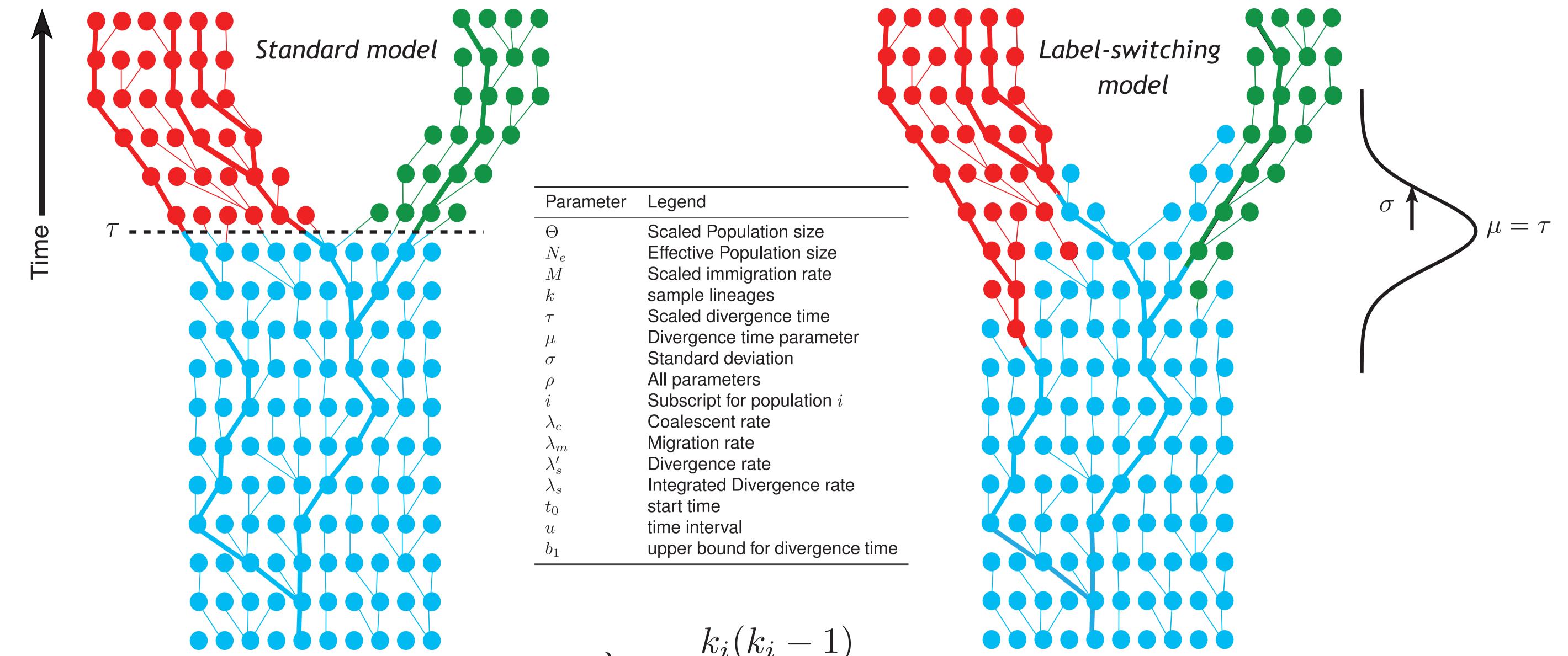
Population divergence estimation using lineage-label switching



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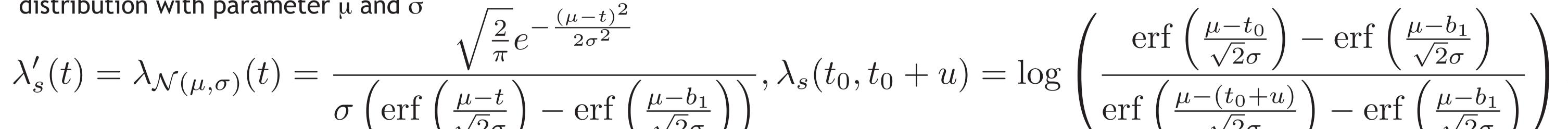
In the standard model the divergence time is a fixed parameter; in inferences this parameter is changed using an arbitrary prior distribution. In contrast, the label-switching model treats the divergence time as a random varable with a truncated normal distribution with parameter μ and σ

Standard deviation
All parameters
Subscript for population <i>i</i>
Coalescent rate
Migration rate
Divergence rate
Integrated Divergence rate
start time
time interval
upper bound for divergence time

$$\lambda_{c_i} = \frac{k_i(k_i - 1)}{\Theta_i},$$

$$\lambda_{M_{.i}} = \sum_{j=1}^{n_p} k_i M_{ji};$$

We use a hazard function to evaluate the risk of switching the label looking backwards in time; this leads to a mixture of watiting times, in the simplest case we consider coalescent and divergence events, in more complex cases we can add immigration events.

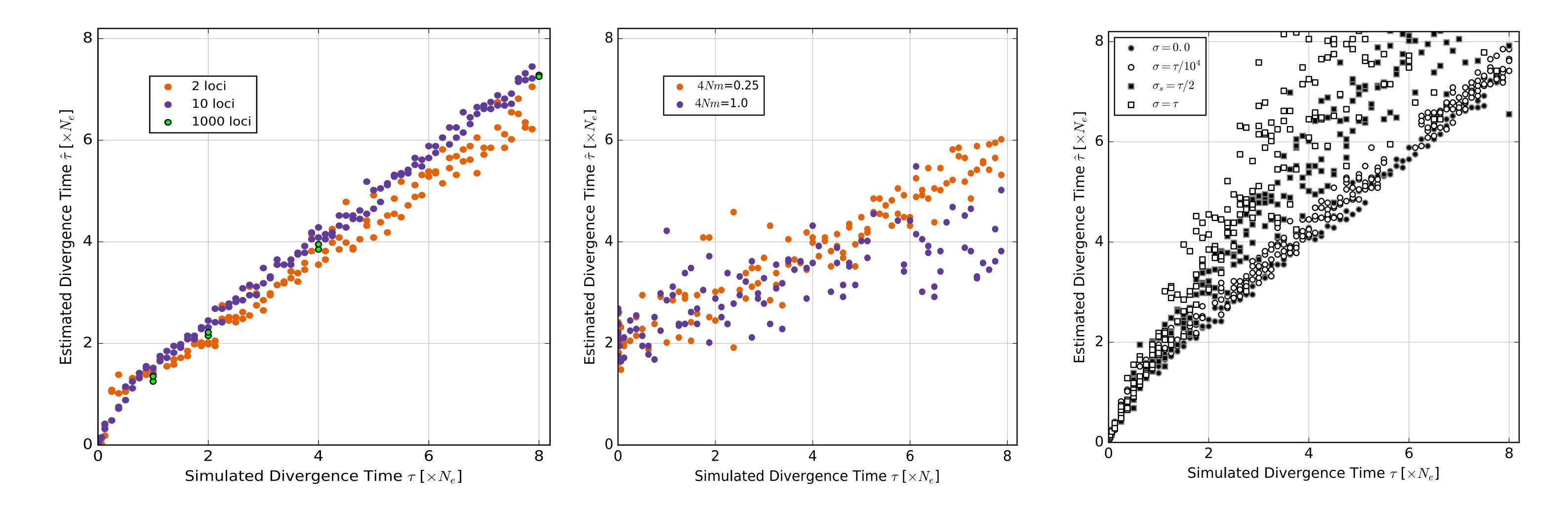


$$p_d(u|G, t_0, \rho) = \frac{1}{k} e^{-u(\lambda_c + \lambda_m) + \lambda_s(t_0 + u)} [\lambda_c + \lambda_m + \lambda'_s(t_0 + u)] \int_0^\infty e^{-u\lambda_c} e^{-u\lambda_m} \lambda'_s(t) \ e^{\lambda_s(t_0, t_0 + u)} du.$$

Unfortunately, the integral needs to be solved numerically. This makes the above calculation very slow. Instead of solving the integral numerically, we approximate using the midpoint rule, this approximation leads to a simpler, approximate, solution:

$$p_s(u|G, t_0, \rho) = e^{-u(\frac{k(k-1)}{\Theta} + kM + \lambda'_s(t_0 + \epsilon))} \frac{\lambda'_s(t_0 + \epsilon)}{k}$$

We implemented this method in the program MIGRATE version 4, which is available from the MIGRATE website (int the preview section): http://peterbeerli.com/migrate-html5 or http://popgen.sc.fsu.edu



Disclaimer: figures will most likely change for the publication.