Rate matrix for an MG-style codon model

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

X,Y = AAA...TTT (excluding stop codons),
π_t - frequency of the target nucleotide.
Example substitutions:
AAC→AAT (one step, synonymous - Aspargine) αR_{CT}
CAC→GAC (one step, non-synonymous - Histidine to Aspartic Acid) βR_{CG}
AAC→GTC (multi-step).

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 **`T(t)`** from the rate matrix **`Q`**, one computes the matrix exponential **`T(t) = exp (Qt),`** 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