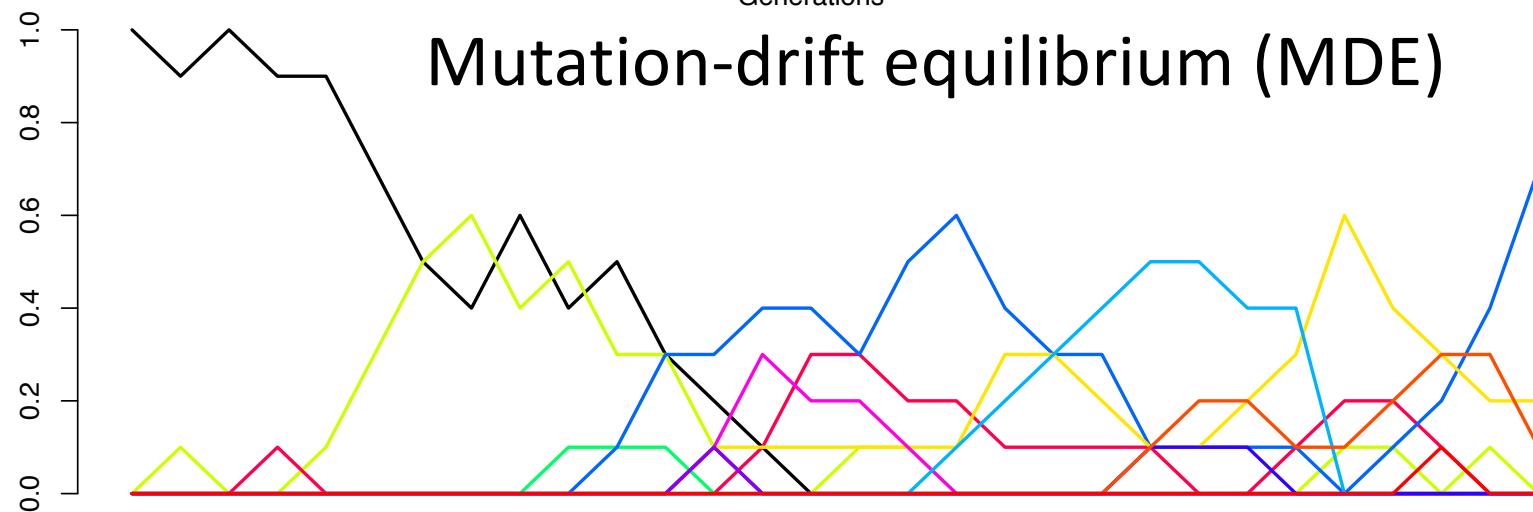
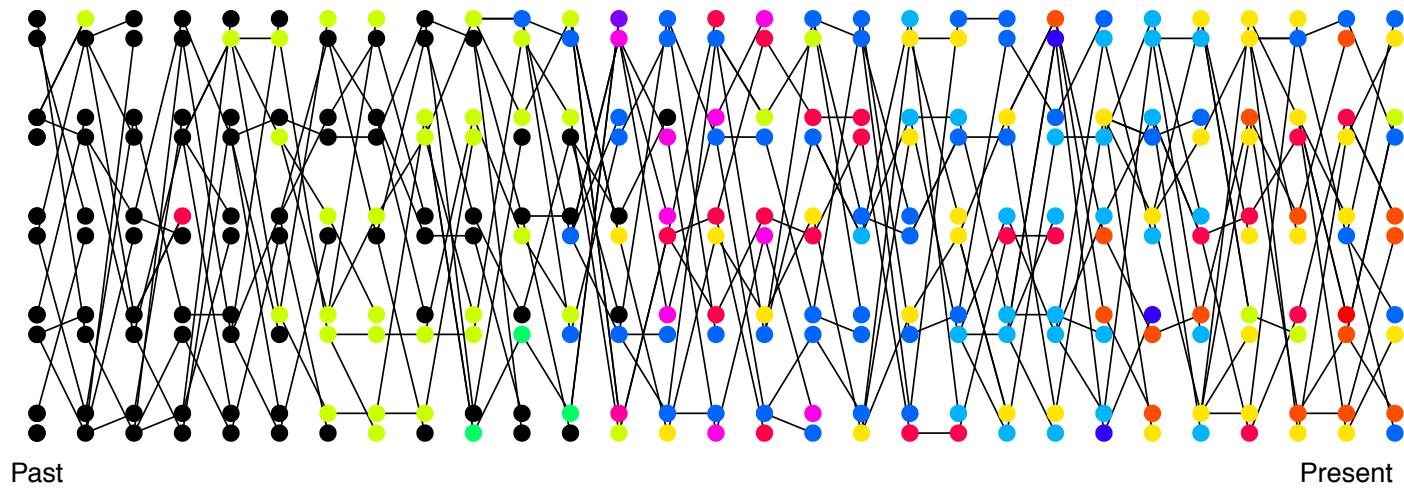


Lecture 9



Mutation-drift equilibrium (MDE)

Mutation-drift equilibrium (MDE)

- Variation lost by drift = variation introduced by mutation
- N_e = effective population size,
 μ = mutation rate to new neutral alleles

At MDE, heterozygosity = $H \approx 4 N_e \mu$

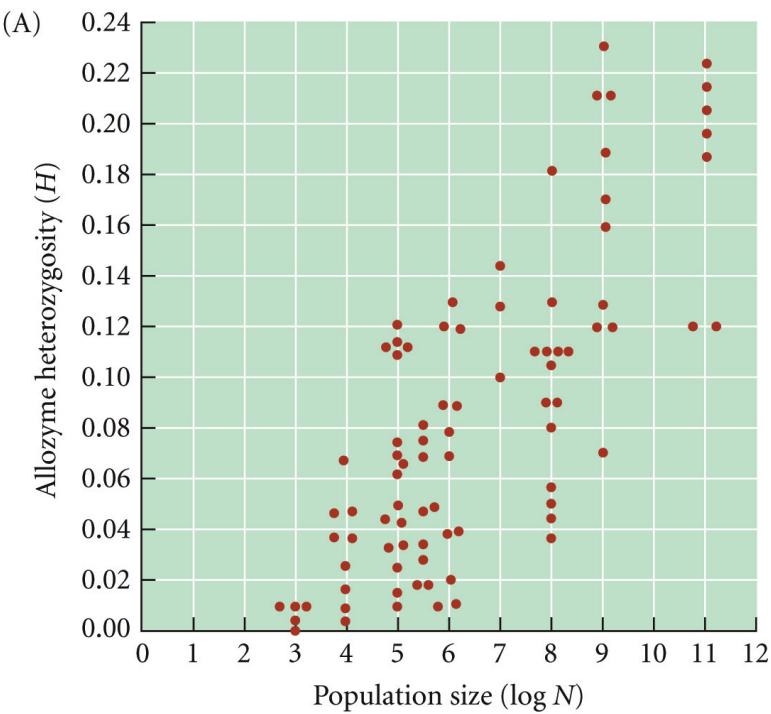
The rate of genetic drift is slower in larger populations and the input of new mutations is higher. Large populations have a higher level of neutral polymorphism

Neutral theory of molecular evolution

- Kimura 1968; King and Jukes 1969
- Claim: Most of the observed molecular polymorphism is neutral

Consistent with Neutral theory

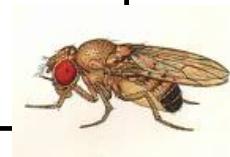
Levels of genetic variability within Populations (i.e. heterozygosity) are high and are broadly correlated with population size



EVOLUTION 2e, Figure 10.9 (Part 1)

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We can estimate effective population sizes
 $H=4N_e\mu$:

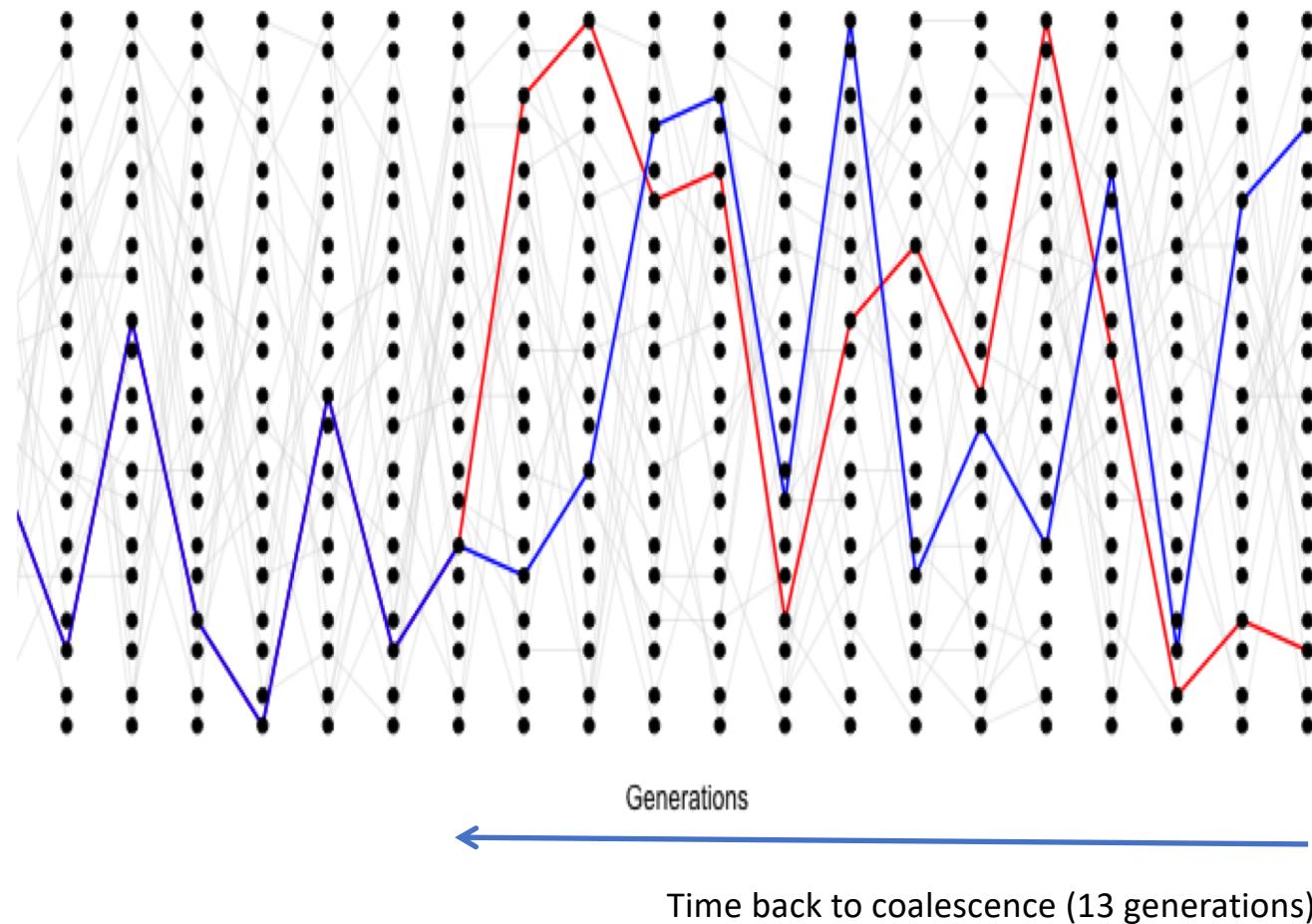
	H	μ (per gen)	N	
Human	0.1%	2×10^{-8}	10^4	
Chimpanzee	0.3%	2×10^{-8}	3×10^4	
<i>Drosophila melanogaster</i>	2%	5×10^{-9}	10^6	

Human census population~ 7×10^9 ; Chimp~ 2×10^5

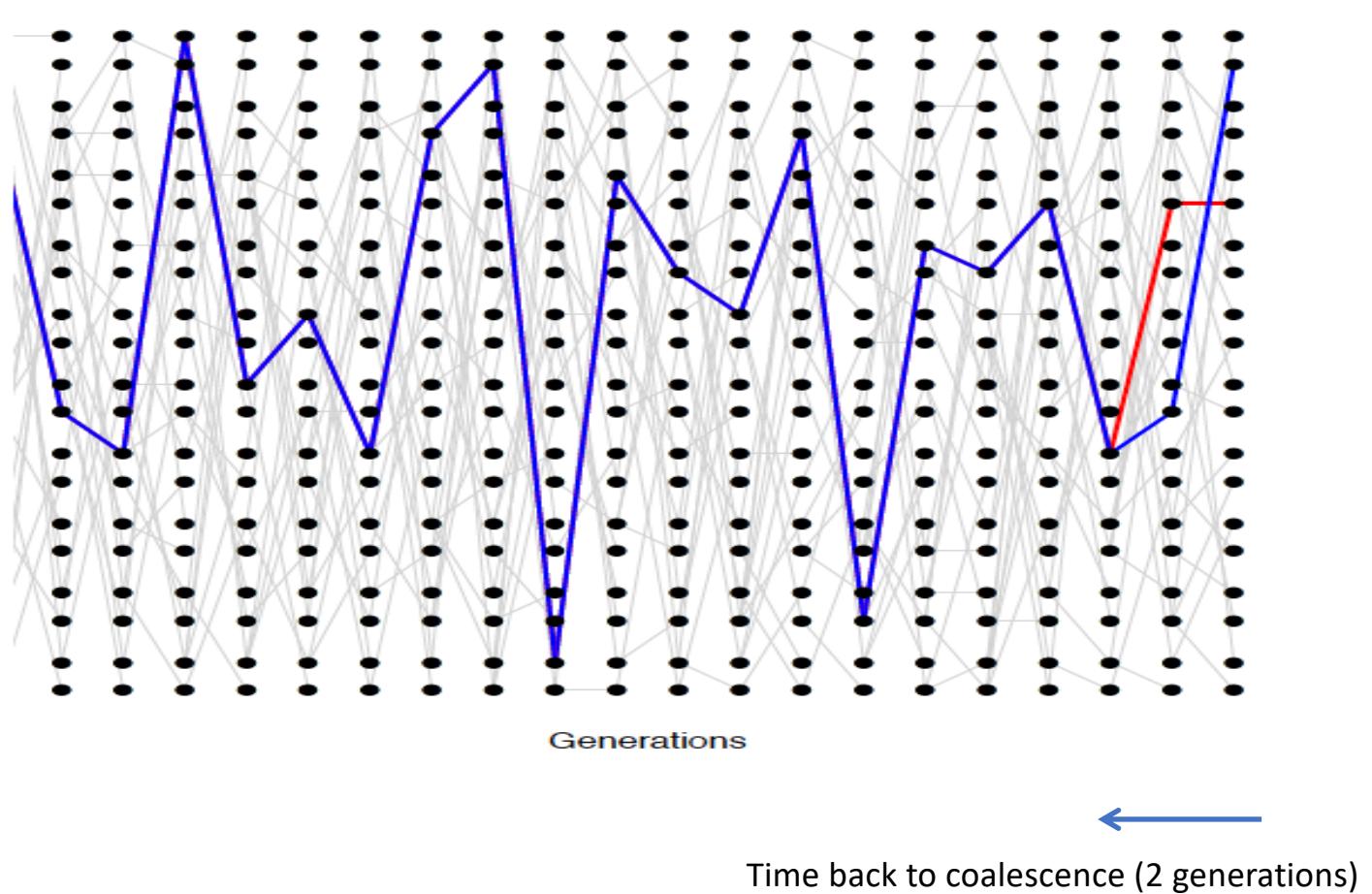
Do these low effective population sizes reflect repeated bottlenecks

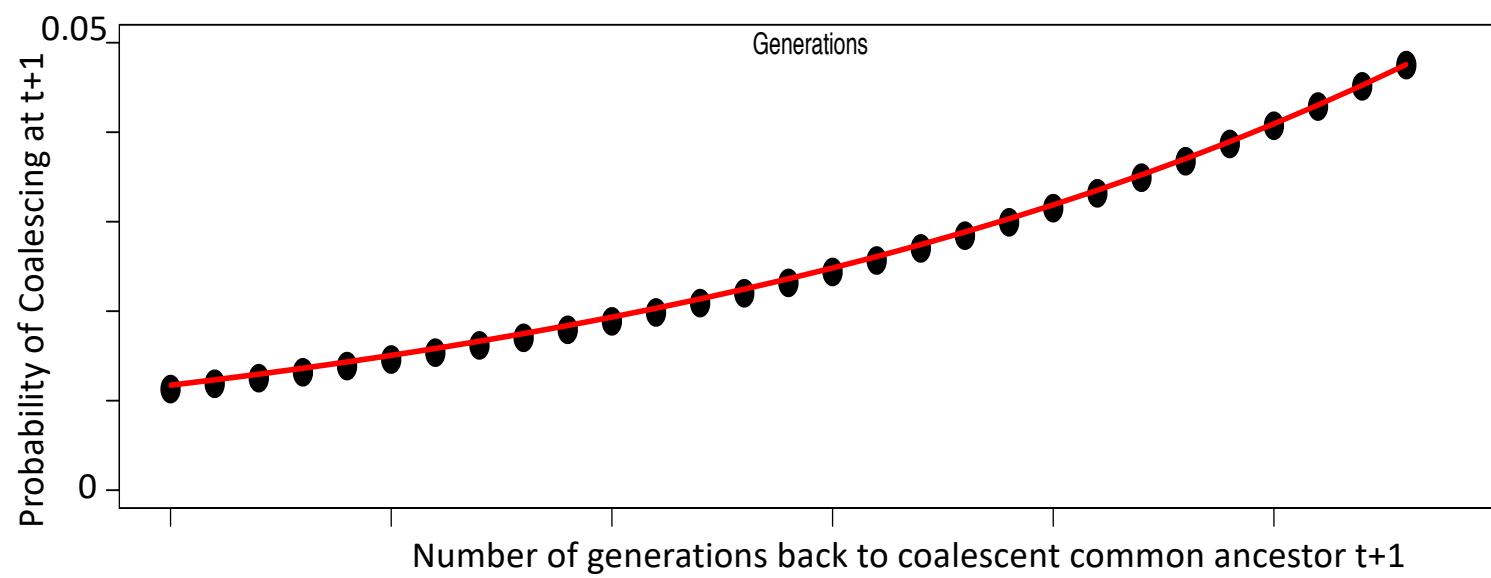
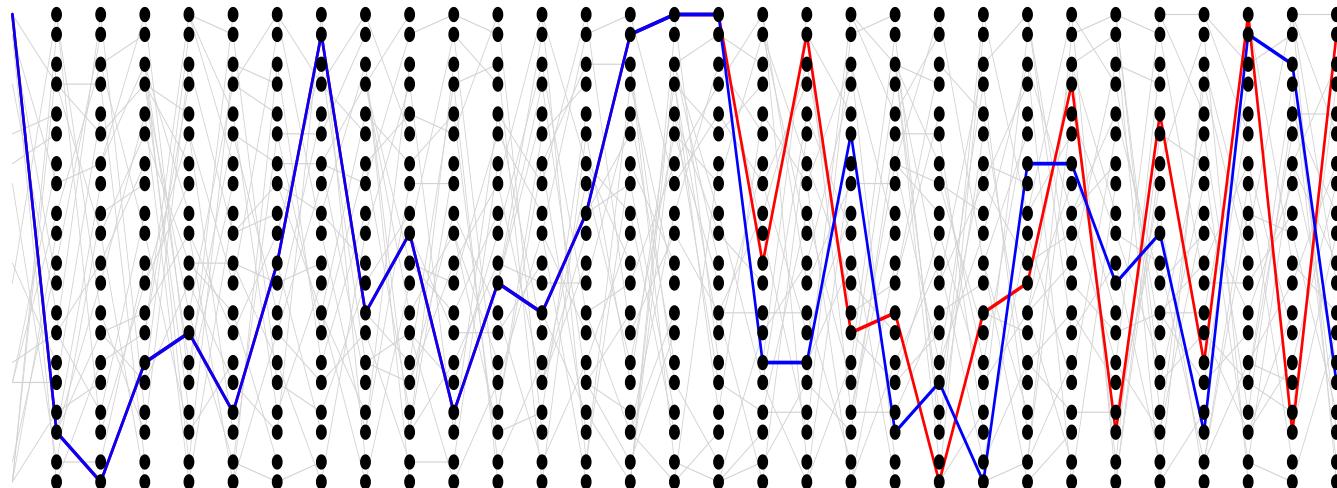
Or is neutral theory only partially correct?

Coalescent process w. 2 lineages



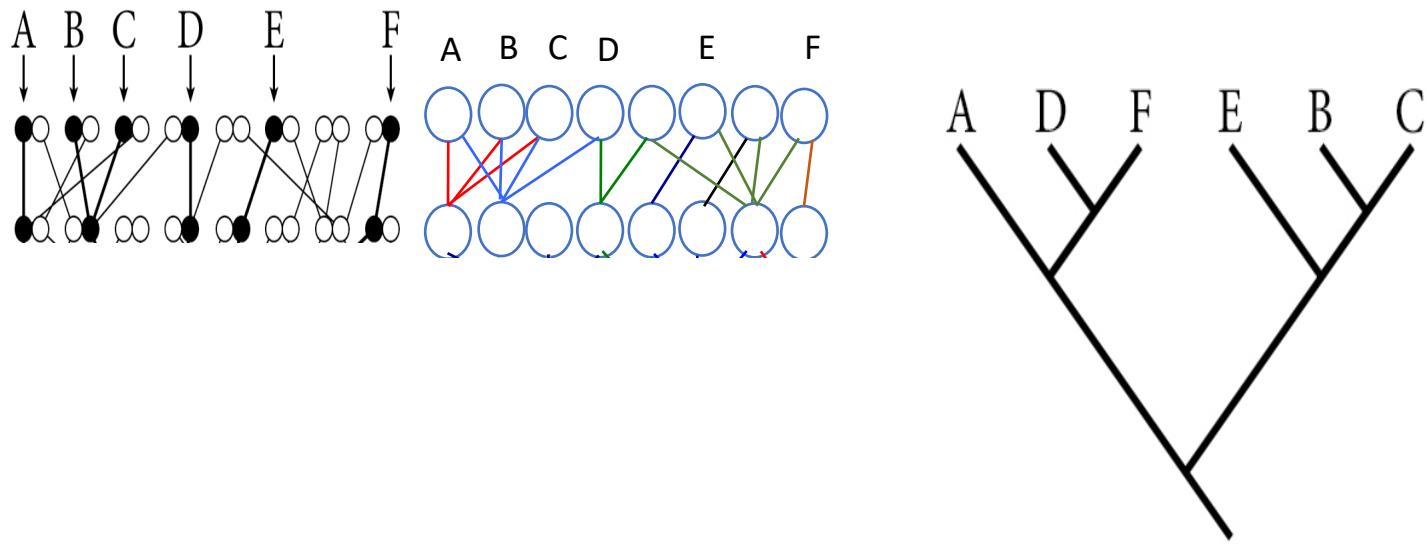
Coalescent process w. 2 lineages



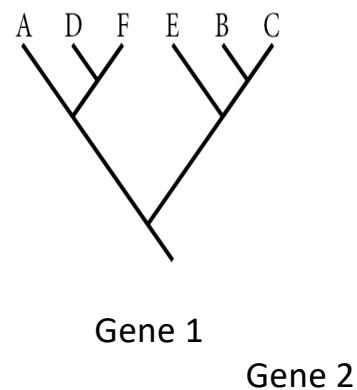
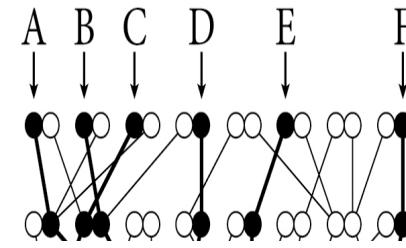
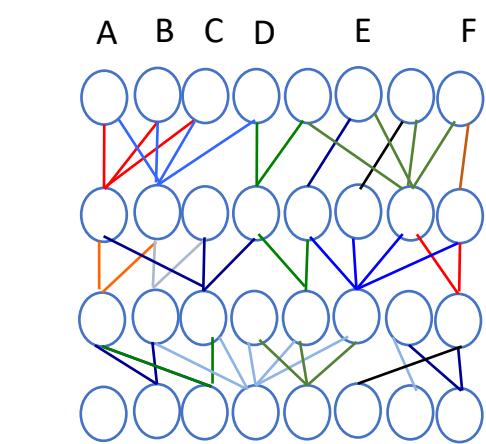
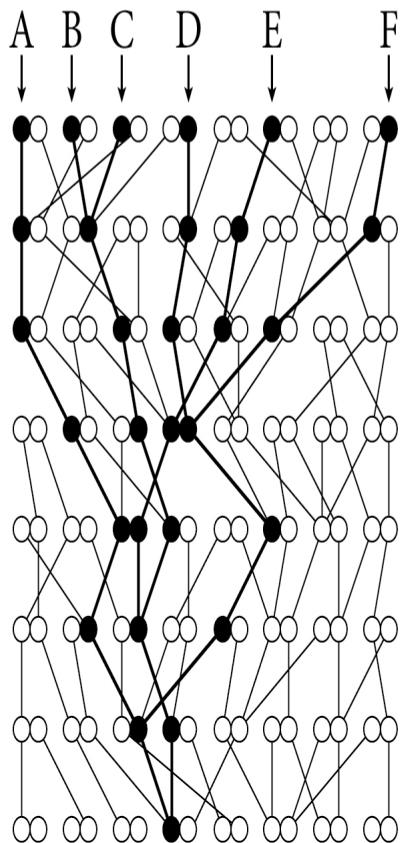


Pairwise diversity

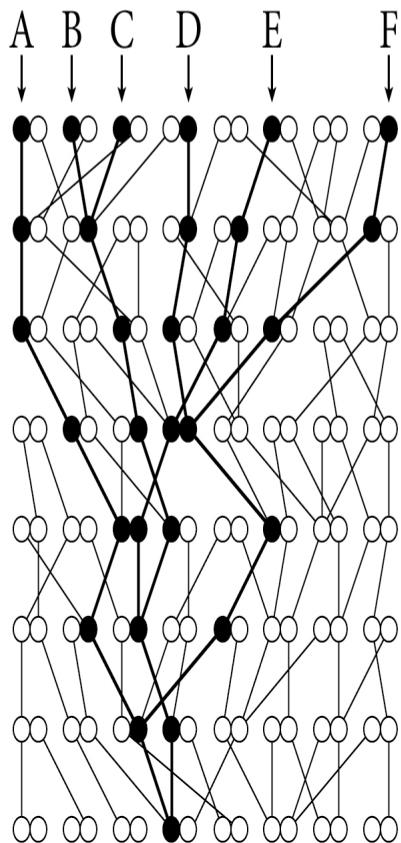
A sexual population over time
is a giant pedigree



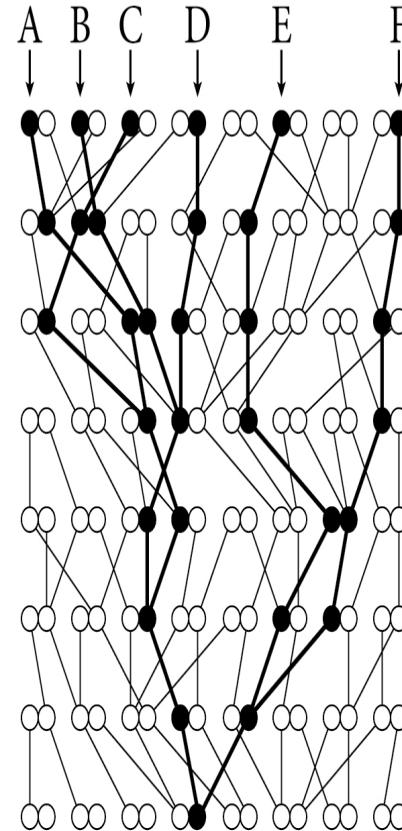
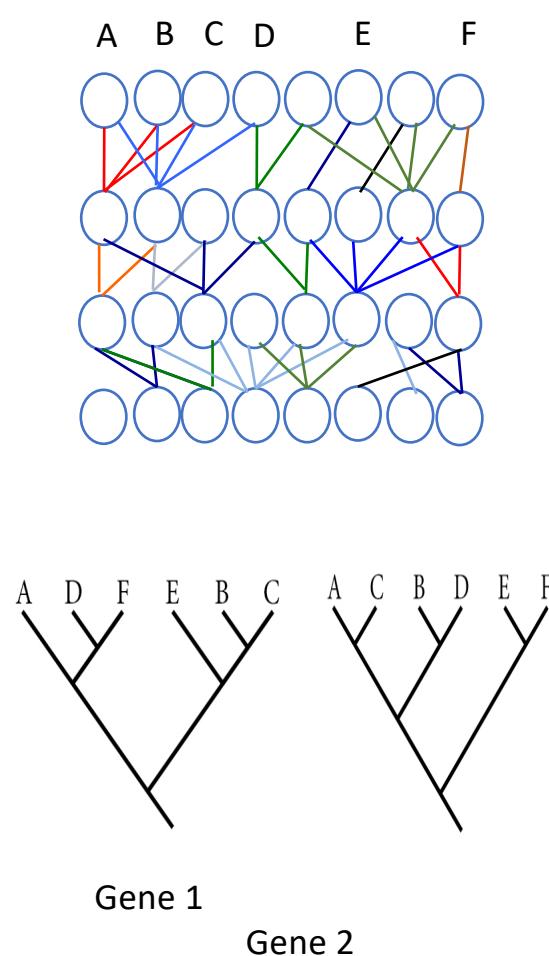
A sexual population over time
is a giant pedigree. Gene trees of alleles from within a
population will differ across loci.



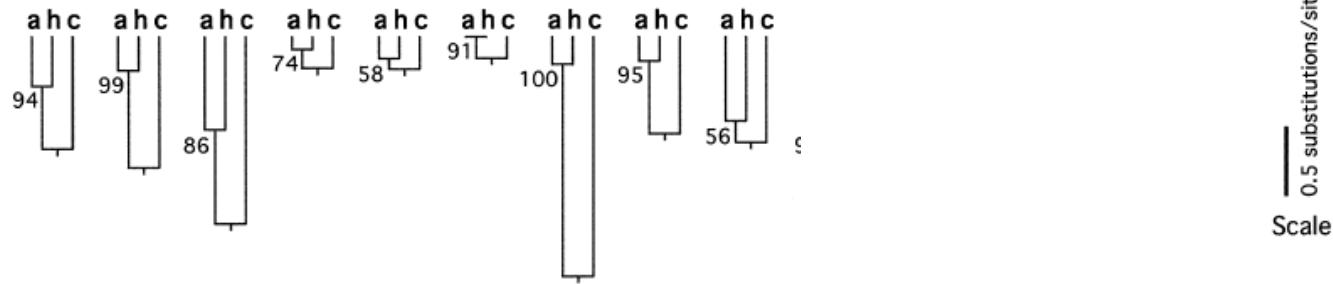
A sexual population over time
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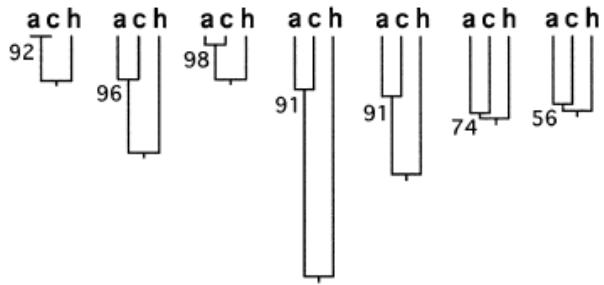
Transmission of alleles
At gene 1



Transmission of alleles
At gene 2

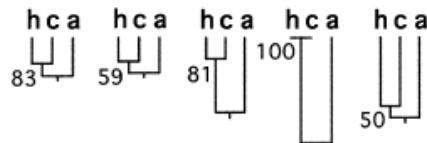


B Pa-17 Pa-18 Pa-19 Pa-20 Pa-21 Pa-22 Pa-23

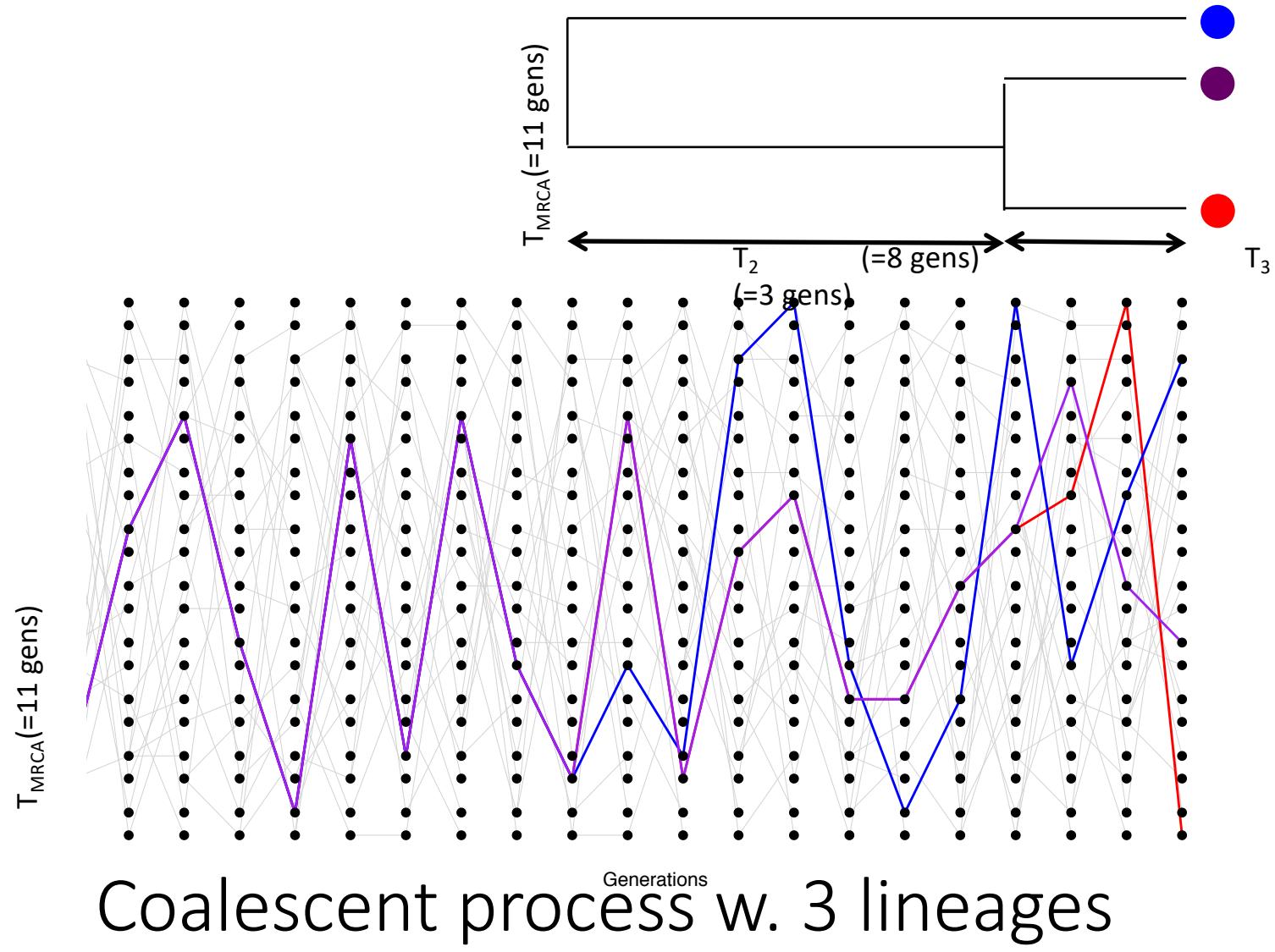


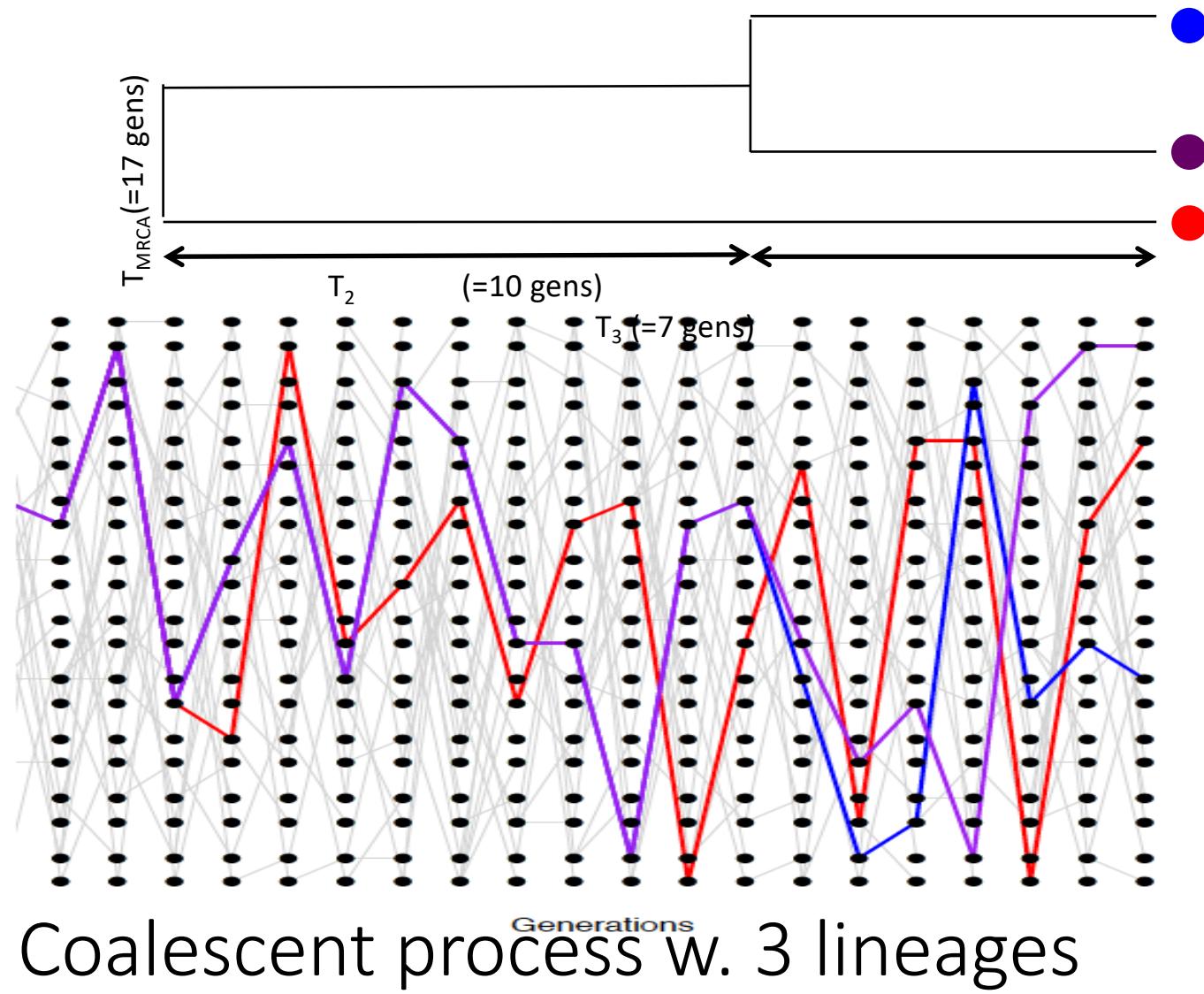
C

Pa-24 Pa-25 Pa-26 Pa-27 Pa-28

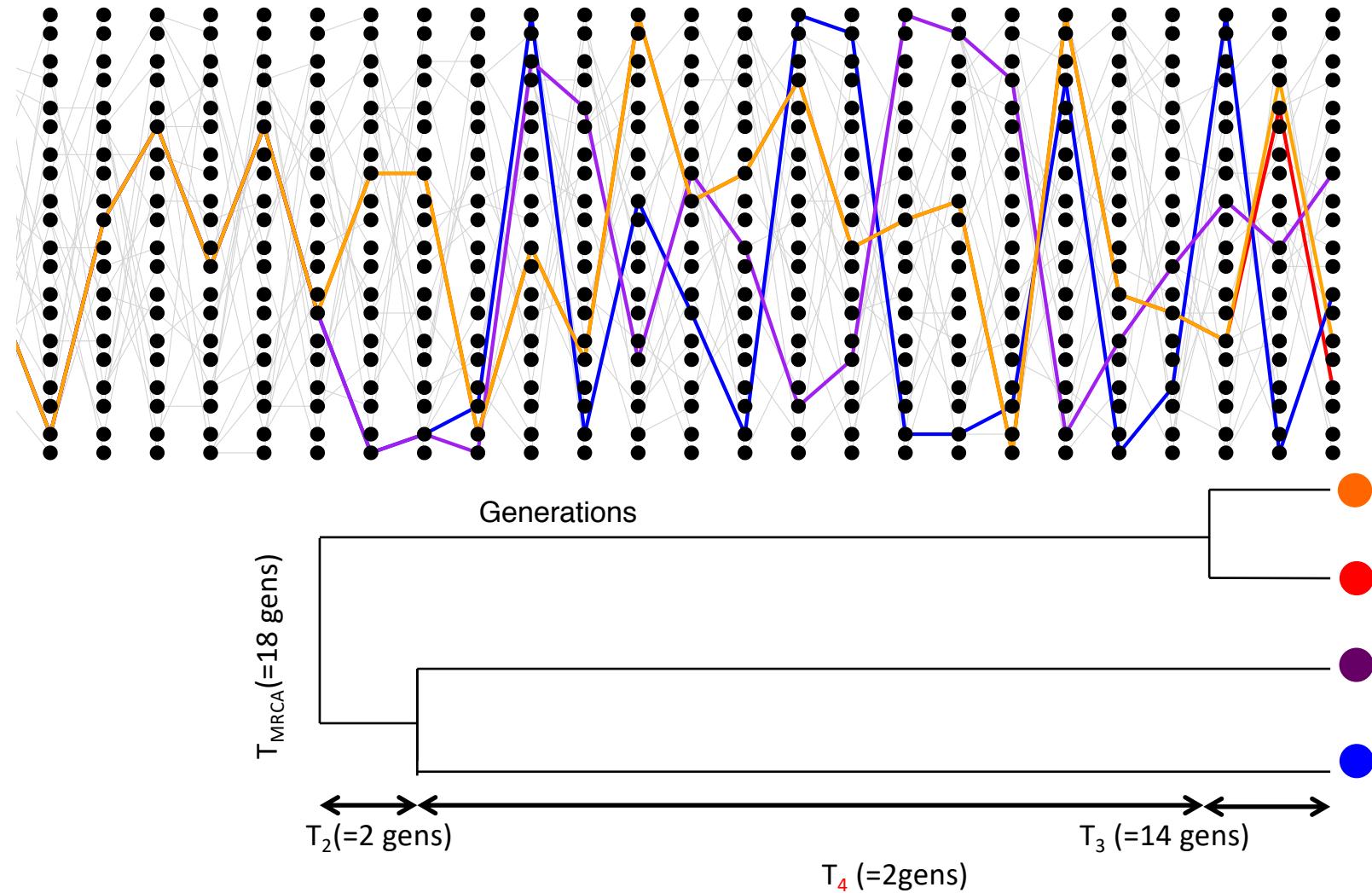


28 gene trees for 3
AUSTRALIAN
GRASS FINCHES (POEPHILA)
JENNINGS & EDWARDS 2005

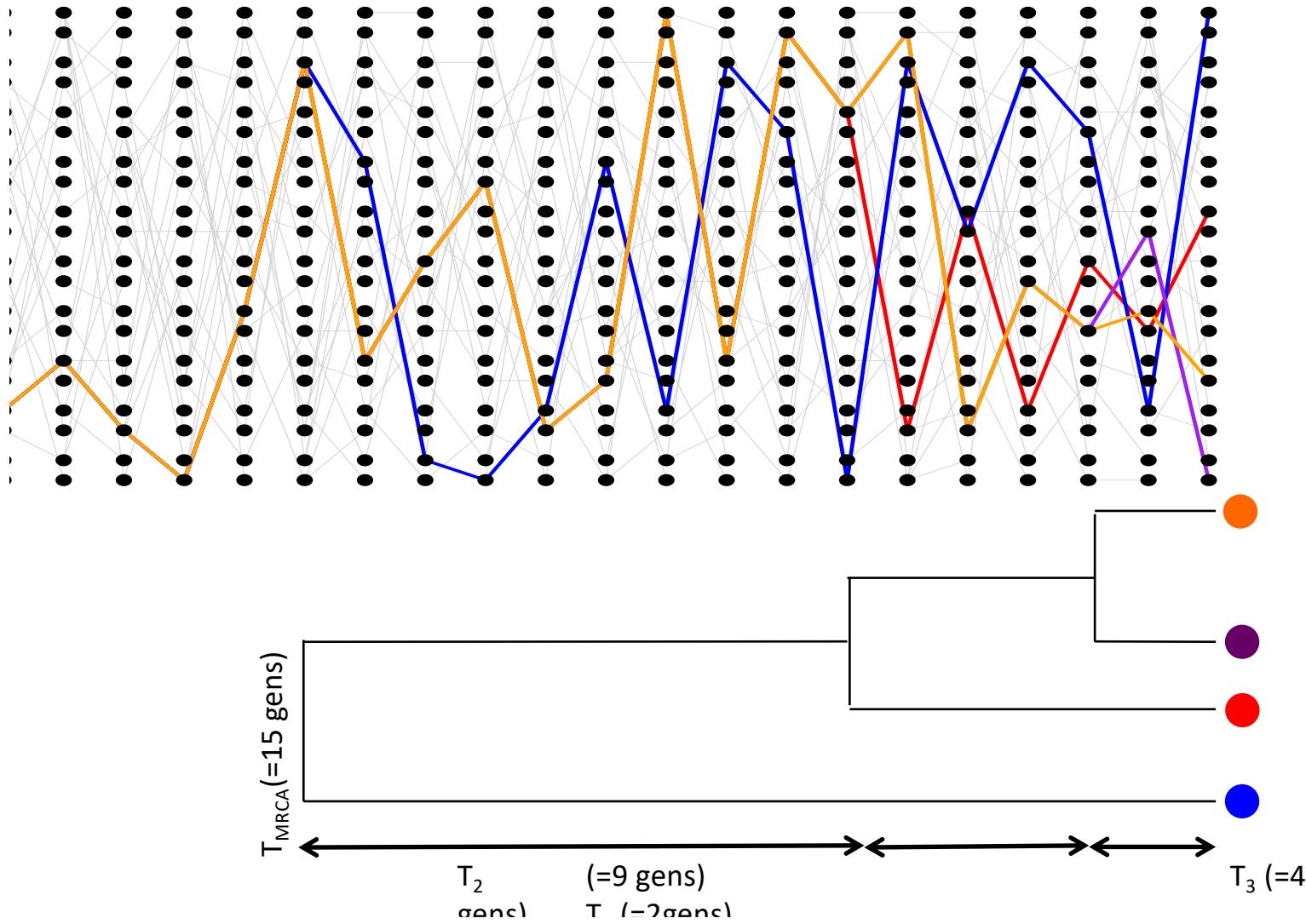




The coalescent for sample sizes greater than two



The coalescent for sample sizes greater than two



The coalescent for sample sizes greater than two

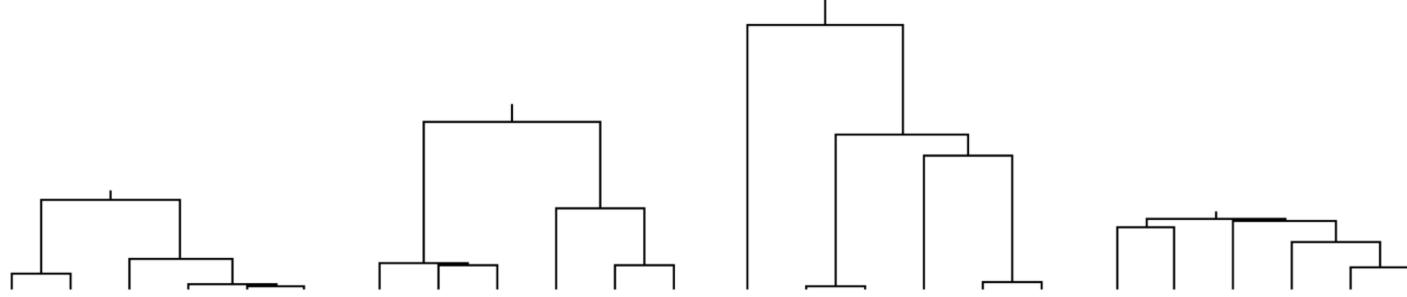


Figure 4: Four realizations of the coalescent for $n = 6$, drawn on the same scale (the labels 1–6 should be assigned randomly to the tips).

There is little information about
underlying processes in a single genealogy

From Nordborg 2000

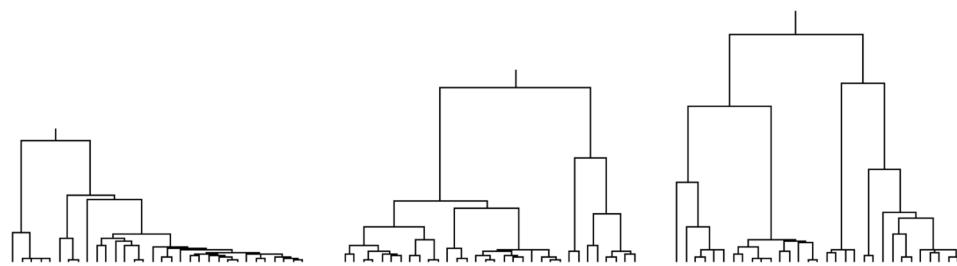


Figure 5: Three realizations of the coalescent for $n = 32$, drawn on the same scale (the labels 1–32 should be assigned randomly to the tips). From Nordborg review

→ You don't increase the information about the tree much from increasing your
sample size

The coalescent for sample sizes greater than two

