

Two requirements for working with data and trees are:

- 1) Tree is ultrametric - All tips are reaching the present and tree is time-calibrated
- 2) Tree is binary (bifurcating)

## Discrete trait models

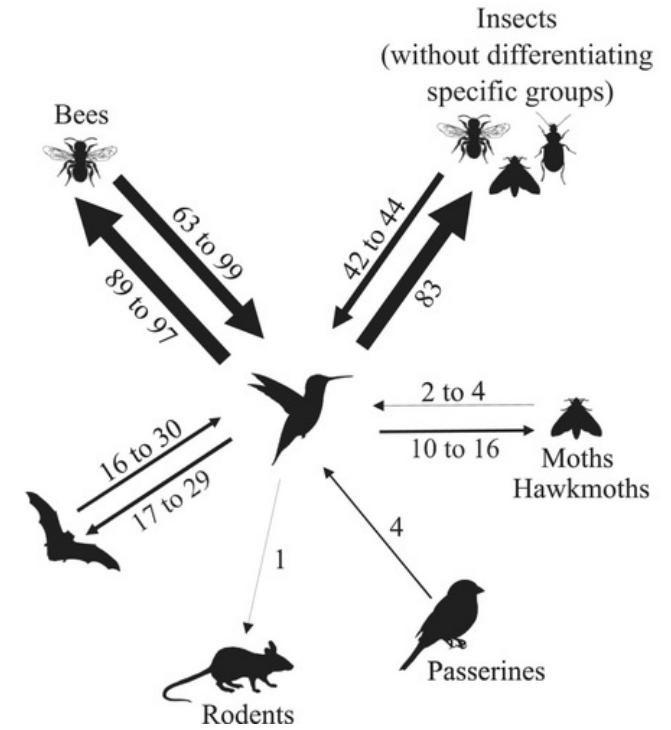
Introduction to phylogenetic comparative methods

In R the functions you would use to check for your tree shape are

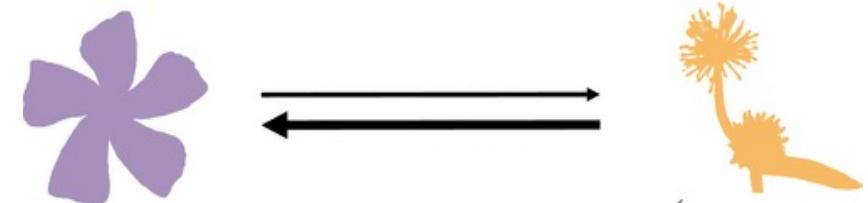
- (1) `is.ultrametric(Φ)`
- (2) `is.binary(Φ)`

# Pollination

- Plants depend on pollination to start the breeding process
- Pollen can be transferred from plant to plant by insects, wind, vertebrates, or even water
- There are multiple types of pollination, and frequently within a flowering plant/genus or family we can find different strategies for pollination.
- Often flower shape tells us something about the type of pollination we can expect.



Barreto et al. 2024



How do we estimate the number of transitions and the tempo?

# Cumberland Falls State Park, KY



*Thalictrum*  
*multiple changes between*  
*insect and wind pollination*

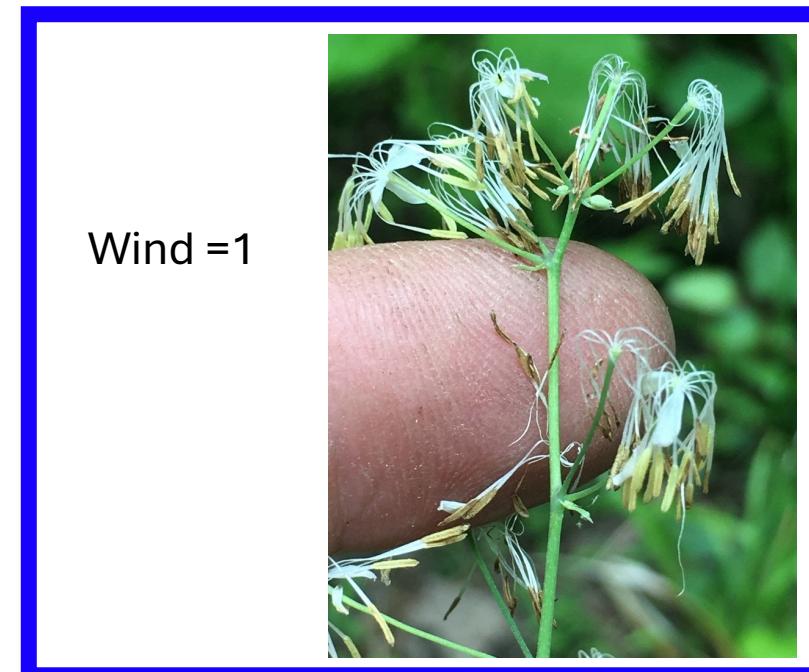
Verónica di Stilio  
University of Washington

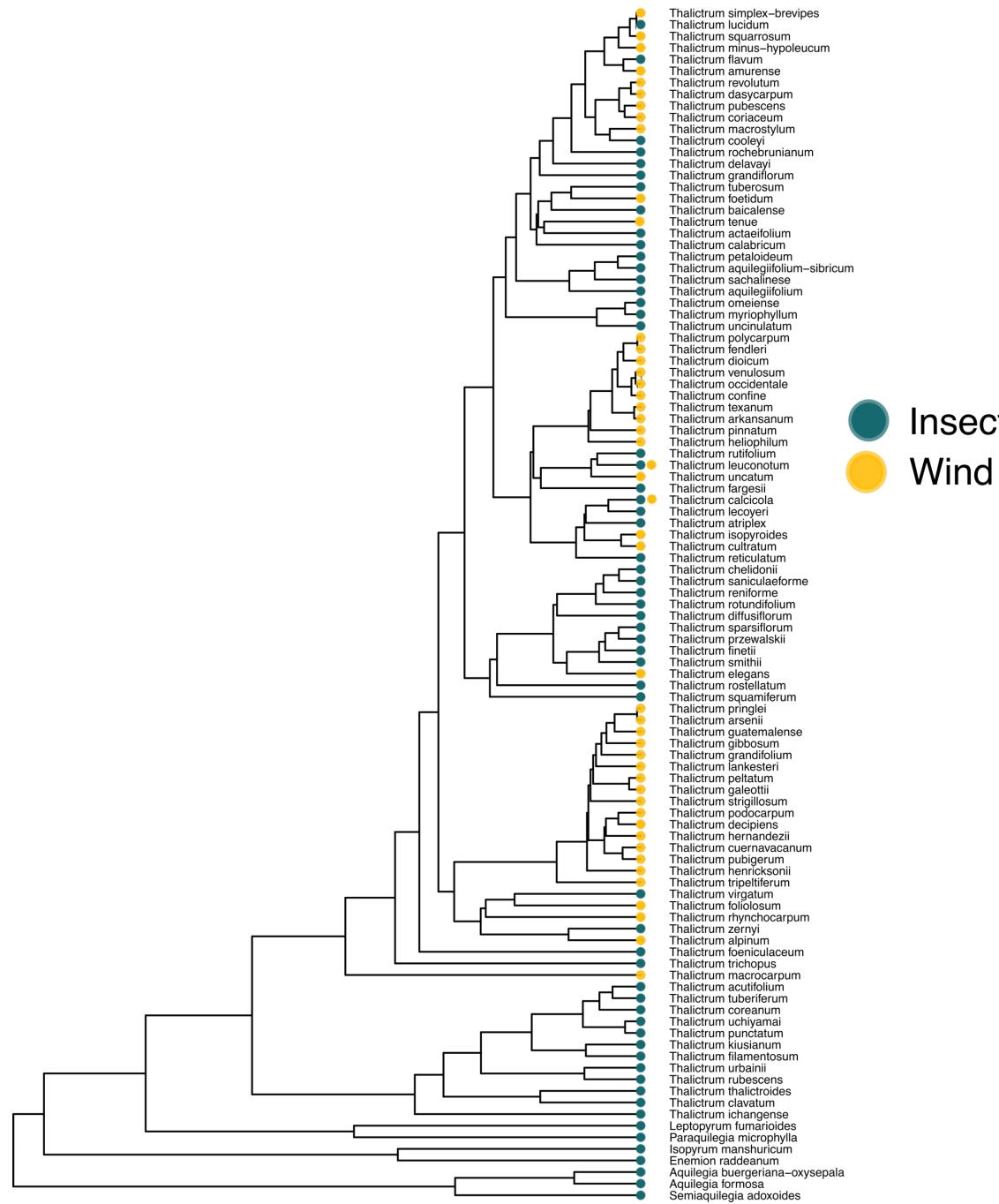


# Pollination modes

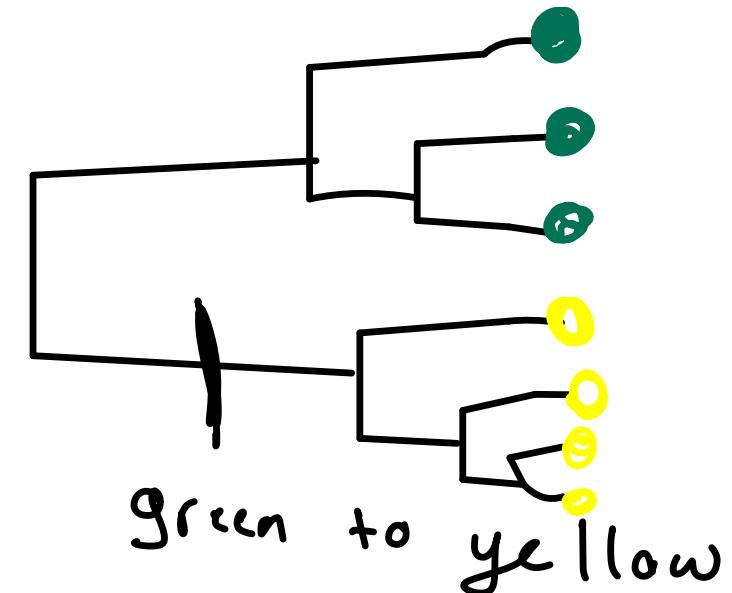


many pollination  
mode changes

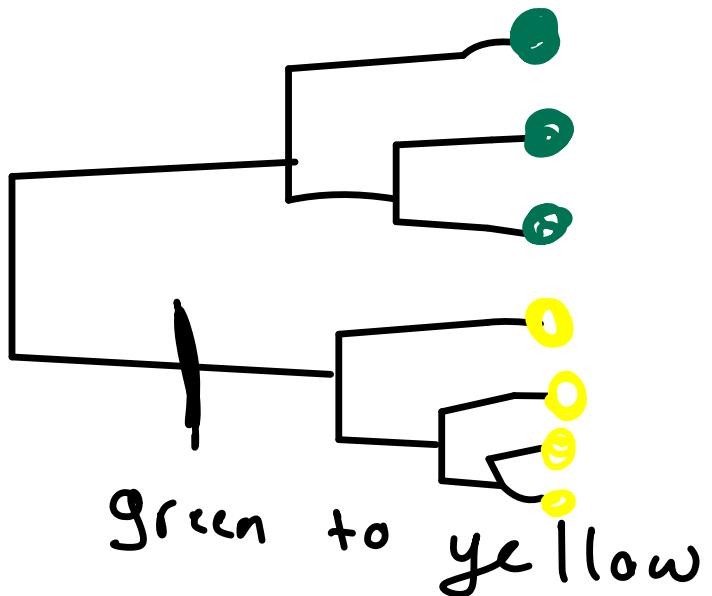




- Always plot your data!
- Check for nestedness of trait!
- Transitions are the effective sample size for these analyses



# Felsenstein's worst case scenario



- 1 transition
- 2 clear groups with the same trait
- NO COMPAREATIVE METHODS  
WORK

# Random variable definition

Variable - Trait

Random - Probability

Random variables : Function takes me from trait value to number

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$$X(t) = \begin{cases} 0 & \text{if insect pollinated} \\ 1 & \text{if wind pollinated} \end{cases}$$

time is  
the branch lengths  
of phylogeny

Trait values are called  
discrete states

# Continuous-Time Markov Chains (CTMC)

$$\{X(t), t \geq 0\}$$

Stochastic models that follow change in time with an associated **probability**

$X(t)$ = phenotype (trait) value at time t

t= millions of years

What is Probability of  $X(t)$ ?

# Discrete models of evolution

$X(t)$ = phenotype (trait) value at time t

$X(t)$ = Insect (0), Wind (1)

We use conditional probabilities. For example:

$P(X(t) = 1 | X(0) = 0)$

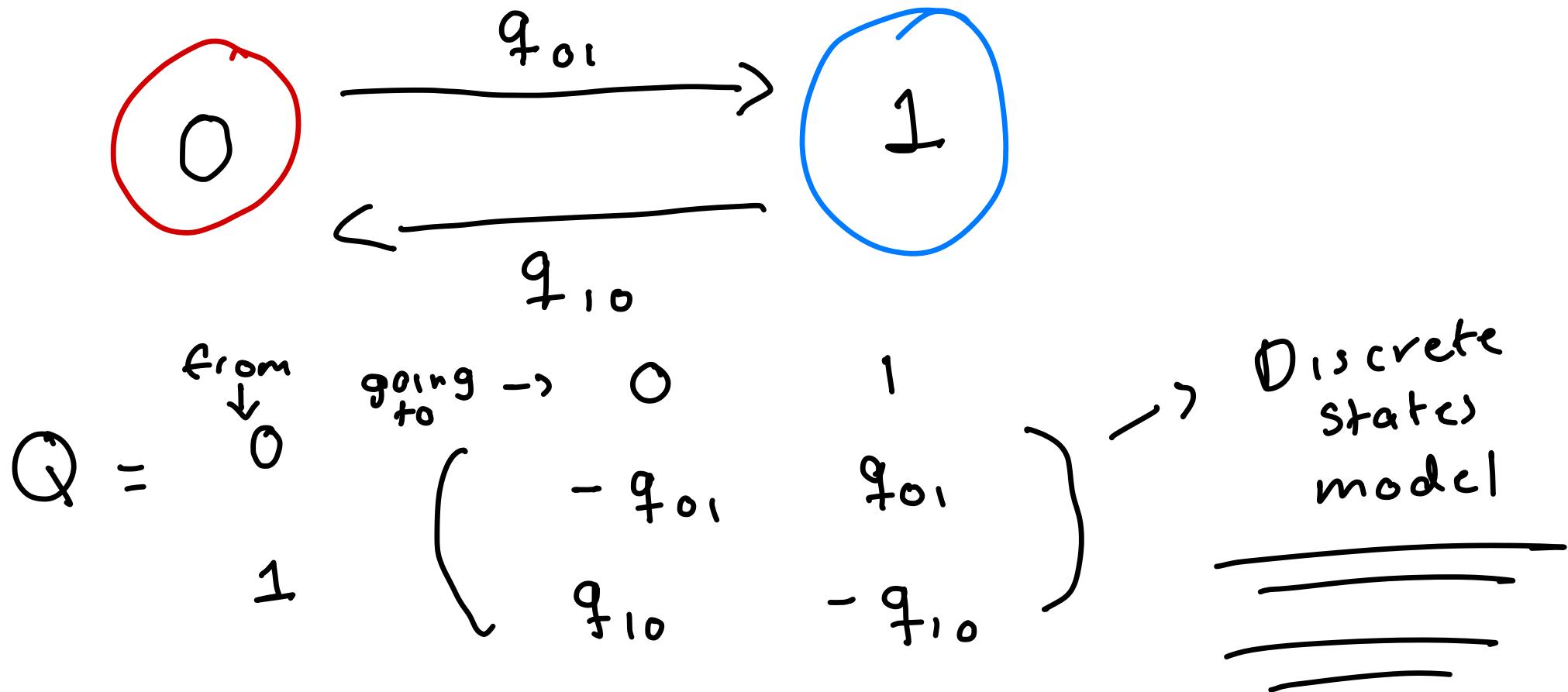
trait value equal at time 0 equal to insect pollinated

wind pollinated

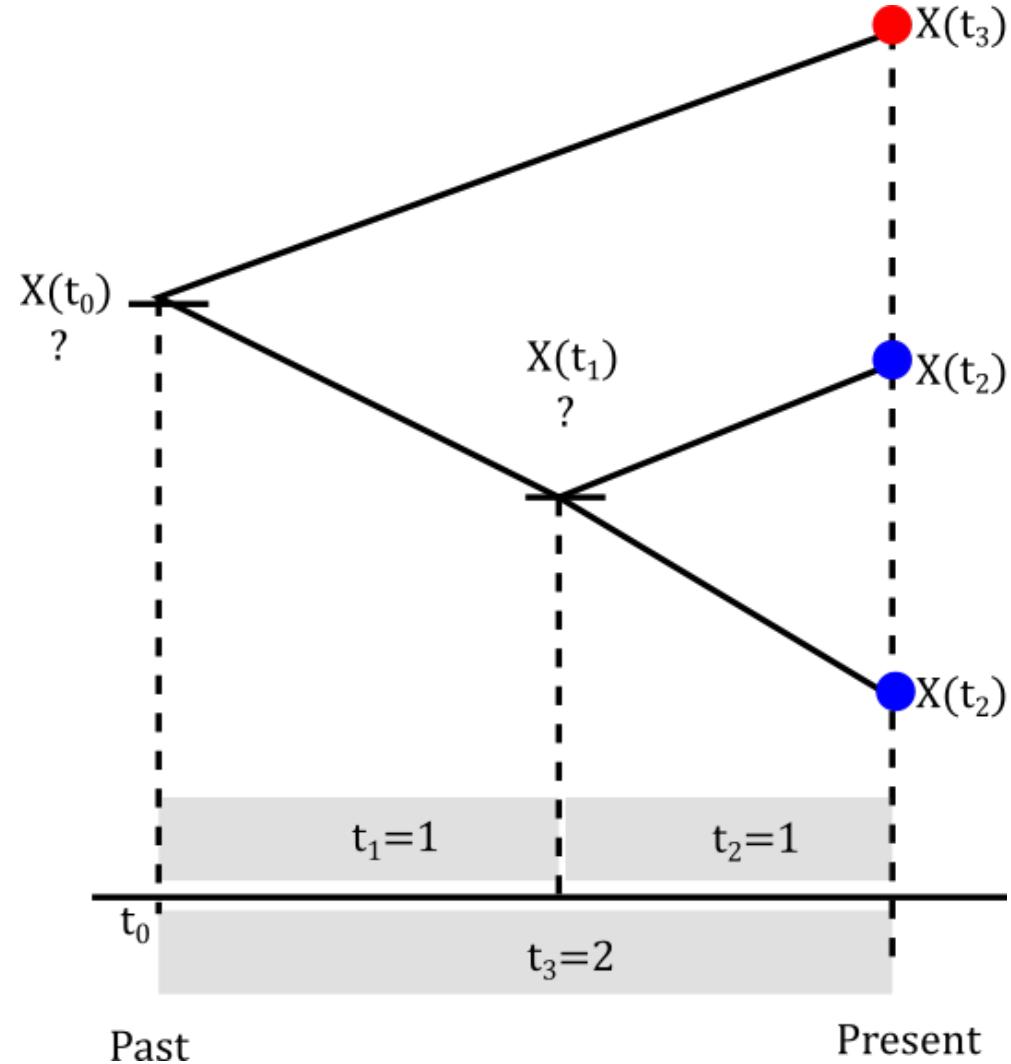
GIVEN

(conditional)

# Drawing the model



# Data: Phylogenetic tree and traits

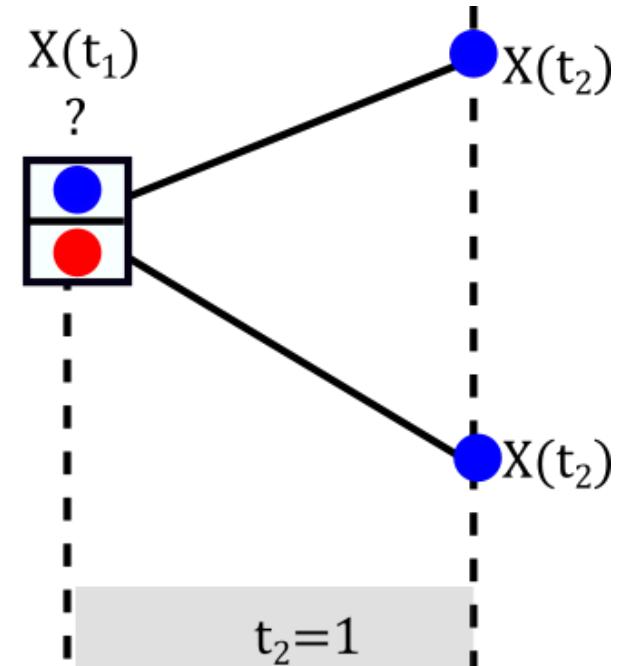


# Calculating transition probabilities

$$P(X(t) = 1 | X(0) = 0) = \frac{1}{q_{01} + q_{10}} (q_{10} - q_{01} e^{-(q_{01} + q_{10})t})$$

Past

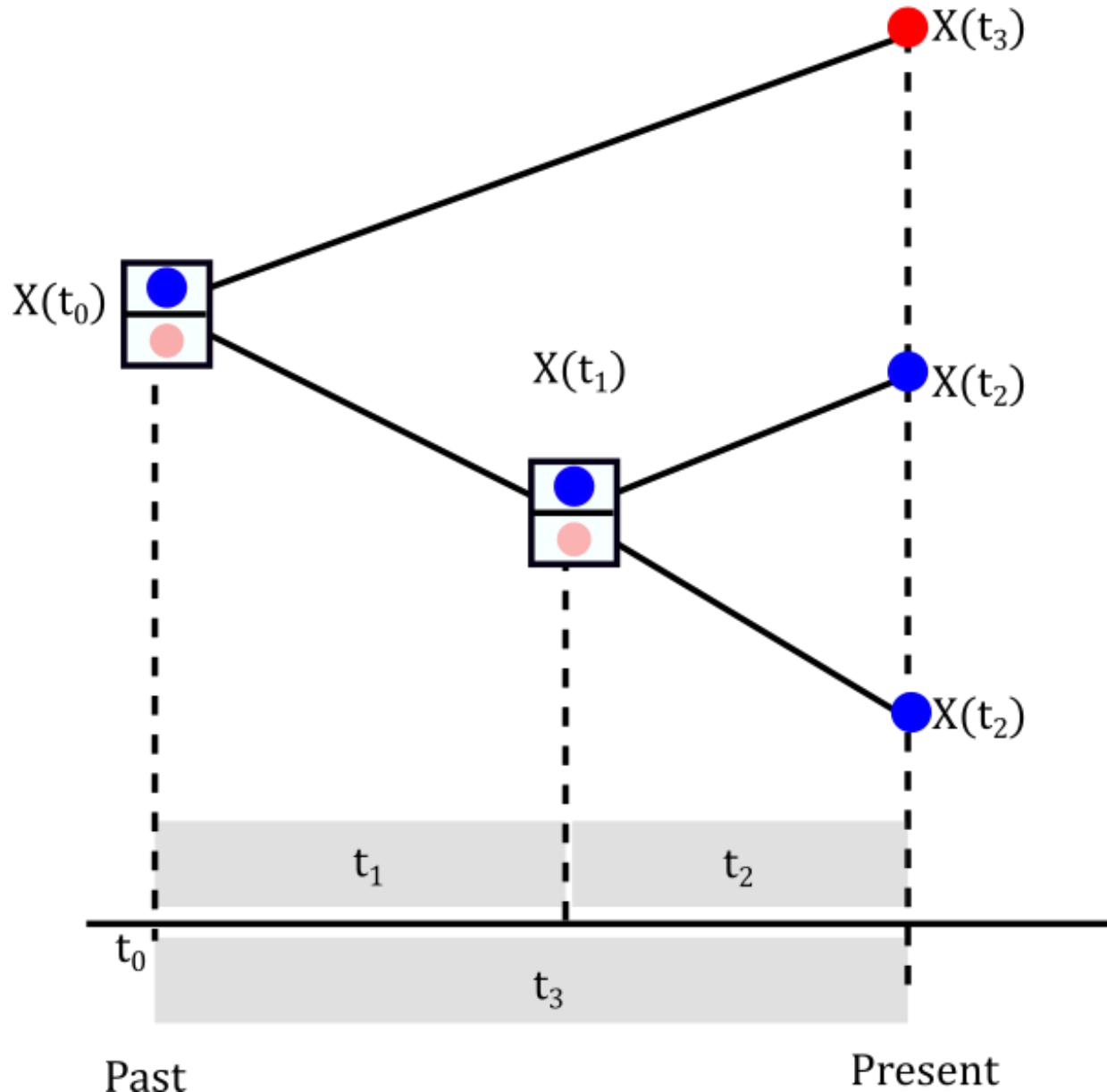
Present



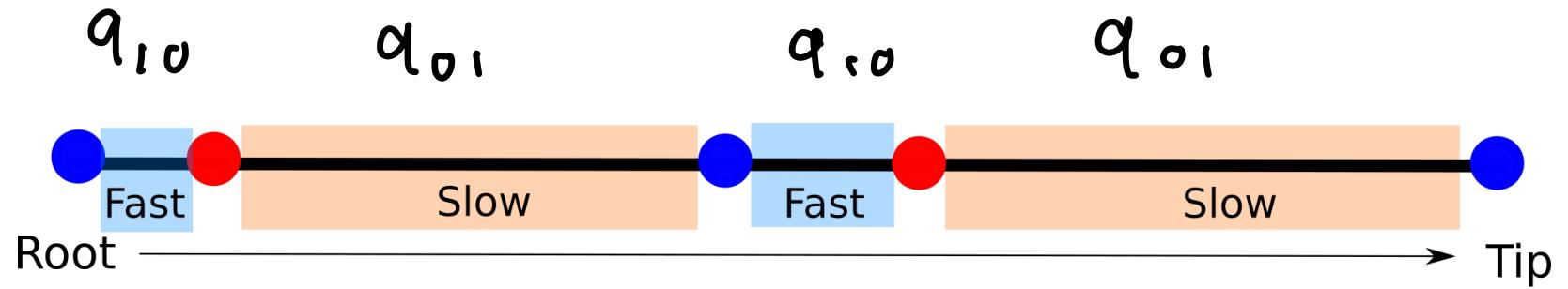
# Probabilities and the Q-matrix

$$P(t) = \frac{1}{q_{01} + q_{10}} \begin{pmatrix} q_{10} + q_{01}e^{-(q_{01}+q_{10})t} & q_{01} - q_{01}e^{-(q_{01}+q_{10})t} \\ q_{10} - q_{10}e^{-(q_{01}+q_{10})t} & q_{01} + q_{10}e^{-(q_{01}+q_{10})t} \end{pmatrix} \begin{pmatrix} 0 \\ 1 \end{pmatrix} \quad P(t) = e^{Qt}$$
$$q_{01} - q_{01}e^{- (q_{01} + q_{10}) t} = \underbrace{P(X(t) = 1 \mid X(0) = 0)}_{\text{what you need for your random variable}}$$

# What about the rest of the tree?



# Rates: Change per time

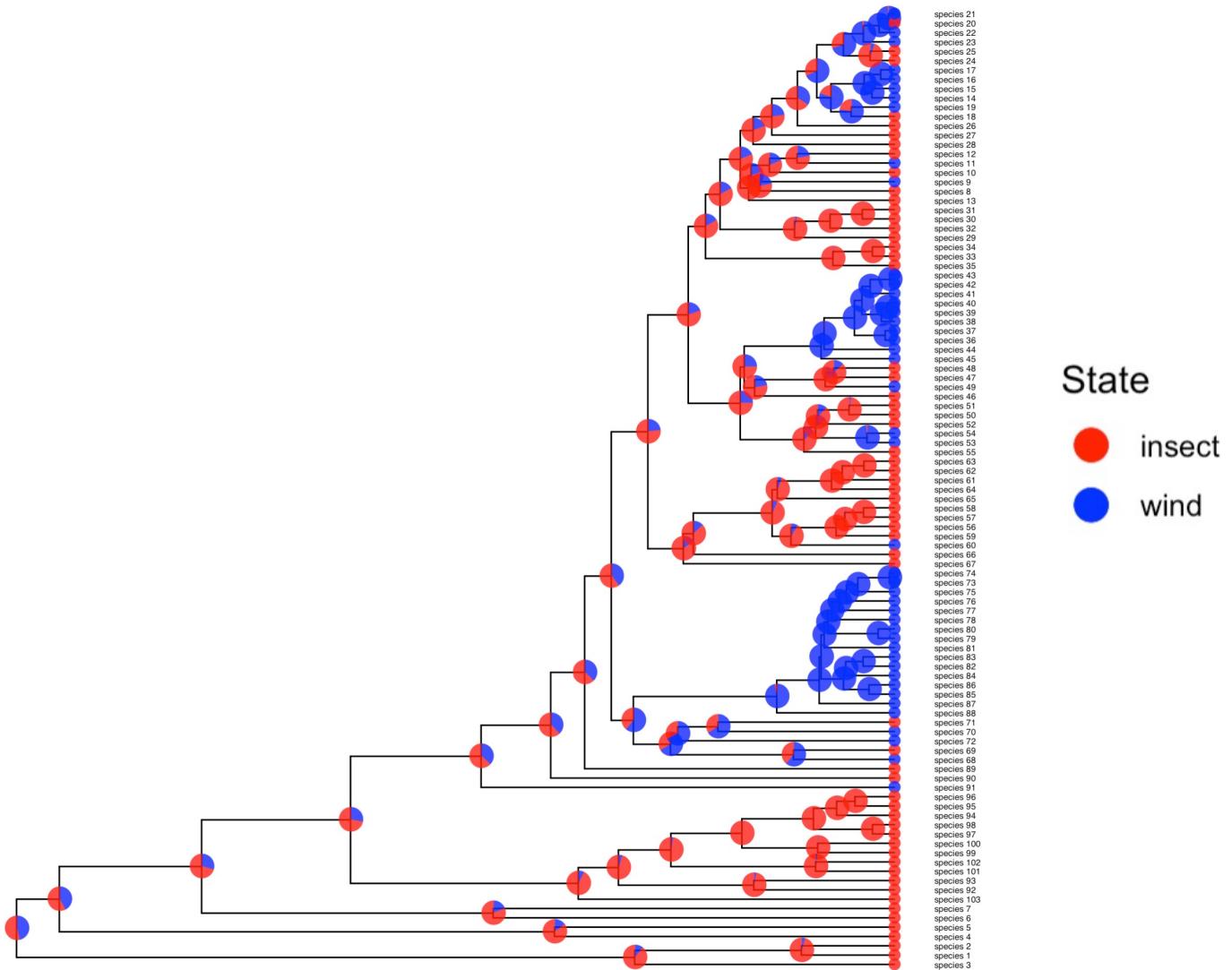


# Hypothesis testing- Likelihood

Null hypothesis  $H_0: q_{01} = q_{10}$

are the rates between  
states equal ?

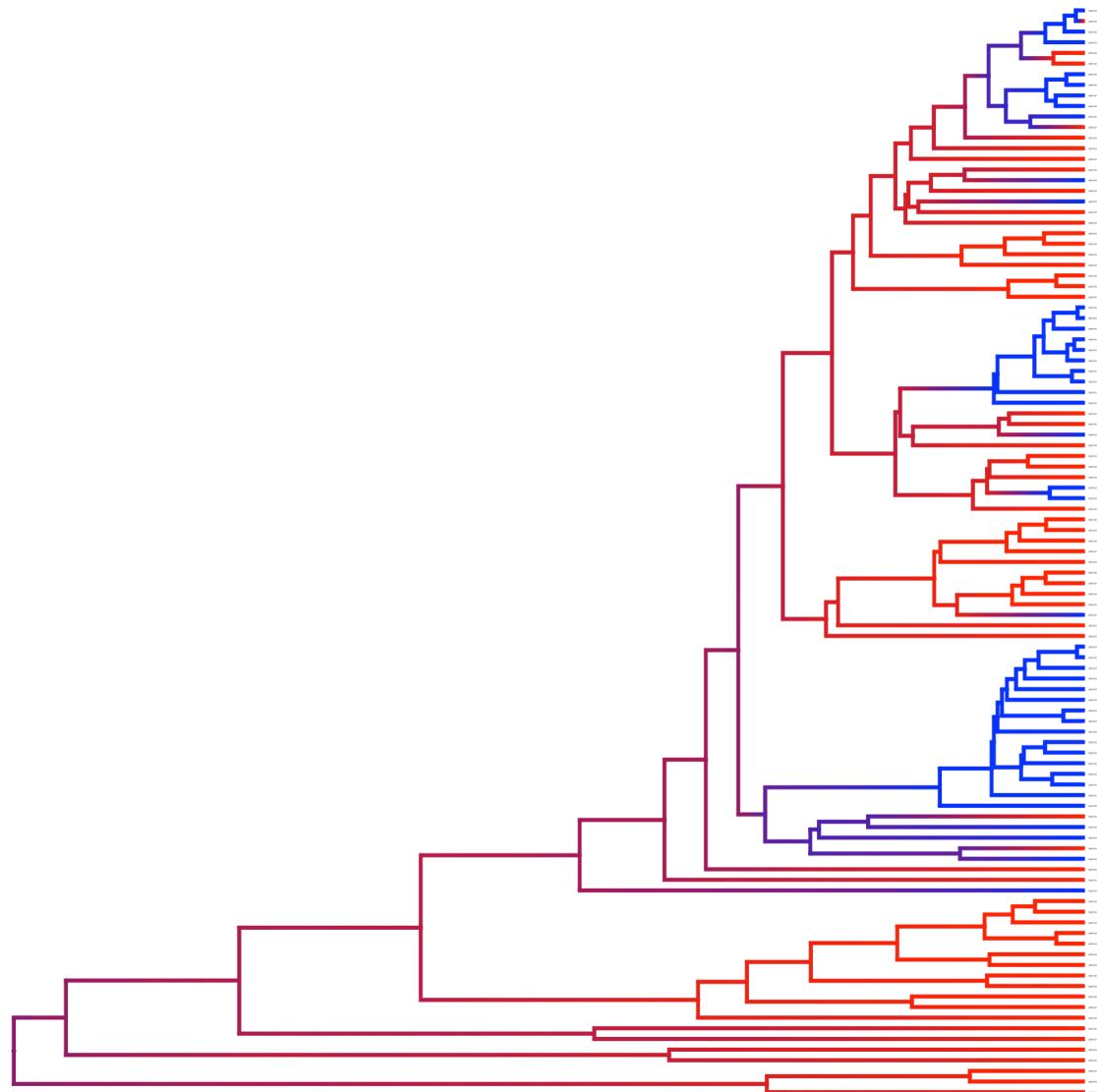
# Ancestral state reconstruction (marginal)



- Marginal likelihood function

This is a posterior distribution pie

# Stochastic mapping



- Many simulations= stochastic maps
- Posterior distribution in small time slices along branches (summarized as the MAP in each of the chunks)
- \*Can be summarized with other statistics

**Can you talk about the number of transitions with an stochastic map?**