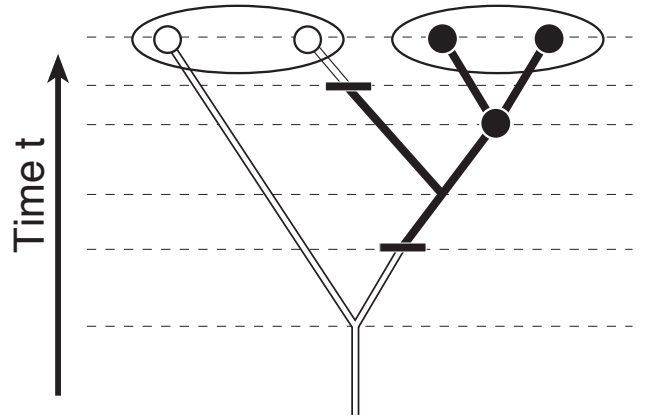# Integration and the Structured Coalescent

Michal Palczewski (Advisor: Peter Beerli)

$$P(G|\theta) = \prod_{i=2}^{K} \frac{\exp \frac{-k(k-1)u_i}{\theta}}{\theta}$$

θ is the mutation rate scaled population size
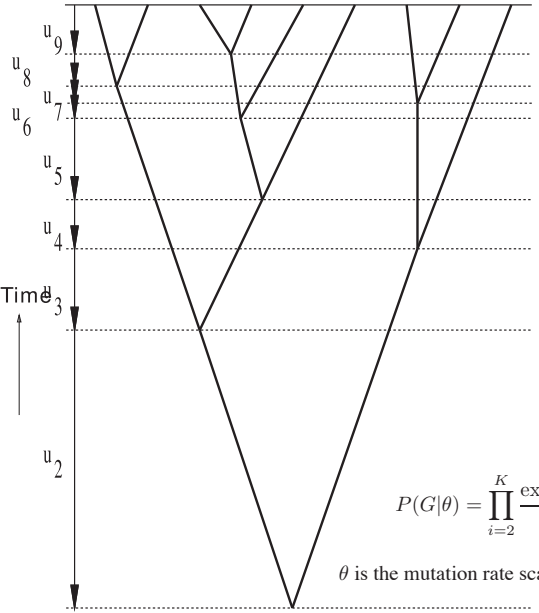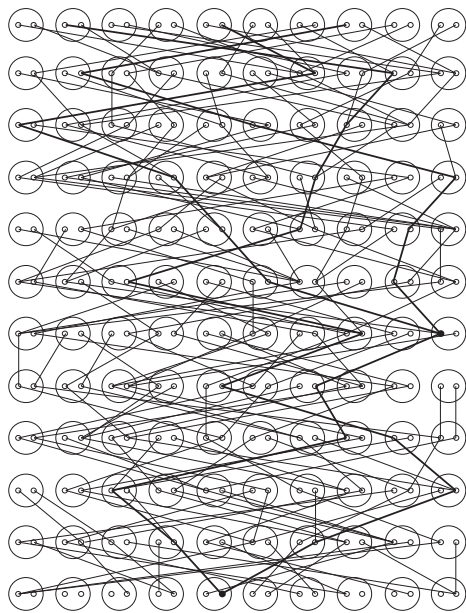
Typically MCMC is used to sample trees like the one above. This includes sampling migration events in addition to different tree topologies.

The Wright Fisher Model describes a randomly mating population. Where every individual in a generation comes from a random union of gamates. When looking backward in time all individuals have a common ancestor. The relationships form a tree. The length of time until a coalescense is proportional to the population size.
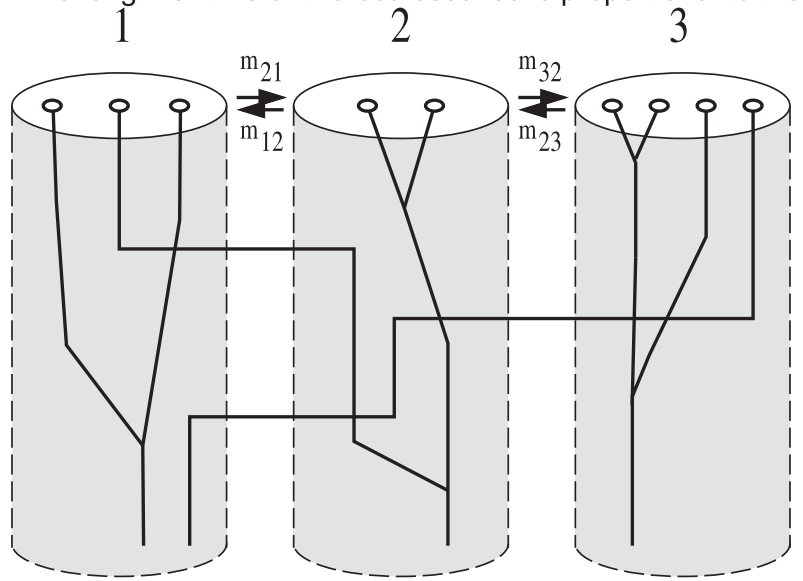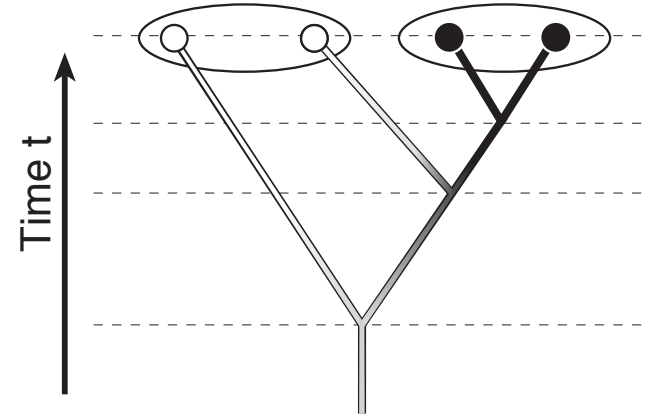
The coalescent framework can be extended to a non random mating population. The example to the left shows three populations exchanging migrants. This is known as

$$\lambda(t) = \sum_k \sum_i \sum_{j, i \neq j} \frac{P(L_i \in k|t) P(L_j \in k|t)}{\Theta_k}$$

$$P(\epsilon|t, t_0) = \lambda(t) e^{\int_{t_0}^{t} \lambda(x)dx}$$

$$P(G|M, \Theta) = \prod_{i=1}^{k-1} P(\epsilon|u_i, u_{i-1})$$

We use a time continuous Markov chain model for location probability and a non-homogeneous Poisson process for coalescent times one can calculate the probability of just the topology. This allows us to sample from a much smaller sample space.