

Allowing multi-nucleotide substitutions

- Some of the methods (e.g. BUSTED, aBSREL, RELAX) can extend substitution models to allow instantaneous double- and triple-“hits” (e.g. ACC to AGG)
- Sometimes multi-nucleotide changes along short branches at a single site can drive selection signal (possible false positives?)
- HyPhy includes a simple standard analysis for estimating alignment-wide multiple-hit rates.

Extra base hits: Widespread empirical support for instantaneous multiple-nucleotide changes

Alexander G. Lucaci , Sadie R. Wisotsky , Stephen D. Shank, Steven Weaver, Sergei L. Kosakovsky Pond 

Published: March 12, 2021 • <https://doi.org/10.1371/journal.pone.0248337>

[See the preprint](#)

