Many molecular phylogenetic studies use nucleotide or amino-acid sequences to infer the tree of evolution. The input data consists of a $K \times N$ matrix where K denotes the number of taxa (or species) and N denotes the number of matched nucleotide or amino-acid sites. The output is a phylogenetic tree with $2K-1$ nodes and $2K-2$ edges. Here, a node represents either an extinct ancestral species or an extant species and an edge represents the link between two adjacent nodes. The evolutionary process over an edge is usually represented as a time-homogeneous Markov process with an associated rate matrix. Let U denote the number of distinct rate matrices over the phylogenetic tree, where $1 \le U \le 2K-2$, and let M_U denote the associated Markov model. The most commonly used model for phylogenetic analysis is the M_1 model that assumes the same rate matrix over the entire tree. However, this model usually does not provide a good fit for the data suggesting that a model with $U \ge 2$ is needed. At the same time, the M_{2K-2} model is too complex.

For $2 \le U < 2K-2$, each of the $2K-2$ edges can be assigned one of the U rate matrices and the total number of arrangements is too large to be tried exhaustively. For example, for $U=2$, the total number of possible arrangements is $2^{2K-3}-1$. First, we describe a maximum-likelihood method for the estimation of model parameters for any U and any arrangement of these U rate matrices. Next, we describe a heuristic for identifying the optimal number of rate matrices. We use simulated data sets to show that the heuristic is successful in identifying the correct rate matrix per edge in most of the cases. We also analyze a biological data set and successfully recover the correct assignment of rate matrices to the edges.