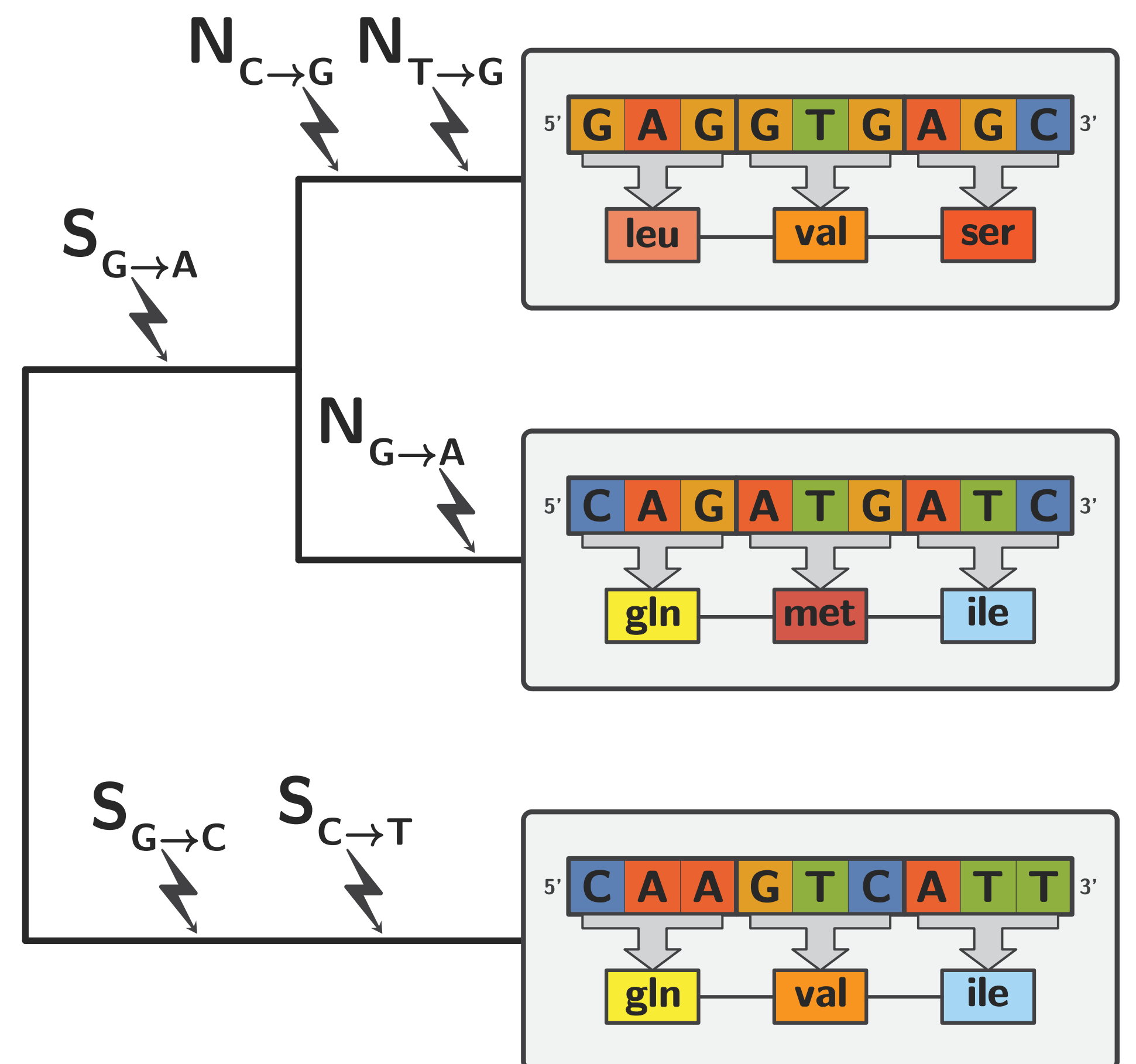
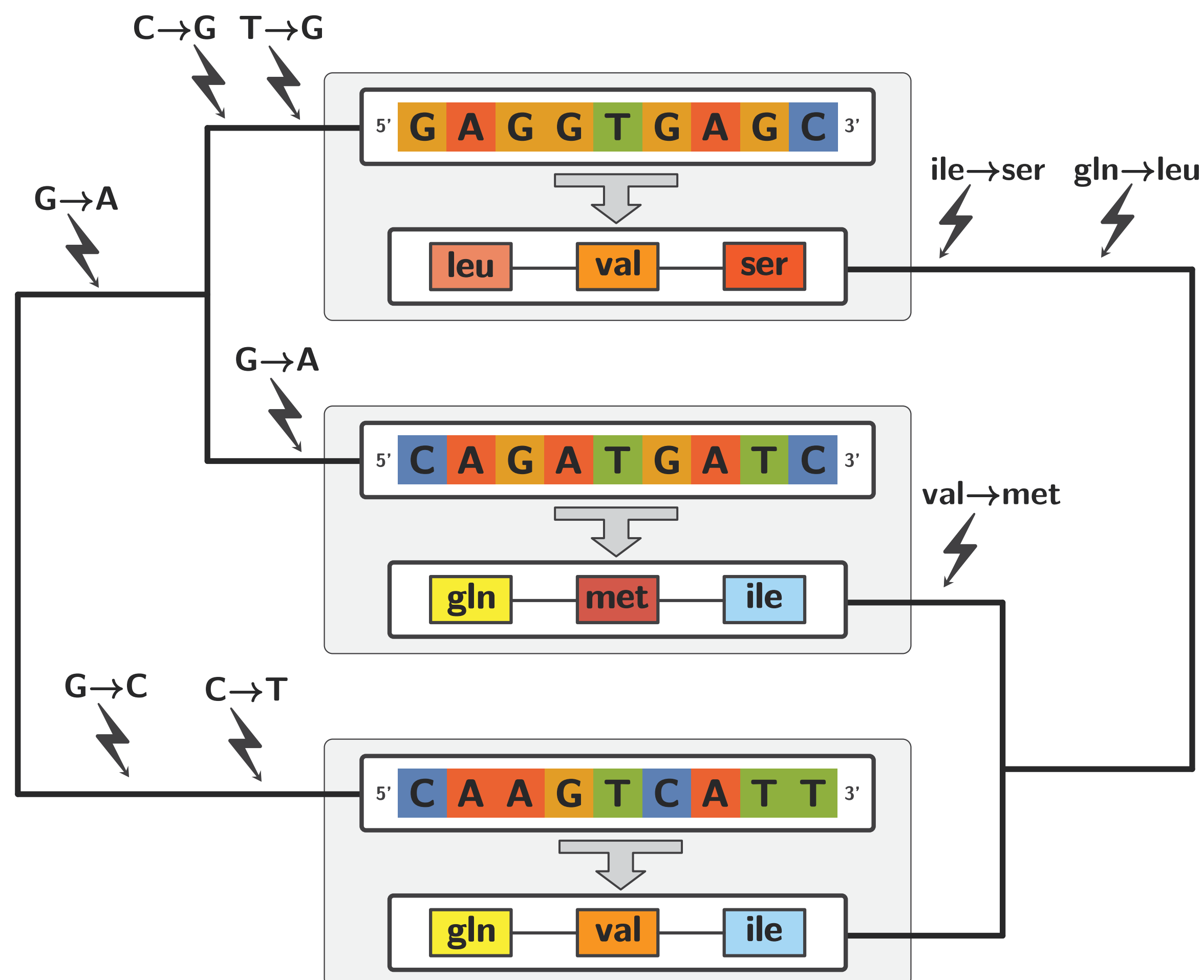


A: Synonymous and non-synonymous DNA mutations

Phylogenetic tree reconstruction using three hypothetical DNA sequences



B: DNA (left) and amino-acid (right) substitution models

C: Codon substitution model