Discrete characters are traits that are shared among groups in different temporal states

-use them in making trees to trace a trait

-often used with molecular markers, morphology

-determine ancestry of traits, rates of transition, trait complexity, correlated traits

If you have a matrix of states a,b,c, rate of going from one to another can be mathematically stated with a given value

-higher rate = spend more time at that state

There are a lot of models to represent rates in this matrix. Can take a matrix to test on biological data

Things that can go wrong:

-different methods leading to different answers

-transition rates may not be constant

-does not take into account things such as extinction events

-branch lengths matter, so if they are wrong this affects results

-assumptions given to root can matter

Joint vs marginal: what the states are at what position in the tree. Ancestral states are typically counted as nodes

-joint uses all nodes at once, finding the best estimate

-marginal does them one at a time (0 vs 1 at one node, then move on to next node)

O’Meara paper:

Figure 2

Pagel paper:

Lewis paper:

Applying discrete data to morphological data instead of parsimony

Pick traits that not everything has (maximum likelihood is only method that works with traits everyone has/lacks)