

Introduction

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Exercise is in Section sect:RB-ExerciseMain.

Models

Sequence Evolution

Point to other tutorials (e.g., GTR stuff)

Morphological Character Change

The incorporation of morphological data from fossils into phylogenetic analyses allows us to directly observe organisms that existed in the past. In 2001, Paul Lewis described a model, the Mk model, to allow for the incorporation of morphology into likelihood and Bayesian analyses. The Mk model uses a generalized Jukes-Cantor matrix. This introduces a number of assumptions. One key assumption is that characters exhibit symmetrical change - that a given character is as likely to transition from a one state to another as it is to reverse. For example, this assumption applied to a binary character would mean that a change from a 0 state to a 1 state is as likely as a change from a 1 state to a 0 state.

In the tutorial, we will relax this assumption through the use of a prior on stationary state frequencies. This prior is visualized in Fig. 1. 