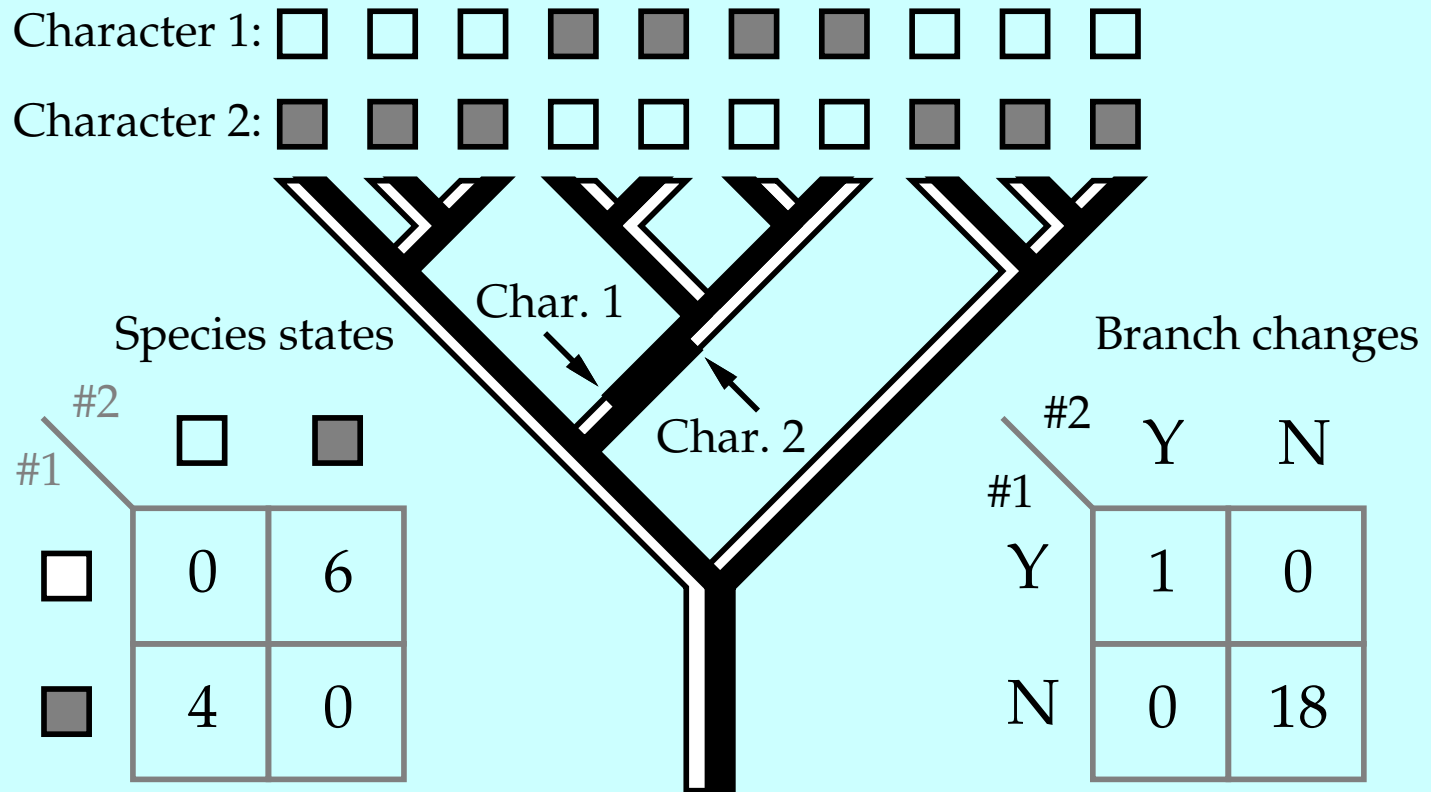


Comparative method, coalescents, and the future

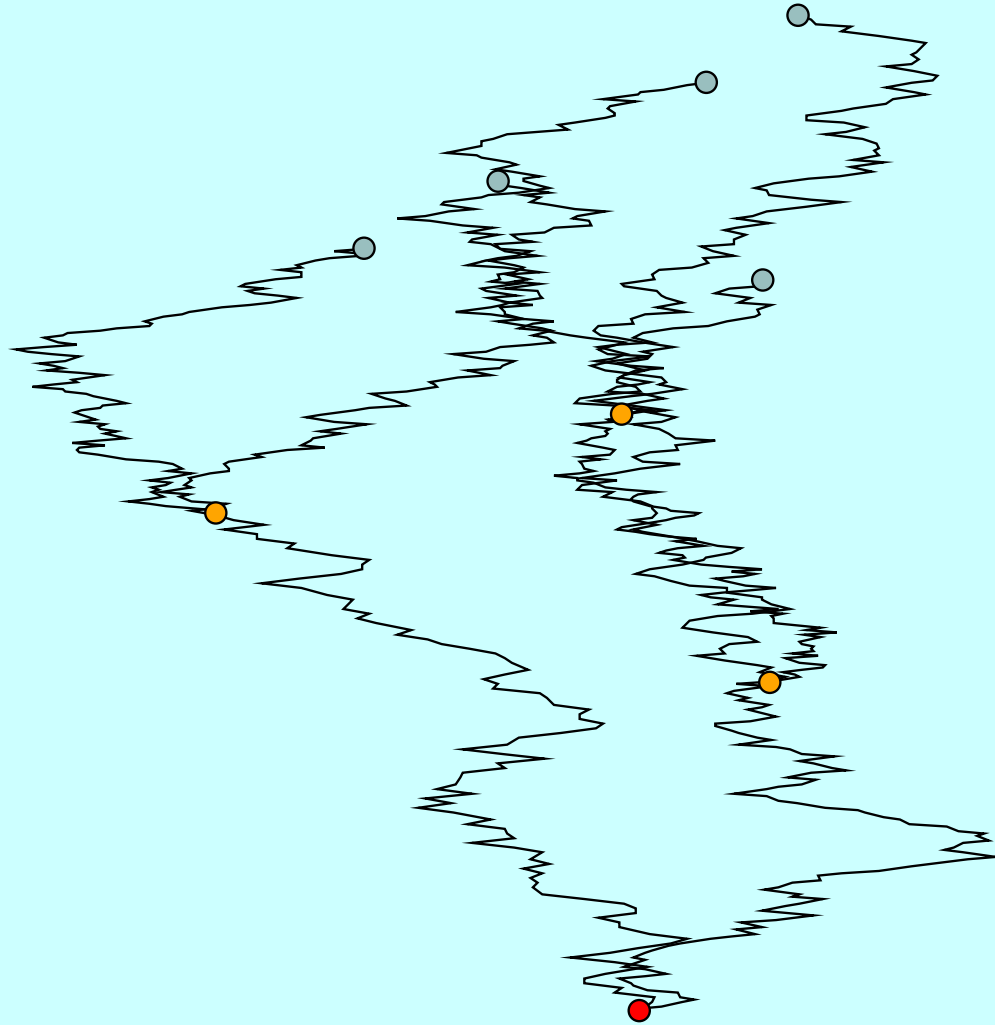
Joe Felsenstein

Depts. of Genome Sciences and of Biology, University of Washington

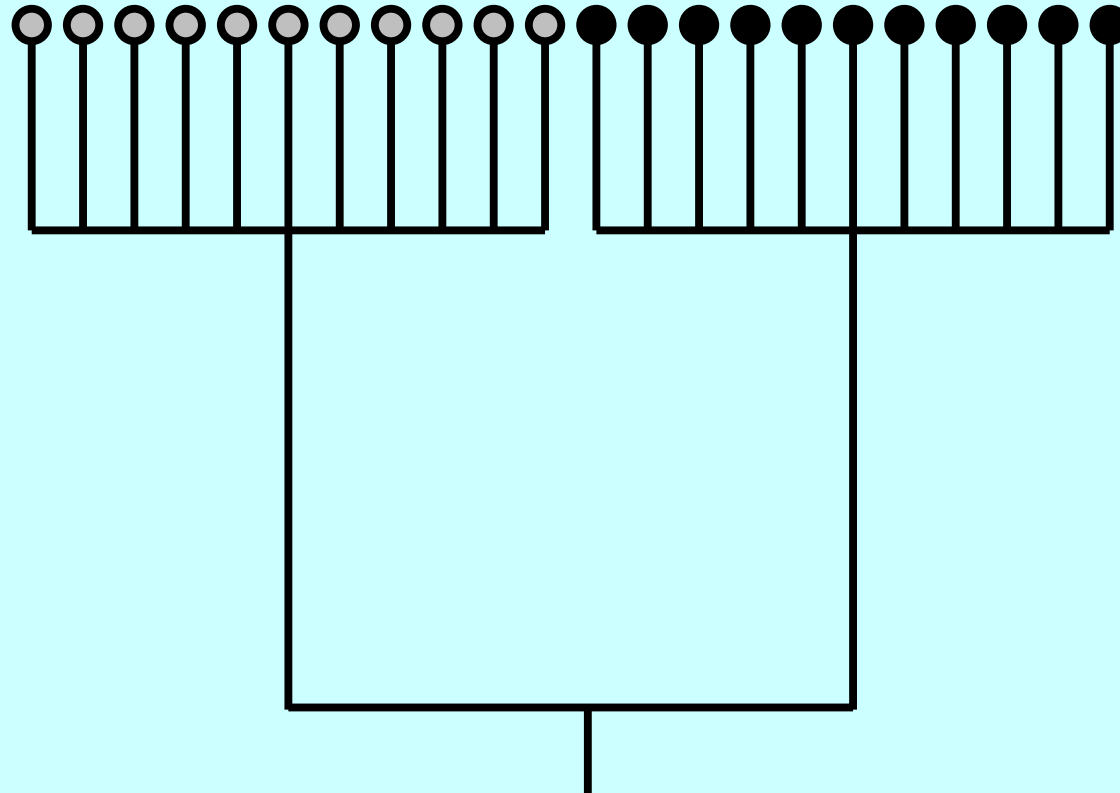
Correlation of states in a discrete-state model



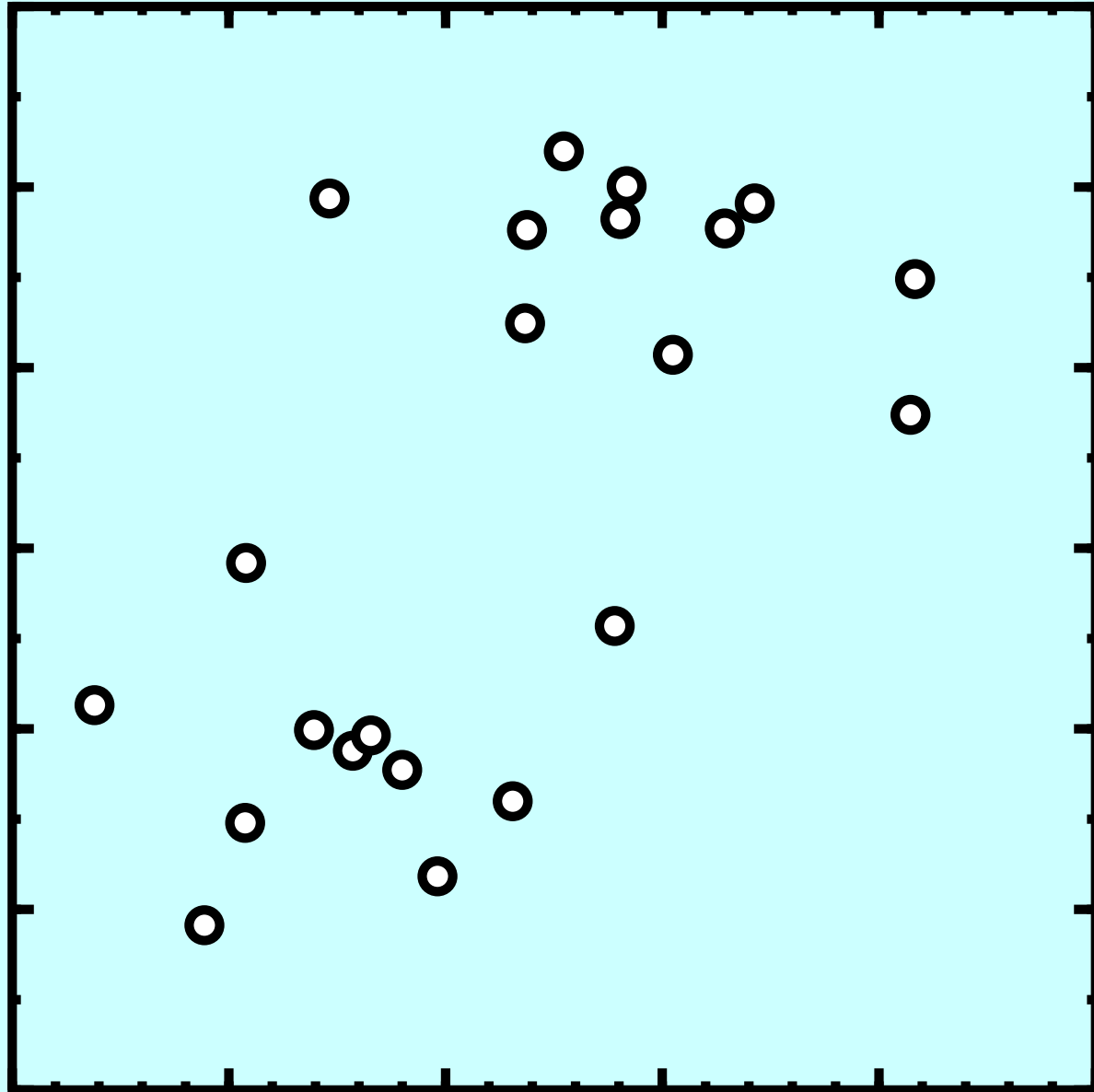
A simple model: Brownian motion



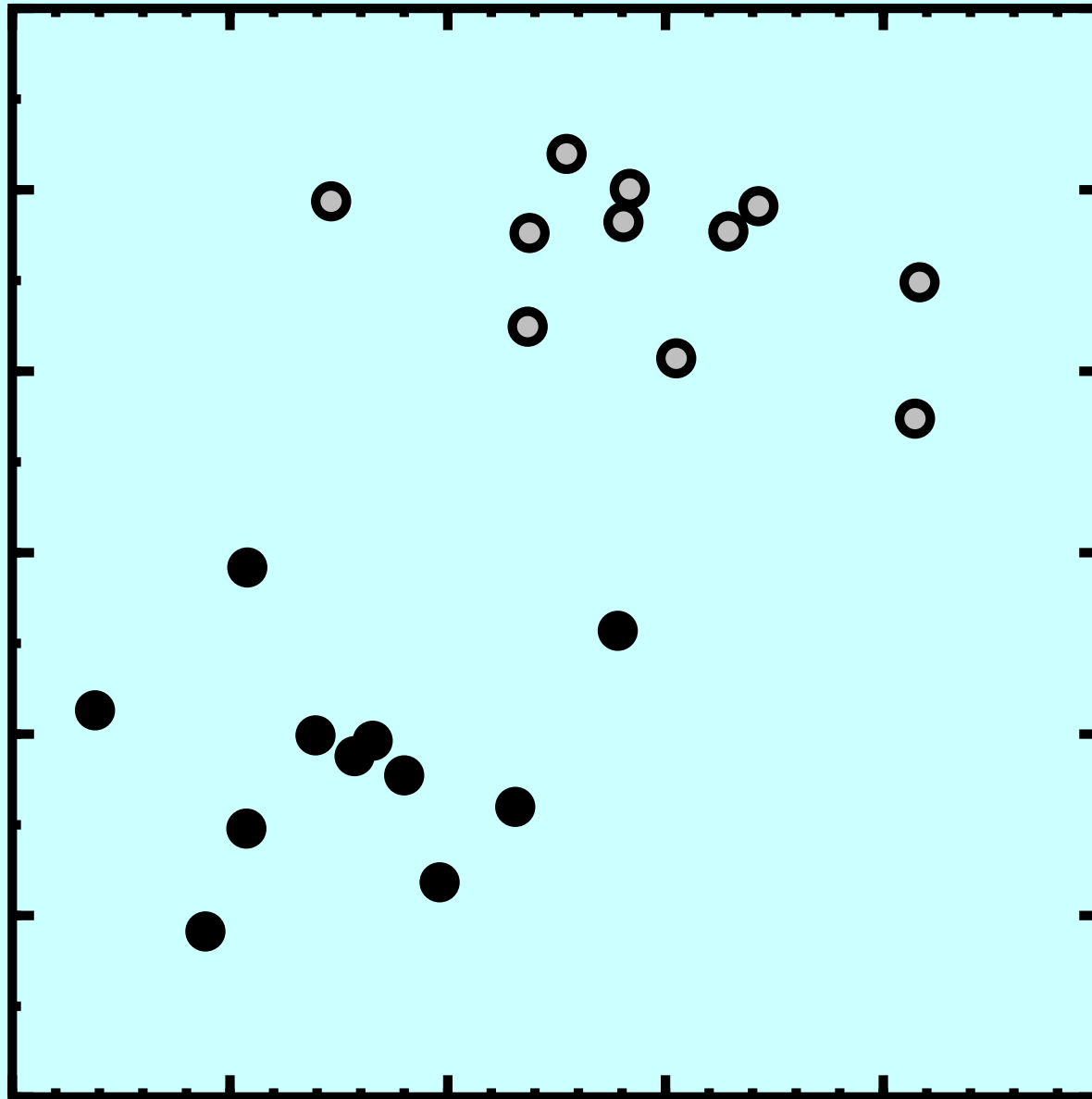
A simple case to show effects of phylogeny



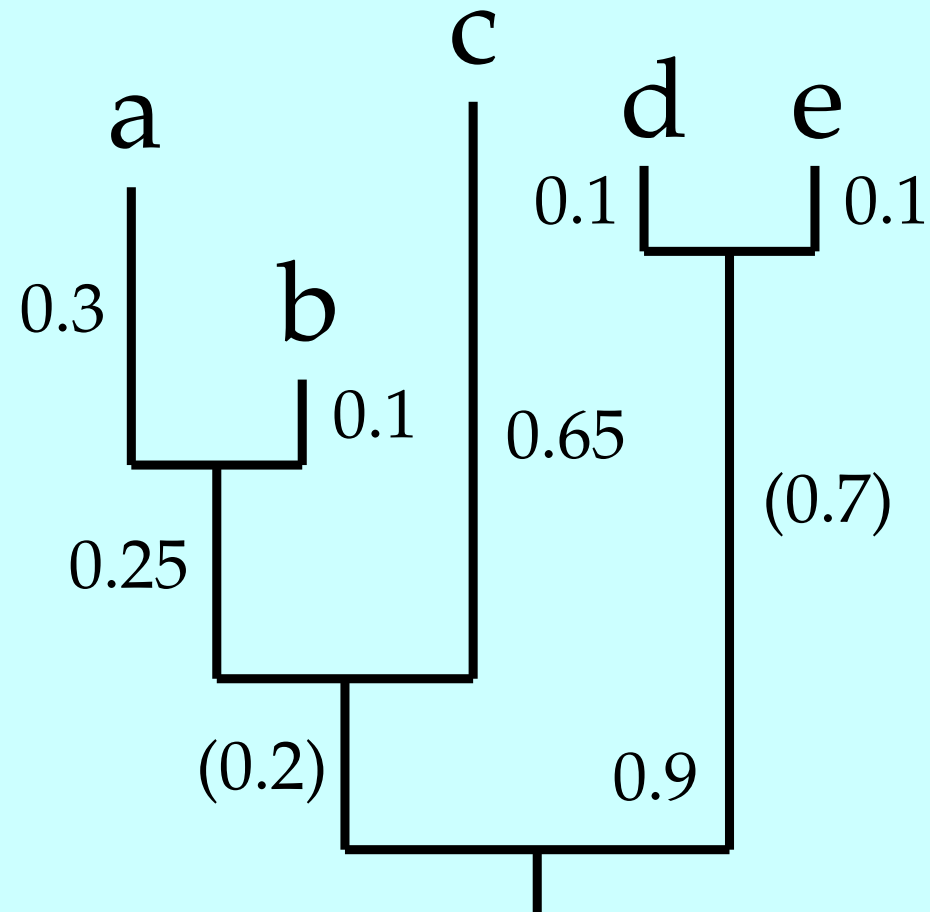
Two uncorrelated characters evolving on that tree



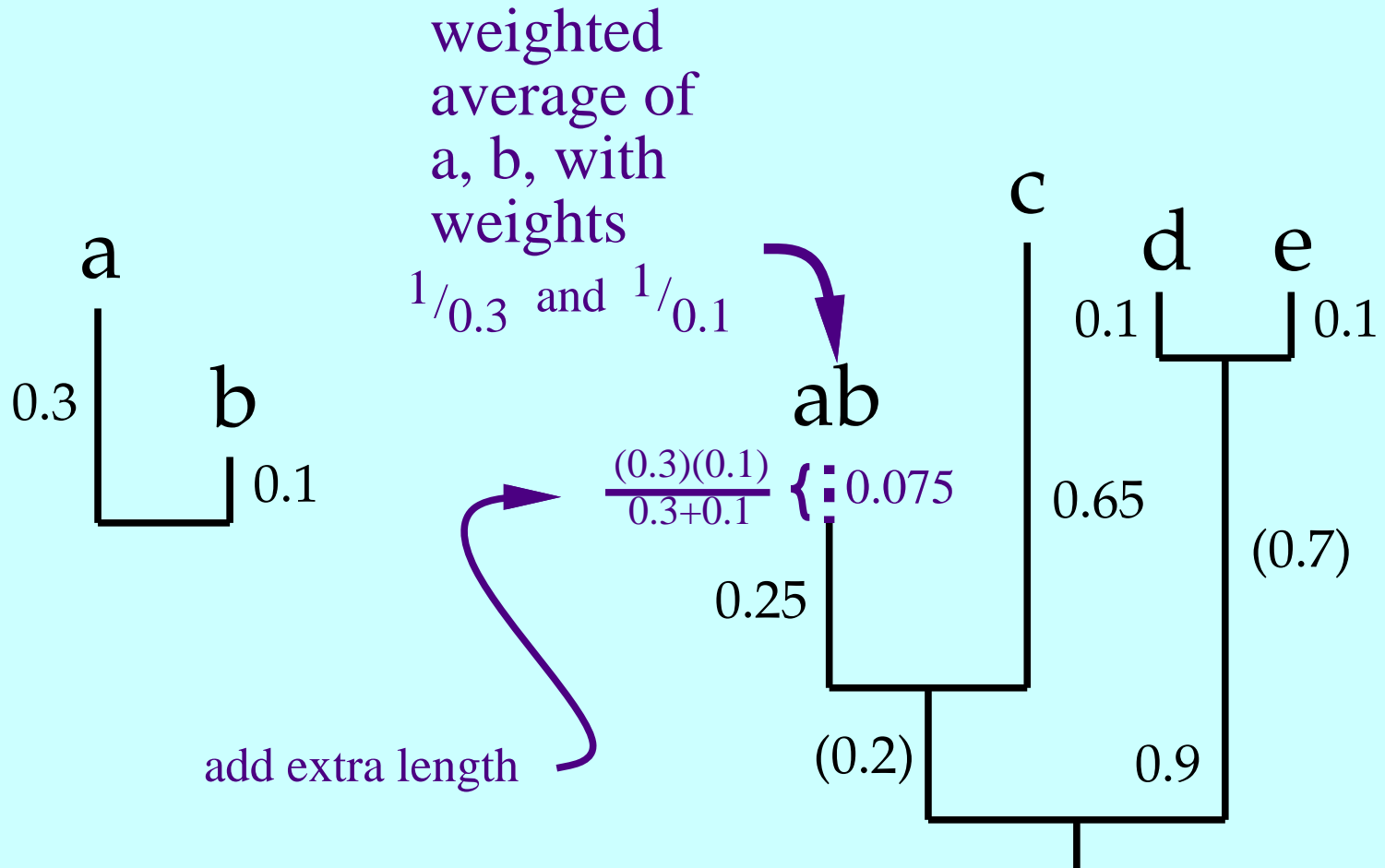
Identifying the two clades



A tree on which we are to observe two characters



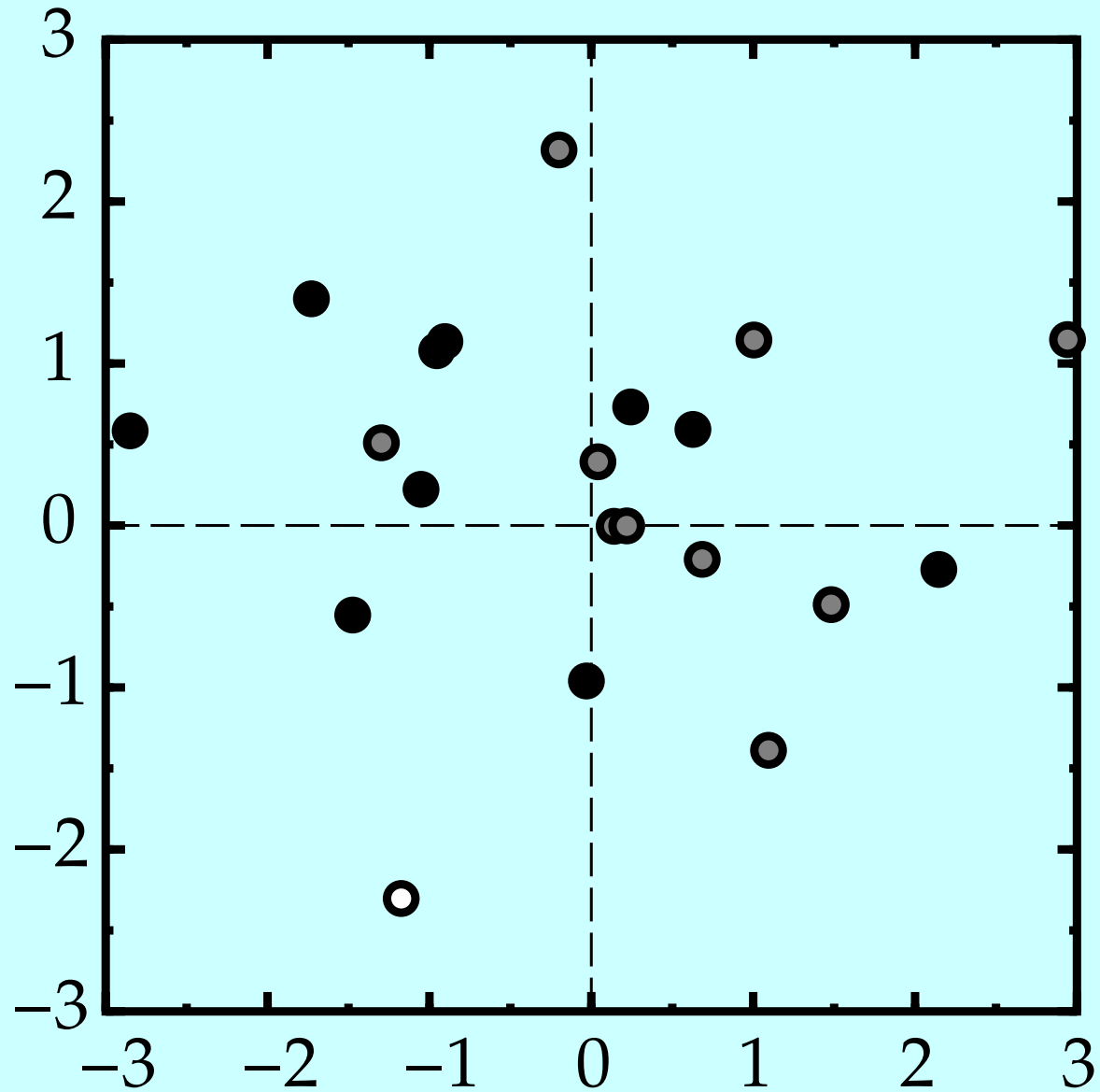
This turns out to be statistically equivalent to ...



Contrasts on that tree

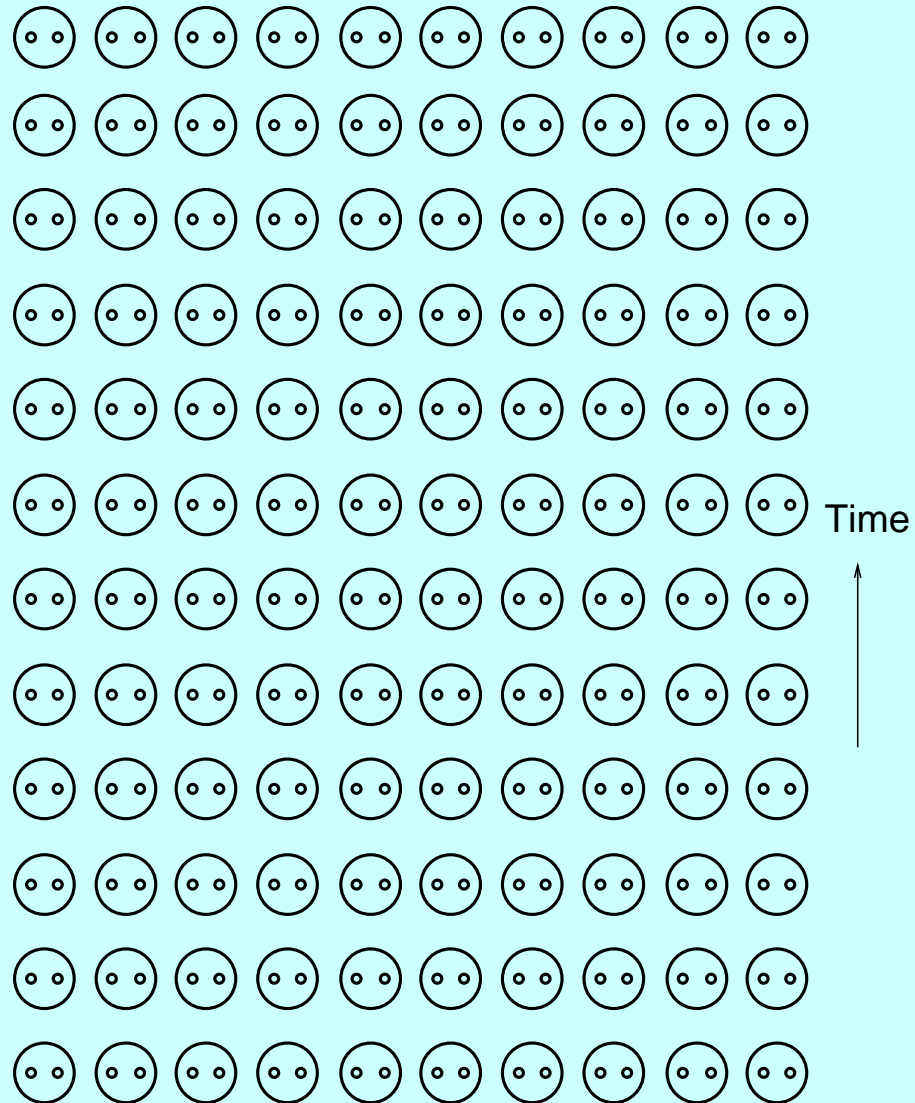
	Contrast	Variance proportional to
y_1	$= x_a - x_b$	0.4
y_2	$= \frac{1}{4} x_a + \frac{3}{4} x_b - x_c$	0.975
y_3	$= x_d - x_e$	0.2
y_4	$= \frac{1}{6} x_a + \frac{1}{2} x_b + \frac{1}{3} x_c - \frac{1}{2} x_d - \frac{1}{2} x_e$	1.11666

Plot standardized contrasts against each other



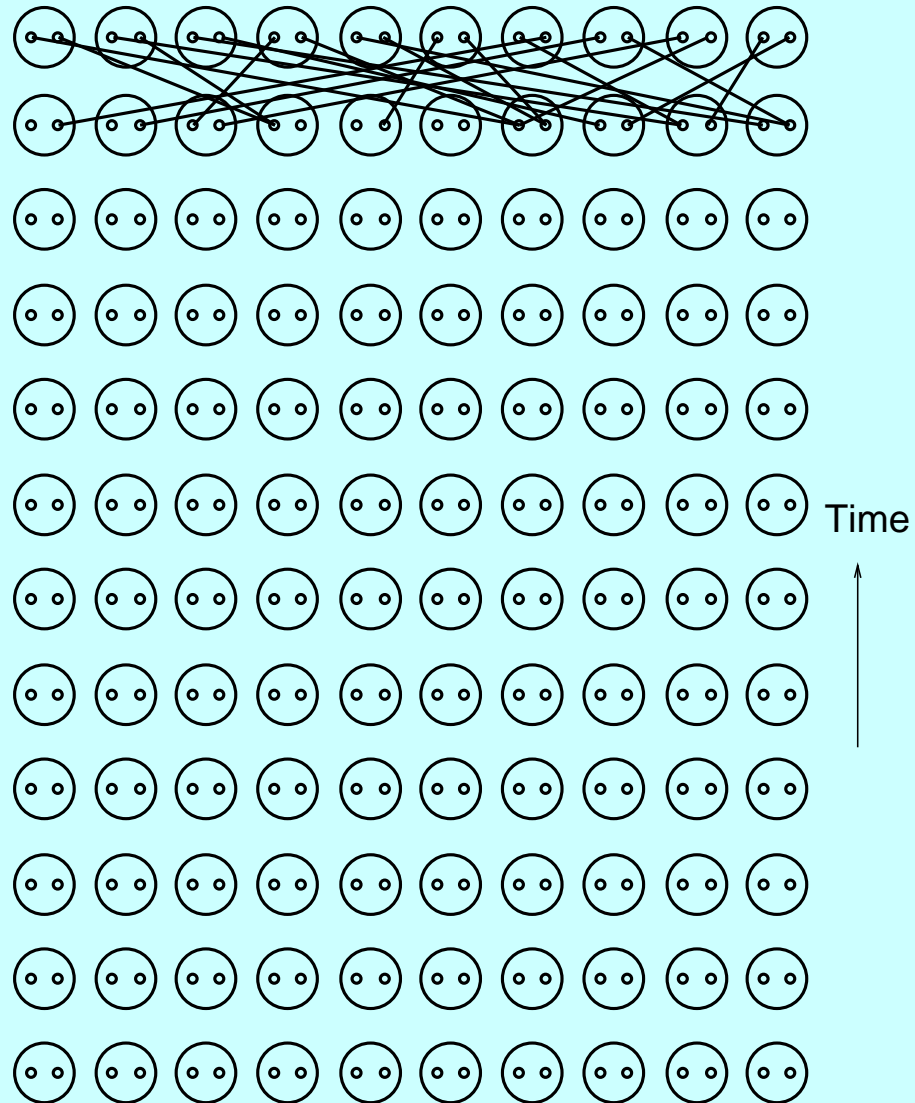
Gene copies in a population of 10 individuals

A random-mating population



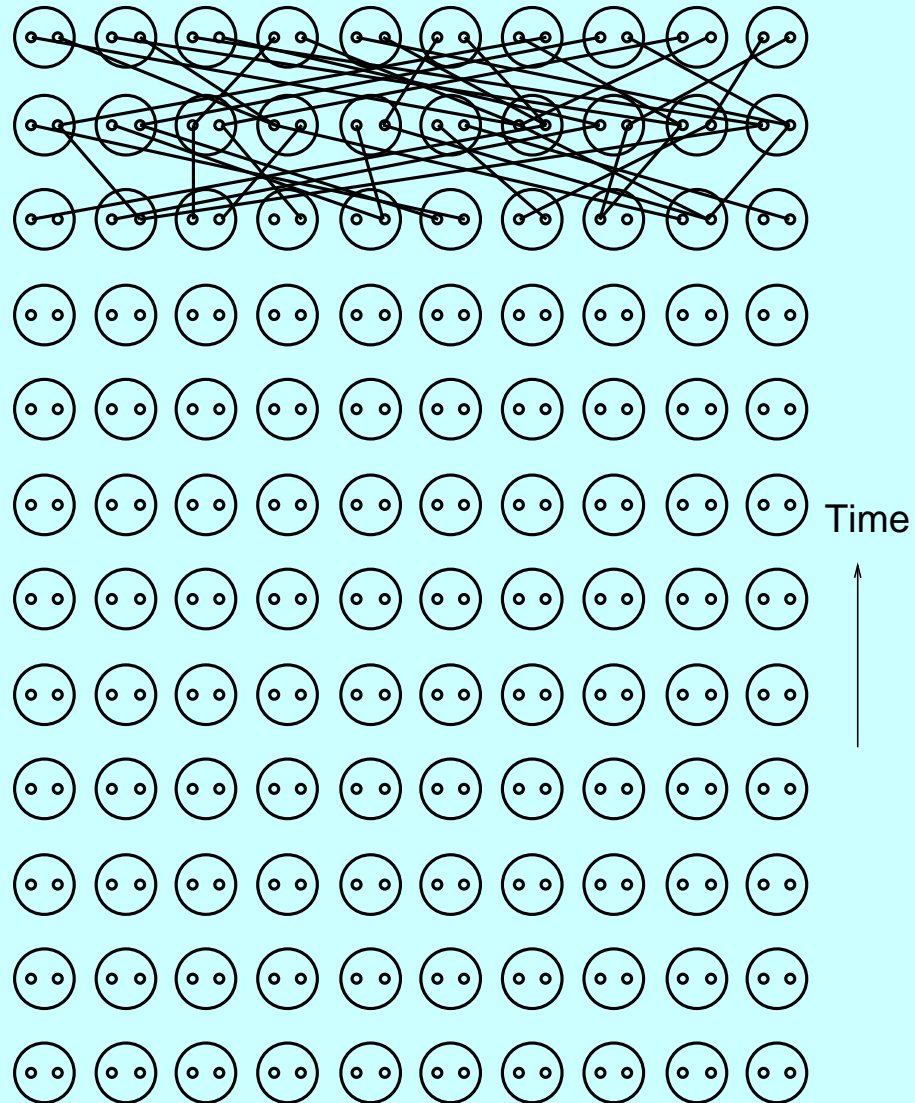
Going back one generation

A random-mating population



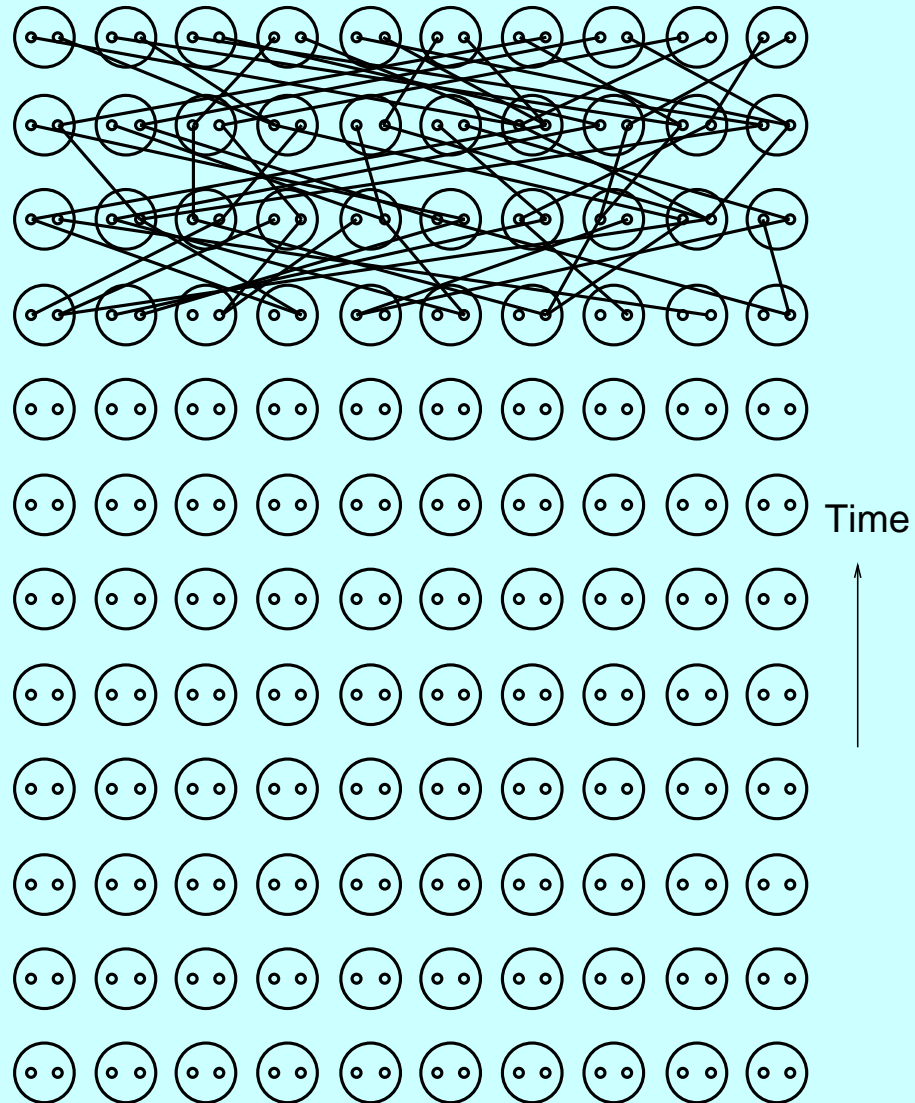
... and one more

A random-mating population



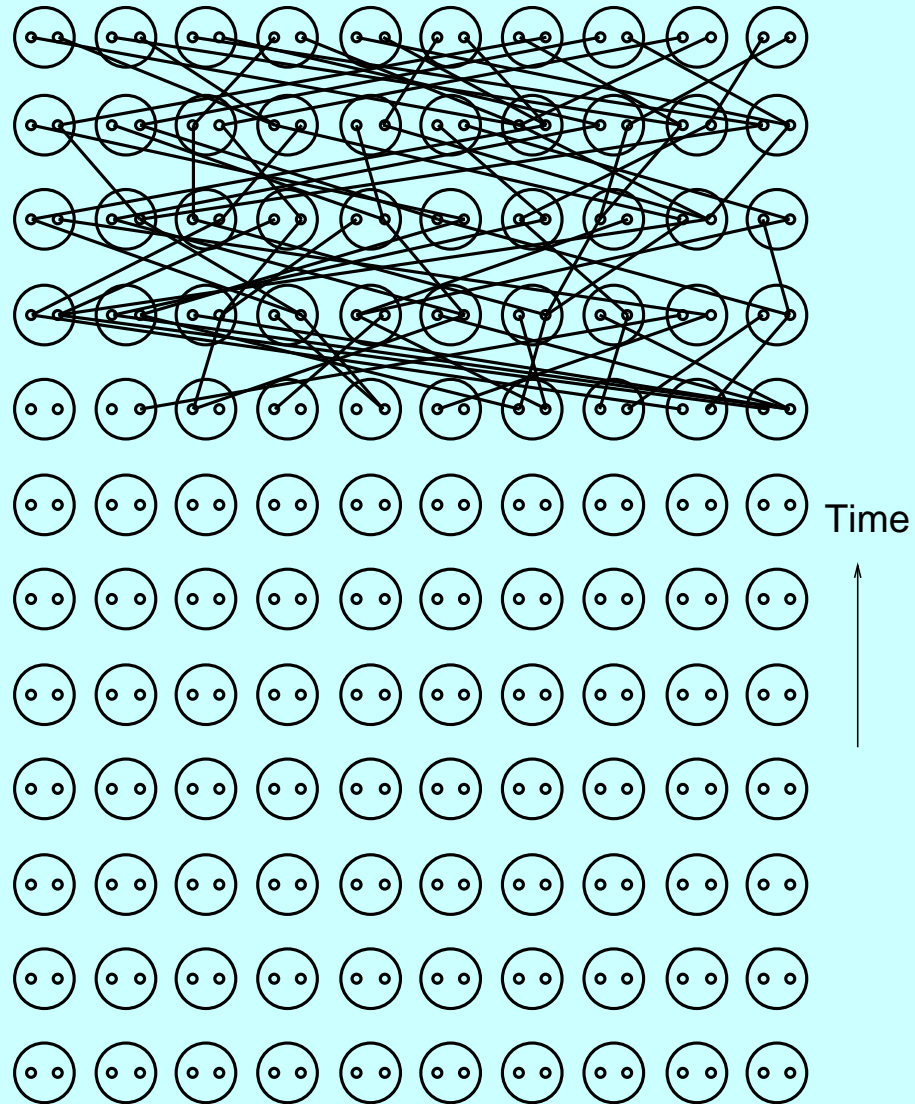
... and one more

A random-mating population



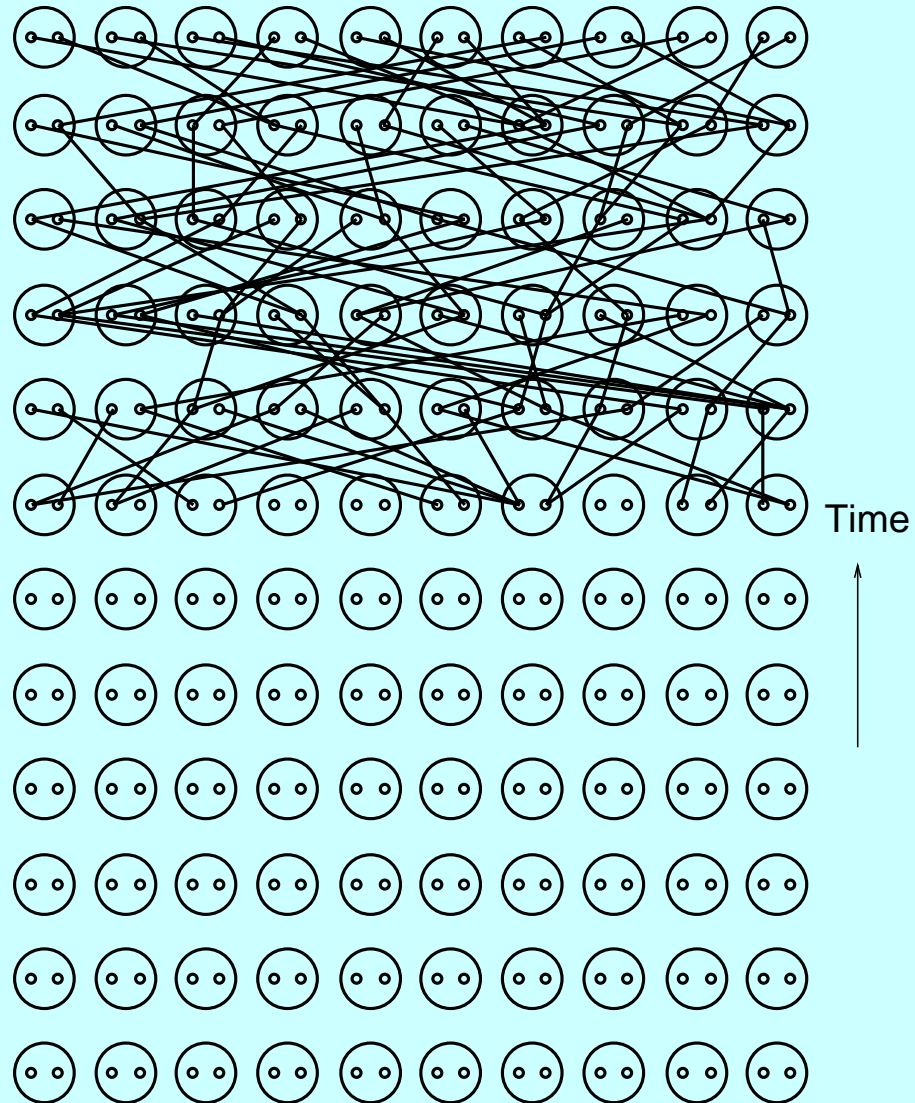
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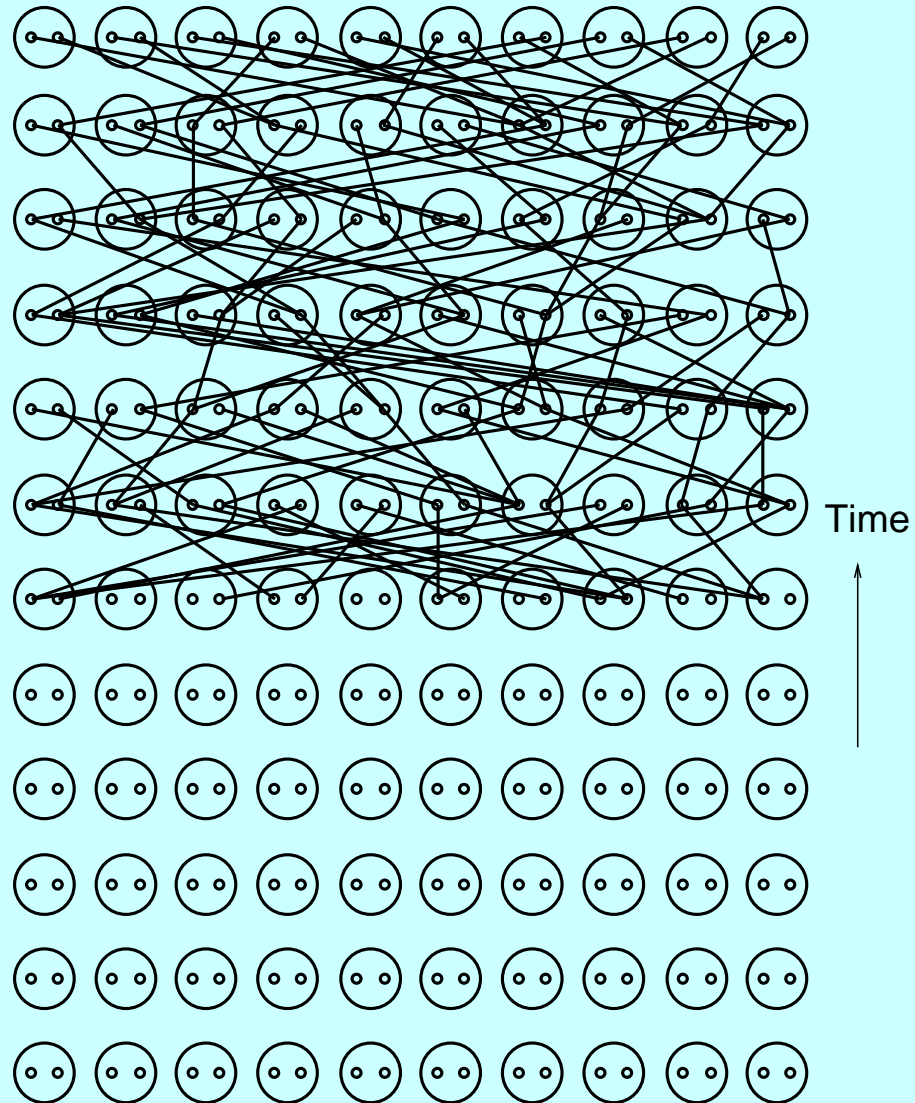
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A random-mating population



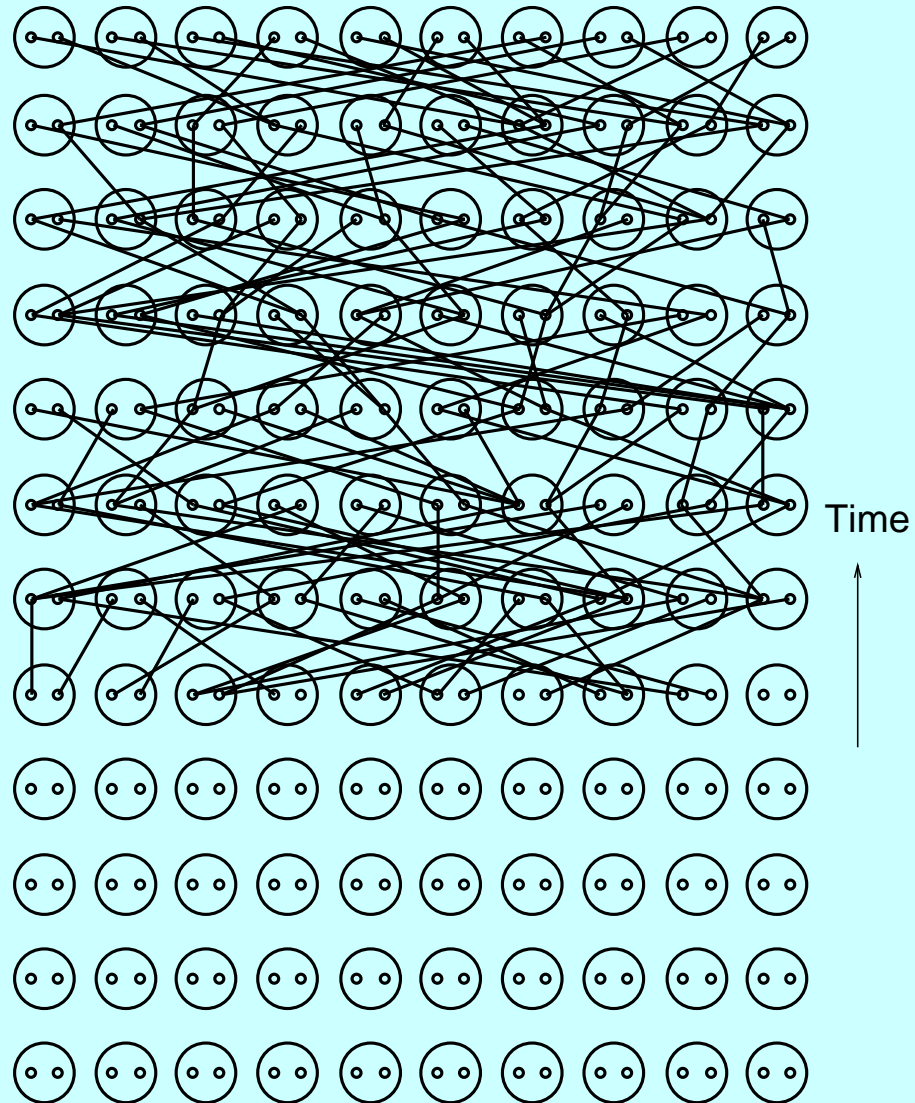
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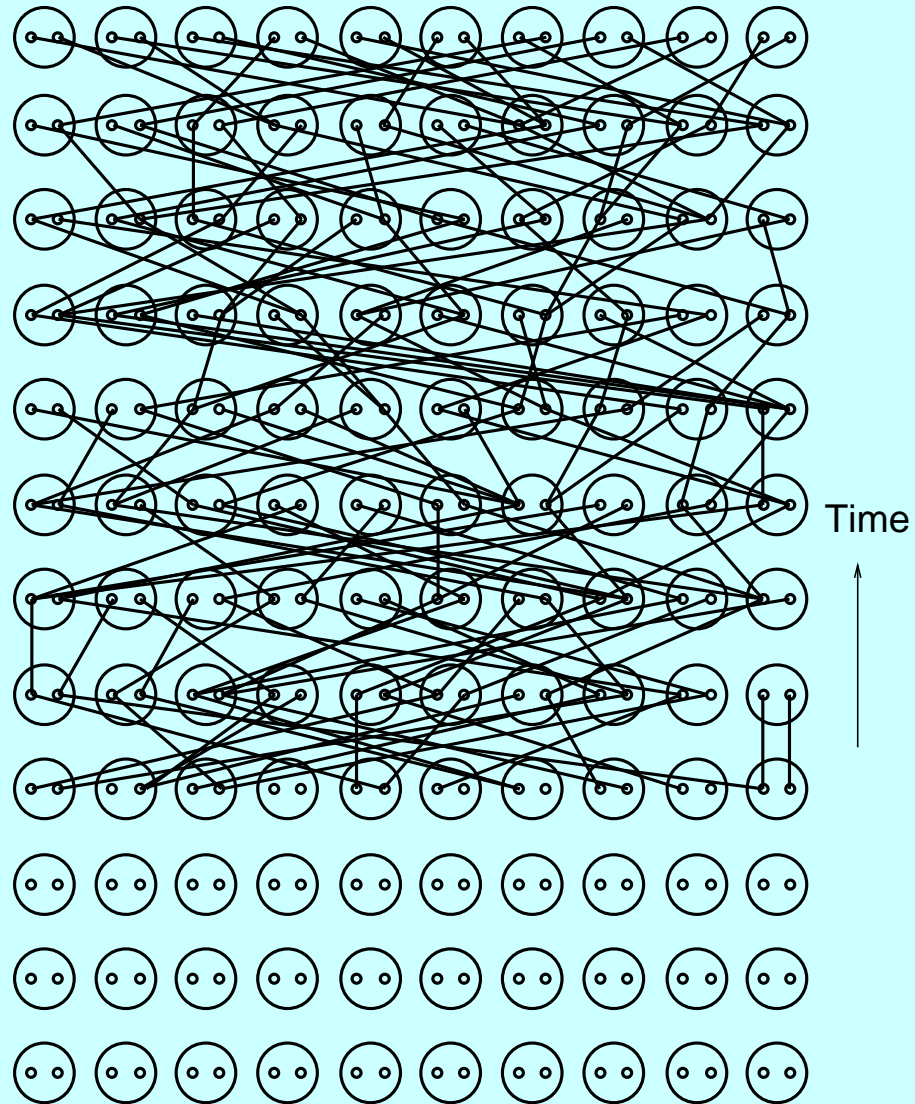
... and one more

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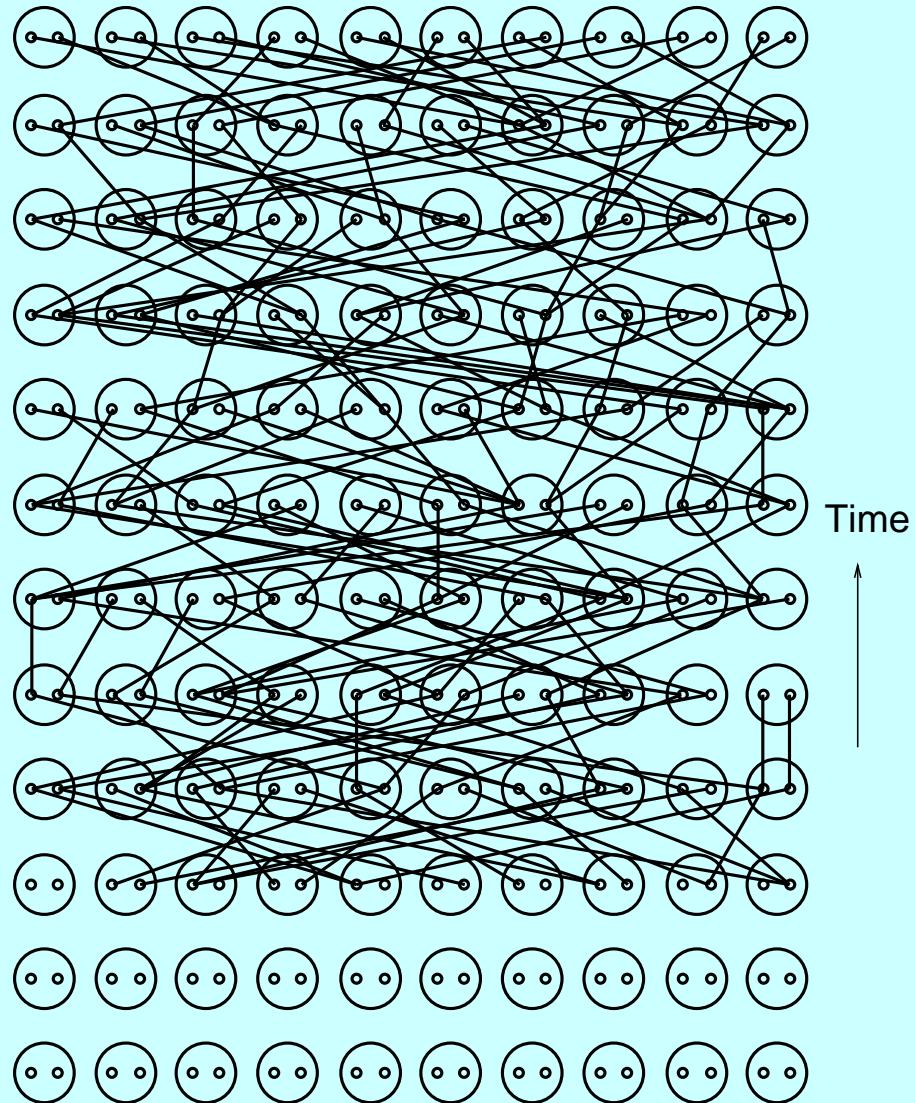
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A random-mating population



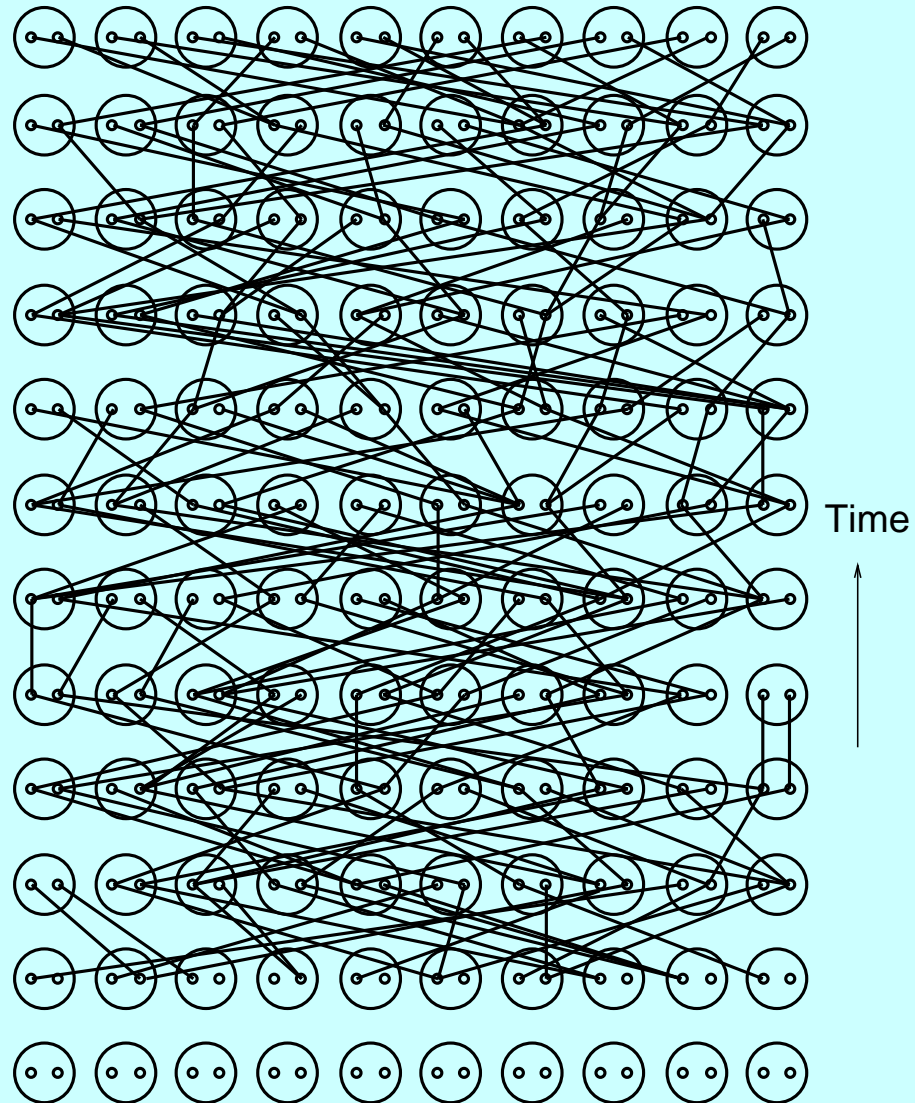
... and one more

A random-mating population



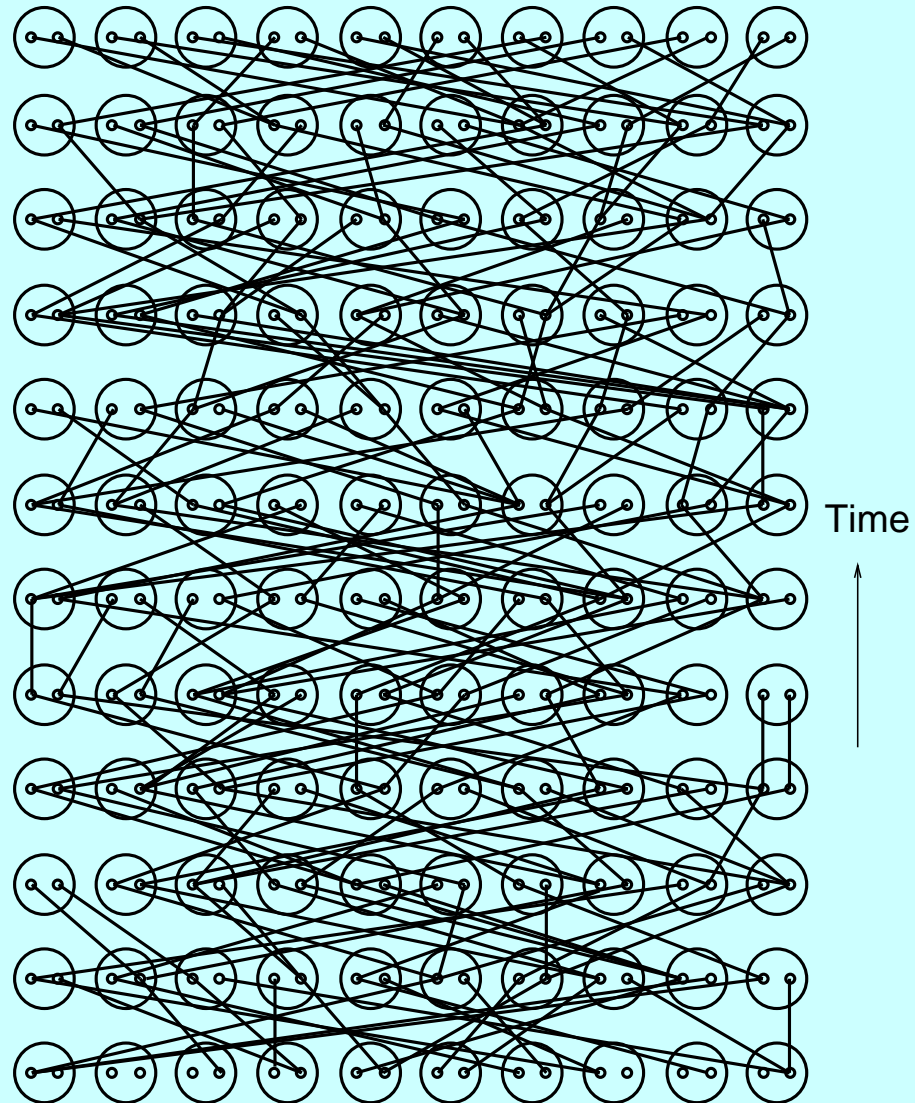
... and one more

A random-mating population



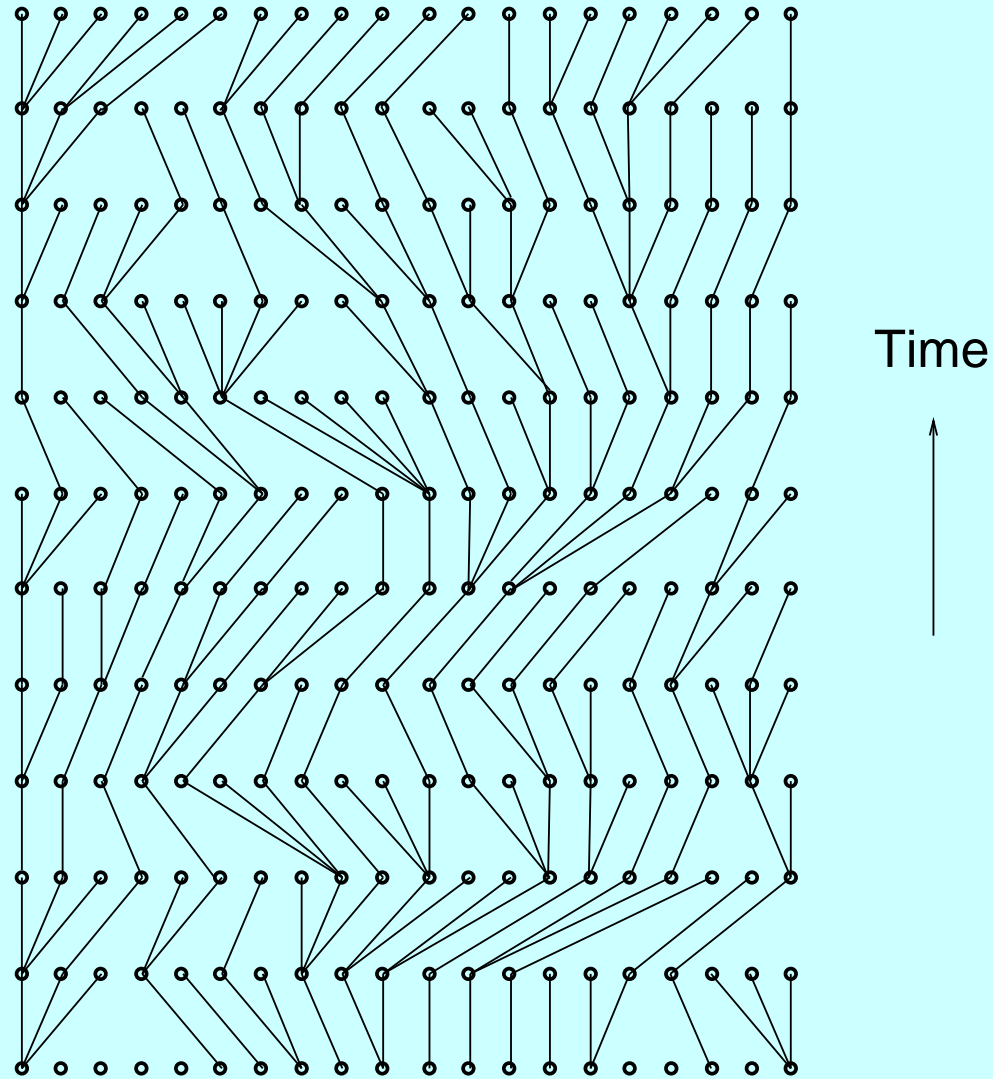
showing ancestry of gene copies

A random-mating population



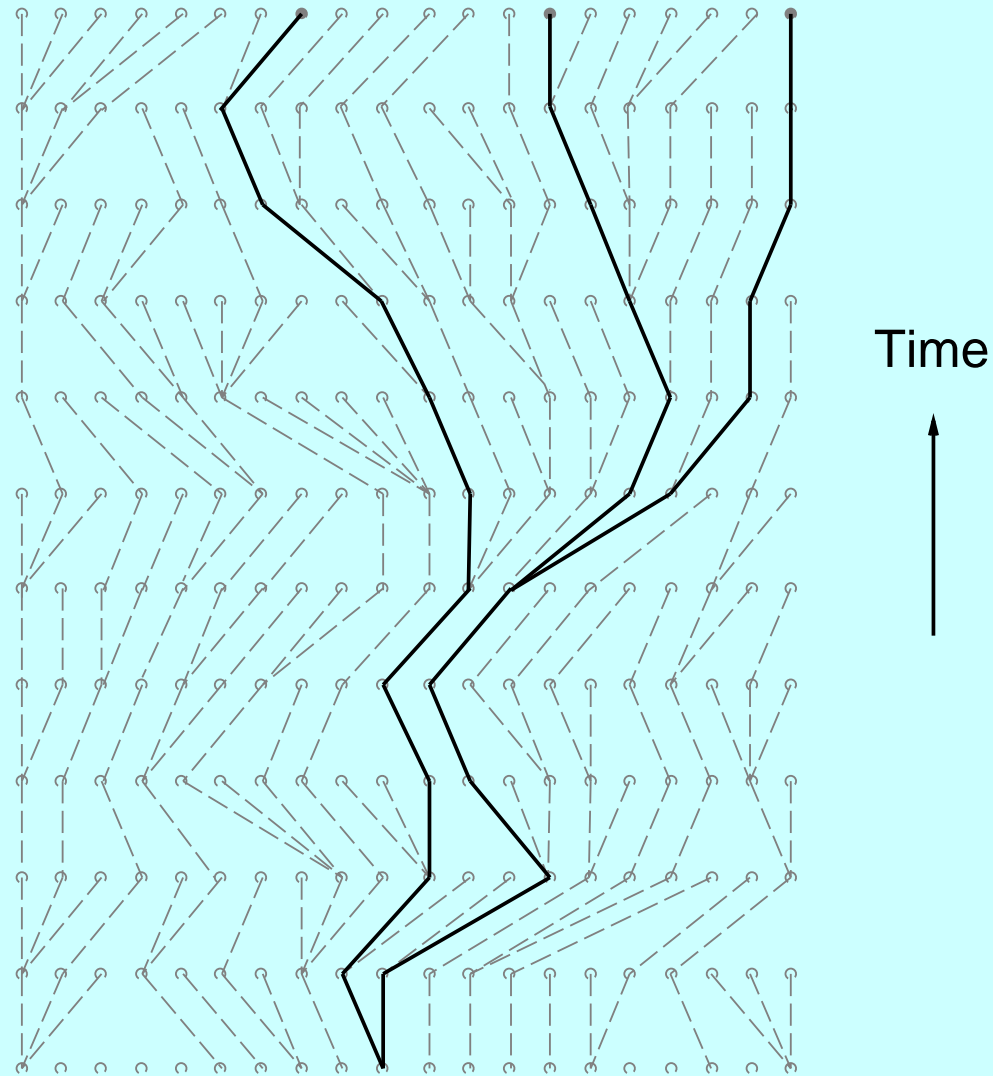
The genealogy of gene copies is a tree

Genealogy of gene copies, after reordering the copies

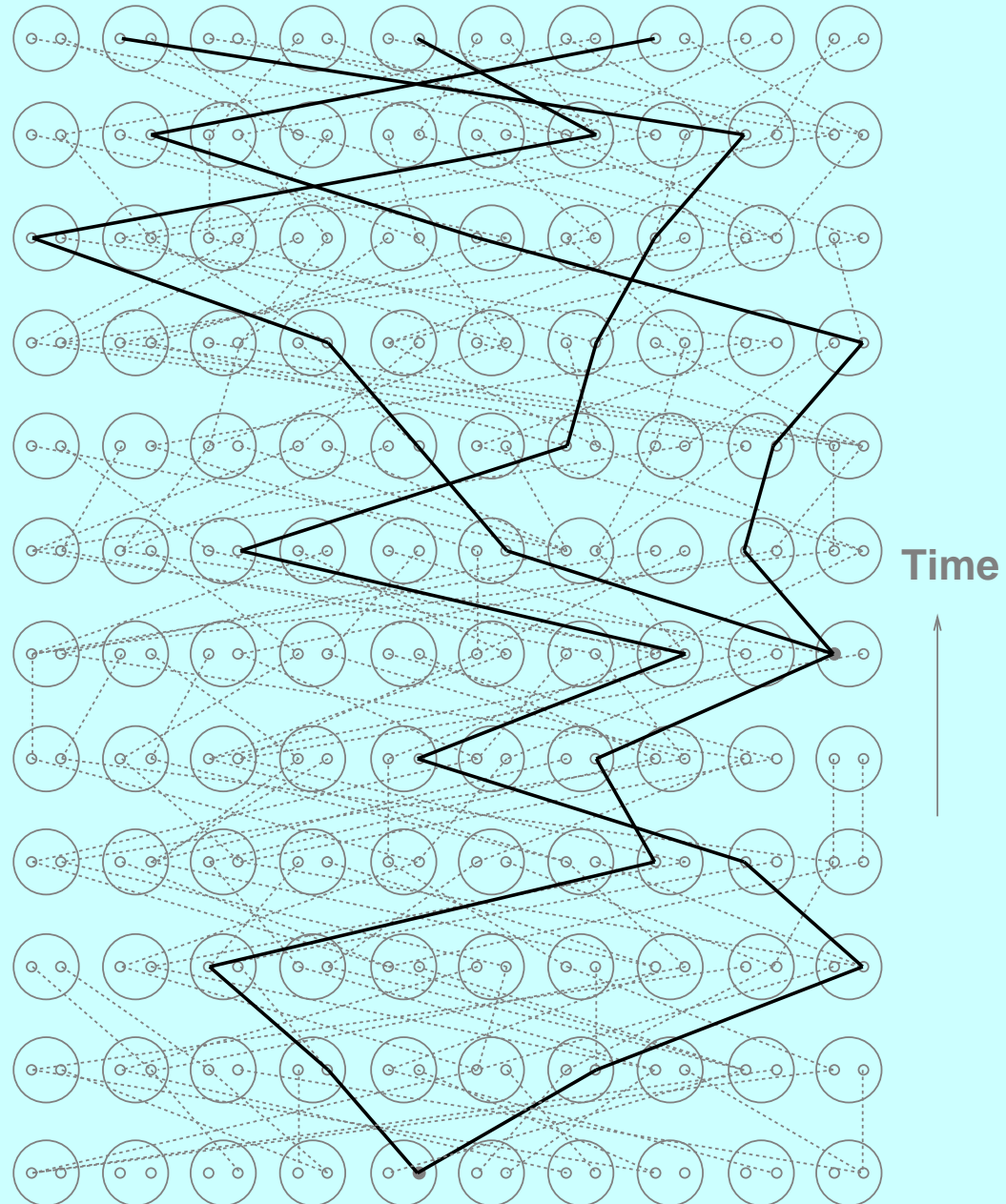


Ancestry of a sample of 3 copies

Genealogy of a small sample of genes from the population



Here is that tree of 3 copies in the pedigree



Kingman's coalescent

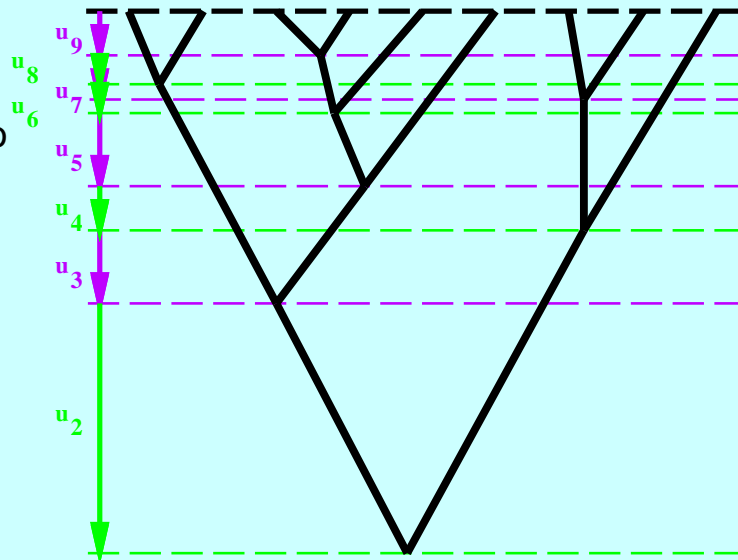
Coalescent trees of gene copies within species (Kingman, 1982)

Random collision of lineages as go back in time (sans recombination)
Collision is faster the smaller the effective population size

Average time for
k copies to coalesce to

$$k-1 = \frac{4N}{k(k-1)}$$

Average time for
two copies to coalesce
= 2N generations



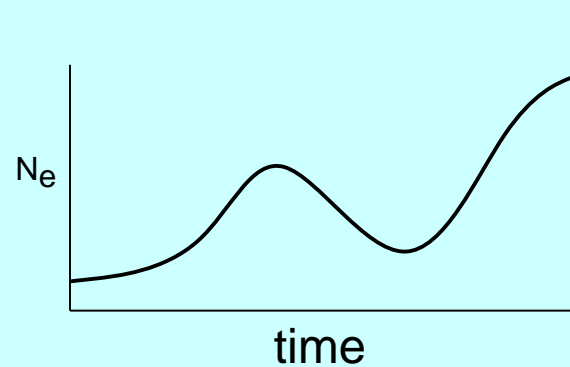
In a diploid population of
effective population size N,

Average time for n
copies to coalesce

$$= 4N \left(1 - \frac{1}{n}\right) \text{ generations}$$

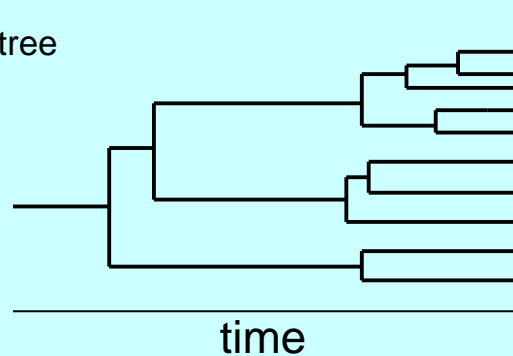
Coalescence is faster in small populations

Change of population size and coalescents

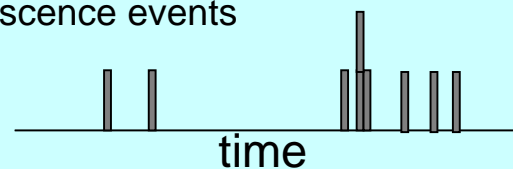


the changes in population size will produce waves of coalescence

the tree

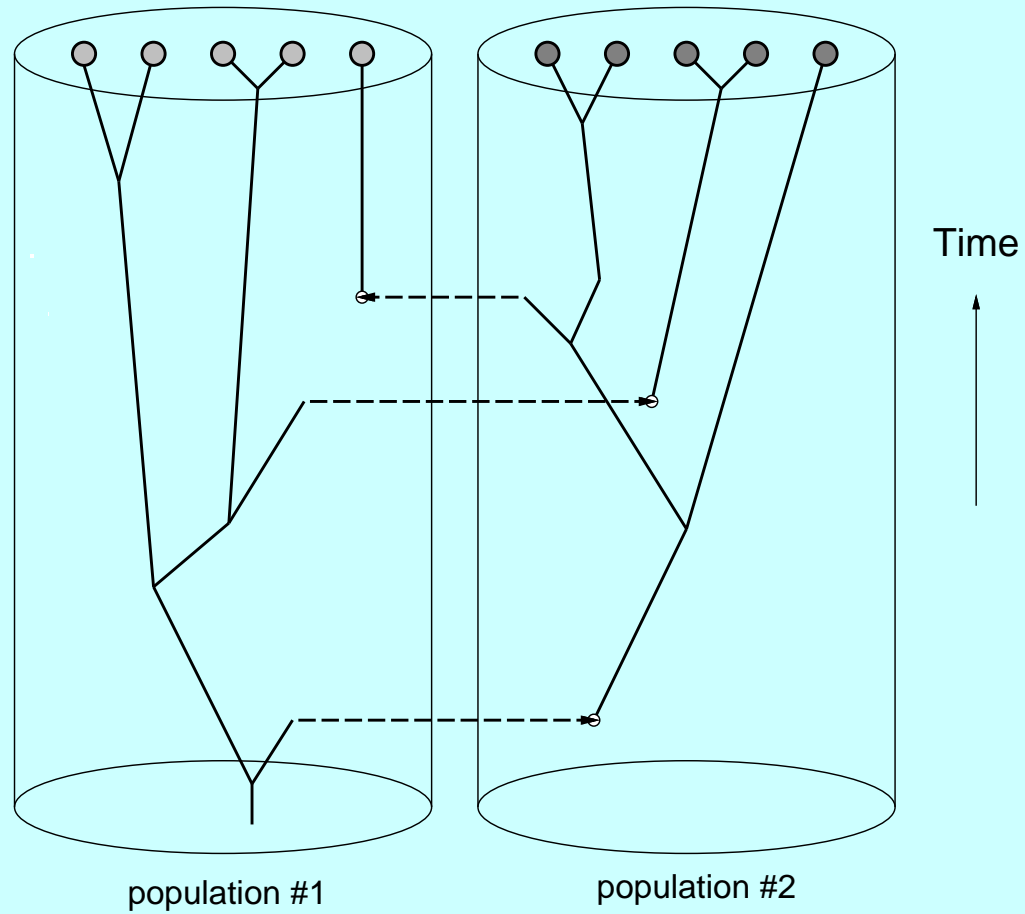


Coalescence events

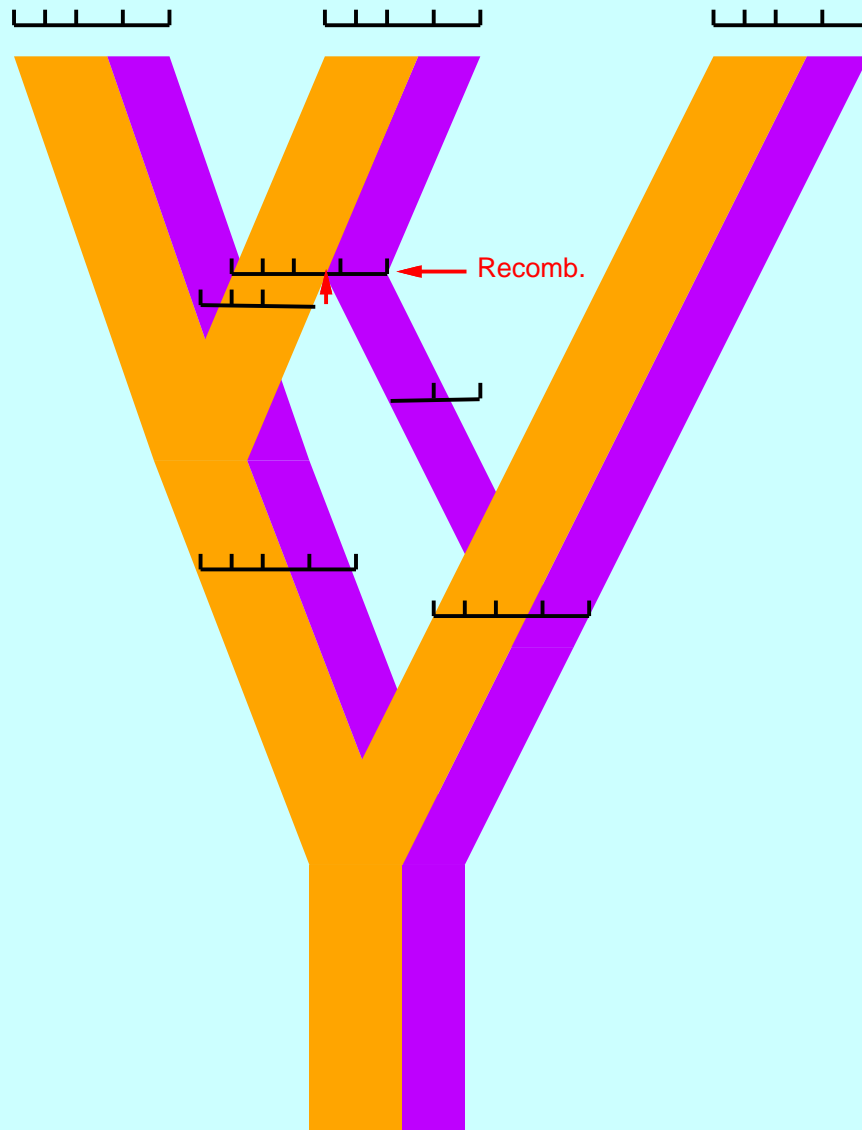


The parameters of the growth curve for N_e can be inferred by likelihood methods as they affect the prior probabilities of those trees that fit the data.

Migration can be taken into account



Recombination creates loops



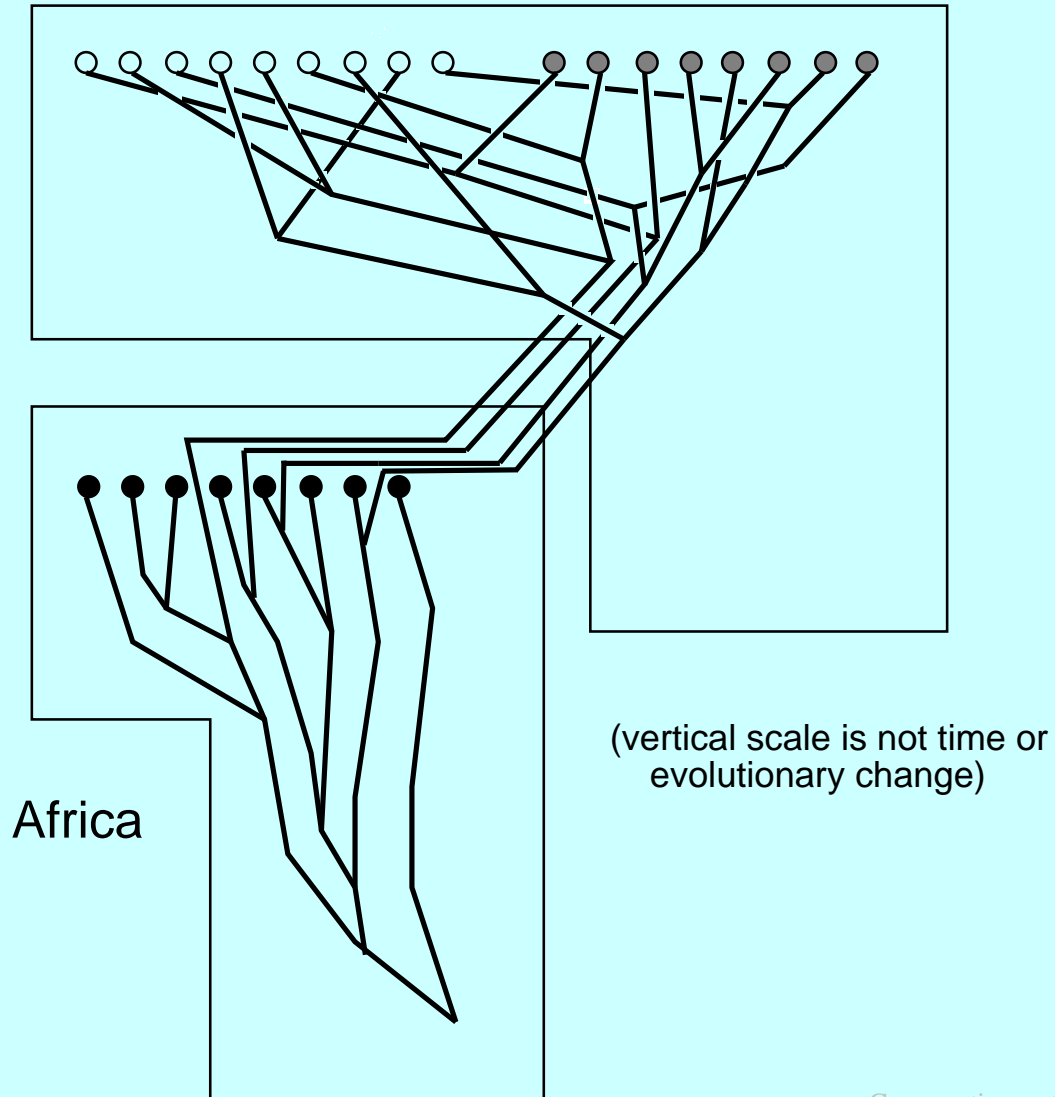
Different markers have slightly different coalescent trees

We want to be able to analyze human evolution

"Out of Africa" hypothesis

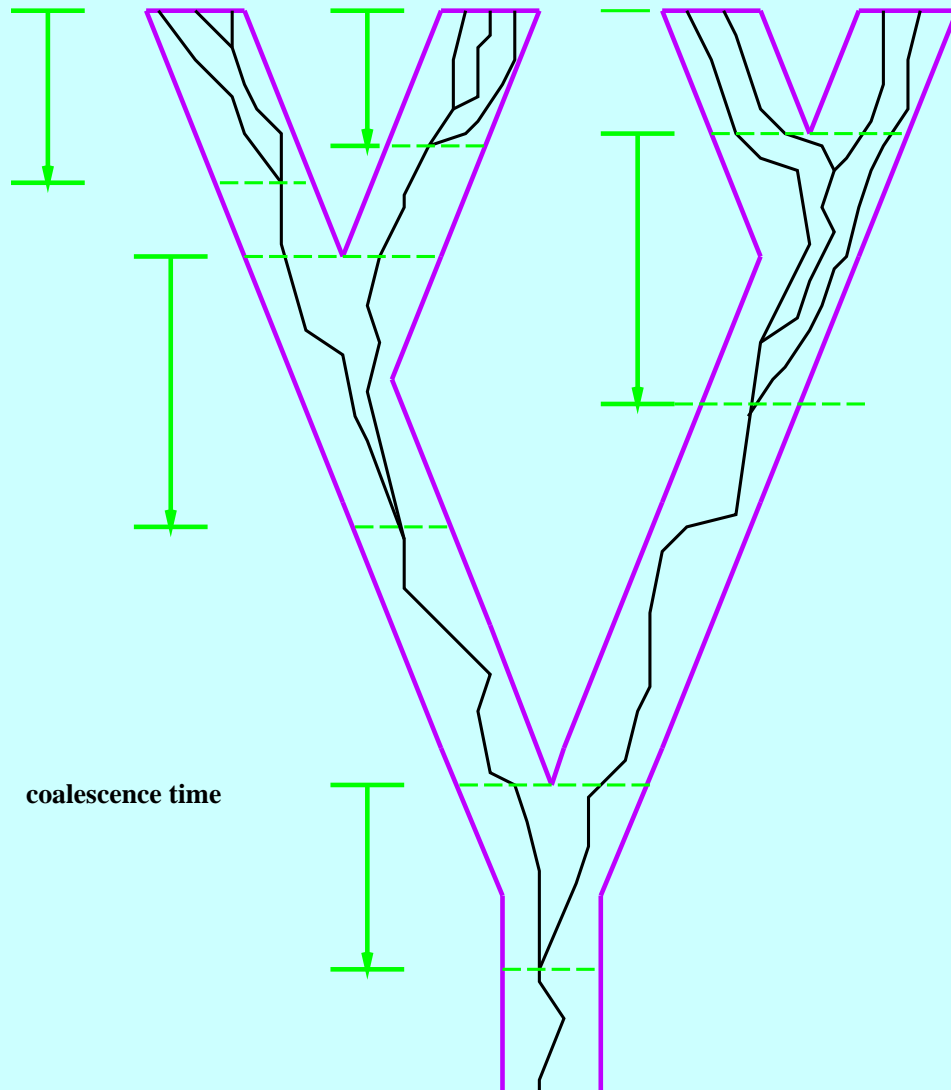
Europe

Asia



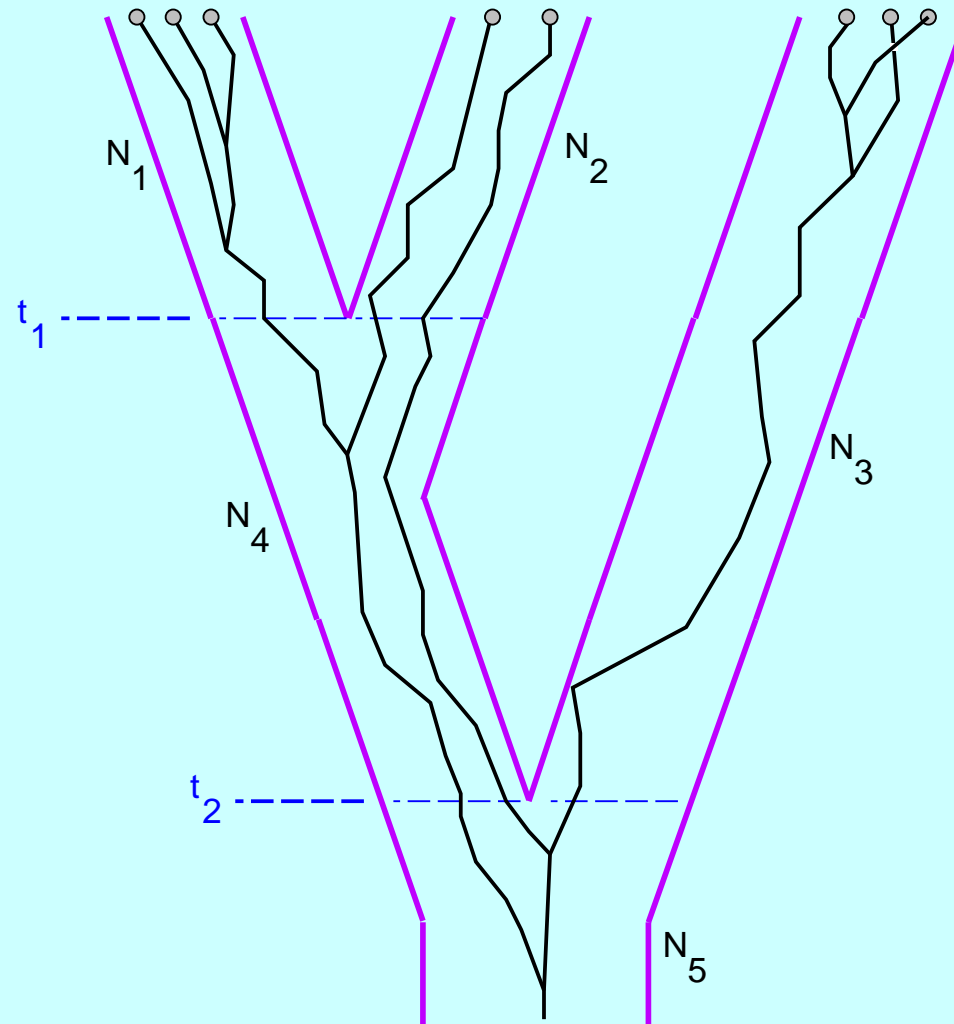
coalescent and “gene trees” versus species trees

Consistency of gene tree with species tree



If the branch is more than N_e generations long ...

Gene tree and Species tree



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- ... and more approximately by Approximate Bayesian Computation (ABC) methods. Faster but not necessarily as efficient statistically.

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References

Comparative methods

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Harvey, P. H. and M. D. Pagel. 1991. *The Comparative Method in Evolutionary Biology*. Oxford University Press, Oxford. [Reviews early work by me, Mark Ridley and the authors on comparative methods]

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The coalescent

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(continued)

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Wakeley, J. 2008. *Coalescent Theory*. Roberts and Co., Greenwood Village, Colorado. [One of two books so far on coalescents. Light on estimation issues.]

Nielsen, R. and M. Slatkin. 2013. *An Introduction to Population Genetics. Theory and Applications*. Sinauer Associates, Sunderland, Massachusetts. Population genetics textbook with more coverage of coalescents than usual.

Felsenstein, J. 2004. *Inferring Phylogenies*. Sinauer Associates, Sunderland, Massachusetts. [Especially chapter 27 which covers MCMC likelihood approaches (but explanation of logic of Griffiths/Tavaré method is wrong)]

Felsenstein, J. 2007. Trees of genes in populations. pp. 3-29 in *Reconstructing Evolution. New Mathematical and Computational Advances*, pp. 3-27 in by O. Gascuel and M. Steel. Oxford University Press, Oxford. [Review of coalescents including MCMC, for a somewhat mathematical audience]