



GENETIC DRIFT: Rate of neutral molecular evolution



Are long-term effects of mutations + genetic drift predictable?

- New mutations arise at some rate
- Mutations in some parts of genome have no effect on fitness
 - Might spread or be lost by drift
 - Can we predict the *rate* at which they arise and spread to fixation?
 - Ancient population sizes unknown





Break this up into pieces...

- Mutations arise— rate “ μ ”
 - Can be “mutations per year” or “per generation”
 - Example: $\mu = 1 \times 10^{-9}$ mutations per year per basepair studied
- In bigger populations, more likely to get a mutation (just because more alleles present)
 - Rate $2N\mu$ of *getting* new mutations



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- In bigger populations, more likely to get a mutation (just because more alleles present)
 - Rate $2N\mu$ of *getting* new mutations
- Mutation must then also fix by drift
 - Probability of fixation of new mutation in diploids?

Rate of neutral molecular evolution

Probability of new mutation arising \times

Probability of new mutation fixing

$$= 2N\mu \times 1/(2N) =$$

Rate of neutral molecular evolution

Probability of new mutation arising \times
Probability of new mutation fixing

$$= 2N\mu \times 1/(2N) = \mu$$



- Large populations have more chance mutation will arise, BUT smaller chance it will fix.
- Rate of neutral molecular evolution does not depend on population size!

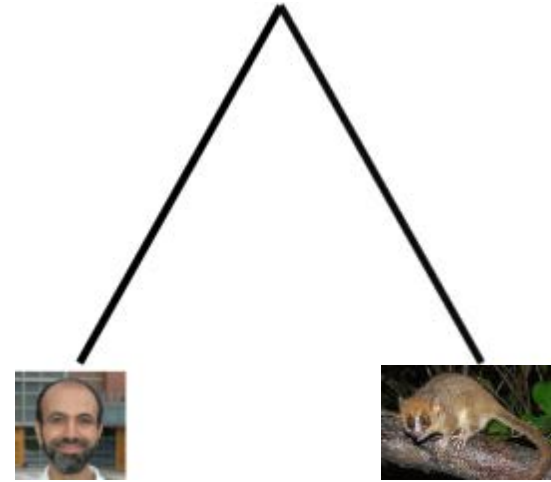
Application of this calculation

- Mutation rate for human pseudogenes is roughly 1×10^{-9} mutations/ year/ bp
- Want to know divergence time between humans and mouse lemurs
- Sequence a pseudogene and see 150 base differences in 1000bp between human and mouse lemur



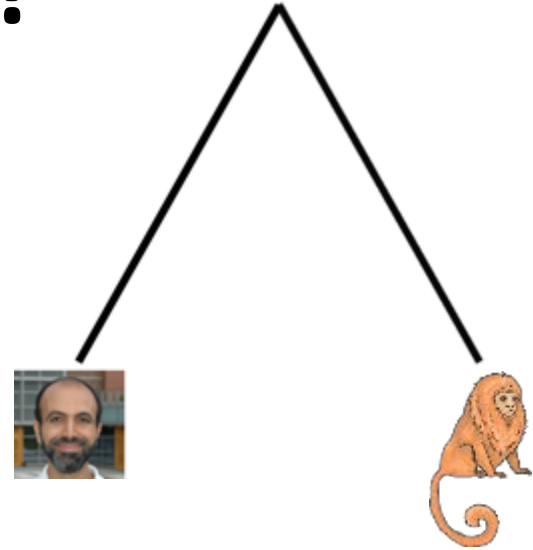
Time to ancestor: human - mouse lemur?

- 1×10^{-9} mutations/ bp/ year
 1×10^{-6} mutations in 1000bp/ year
so, 10^6 years/ 1 mutation in 1000bp
- see 150 mutations:
 $150 \text{ mutations} \times 10^6 \text{ years/mutation} =$
 1.5×10^8 years *total* divergence
- BUT, *two* branches 7.5×10^7 years
to ancestor (75 million years)



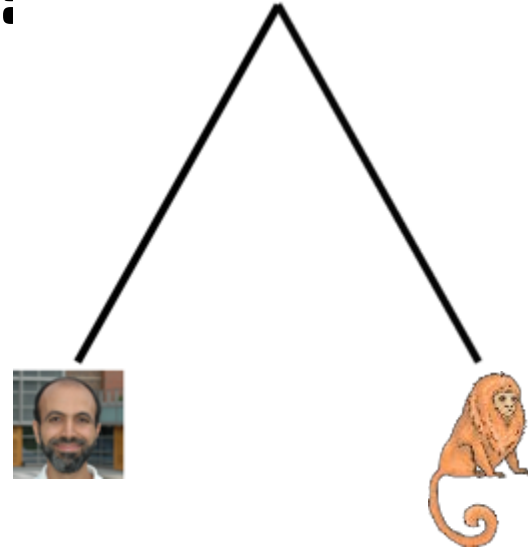
Time to ancestor: human - tamarin?

- 1×10^{-9} mutations/ bp/ year
- Screened 10,000bp of sequence
- Found 860 mutations



Time to ancestor: human - tamarin?

- 1×10^{-9} mutations/ bp/ year
- Screened 10,000bp of sequence
- Found 860 mutations
 1×10^{-5} mutations in 10,000bp/ year
so, 10^5 years/ 1 mutation in 10,000bp
- 860 mutations $\times 10^5$ years/1 mutation =
 8.6×10^7 years *total* divergence
- BUT, *two* branches, so
 4.3×10^7 years to ancestor (43 million years)



**Want to look up some molecular
estimates of divergence times
between species?**

<http://www.timetree.org>

Also have free iPhone app



Nucleotide variation within species and between species

Species 1, indiv 1: AACAGCTGACGTTGTTTAA

Species 1, indiv 2: AACAGCTGACATTGTTTAA

Species 1, indiv 3: AACAGCTGACATTGTTTAA

Species 1, indiv 4: AACAGCTGACGTTGTTTAA

Species 2, indiv 1: AAGAGCTGACGTTGTTTAA

Species 2, indiv 2: AAGAGCTGACGTTGTTTAA

Species 2, indiv 3: AAGAGCTGACGTTGTTTAA

Species 2, indiv 4: AAGAGCTGACGTTGTTTAG

1

2

3

Big question...



- Some mutations are advantageous
 - Many mutations are bad
 - How much of the genome *actually* evolves solely via mutation and genetic drift (ie, “neutrally”)???
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- **Neutralists** – most nucleotide variation within and between species is neutral
 - **Selectionists** – very little nucleotide variation is neutral

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