

Beyond binary rate matrices `sec:dm_matrix`

The instantaneous rate matrix encodes the transition rates between all pairs of evolutionary states. It is important to emphasize that all rate matrices are assertions about how morphological evolution operates. Depending on how one populates the rate matrix elements, different evolutionary hypotheses may be expressed.

When we model the evolution of morphological data, unlike nucleotide data, each change may require a sequence of intermediate changes. Getting to one state may require going through another. In short, it is probably not likely that one single model describes all characters well.

Symmetric unordered

The standard Mk model of character evolution, where M denotes it is a Markov model and K denotes the number of states for the character. The lineage may transition directly from state 1 to state 4 without going through states 2 and 3, which is representative of a character with *unordered* states. In addition, all transition rates are equal as they are in the Jukes-Cantor rate matrix `jukes69`. Here is an example of a symmetric unordered Mk model for $K = 4$.

equation* $Q = \text{pmatrix} - r \ r \ r$

Define the single shared rate parameter `snugshade* lstlisting r <- 1.0`