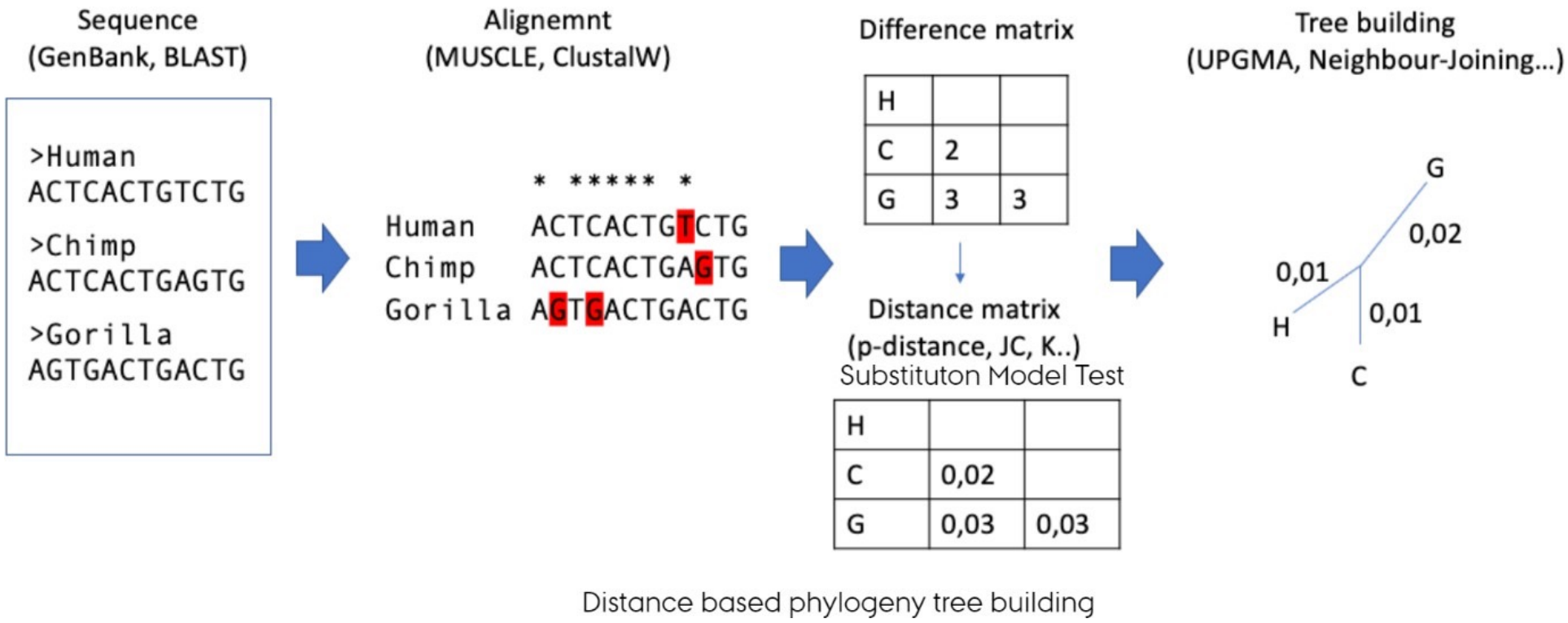
MOLECULAR CLOCK, ZOONOMIA PAPER

AARHUS
UNIVERSITY
DEPARTMENT OF MOLECULAR BIOLOGY AND GENETICS

EVOLUTIONARY THINKING 2023
WEEK 37

JANEK SENDROWSKI
PHD STUDENT

BRIEF RECAP



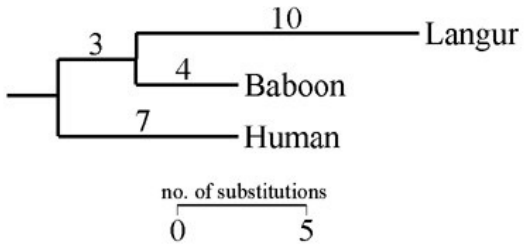
Distance based phylogeny tree building

MOLECULAR CLOCK

- sequence evolution rate constant across time or among lineages?

- discrepancy between molecular divergence dates and fossil-based estimates
  - why?

- substitution rate heterozygosity
  - also why? And how to circumvent this?



Amino acid substitutions in lysozyme C in some primates

Data from C-B Stewart & A.C. Wilson 1987, Sequence convergence and functional adaptation of stomach lysozymes from foregut fermenters. Cold Spring Harb. Symp. Quant. Biol. 52: 891-899

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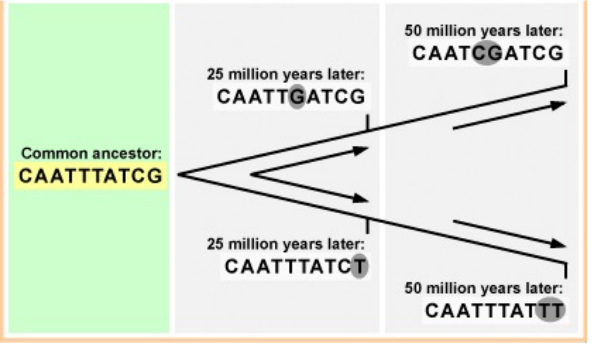
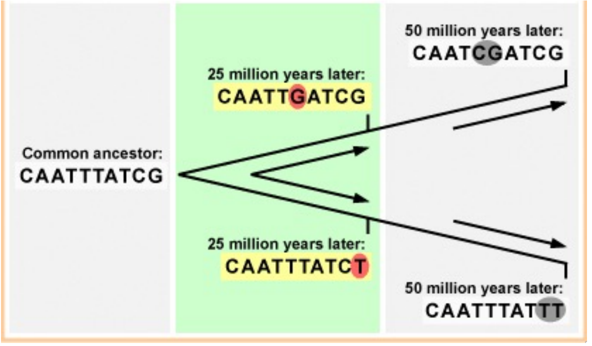
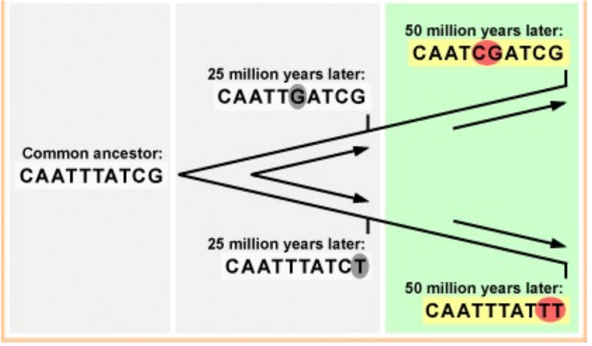
12:15-12:25







But!

Molecular clock mirages (Ayala 1999) – nice summary on Wikipedia:

- Changing generation times (If the rate of new mutations depends at least partly on the number of generations rather than the number of years)
- Population size (Genetic drift is stronger in small populations, and so more mutations are effectively neutral)
- Species-specific differences (due to differing metabolism, ecology, evolutionary history, ...)
- Change in function of the protein studied (can be avoided in closely related species by utilizing non-coding DNA sequences or emphasizing silent mutations)
- Changes in the intensity of natural selection.

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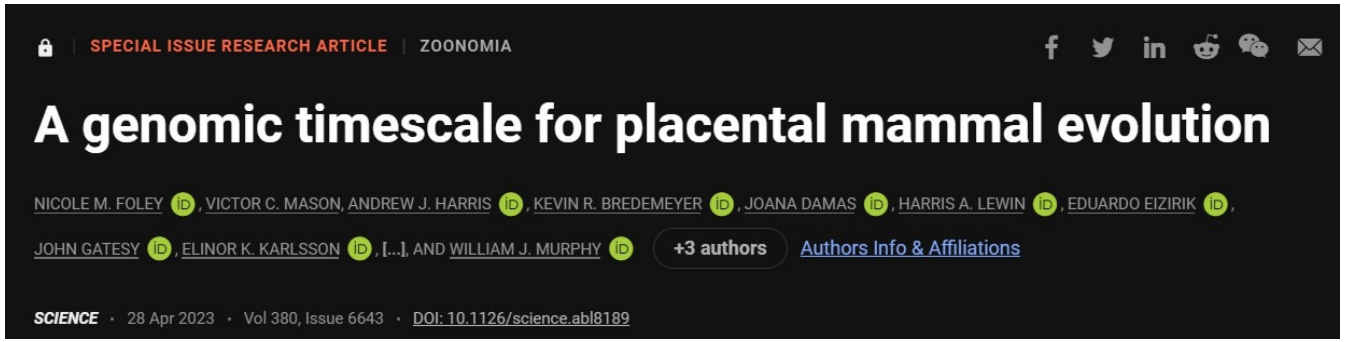

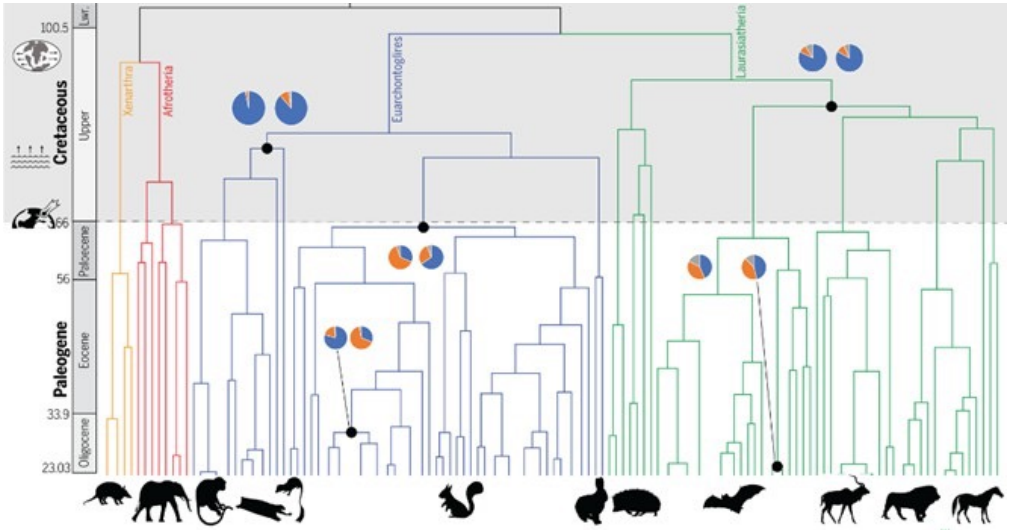

- A look into estimating divergence times based on multiple clock models
- Simple idea: look at how differently recombining chromosomes evolve
- Let's see how that went!

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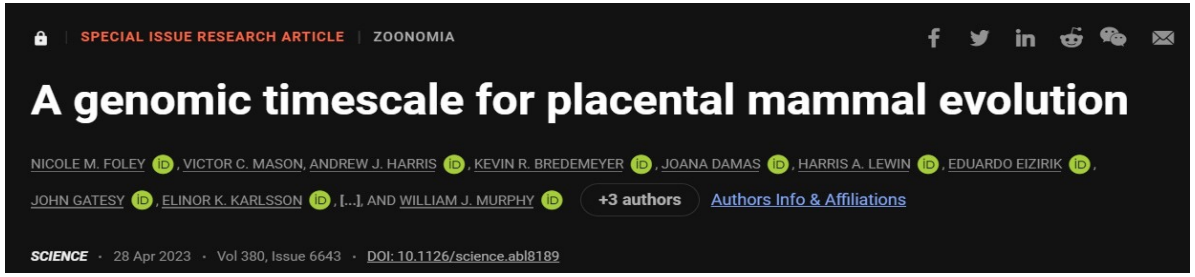

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GROUP DISCUSSIONS

Group 1

Last Name	First Name	Username	Org Defined ID
Bondia Portoles, Pablo Javier, au777573, 777573			
Cerniauskaite, Migle, au777576, 777576			
Hegedus, Mark, au777578, 777578			
Svenningsen, Laurids, au632957, 632957			

Group 2

Last Name	First Name	Username	Org Defined ID
Andersen, Line Witt, au668392, 668392			
Dyhr, Sebastian Steenstrup, au676699, 676699			
Stankeviciute, Martyna, au777575, 777575			
Zhang, Ruiqi, au779759, 779759			

Group 3

Last Name	First Name	Username	Org Defined ID
Lück, Kjeld Janke, au691027, 691027			
Matthiesen, Olivia Scharf, au696268, 696268			
Mehlig, Antonia Christine, au777579, 777579			
Singh, Aakriti, au779761, 779761			

Group 4

Last Name	First Name	Username	Org Defined ID
Christensen, Svend Bechmann Vang, au706411, 706411			
Danger, Stinna Weisberg, au643227, 643227			
Olesen, Johan, au700629, 700629			

Group 5

Last Name	First Name	Username	Org Defined ID
Cavallo, Giovanni Vincenzo, au777577, 777577			
Gergely, Péter, au777945, 777945			
Ramírez, Marina, au777574, 777574			
Wang, Chunni, au779762, 779762			

Group 6

Last Name	First Name	Username	Org Defined ID
Lopez Errasti, Unai, au777552, 777552			
Lütken, Gorm Hjorth, au681865, 681865			
Núñez Martínez, Diego, au777550, 777550			
Rico, Grace Adalia, au779763, 779763			

Group 7

Last Name	First Name	Username	Org Defined ID
Hansen, Lærke Brandt, au681665, 681665			
Manginas, Ilias, au777554, 777554			
Svendsen, Cecilie, au682949, 682949			
Vilstrøm, Victoria Hagelskjær, au638823, 638823			

Group 8

Last Name	First Name	Username	Org Defined ID
Cooper, Helena Charlotte Carlsen, au640170, 640170			
Jerideh, Aban Radwan, au603885, 603885			

Group 9

Last Name	First Name	Username	Org Defined ID
Birkmose, Sidsel, au683834, 683834			
Daskalaki, Eftychia, au777555, 777555			
Jensen, Elise Ledet, au702432, 702432			
Nielsen, Rasmine Andersson, au483502, 483502			

BREAK

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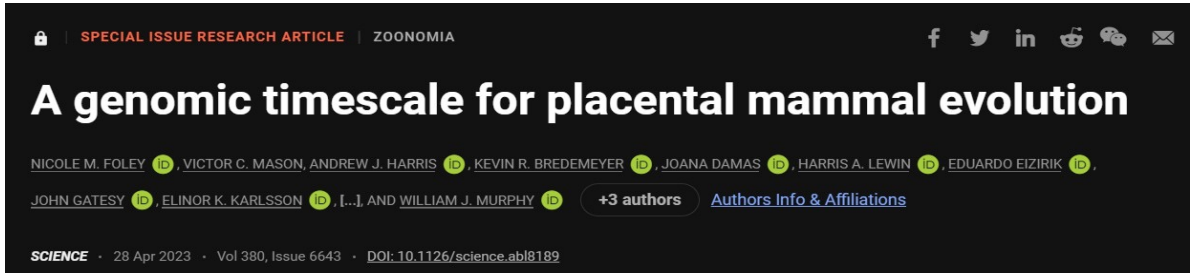

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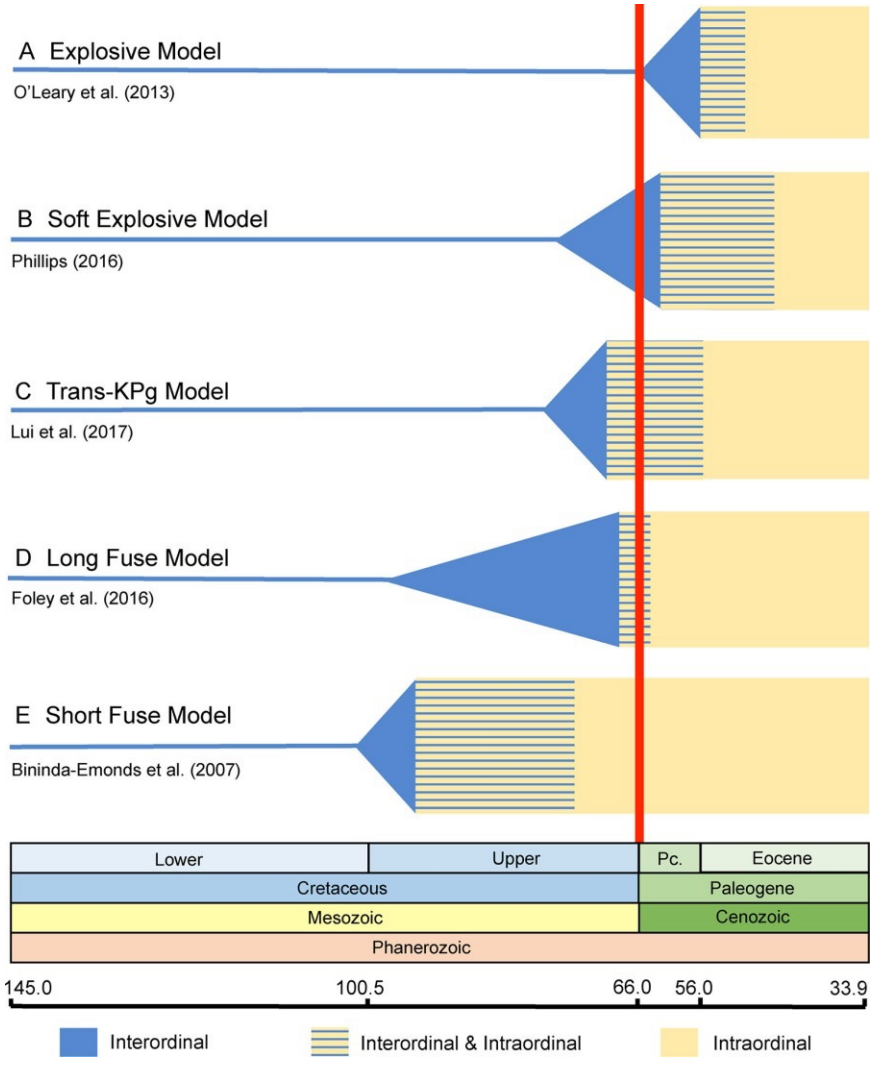
EUTHERIAN DIVERSIFICATION

Very brief discussion on the models

Use your intuition from the Zoonomia paper: does the long fuse model make sense?

What arguments supporting the other models can you think of?



Cake?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