

Nee et al., 1994

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March 20, 2015

1 Likelihood

The likelihood calculation is based on Nee et al., 1994.

To calculate the likelihood of a phylogeny and parameters, the phylogeny is cut into pieces (1), as all we need are braching times (ts) and branch lengths (xs). The shape of the tree is unimportant for this model.

$$u(\lambda, \mu, x) = \frac{\lambda(1 - \exp(-(\lambda - \mu)x))}{\lambda - \mu(-(\lambda - \mu)x)} \quad (1)$$

$$P(\lambda, \mu, t, T) = \frac{\lambda - \mu}{\lambda - \mu \exp(-(\lambda - \mu)(T - t))} \quad (2)$$

$P(\lambda, \mu, t, T)$ is the chance a lineage alive at time t is still present at time T . The likelihood function, equation 3, is:

$$\mathcal{L}(\lambda, \mu, ts, T) = (N - 1)! \left[\prod_{i=3}^N P(\lambda, \mu, t_i, T) \right] (1 - u(\lambda, \mu, x_2))^2 \left[\prod_{i=3}^N (1 - u(\lambda, \mu, x_i)) \right] \quad (3)$$

2 Acknowledgements

Thanks to César Martinez for helpfull discussion.

3 References

- Nee, Sean, Robert M. May, and Paul H. Harvey. "The reconstructed evolutionary process." Philosophical Transactions of the Royal Society B: Biological Sciences 344.1309 (1994): 305-311.

Symbol	Description
\mathcal{L}	Likelihood
λ	Speciation rate
μ	Extinction rate
N	number of lineages at the current time, time T
t_1	Root time
t_2	Crown age, time of first branching
t_i	Time of $(i - 1)$ th branching, $i \in [1, N]$
ts	Vector of branching time, $ts = \{t_1, t_2, \dots, t_n\}$
T	Current time
x_2	Time between t_2 and T , time since first branching, $i \in [1, N]$
x_3	Time between t_3 and T , branch length of branch originating at t_3
x_i	Time between t_i and T , branch length of branch originating at t_i
xs	Vector of branch lengths, $xs = \{x_1, x_2, \dots, x_n\}$

Table 1: Symbol descriptions

Original number	Original form	Equation number	Form used here
1	u_t	1	$u(\lambda, \mu, x)$
2	$P(t, T)$	2	$P(\lambda, \mu, t, T)$
20	lik	3	$\mathcal{L}(\lambda, \mu, ts, T)$

Table 2: Equation comparisons of the original equations by Nee et al., 1994 and the numbers and form used here

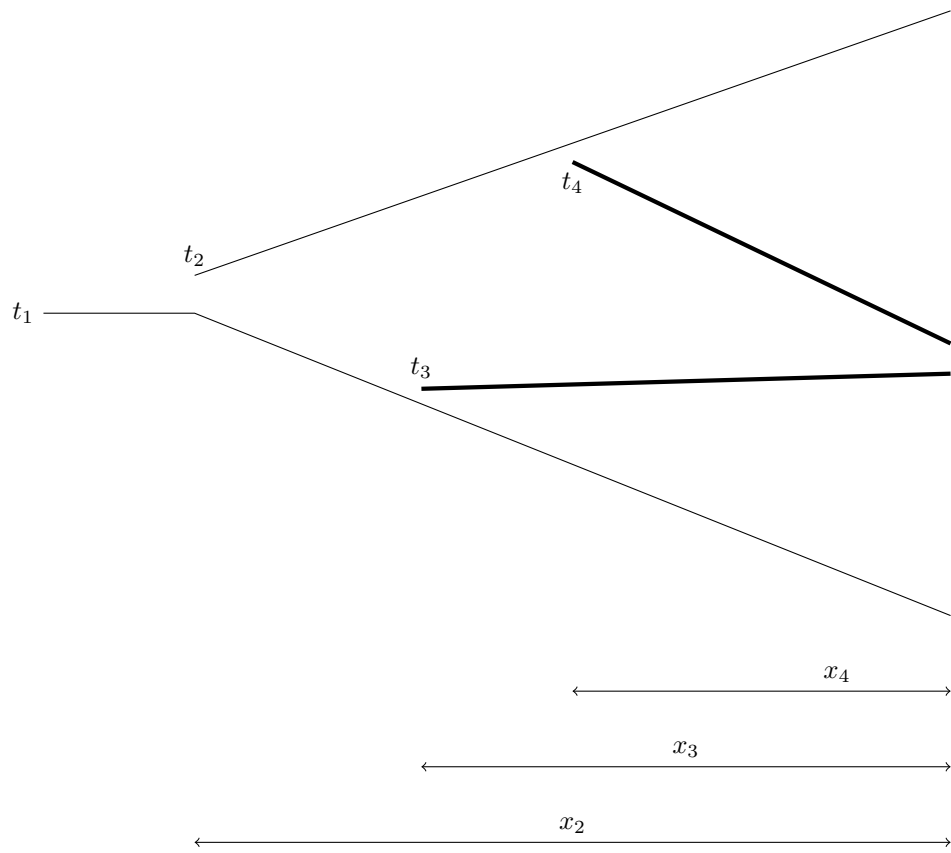


Figure 1: Tree similar to figure 2 of Nee et al.