

Rate matrix for an MG-style codon model

$$(\text{Rate})_{X,Y}(dt) = \begin{cases} \alpha & \pi_t dt & , \text{ one-step, synonymous substitution,} \\ \beta & \pi_t dt & , \text{ one-step, non-synonymous substitution,} \\ 0 & & , \text{ multi-step.} \end{cases}$$

$X, Y = \text{AAA} \dots \text{TTT}$ (excluding stop codons),
 π_t - frequency of the target nucleotide.

Example substitutions:

$\text{AAC} \rightarrow \text{AAT}$ (one step, synonymous - Asparagine)

$\text{CAC} \rightarrow \text{GAC}$ (one step, non-synonymous - Histidine to Aspartic Acid)

$\text{AAC} \rightarrow \text{GTC}$ (multi-step).

αR_{CT}
 βR_{CG}

α (syn. rate) and β (non-syn. rate) are the key quantities for all selection analyses

Computing the transition probabilities

- In order to recover transition probabilities $\mathbf{T}(t)$ from the rate matrix \mathbf{Q} , one computes the matrix exponential $\mathbf{T}(t) = \exp(\mathbf{Q}t)$, same as with standard nucleotide models, e.g. HKY85 or GTR.
- Because the computational complexity of matrix exponentiation scales as the cube of the matrix dimension, codon based models require roughly $(61/4)^3 \approx 3500$ more operations than nucleotide models.
- This explains why codon probabilistic models were not introduced until the 1990s, even though they are relatively straightforward extensions of 4x4 nucleotide models