Evolutionary Thinking 2022
TA session
week 3 – Molecular Clock

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Outline

1. Recap

2. Learning outcome of this week - Molecular Clock

What is it ?

Assumption

Overview of the paper

3. Paper Discussion

Recap

Sequence
(GenBank, BLAST)

```
>Human
ACTCACTGTCTG
>Chimp
ACTCACTGAGTG
>Gorilla
AGTGACTGACTG
```

Alignemnt
(MUSCLE, ClustalW)

```
          *  *****  *
Human     ACTCACTGTCTG
Chimp     ACTCACTGAGTG
Gorilla   AGTGACTGACTG
```

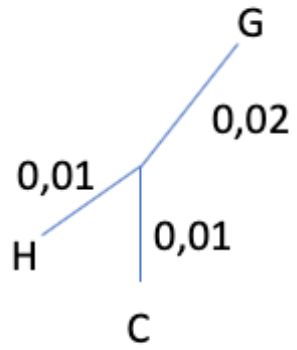
Difference matrix

H		
C	2	
G	3	3

Distance matrix
(p-distance, JC, K..)
Substituton Model Test

H		
C	0,02	
G	0,03	0,03

Tree building
(UPGMA, Neighbour-Joining...)



Distance based phylogeny tree building

Learning outcome of this week

Molecular clock

Q: What it is and the underlying assumption

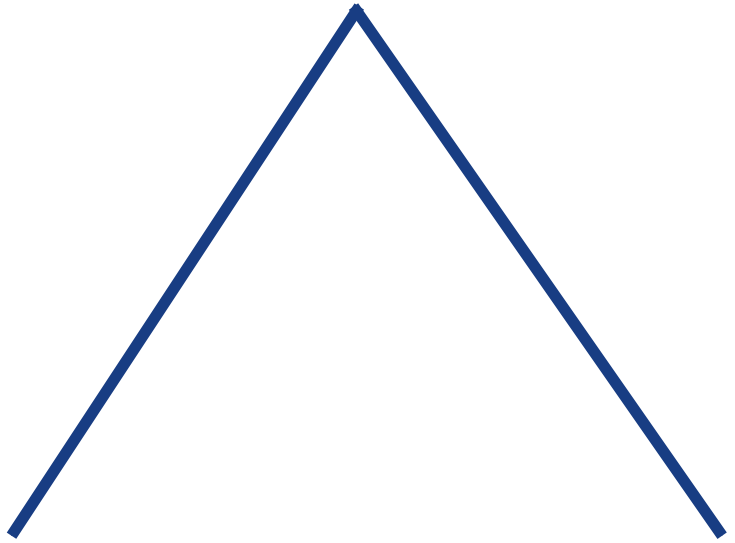
According to Wikipedia:
"Uses the mutation rate of biomolecules to deduce the time in prehistory when two or more life forms diverged."

Assumption:
The rate of molecular evolution is approximately constant over time in all lineages

Learning outcome of this week

Molecular clock

Examples



alpha-globins divergence
Observe 0.093 substition per site

rate: 5.6e-10 substitution per site per year

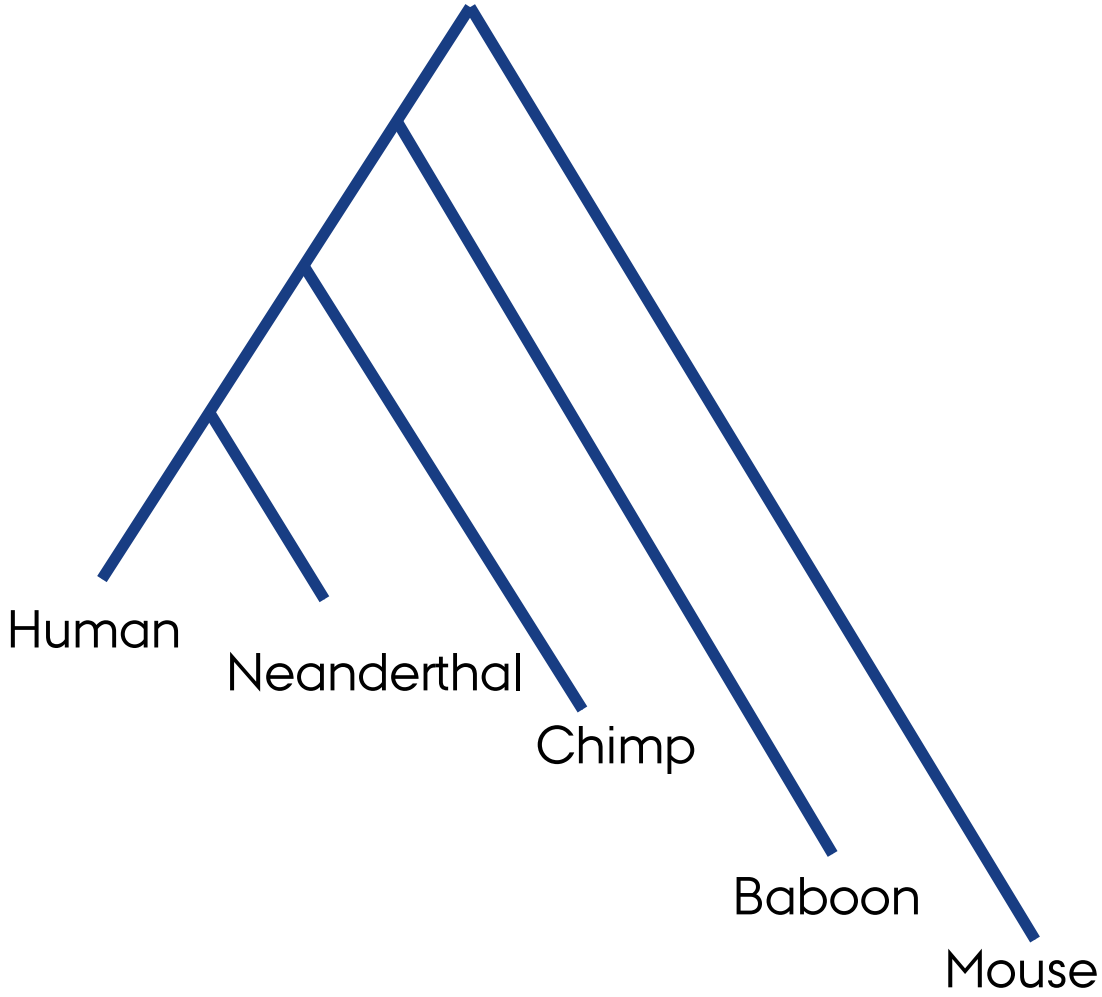
Learning outcome of this week

Molecular clock

Violation of the assumption

Rate Heterozygosity

Walk around solutions?
(3 min discussion)



Learning outcome of this week

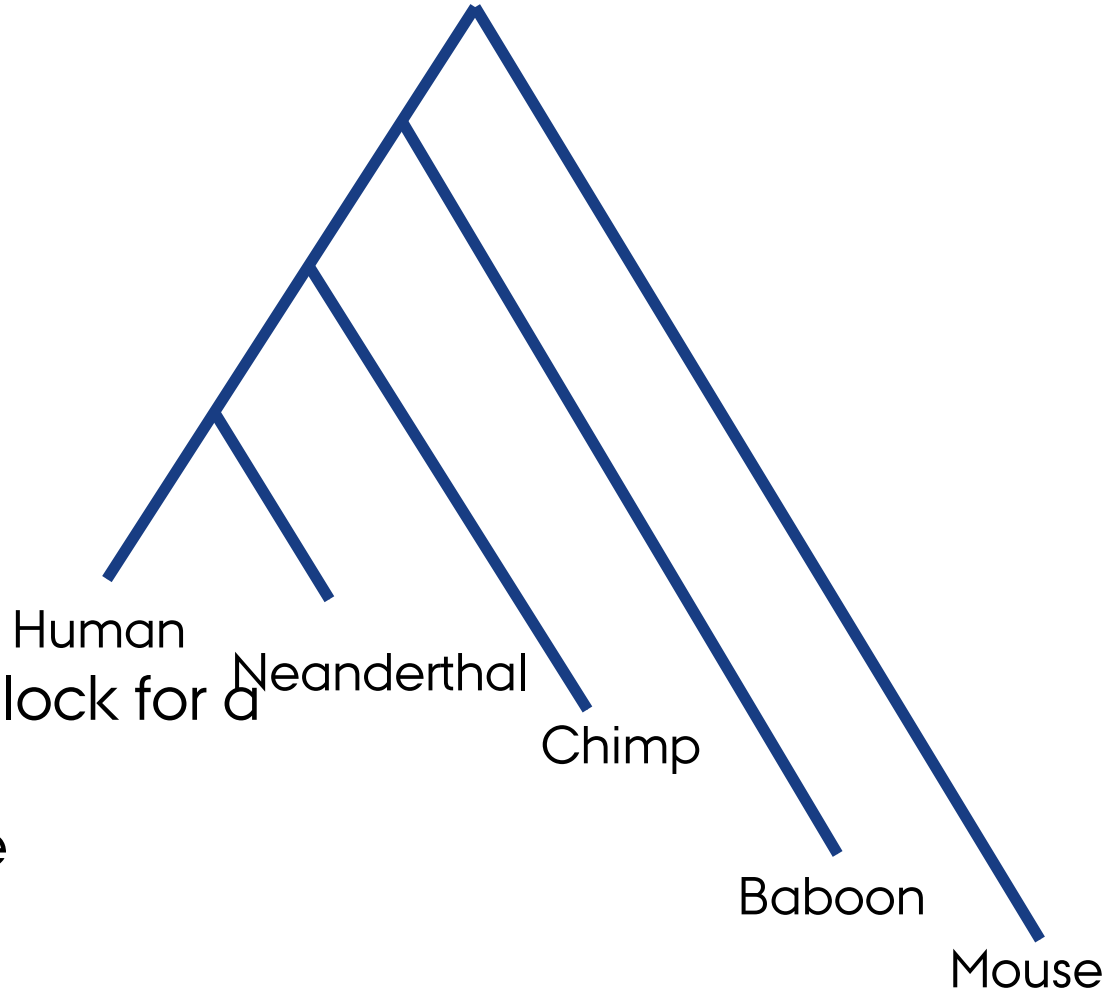
Molecular clock

Violation of the assumption

Rate Heterozygosity

Walk around solutions?

1. Local clocks – whether there is a clock for a particular group of organisms.
2. Looking for regions where the rate heterozygosity is minimized



Overview of the paper

Purpose: Dates the origins of Insects

Data: sequence from 16S, 18S, cytochrome b (cob), cytochrome oxidase I (cox1), and elongation factor 1α (EF-1α)

Overview of the paper

Step by step:

1. Finding which sequence has the relatively more constant substitution rate? (How)

2. Calibrate the molecular clock. (number of substitutions per million years)

3. Relax to the local molecular clock

4. Estimate the time and check the robustness. (How)

Overview of the paper

Step by step:

1. Finding which sequence has the relatively more constant substitution rate? (How)
   using the phylogeny built from cox1
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   Approach to getting different mutation models
4. Estimate the time and check the robustness. (How)
   Fossil records and biogeographical landmarks

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