#### A very small intro to CTMC in phylogenetics

Rosana Zenil-Ferguson

University of Hawai'i

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#### We are always interested in knowing the posterior distribution







#### X(t) = Evolution of flower color at time changes according time t

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*M* is our Model (a.k.a.the hypothesis) Blue flowers evolve to red and viceversa

 $\boldsymbol{\theta} = (q_{BR}, q_{RB})$ 

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#### The prior distribution: $P(\theta)$



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#### How are these assumptions represented graphically?



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*D* is our data We go into our favorite herbarium, field site, or green house and we collect color of multiple species

How do we integrate our model  $\theta$  and our data D ?

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### Calculating the likelihood $P(D|\theta)$

• We assume a phylogenetic tree  $\Psi$  (for this example is fixed)

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### Calculating the likelihood $P(D|\theta)$

- We assume a phylogenetic tree  $\Psi$  (for this example is fixed)
- Data: a sample of red and blue flowers on the tips of our phylogeny tree

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### Likelihood function: The probability of the sample given our hypothesis $\theta$



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## The probability of a single possible story in phylogenetics

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# Calculating the likelihood is computationally challenging

Felsenstein (1981)= Pruning algorithm, reduces the complexity in the calculation.

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- Reminder: Optimizations to find maximum likelihood estimates and confident intervals require challenging numerical algorithms

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#### How do the rates connect with the probabilities?

Q-matrix= The infinitesimal probability matrix is the derivative of the probability



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Likelihood in graphical form  $P(D|\theta)$ 



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The posterior distribution: the model conditional to the observed data



Explicit notation: In RevBayes we have notation for fixed variables, random variables, observed data, deterministic function,...

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- Explicit notation: In RevBayes we have notation for fixed variables, random variables, observed data, deterministic function,...
- Modularity: Once I have built a model I can connect other as a module (building blocks!)

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