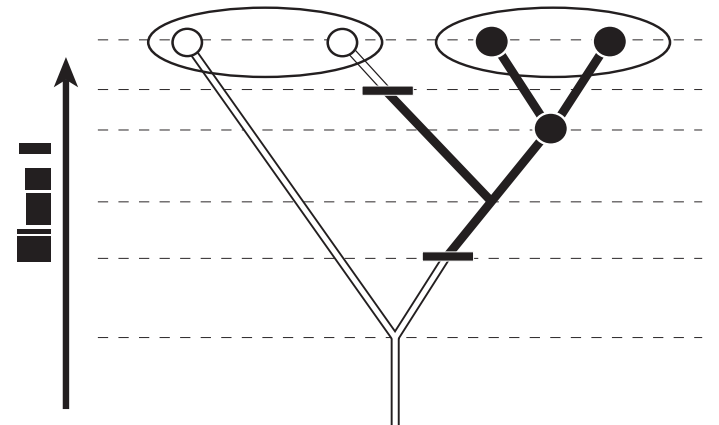
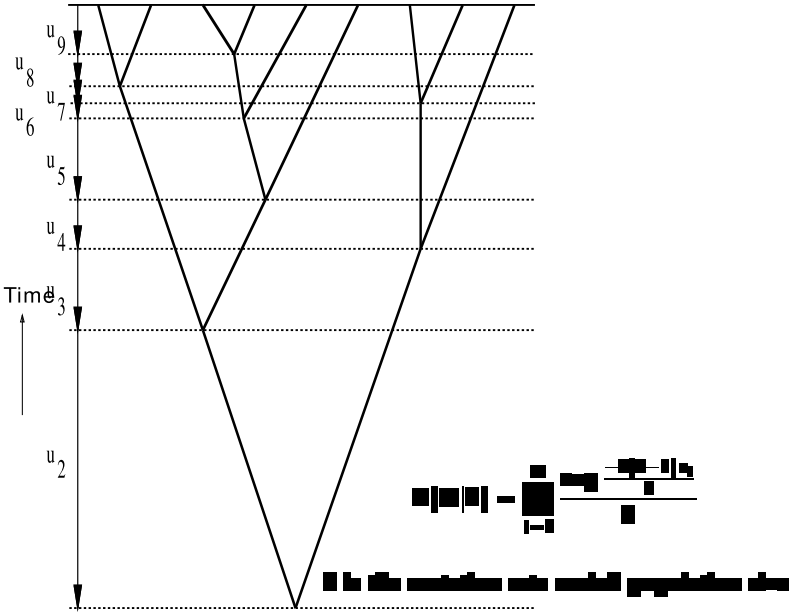
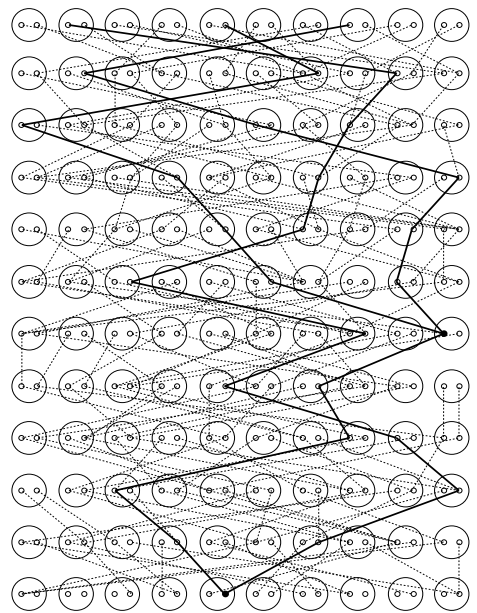


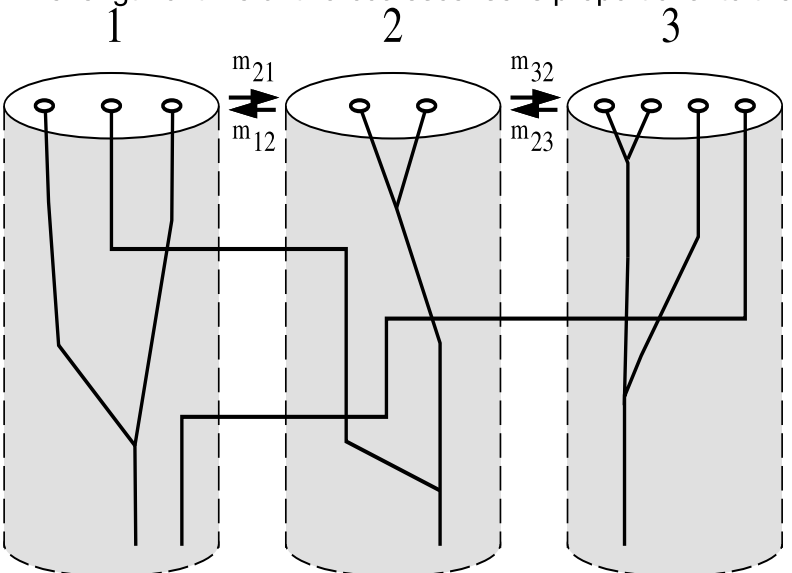
Integration and the Structured Coalescent

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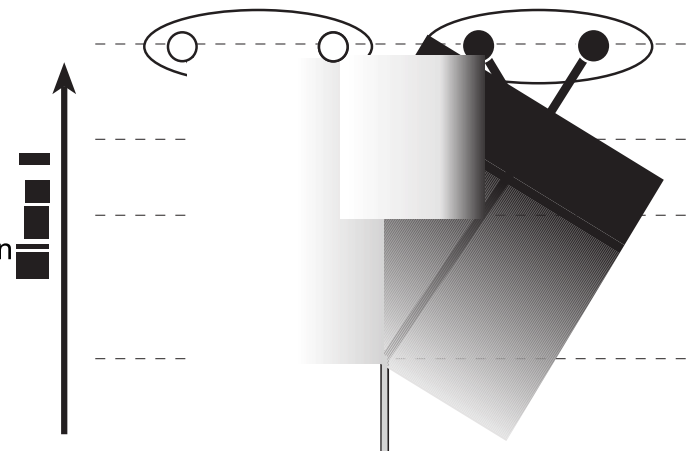
Typically MCMC is used to sample trees like the one above. This includes sampling migration events in addition to different tree topologies.

The Wright Fisher Model describes a randomly mating population. Where every individual in a generation comes from a random union of gametes. When looking backward in time all individuals have a common ancestor. The relationships form a tree. The length of time until a coalescence 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 the structured coalescent.

$$P[G|M, \mathbf{u}] = \sum_{\mathbf{k}} \sum_{\mathbf{l}} \sum_{\mathbf{t}} \frac{P[L_1 \in k | t] P[L_2 \in l | t]}{P[\mathbf{L} \in \mathbf{k} | t]} P[\mathbf{G} | \mathbf{t}, \mathbf{u}] = P[\mathbf{G} | \mathbf{t}, \mathbf{u}] e^{-\sum_{i=1}^n \lambda_i t} \prod_{i=1}^n P[\mathbf{L}_i \in k_i | t]$$



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.