

Modeling transition/transversion bias of nucleotide substitution over time

Case study 4

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Estimate nucleotide frequencies from the pairwise alignment of human and mouse cytochrome b gene as given in the file "mt-cyb-human- mouse_cDNAalignment.fasta". Use these values to parameterize the model.

One way to estimate the nucleotide frequencies is to count them.

Since we're working with a pairwise alignment without indels, the total length of both sequences is the same (1140 nt). The detailed composition is listed in Table 1.

Table 1: Nucleotide frequencies

nucleotide	human	mouse
T	286	327
C	391	312
A	326	361
G	137	140