Models of Sequence Evolution With Selection

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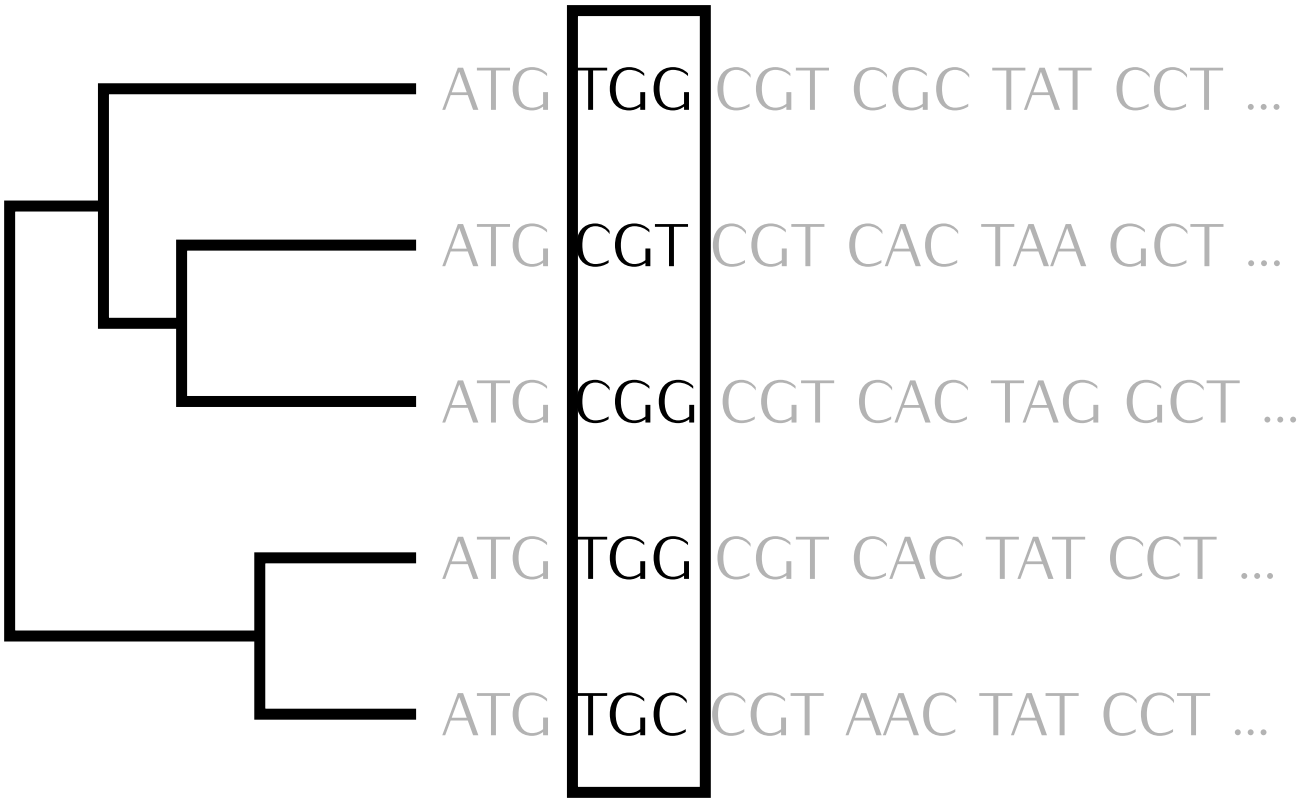

- We assume that all columns (sites) are independent

Modeling the evolution on a branch

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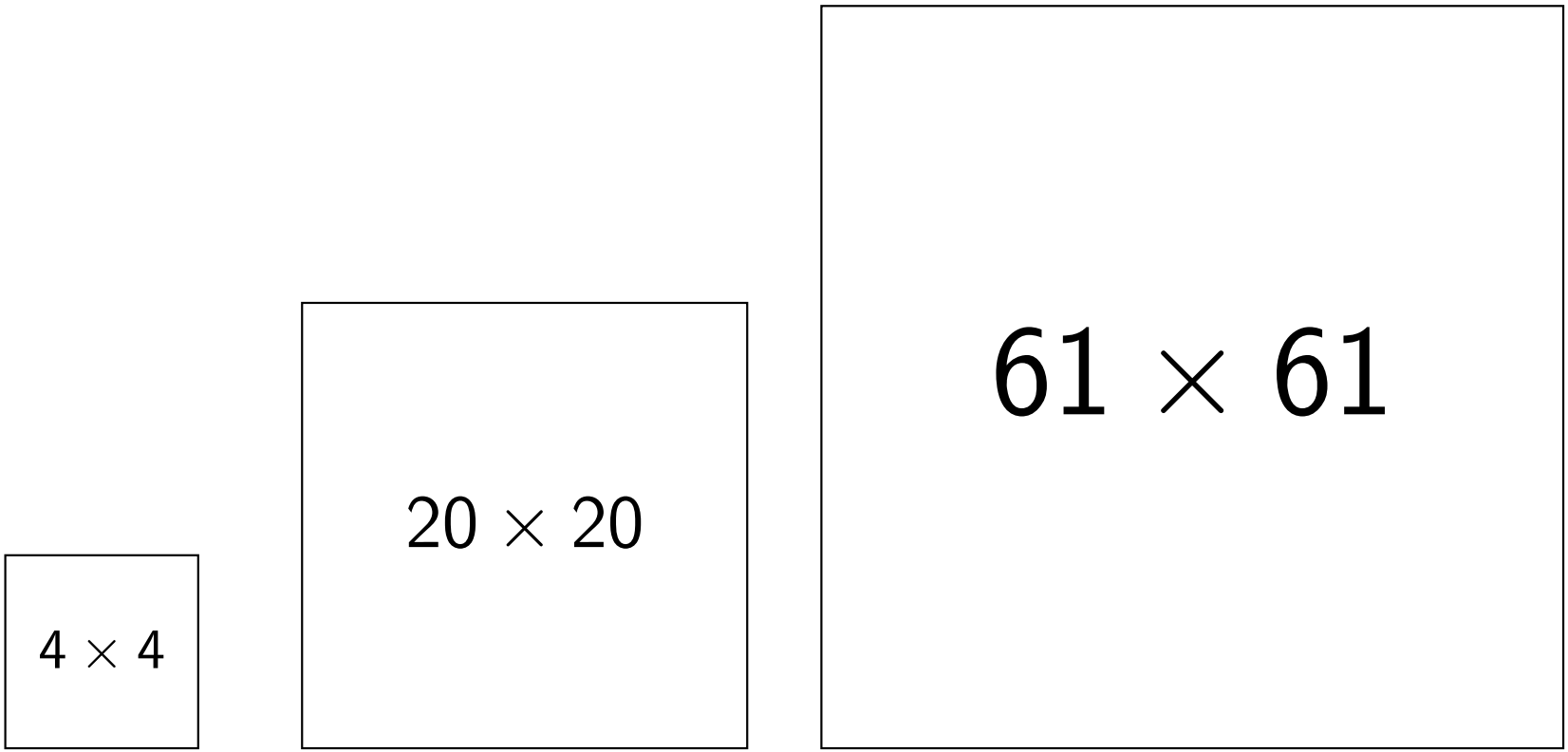
- The probability of each type of mutation is given by a matrix:



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  - We consider only 2 types of mutations: synonymous and non-synonymous. The ratio of the two is noted *omega*
  - We allow nucleotide transitions and transversions to occur at a distinct rate. The ratio of the two is noted *kappa*
- We can therefore express all mutation probabilities with only two parameters

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3. Summing over all possible ancestral states
4. Multiplying for all sites in the alignment

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Note

Even though this is not a requirement, in practice, codon models are not used for phylogenetic inference. The phylogenetic tree / sequence genealogy is assumed to be known.