

# Likelihood Function of Some Time-Dependent Coalescent Models

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October 27, 2013

Coalescent models describe the distribution of ancestry in a population under some assumptions on the variation in the parameter  $\Theta = 4N_e\nu$ , with  $N_e$  the effective size of the population and  $\nu$  the mutation rate. The present document gives the likelihood function, and some computational details, for several models with  $\Theta$  varying through time. These models are available in `coalescentMCMC` as R functions (see below).

The general mathematical framework has been given by Griffiths & Tavaré [1]. If  $\Theta$  is constant, the probability of observing the coalescent times  $t_1, \dots, t_n$  is:

$$\prod_{i=2}^n \binom{i}{2} \frac{1}{\Theta} \exp \left[ - \binom{i}{2} \frac{t_i - t_{i-1}}{\Theta} \right]$$

where  $t_1 = 0$  is the present time and  $t_n = T_{\text{MRCA}}$ . The general formula for  $\Theta(t)$  varying through time is:

$$\prod_{i=2}^n \binom{i}{2} \frac{1}{\Theta(t_i)} \exp \left[ - \binom{i}{2} \int_{t_{i-1}}^{t_i} \frac{1}{\Theta(u)} du \right] \quad (1)$$

Four specific temporal models are considered below. The time to the most recent ancestor, denoted as  $T_{\text{MRCA}}$ , is assumed to be known—this assumption could be relaxed though this is not considered here.

## 1 Models

The *exponential growth model* assumes  $\Theta(t) = \Theta_0 e^{\rho t}$ , with  $\Theta_0$  is the value of  $\Theta$  at present and  $\rho$  is the population growth rate [2]. Because of the exponential function,  $\Theta$  may reach very high (or low) values. To avoid this, the *linear model* formulated as  $\Theta(t) = \Theta_0 + t(\Theta_{T_{\text{MRCA}}} - \Theta_0)/T_{\text{MRCA}}$ . This model, like the previous one, has two free parameters:  $\Theta_0$  and  $\Theta_{T_{\text{MRCA}}}$ .

The third model (*step model*) assumes two constant values of  $\Theta$  before and after a point in time denoted as  $\tau$ :

$$\Theta(t) = \begin{cases} \Theta_0 & t \leq \tau \\ \Theta_1 & t > \tau \end{cases}$$

The last model (*exponential double growth model*) assumes that the population experienced two different phases of exponential growth:

$$\Theta(t) = \begin{cases} \Theta_0 e^{\rho_1 t} & t \leq \tau \\ \Theta(\tau) e^{\rho_2(t-\tau)} = \Theta_0 e^{\rho_2 t + (\rho_1 - \rho_2)\tau} & t \geq \tau \end{cases}$$

which reduces to the first model if  $\rho_1 = \rho_2$ . These two last models have three free parameters.

### 1.1 Constant- $\Theta$ Model

The log-likelihood is:

$$\ln L = \sum_{i=2}^n \ln \binom{i}{2} - \ln \Theta - \binom{i}{2} \frac{t_i - t_{i-1}}{\Theta}.$$

Its partial derivative with respect to  $\Theta$  is:

$$\frac{\partial \ln L}{\partial \Theta} = \sum_{i=2}^n -\frac{1}{\Theta} + \binom{i}{2} \frac{t_i - t_{i-1}}{\Theta^2},$$

which, after setting  $\partial \ln L / \partial \Theta = 0$  can be solved to find the maximum likelihood estimator (MLE):

$$\hat{\Theta} = \frac{1}{n-1} \sum_{i=2}^n \binom{i}{2} (t_i - t_{i-1}).$$

Under the normal approximation of the likelihood function, the variance of  $\hat{\Theta}$  is calculated through the second derivative of  $\ln L$ :

$$\frac{\partial^2 \ln L}{\partial \Theta^2} = \sum_{i=2}^n \frac{1}{\Theta^2} - 2 \times \binom{i}{2} \frac{t_i - t_{i-1}}{\Theta^3},$$

and:

$$\widehat{\text{var}}(\hat{\Theta}) = - \left[ \frac{n-1}{\hat{\Theta}^2} - \frac{2}{\hat{\Theta}^3} \sum_{i=2}^n \binom{i}{2} (t_i - t_{i-1}) \right]^{-1}.$$

This estimator is implemented in `pegas` with the function `theta.tree`.

### 1.2 Exponential Growth Model

The integral in equation (1) is:

$$\int_{t_{i-1}}^{t_i} \frac{1}{\Theta(u)} du = -\frac{1}{\rho \Theta_0} (e^{-\rho t_i} - e^{-\rho t_{i-1}}),$$

leading to the log-likelihood:

$$\ln L = \sum_{i=2}^n \ln \binom{i}{2} - \ln \Theta_0 - \rho t_i + \binom{i}{2} \frac{1}{\rho \Theta_0} (e^{-\rho t_i} - e^{-\rho t_{i-1}}),$$

with its first partial derivatives being:

$$\begin{aligned}\frac{\partial \ln L}{\partial \Theta_0} &= \sum_{i=2}^n -\frac{1}{\Theta_0} - \binom{i}{2} \frac{1}{\rho \Theta_0^2} (e^{-\rho t_i} - e^{-\rho t_{i-1}}), \\ \frac{\partial \ln L}{\partial \rho} &= \sum_{i=2}^n -t_i + \binom{i}{2} \frac{1}{\Theta_0} \left[ -\frac{1}{\rho^2} (e^{-\rho t_i} - e^{-\rho t_{i-1}}) + \frac{1}{\rho} (-t_i e^{-\rho t_i} + t_{i-1} e^{-\rho t_{i-1}}) \right].\end{aligned}$$

These cannot be solved analytically to find the MLEs  $\hat{\Theta}_0$  and  $\hat{\rho}$  but they may be used to speed-up an optimization procedure with analytical gradients.

### 1.3 Linear Growth Model

Let  $\kappa = (\Theta_{T_{\text{MRCA}}} - \Theta_0)/T_{\text{MRCA}}$ , so  $\Theta(t) = \Theta_0 + \kappa t$ . The integral in equation~(1) is:

$$\begin{aligned}\int_{t_{i-1}}^{t_i} \frac{1}{\Theta(u)} du &= \frac{\ln(\Theta_0 + \kappa t_i)}{\kappa} - \frac{\ln(\Theta_0 + \kappa t_{i-1})}{\kappa} \\ &= \frac{1}{\kappa} \ln \frac{\Theta_0 + \kappa t_i}{\Theta_0 + \kappa t_{i-1}}.\end{aligned}$$

The log-likelihood is thus:

$$\ln L = \sum_{i=2}^n \ln \binom{i}{2} - \ln(\Theta_0 + \kappa t_i) - \binom{i}{2} \frac{1}{\kappa} \ln \frac{\Theta_0 + \kappa t_i}{\Theta_0 + \kappa t_{i-1}}.$$

The partial derivatives can be calculated analytically.

### 1.4 Step Model

It is easier to calculate the integral in equation~1 with the difference:

$$\int_{t_{i-1}}^{t_i} \frac{1}{\Theta(u)} du = \int_0^{t_i} \frac{1}{\Theta(u)} du - \int_0^{t_{i-1}} \frac{1}{\Theta(u)} du. \quad (2)$$

The integral from the origin is:

$$\int_0^t \frac{1}{\Theta(u)} du = \begin{cases} \frac{t}{\Theta_0} & t \leq \tau \\ \frac{\tau}{\Theta_0} + \frac{t - \tau}{\Theta_1} & t > \tau. \end{cases}$$

This is then plugged into equation~1 with a simple Dirac delta function.

### 1.5 Exponential Double Growth Model

In this model the inverse of  $\Theta(t)$  is:

$$\frac{1}{\Theta(t)} = \begin{cases} \frac{e^{-\rho_1 t}}{\Theta_0} & t \leq \tau \\ \frac{e^{-\rho_2 t - (\rho_1 - \rho_2)\tau}}{\Theta_0} & t \geq \tau \end{cases}$$

Again, it is easier to calculate the integral in equation~(1) with equation~(2). The integral from the origin is:

$$\int_0^t \frac{1}{\Theta(u)} du = \begin{cases} -\frac{1}{\rho_1 \Theta_0} (e^{-\rho_1 t} - 1) & t \leq \tau \\ -\frac{1}{\rho_1 \Theta_0} (e^{-\rho_1 \tau} - 1) - \frac{1}{\rho_2 \Theta_0} [e^{-\rho_2 t - (\rho_1 - \rho_2)\tau} - e^{-\rho_1 \tau}] & t \geq \tau \end{cases}$$

This is then plugged into equation~(1) with a simple Dirac delta function.

## 2 Simulation of Coalescent Times

It is generally possible to simulate coalescent times from a time-dependent model by rescaling a set of coalescent times simulated with constant  $\Theta$ , denoted as  $t$ , with:

$$t' = \frac{\int_0^t \Theta(u) du}{\Theta(0)}.$$

This gives for the exponential growth model [2]:

$$t' = \frac{e^{\rho t} - 1}{\rho},$$

for the linear growth model:

$$t' = t + t^2 (\Theta_{T_{\text{MRCA}}} / \Theta_0 - 1) / T_{\text{MRCA}},$$

for the step model:

$$t' = \tau + (t - \tau) \Theta_1 / \Theta_0 \quad \text{if } t > \tau,$$

and for the exponential double growth model:

$$t' = \begin{cases} \frac{e^{\rho_1 t} - 1}{\rho_1} & t \leq \tau \\ \frac{e^{\rho_1 \tau} - 1}{\rho_1} + \frac{e^{\rho_2 t + (\rho_1 - \rho_2)\tau} - e^{\rho_1 \tau}}{\rho_2} & t \geq \tau \end{cases}$$

## 3 Implementation in coalescentMCMC

Five functions are available in `coalescentMCMC` which compute the likelihood of the constant- $\Theta$  model as well as the four above ones:

```
dcoal(phy, theta, log = FALSE)
dcoal.time(phy, theta0, rho, log = FALSE)
dcoal.linear(phy, theta0, thetaT, TMRCA, log = FALSE)
dcoal.step(phy, theta0, theta1, tau, log = FALSE)
dcoal.time2(phy, theta0, rho1, rho2, tau, log = FALSE)
```

The two arguments common to all functions are:

**phy:** a tree as an object of class "phylo";

**log:** a logical value, if **TRUE** the values are returned log-transformed which is recommended for computing log-likelihoods.

The other arguments are the parameters of the models.

## References

- [1] R. C. Griffiths and S. Tavaré. Sampling theory for neutral alleles in a varying environment. *Philosophical Transactions of the Royal Society of London. Series B. Biological Sciences*, 344:403–410, 1994.
- [2] M. K. Kuhner, J. Yamato, and J. Felsenstein. Maximum likelihood estimation of population growth rates based on the coalescent. *Genetics*, 149:429–434, 1998.