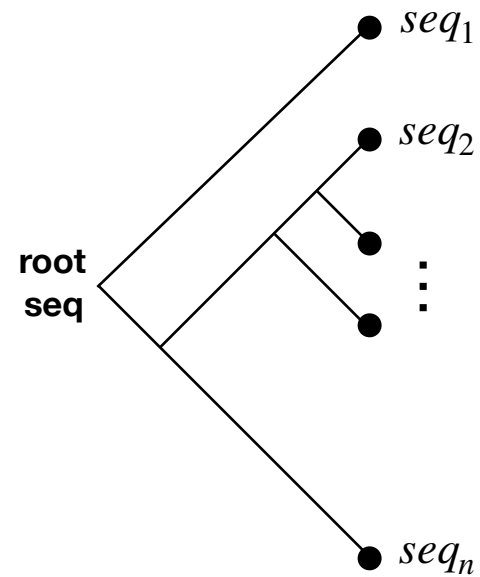


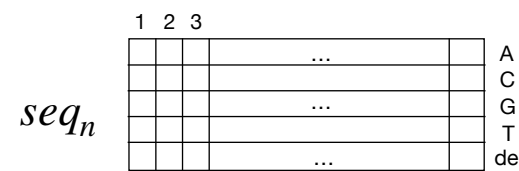
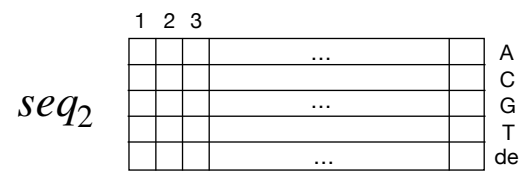
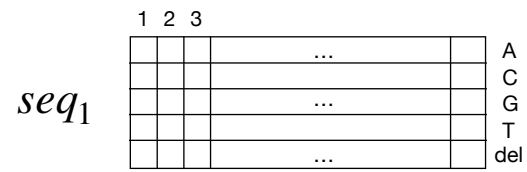
Step 1

Generate benchmark phylogeny from root sequence



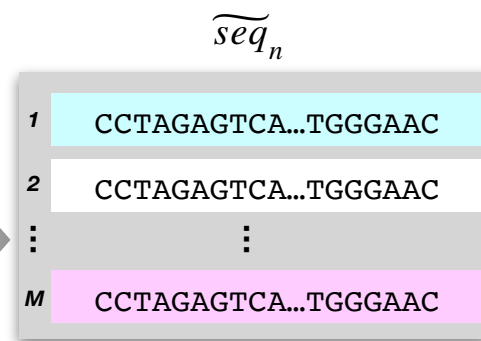
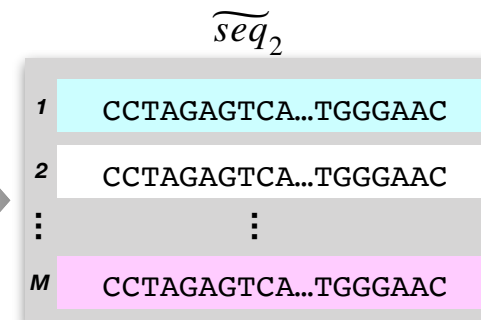
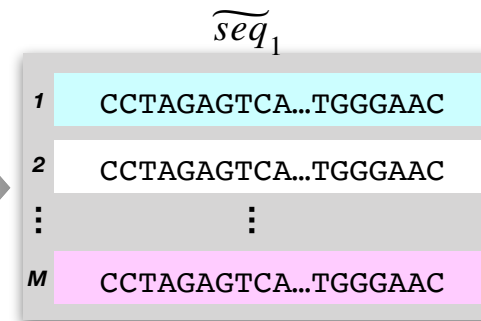
Step 2

Add sequence uncertainty with a nucleotide-level probabilistic sequence



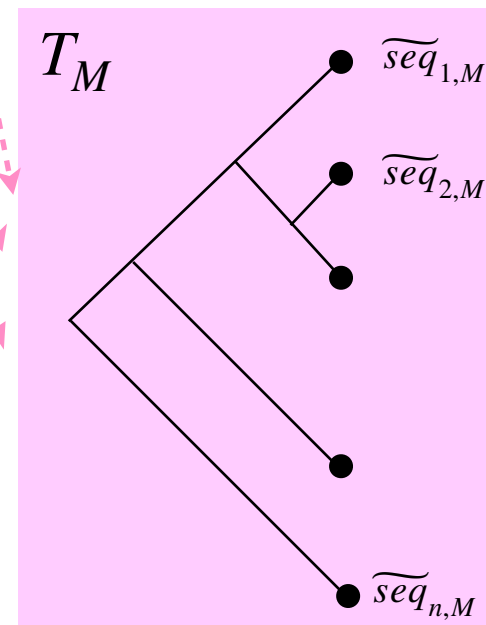
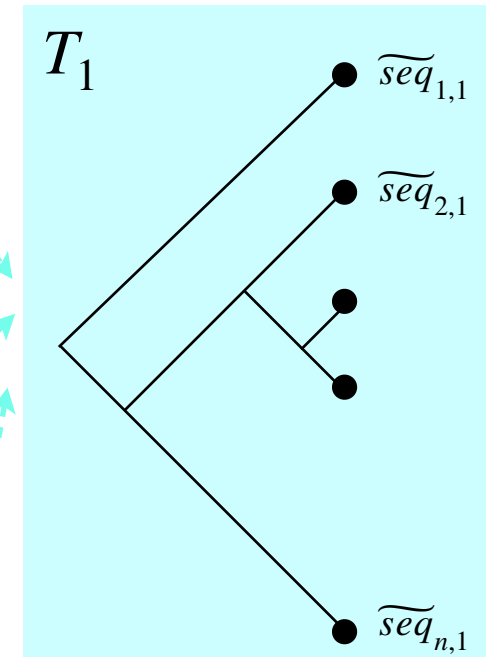
Step 3

Draw M times from each probabilistic sequence



Step 4

For each Monte-Carlo iteration, reconstruct phylogeny



Step 5

Calculate pairwise distances between all trees

$$d(T_i, T_j)$$