### **Review Questions**

What is a Markov chain? What is the Markov property?

What are the differences between discrete- and continuous-time Markov chains?

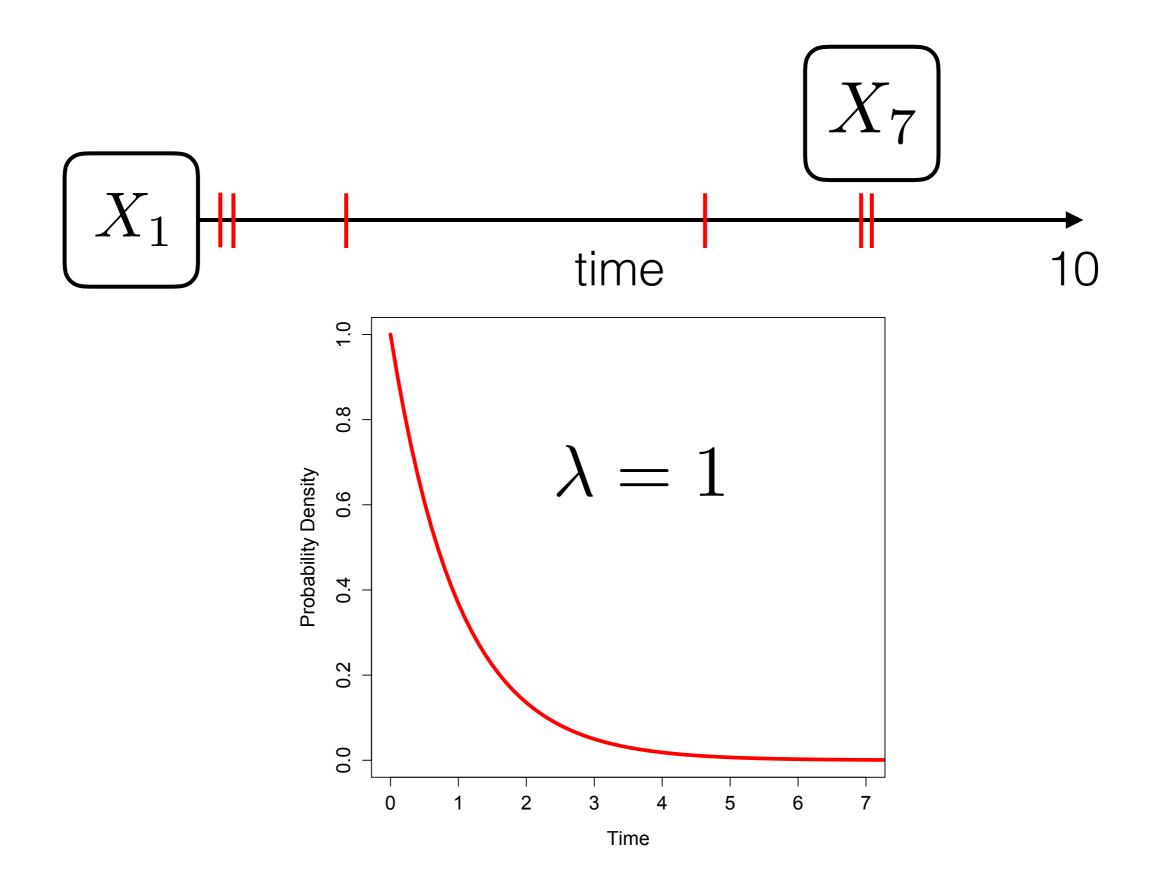
What is the state space for a typical phylogenetic model?

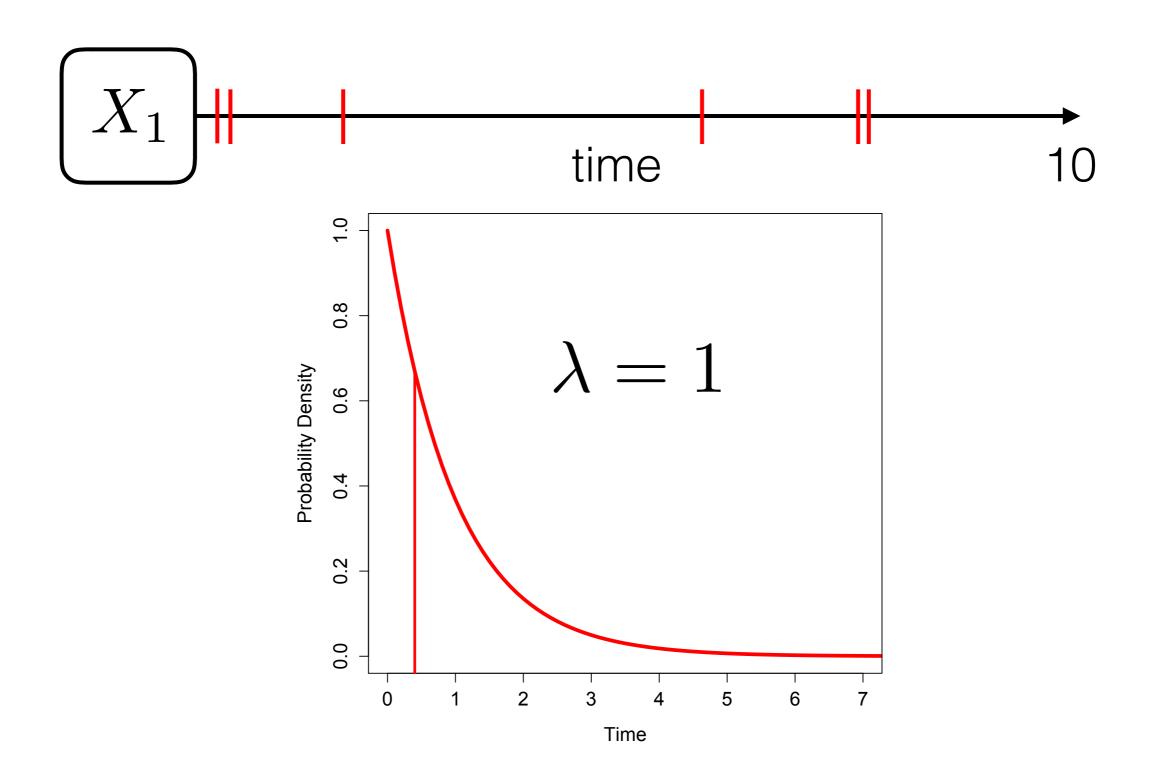
What does the stationary distribution tell us?

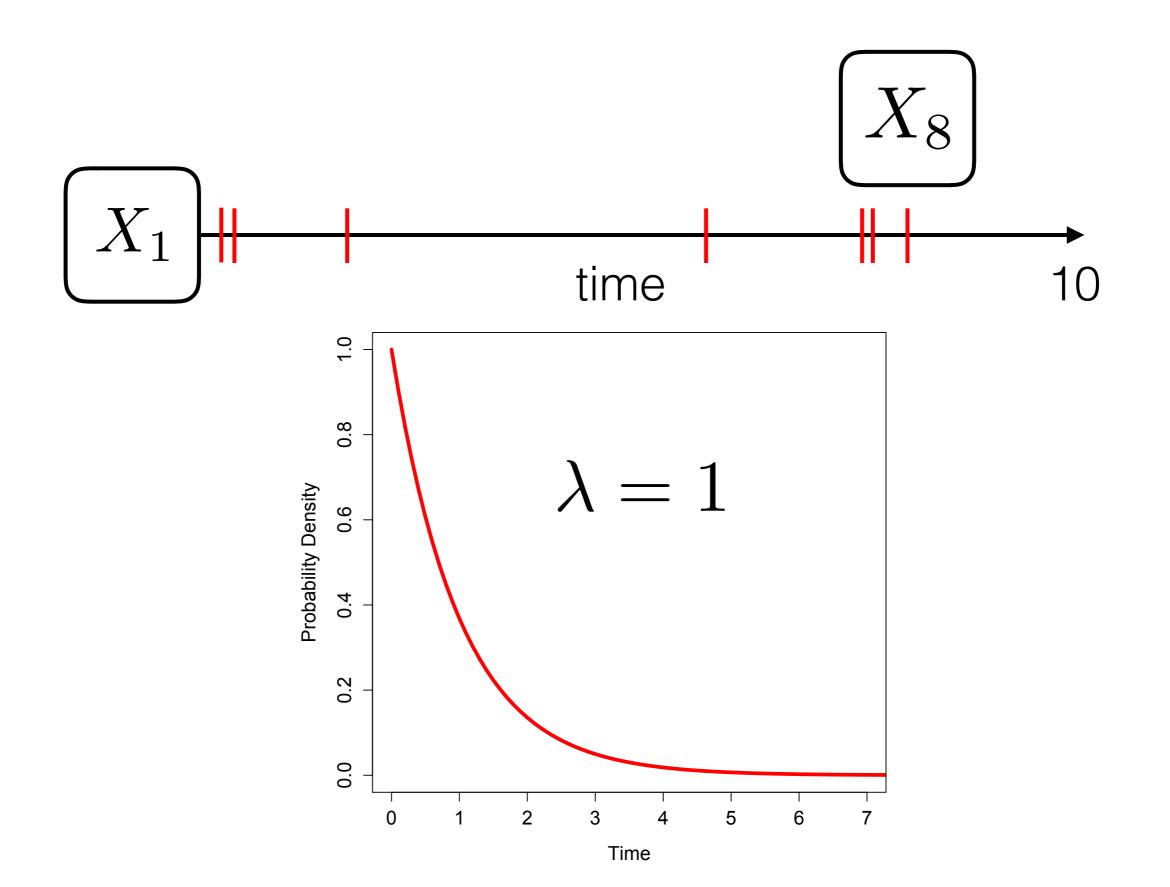
What does it mean for a chain to be reversible?

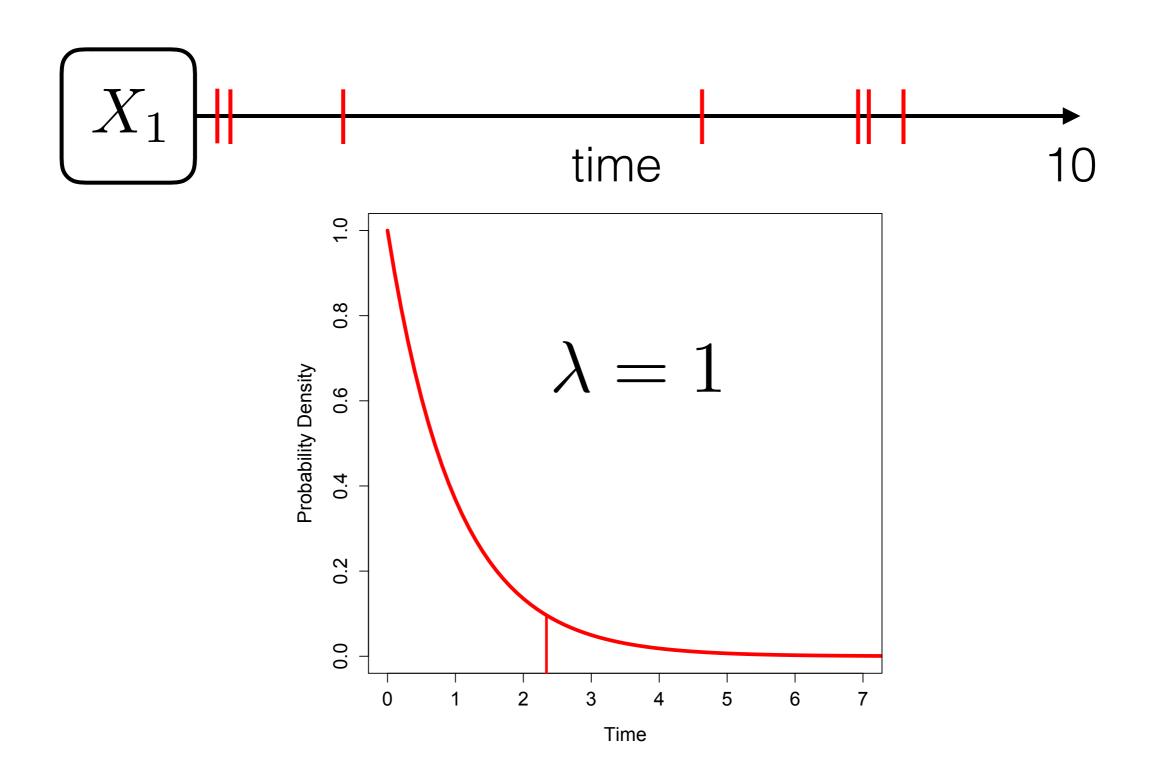
### Simulating Sequence Evolution Assignment

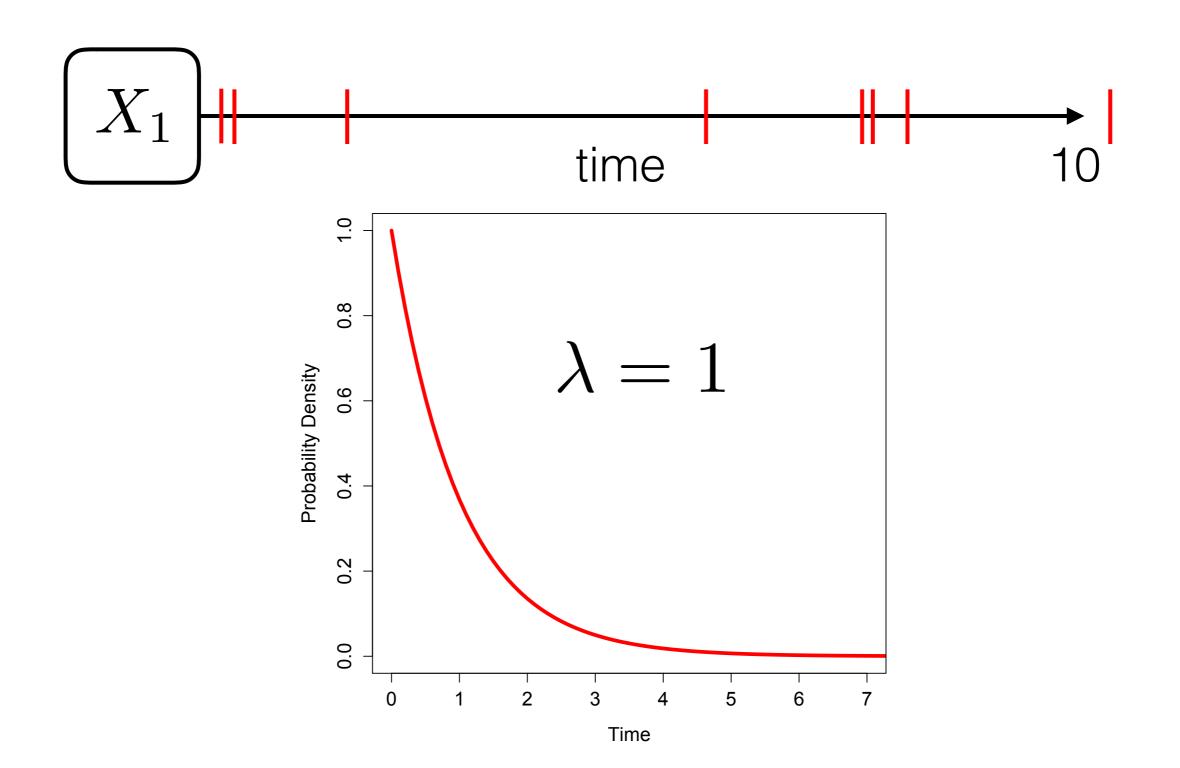
PSEUDOCODE! What are the steps?













Simulation stops when a waiting time is drawn that exceeds the total length of the simulation (for phylogenetics, think of this as a branch length).

The state of the chain at the end of the simulation is the state last sampled before the branch length was exceeded ( $X_8$ , in this case).



If the rate parameter ( $\lambda$ ) is 1, what is the expected number of events in a Poisson distribution? What does this mean if we're thinking about a phylogenetic tree with branch lengths?

#### **Poisson Process**

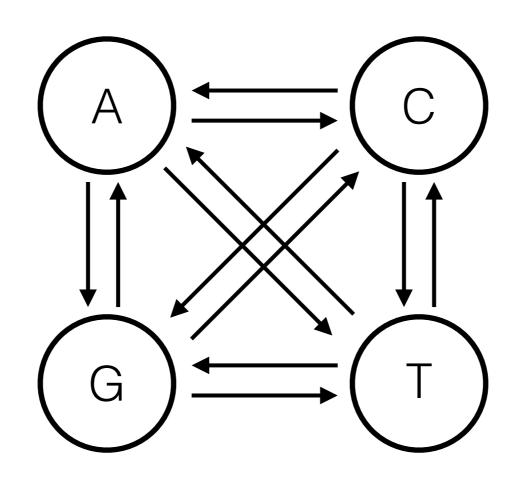


A continuous-time Markov chain is one type of a **Poisson process**, which has these properties:

- (1) The number of events that occur in an interval of length t is a Pois( $\lambda t$ ) random variable.
- (2) The number of events that occur in disjoint intervals are independent of one another.
- (3) The waiting times between events are distributed as:  $T \sim Exp(\lambda)$

Exponential Rate for State A

Relative



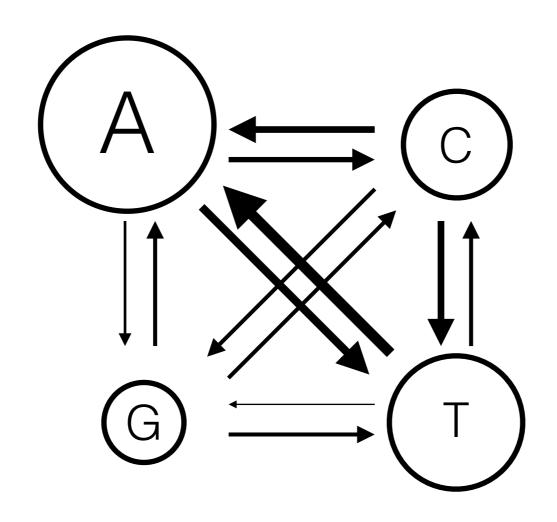
General Time Reversible (GTR; Tavaré 1986)

$$\pi = (\pi_{A}, \pi_{C}, \pi_{G}, \pi_{T}) R = \begin{pmatrix} A & C & G & T \\ A & r_{AC} & r_{AG} & r_{AT} \\ G & & r_{CG} & r_{CT} \\ T & & r_{CG} & r_{CT} \end{pmatrix}$$

$$Q = \begin{pmatrix} A & C & G & T \\ A & C & G & T \\ C & \pi_{C} r_{AC} & \pi_{G} r_{AG} & \pi_{T} r_{AT} \\ \pi_{A} r_{AC} & \pi_{G} r_{CG} & \pi_{T} r_{CT} \\ \pi_{A} r_{AG} & \pi_{C} r_{CG} & \pi_{T} r_{CT} \\ \pi_{A} r_{AT} & \pi_{C} r_{CT} & \pi_{G} r_{GT} \end{pmatrix}$$

General Time Reversible (GTR; Tavaré 1986)

### General Time Reversible (GTR)



### Reversibility

$$\pi_i q_{ij} = \pi_j q_{ji}$$
, for all  $i \neq j$ 

if 
$$i = A$$
 and  $j = C$ ,
$$\pi_A q_{AC} = \pi_C q_{CA}$$

$$\pi_A \pi_C r_{AC} = \pi_C \pi_A r_{AC}$$

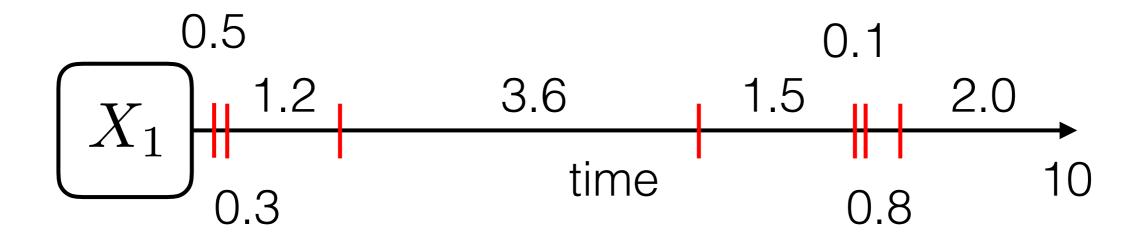
# **Branch-Length Scaling**

$$A$$
  $C$   $G$   $T$ 
 $A$   $A$   $\pi_{C}r_{AC}$   $\pi_{G}r_{AG}$   $\pi_{T}r_{AT}$ 
 $C$   $\pi_{A}r_{AC}$   $\pi_{ust}$   $\pi_{G}r_{CG}$   $\pi_{T}r_{CT}$ 
 $\pi_{A}r_{AG}$   $\pi_{C}r_{CG}$   $\pi_{G}r_{GT}$   $\pi_{T}r_{GT}$ 
 $T$   $\pi_{A}r_{AT}$   $\pi_{C}r_{CT}$   $\pi_{G}r_{GT}$ 

Branch lengths typically denote **expected number of substitutions**. For this to be true, the weighted mean across all states must be 1.

Jukes-Cantor

Instead of thinking about simulating a character history, let's calculate the probability of one that we've been given.



The events in this history are independent. When events are independent how do we combine their probabilities?

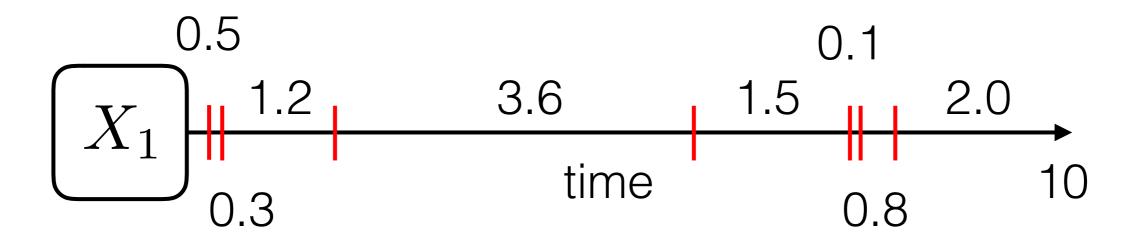
What are the relevant probabilities here?

Jukes-Cantor



Prob(history) =  $Exp(0.5)Exp(0.3)Exp(0.3)Exp(1.2)Exp(3.6)Exp(1.5)Exp(0.1)Exp(0.8)Exp(2.0)(1/3)^7$ 

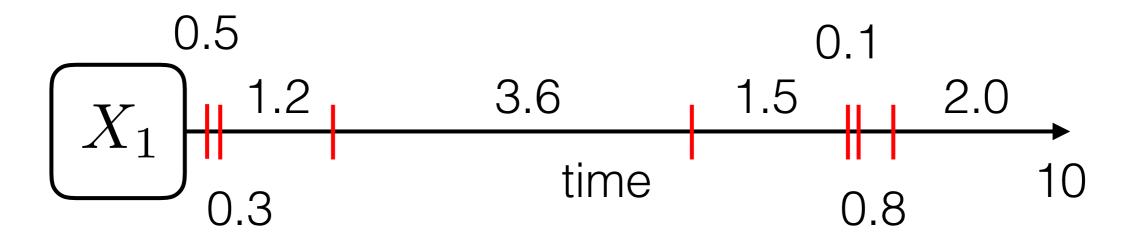
Jukes-Cantor



Prob(history) =  $Exp(0.5)Exp(0.3)Exp(0.3)Exp(1.2)Exp(3.6)Exp(1.5)Exp(0.1)Exp(0.8)Exp(2.0)(1/3)^7$ 

**Waiting Times** 

Jukes-Cantor



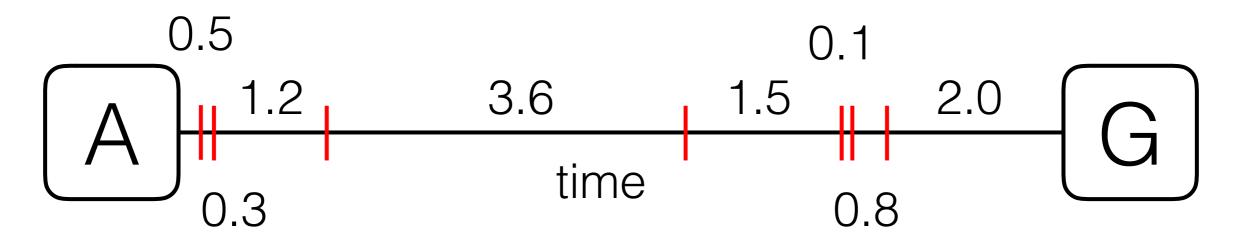
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**Waiting Times** 

Character State Changes

# Probability of Starting and Ending

Jukes-Cantor



Let's say we simulated along our branch of length 10. We started in A and ended in G, with those specific events marked.

# Probability of Starting and Ending

Jukes-Cantor



Let's say we simulated along our branch of length 10. We started in A and ended in G, with those specific events marked.

But now let's say we don't actually know the precise character history. How do we calculate

$$P(A \text{ to } G | t = 10)$$
?

# Probability of Starting and Ending

Jukes-Cantor

$$P(t) = e^{Qt}$$

This is the continuous-time equivalent of the matrix exponentiation we did with the discrete-time matrix!