Species Tree Inference

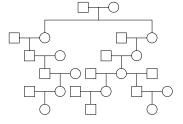
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Outline

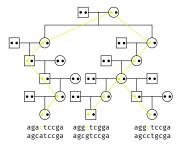
Coalescent Theory

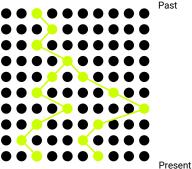
Multispecies Coalescent

Pedigree



Gene Tree Within a Pedigree





Probability of common parent ($P_1 = \frac{1}{2N}$):



Probability of distinct parents ($P_2 = 1 - \frac{1}{2N}$):



Probability no coalescence by generation t

$$P_2^{(t)} = \left(1 - \frac{1}{2N}\right)^t$$

Transform to "diffusion" timescale

$$t = (2N)\tau$$

Unit of time is now 2N generations. One generation on this timescale is

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

so as $N \to \infty$ time appears continuous.

Probability of no coalescence (on the transformed timescale) is

$$P_2^{(\tau)} = \left(1 - \frac{1}{2N}\right)^{\tau(2N)}$$

and for large population size this converges to

$$\lim_{N \to \infty} \left(1 - \frac{1}{2N} \right)^{\tau(2N)} = e^{-\tau}$$

Expectation of Coalescence Time (n = 2)

On the original discrete generation timescale the expected time for 2 sequences to coalesce is

$$\mathbb{E}(t) = \sum_{t=0}^{\infty} t P_2^{(t)}$$
$$= \sum_{t=1}^{\infty} \left(1 - \frac{1}{2N}\right)^{t-1} \frac{1}{2N} = 2N.$$

On the transformed continuous timescale the expected time to coalescence is

$$\mathbb{E}(\tau) = \int P_2^{(\tau)} d\tau = \int_0^\infty \tau e^{-\tau} d\tau = 1.$$

Recall: an exponentially distributed random variable \boldsymbol{x} with rate λ has probability density function

$$f(x) = \lambda e^{-\lambda x},$$

with mean (expectation)

$$\mathbb{E}(x) = 1/\lambda,$$

and variance

$$Var(x) = 1/(\lambda^2).$$

The probability density function of the coalescence time for two sequences on the transformed timescale (2N generations) is

$$f(\tau) = e^{-\tau},$$

which is an exponential distribution with $\lambda=1$. The mean and variance are

$$\mathbb{E}(\tau) = 1,$$

and

$$Var(\tau) = 1.$$

The mean and variance of the coalescence time for two sequences on the original timescale (generations) are

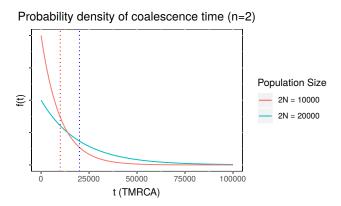
$$\begin{split} \mathbb{E}(t) &=& \mathbb{E}[(2N)\tau] \\ &=& (2N)\mathbb{E}(\tau) \\ &=& 2N, \end{split}$$

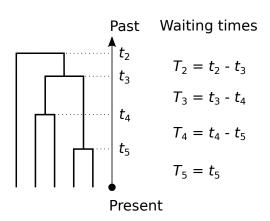
and

$$Var(t) = Var[(2N)\tau]$$

$$= (2N)^{2}Var(\tau)$$

$$= 4N^{2}$$





Waiting time for i lineages to coalesce to i-1 lineages

$$f(\tau_i) = \frac{i(i-1)}{2} e^{-\frac{i(i-1)}{2}\tau_i}$$

This is an exponential distribution with rate parameter

$$\frac{i(i-1)}{2}$$

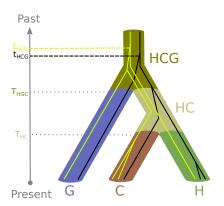
The mean and variance are therefore

$$\mathbb{E}(\tau_i) = \frac{2}{i(i-1)}, \ \operatorname{Var}(\tau_i) = \frac{4}{i^2(i-1)^2}.$$

Gene Trees Within Species Trees

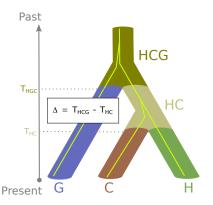


Gene Trees Within Species Trees



Gene Tree Probabilities Within Species Trees

3 species: 1 sequence each



Probability H and C coalesce in HC

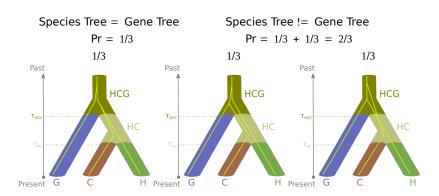
$$\int_{0}^{\Delta} \frac{e^{-\frac{x}{2N_{HC}}}}{2N_{HC}} dx = 1 - e^{-\frac{\Delta}{2N_{HC}}}.$$

Probability H and C do not coalesce in HC

$$e^{-\frac{\Delta}{2N_{HC}}}$$
.

Gene Tree Probabilities Within Species Trees

3 species: 1 sequence each



Gene Tree Probabilities Within Species Trees

3 species: 1 sequence each

$$\Pr(G = S) = 1 - \exp\left(\frac{-\Delta}{2N_{HC}}\right) + \frac{1}{3}\exp\left(\frac{-\Delta}{2N_{HC}}\right)$$
$$= 1 - \frac{2}{3}\exp\left(\frac{-\Delta}{2N_{HC}}\right)$$
$$\Pr(G \neq S) = \frac{2}{3}\exp\left(\frac{-\Delta}{2N_{HC}}\right)$$