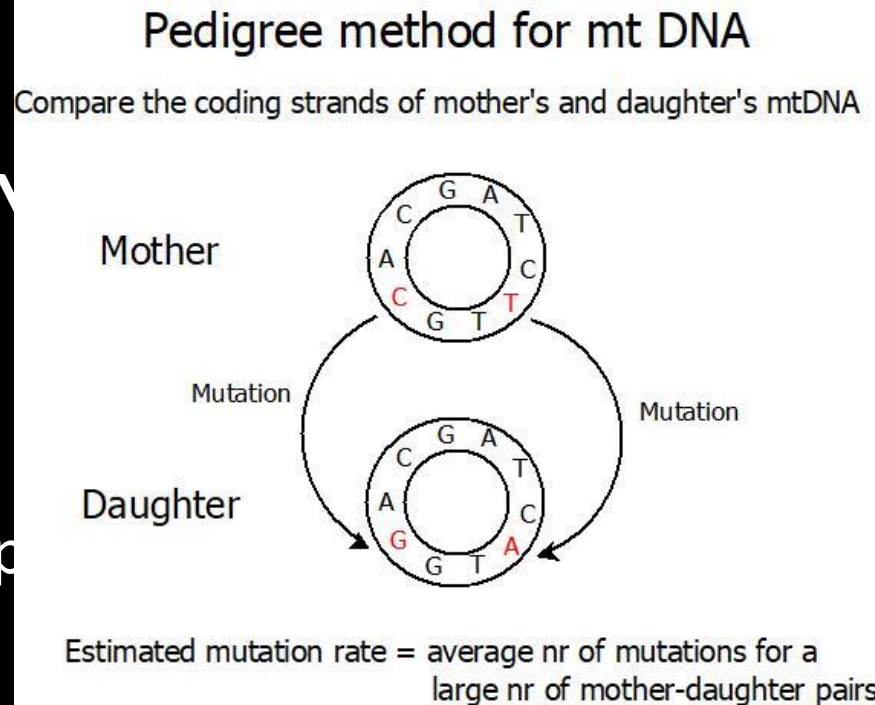
6.3a) MITOCHONDRIAL DNA HUMAN TREE CONSISTENT WITH YEC TIMESCALE

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- 1980s:
 - First estimates of age of MRCA (100 000-200 000 years) rely on evolutionary assumptions (phylogenetic mutation rates)



6.3a) MITOCHONDRIAL DNA MUTATION RATES CONSISTENT WITH Y-CHROMOSOME



- 1980s:
 - First estimates of age of MRCA on evolutionary assumptions (p)
- **Mid 1990s:**
 - First estimates of mutation rates by pedigree method gave conflicting results, but generally the age of the MRCA was found to be at least one order of magnitude smaller

6.3a) MITOCHONDRIAL DNA HUMAN CONSISTENT WITH YEC TIMELINE



- 1980s:
 - First estimates of age of MRCA (100 000-200 000 years) based on evolutionary assumptions (phylogenetic mutation rates)
- Mid 1990s:
 - First estimates of mutation rates by pedigree method gave conflicting results, but generally the age of the MRCA was found to be at least one order of magnitude smaller
- 2013 and 2016:
 - Nathaniel Jeanson pools all these studies and obtains a MRCA less than 10 000 years ago, consistent with Eve
 - He also identifies three major branches from the root (the three daughters-in-law of Noah)

6.3b) Y CHR HUMAN TREE CONSISTENT WITH YEC TIMESCALE & HUMAN HISTORY

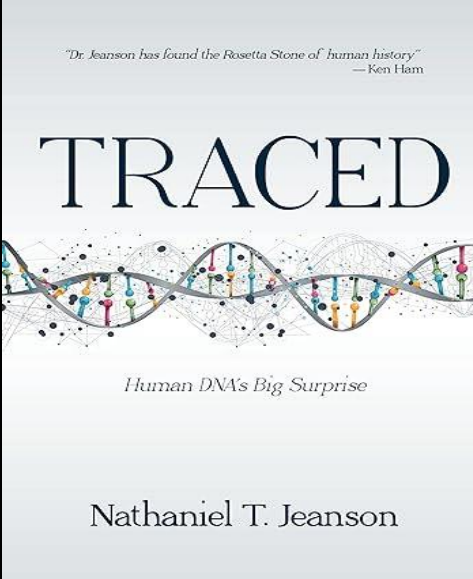
6.3b) Y CHR HUMAN TREE CONSISTENT WITH YEC TIMESCALE & HUMAN HISTORY

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6.3b) Y CHR HUMAN TREE CO WITH YEC TIMESCALE & HUMA



- 1990s
 - First estimates of age of MRCA several hundred years, based on low quality DNA data
- 2019
 - Jeanson and Holland pool several studies with high quality DNA to estimate mutation rate with pedigree method → MRCA lived about 4500 years ago, consistent with Noah



CHR HUMAN TREE CO TIMESCALE & HUMA



ates of age of MRCA several hun
years, based on low quality DNA data

- 2019

- Jeanson and Holland pool several studies with high quality DNA to estimate mutation rate with pedigree method → MRCA lived about 4500 years ago, consistent with Noah

- 2022

- Jeanson publishes Traced. YEC timescale Y-tree used to identify three sons of Noah, descendants of Noah in Genesis Chapter 10, and a number of more recent historical events

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 - **Hopefully, more people will realize how reliable the Bible is, and give their lives to Jesus**

... what may be known about God is plain to them, because God has made it plain to them. For since the creation of the world God's invisible qualities—his eternal power and divine nature—have been clearly seen, being understood from what has been made, so that people are without excuse.

Rom 1:19b-20

THANKS FOR THE ATTENTION!

Please ask questions!

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STATISTICAL BARAMINOLOGY SUPPORTS HUMAN UNIQUENESS

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