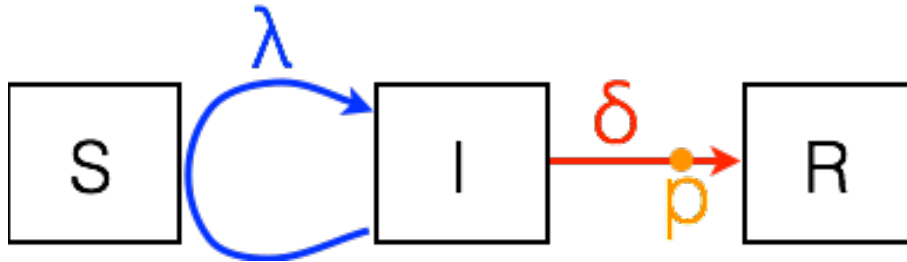


# Epidemiological model



transmission rate  $\lambda$

"becoming-non-infectious" rate  $\delta$

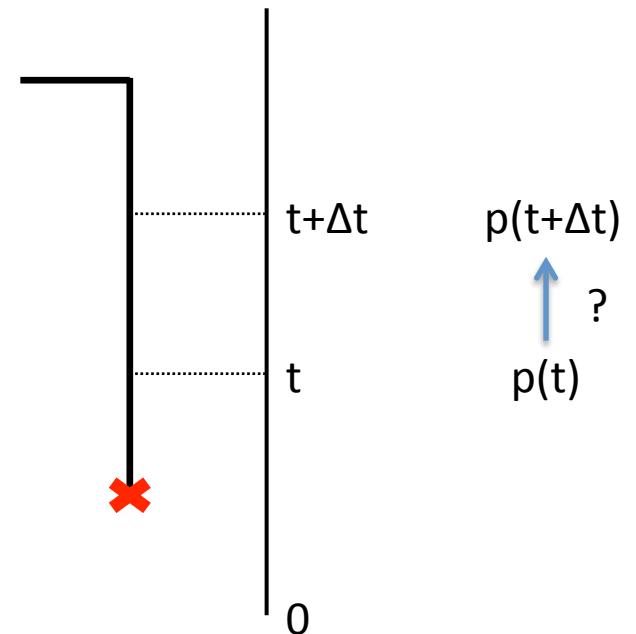
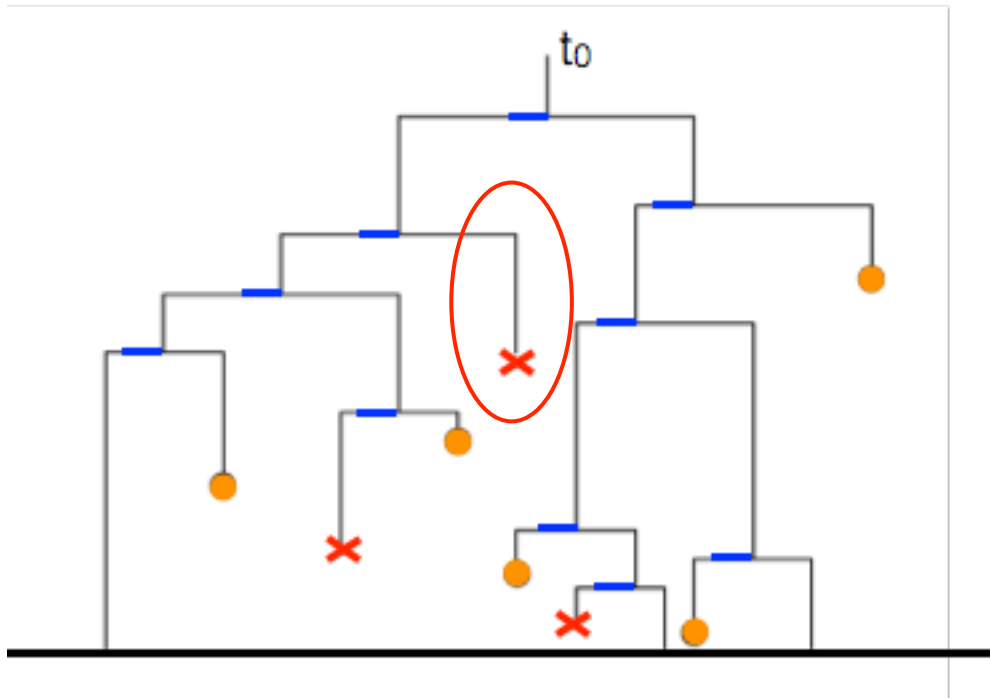
sampling probability  $p$

Lik (  ) ?

today

# Likelihood calculation

$p(t)$  : probability that a given lineage at time  $t$  does NOT appear in the tree

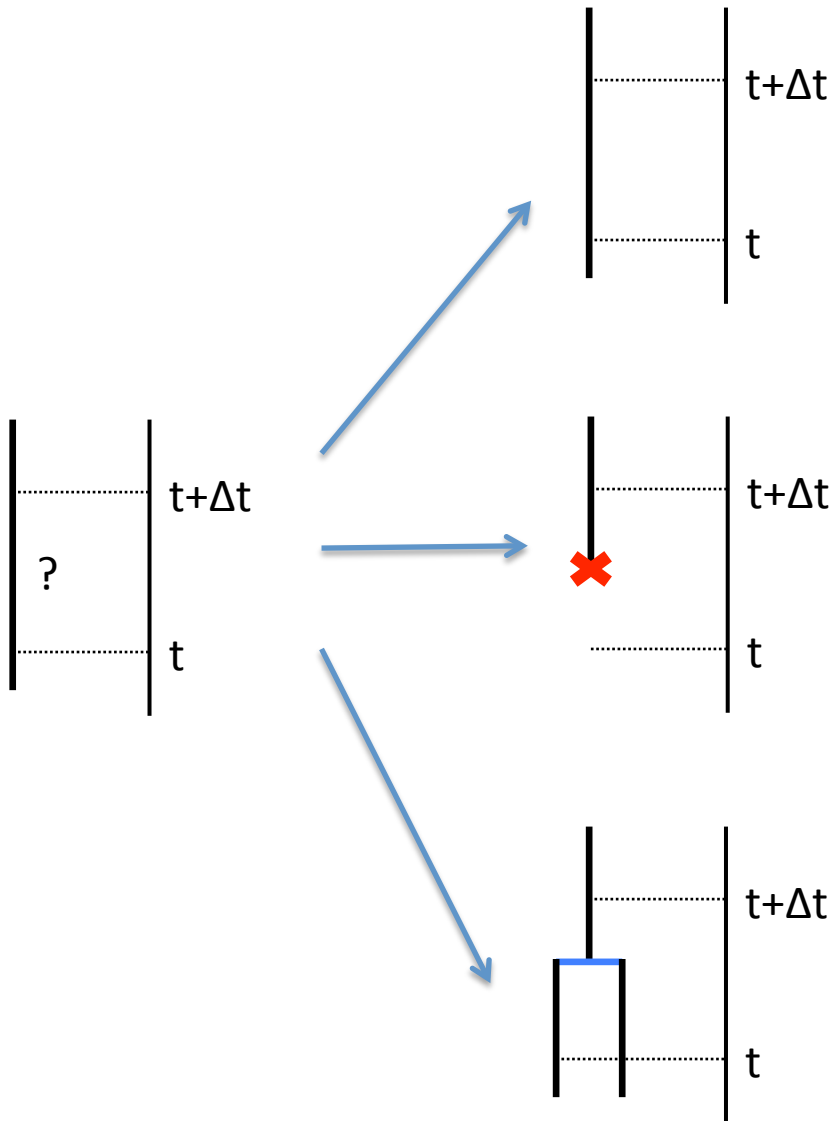


$$p(t + \Delta t) =$$

$$(1 - (\lambda + \delta) \Delta t) p(t)$$

$$+ \delta (1 - p) \Delta t$$

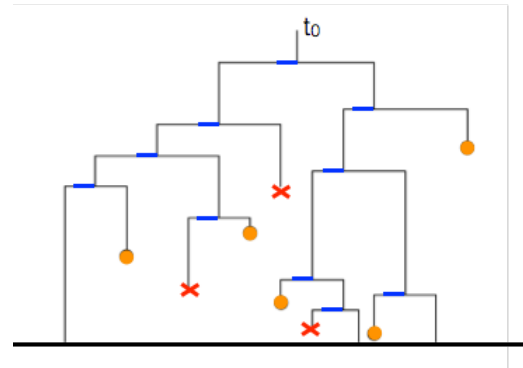
$$+ \lambda \Delta t p(t)^2$$



$$\Delta t \rightarrow 0 \quad \frac{p(t + \Delta t) - p(t)}{\Delta t} = -(\lambda + \delta)p(t) + \delta(1 - p) + \lambda p(t)^2$$

$$\frac{dp(t)}{dt} = -(\lambda + \delta)p(t) + \delta(1 - p) + \lambda p(t)^2$$

Initial condition:  $p(0) = 1$



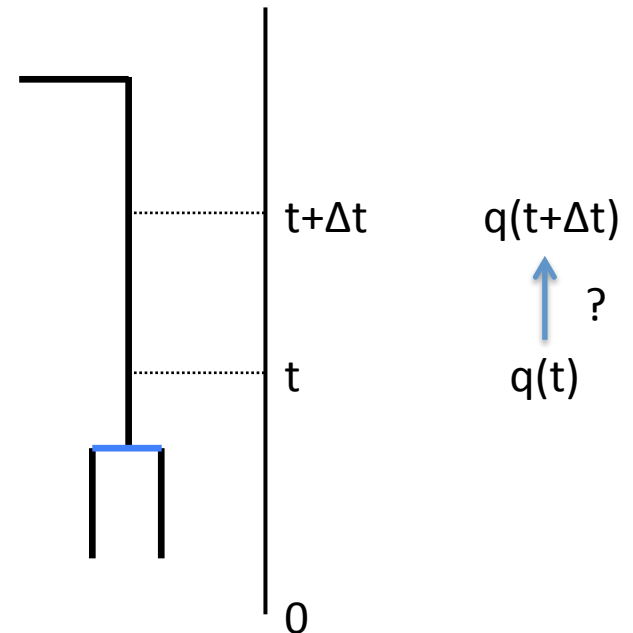
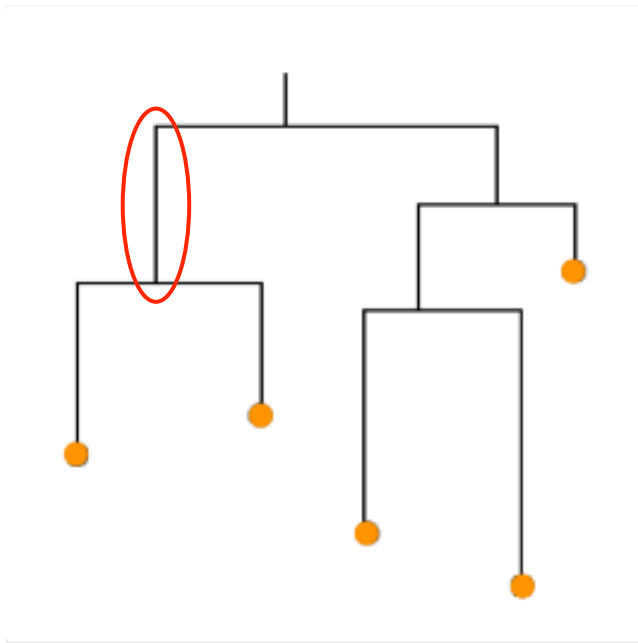
Closed form solution: 
$$p(t) = -\frac{1}{\lambda} \frac{x_1(x_2 + \lambda)e^{-ct} - x_2(x_1 + \lambda)}{(x_2 + \lambda)e^{-ct} - (x_1 + \lambda)}$$

$$x_1 = \frac{-(\lambda + \delta) - c}{2} \quad \text{and} \quad x_2 = \frac{-(\lambda + \delta) + c}{2}$$

$$c = \sqrt{(\lambda + \delta)^2 - 4\delta\lambda(1 - p)}$$

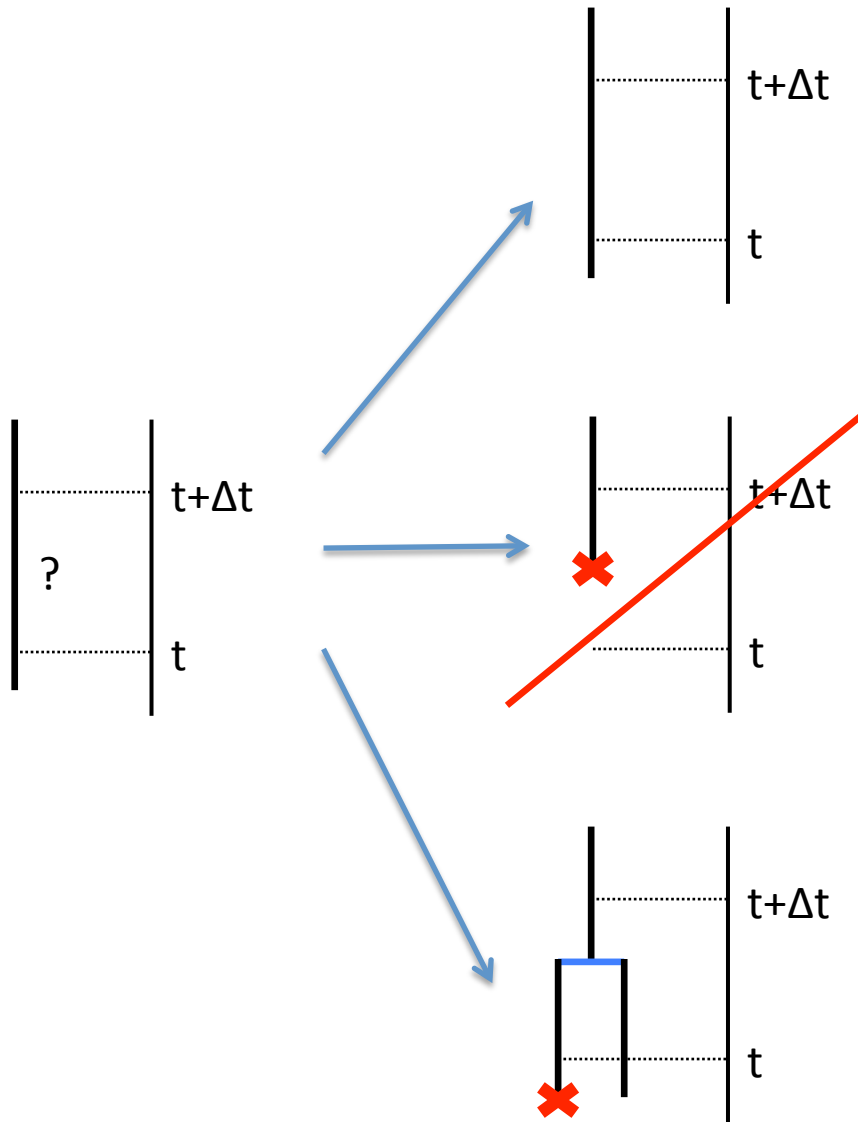
# Likelihood calculation

$q(t)$  : probability that a given lineage at time  $t$  evolves as shown in the tree



$$q(t + \Delta t) =$$

$$(1 - (\lambda + \delta) \Delta t) q(t)$$

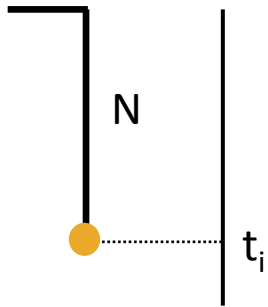


$$+ \lambda \Delta t \times \mathbf{2} q(t) p(t)$$

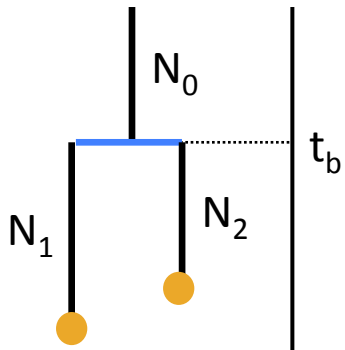
$$\Delta t \rightarrow 0 \quad \frac{q(t + \Delta t) - q(t)}{\Delta t} = -(\lambda + \delta)q(t) + 2\lambda p(t)q(t)$$

$$\frac{dq(t)}{dt} = -(\lambda + \delta)q(t) + 2\lambda p(t)q(t)$$

Initial condition ?



$$q_N(t_i) = \delta p \, dt$$



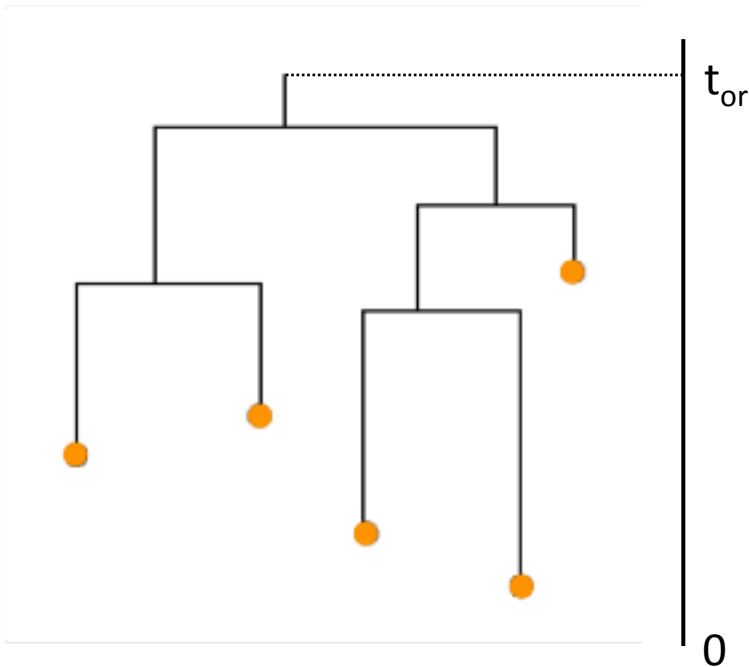
$$q_{N_0}(t_b) = \lambda \, dt \, q_{N_1}(t_b) \, q_{N_2}(t_b)$$



# Final result

$$q_N(t) = \frac{(x_1 + \lambda)^2 C_N}{(x_1 + \lambda - (x_2 + \lambda)e^{-ct})^2 e^{ct}}$$

where  $C_N$  is provided by the initial condition



$$P(\text{tree}) = q_{\text{root}}(t_{or})$$