Coalescent Theory

- the Wright-Fisher model considers changes in the ideal population as time moves forward
- coalescent theory (~1980+) looks backwards in time
- how long does it take for k alleles to coalesce to k - 1 alleles, then k - 2, k - 3, …, and finally a single ancestral allele?

Stochastic elements of the coalescent

- alleles randomly sample their parents in the previous generation
  - results in variation in offspring number
- sample of loci from the genome
  - different loci have different genealogical histories
- sample of alleles from the population
  - different samples of the same locus may have different coalescent trees
- distribution of mutations on the genealogy
  - mutations allow estimates of coalescence times

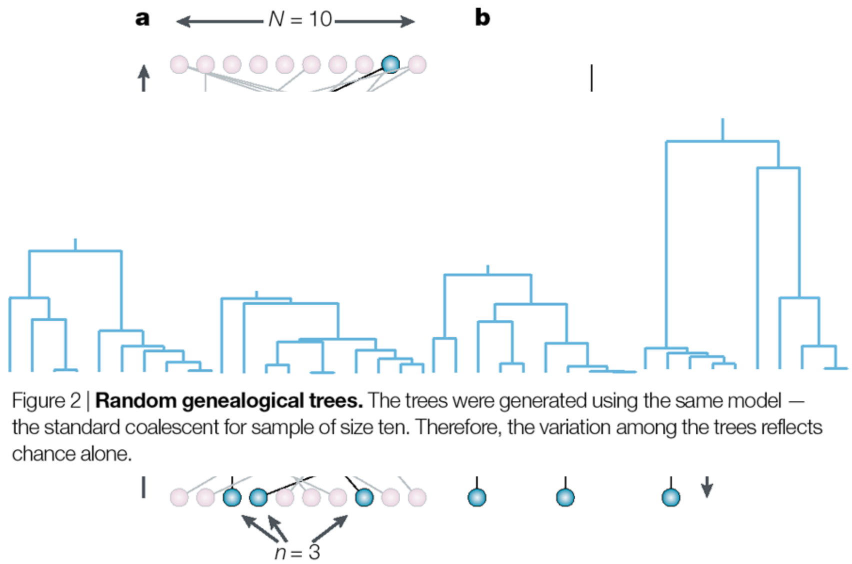


Figure 2 | **Random genealogical trees.** The trees were generated using the same model — the standard coalescent for sample of size ten. Therefore, the variation among the trees reflects chance alone.

Rosenberg & Nordborg 2002 Nat Rev Gen

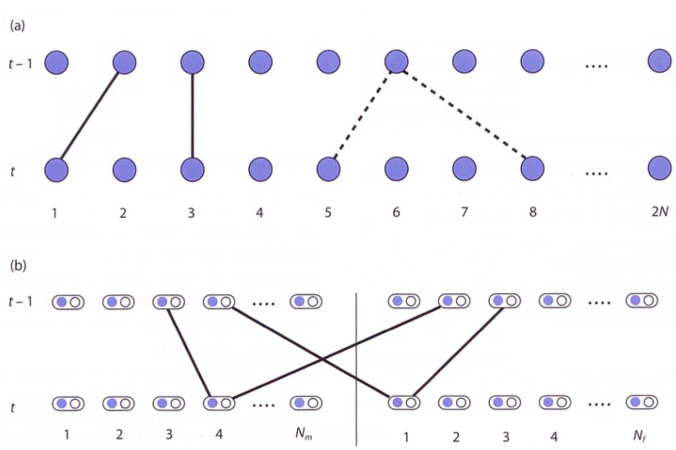


Figure 3.23 Haploid (a) and diploid (b) reproduction in the context of coalescent events. In a haploid population, the probability of coalescence is $\frac{1}{2N}$ (dashed lines) whereas the probability that two lineages do not have a common ancestor in the previous generation is $1-\frac{1}{2N}$ (solid lines). In a diploid population, the two gene or allele copies in one individual in the present time have one ancestor in the female population (N_f) and one ancestor in the male population (N_m). Coalescent events in the diploid population arise when the gene copies in males and females are identical by descent. The haploid model with $2N$ lineages is routinely used to approximate the diploid model with $N = N_f + N_m$ diploid individuals.

Coalescent probabilities 1

- the present is time 0 (zero)
- probability that *two* alleles had a common ancestor in generation 1

$$= \frac{1}{2N}$$

- probability that *two* alleles **did not have** a common ancestor in generation 1

$$= \left(1 - \frac{1}{2N}\right)$$

Coalescent probabilities 2

- probability that *two* alleles have still not coalesced by generation t

$$= \left[1 - \left(\frac{1}{2N}\right)\right]^t$$

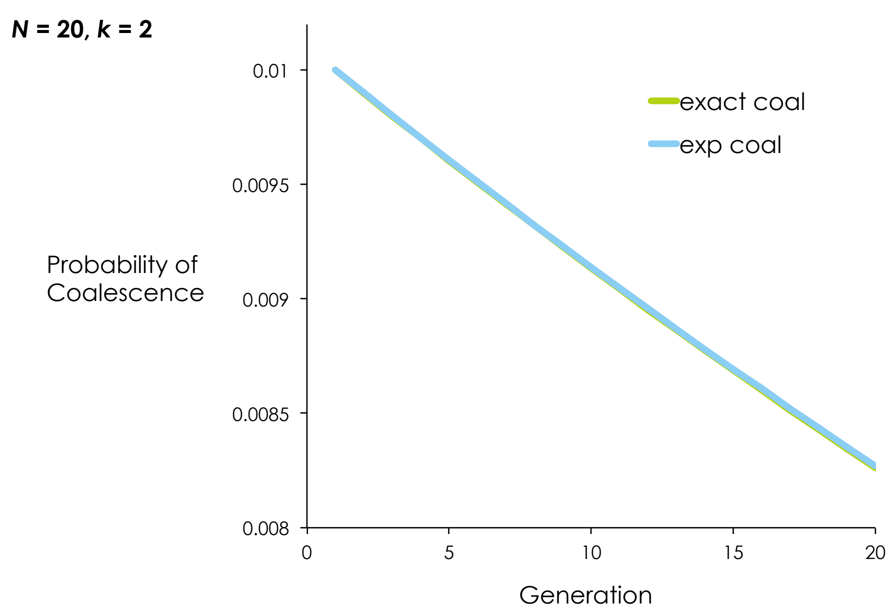
Coalescent probabilities 3

- probability that *two* alleles had a common ancestor in generation t+1

$$= \underbrace{\frac{1}{2N}}_{\text{probability of coalescence in generation } t+1}\underbrace{\left[1-\left(\frac{1}{2N}\right)\right]^{t}}_{\text{probability of NO coalescence in generations 1 through } t}$$

probability of coalescence in generation t + 1

probability of *NO* coalescence in generations 1 through t



Coalescent probabilities 4

- can we randomly choose a coalescence time from the exponential distribution?
  - need to solve for t as a function of a random variable from 0 to 1

$$P_{NC} \approx e^{-t/(2N)} \quad\quad \ln\left(P_{NC}\right) \times 2N \approx -t$$

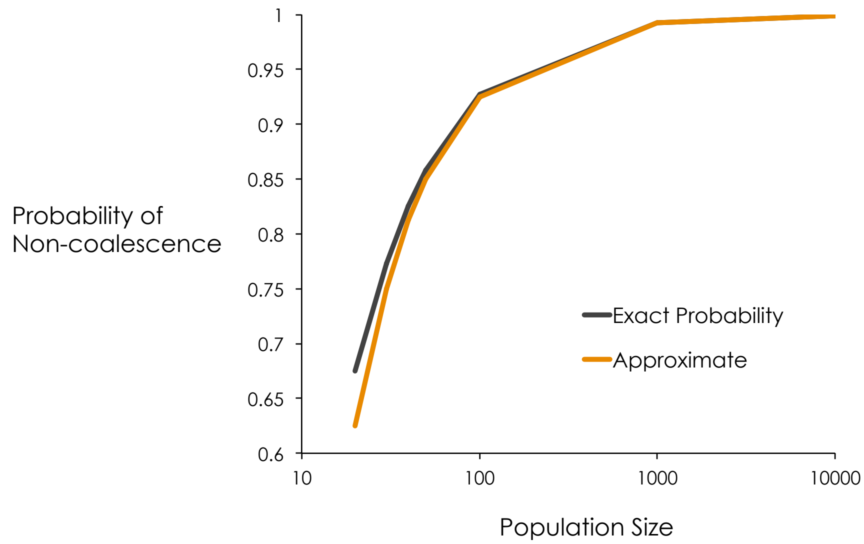
$$\ln\left(P_{NC}\right) \approx -t/(2N) \quad\quad t \approx -\ln\left(P_{NC}\right) \times 2N$$

Coalescent probabilities 5

- what if we consider k alleles and not just 2?
- what is the probability that k alleles had k distinct parental alleles the previous generation?

$$\Pr(k) = \prod_{i=0}^{k-1}\left(1 - \frac{i}{2N}\right) \approx \left(1 - \frac{\binom{k}{2}}{2N}\right)$$

***N* = 20 to 10,000, *k* = 6**



Coalescent probabilities 6

- probability that k alleles *do not* coalesce for t generations

$$P_{NC} = \left(1 - \frac{\binom{k}{2}}{2N}\right)^{t} \approx e^{\left[-\frac{\binom{k}{2}}{2N}t\right]}$$

$$t \approx -\ln\left(P_{NC}\right) \times \frac{2N}{\binom{k}{2}} = -\ln\left(P_{NC}\right) \times \frac{4N}{k\left(k-1\right)}$$

Coalescent probabilities 7

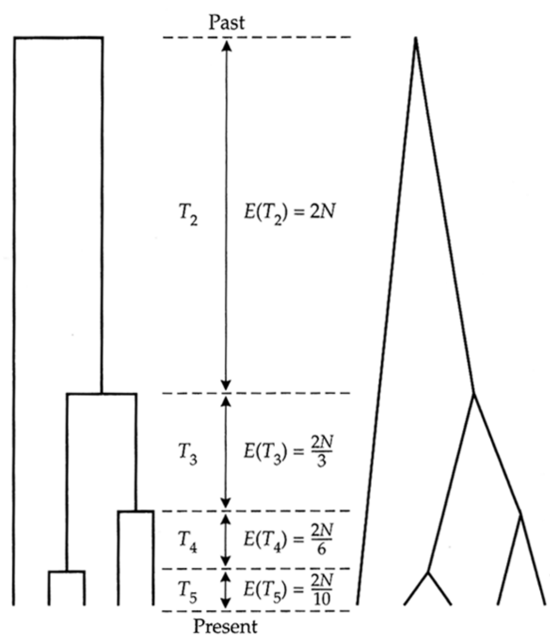
- probability that k alleles *do not* coalesce for t generations, and then *one pair* coalesces to give k - 1 alleles at t + 1 generations

$$= \Pr(k)^t \left[1 - \Pr(k)\right] \approx \frac{\binom{k}{2}}{2N} e^{\left[-\frac{\binom{k}{2}}{2N} t\right]}$$

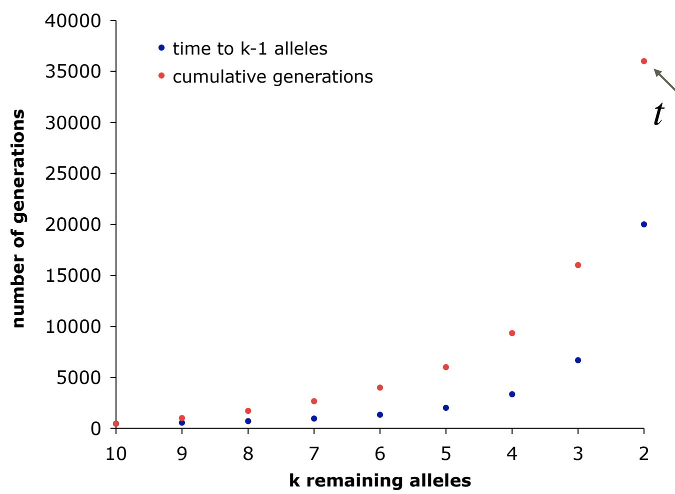
- distribution has mean and variance:

$$\text{Mean} = \frac{4N}{k(k-1)} \text{ generations} \quad \text{Var} = \frac{16N^2}{\left[k(k-1)\right]^2} \text{ generations}^2$$

FIGURE 3.15 Two completely equivalent ways of illustrating the coalescences in a gene tree. On the left, the coalescent events are represented as horizontal lines, on the left they are represented as nodes. In any each generation, if there are k alleles present, the expected time back to the next coalescence is given by $4N/[k(1-k)]$. For example, starting with five alleles, the expected time back to the first coalescence is $4N/[(5)(4)] = 2N/10$. Note that the successive times get longer. When there are only two alleles, the time back to the final coalescence is $2N$ generations.



expected coalescence times for k = 10 and N = 10,000



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