Substitution models in the BUSTED framework

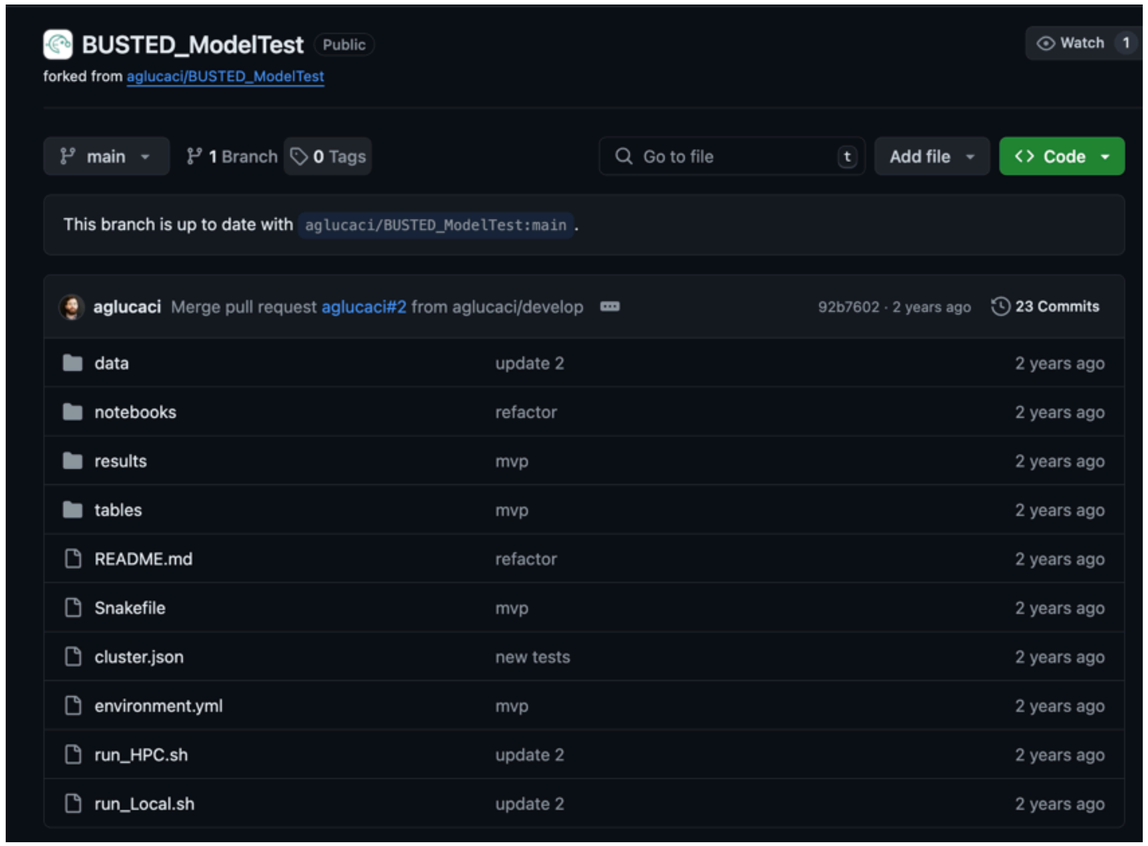
Table 1. Substitution Models Considered in this Paper.

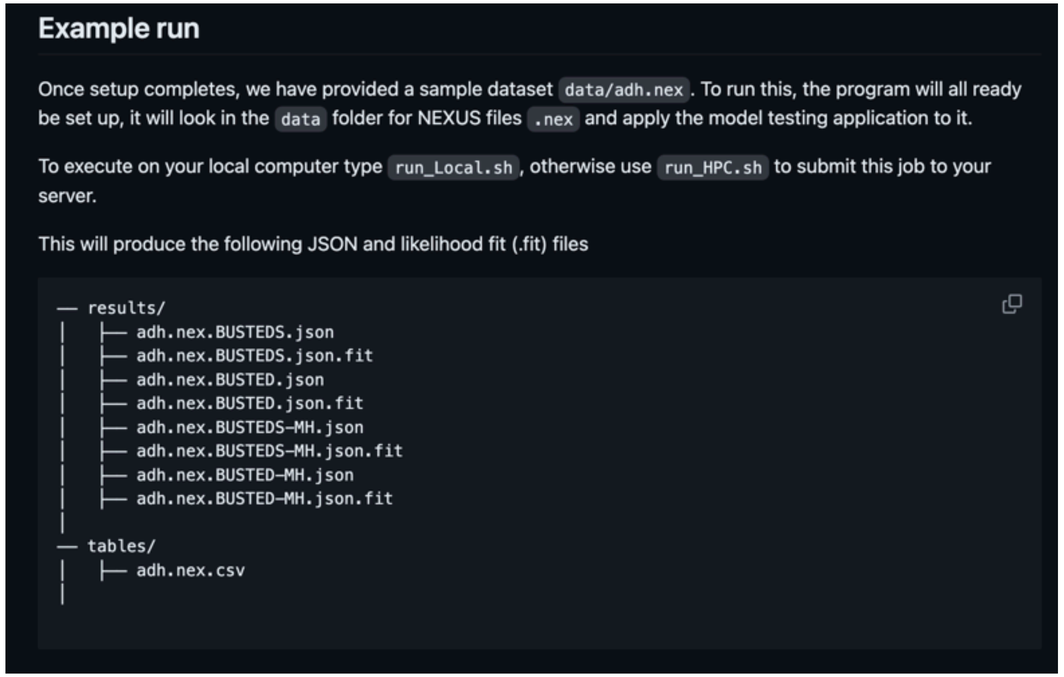
Model	Reference	Nonsynonymous Rates	Synonymous Rates	Multinucleotide Substitutions	Number of Parameters
BUSTED	Murrell et al. (2015)	Random effects branch–site modeled by a $K(=3)$-bin discrete distribution	None	None	$B + 13 + 2 \times K$
+S	Wisotsky et al. (2020)	Random branch–site effects modeled by a $K(=3)$-bin general discrete distribution	Random site effects modeled by an $L(=3)$-bin unit mean general discrete distribution	None	$B + 11 + 2 \times (K + L)$
+MH	Lucaci et al. (2021)	Random branch–site effects modeled by a $K(=3)$-bin general discrete distribution	None	Alignment-wide double- (δ) and triple-(ψ) nucleotide substitution rates	$B + 15 + 2 \times K$
+S+MH	This paper	Random branch–site effects modeled by a $K(=3)$-bin general discrete distribution	Random site effects modeled by an $L(=3)$-bin unit mean general discrete distribution	Alignment-wide double- (δ) and triple-(ψ) nucleotide substitution rates	$B + 13 + 2 \times (K + L)$

NOTE.—B, the number of branches in the phylogenetic tree. K and L are user-tunable parameters, set to 3 each by default.

Lucaci AG, Zehr JD, Enard D, Thornton JW, Kosakovsky Pond SL. Evolutionary Shortcuts via Multinucleotide Substitutions and Their Impact on Natural Selection Analyses. Mol Biol Evol. 2023 Jul 5;40(7):msad150. doi: 10.1093/molbev/msad150. PMID: 37395787; PMCID: PMC10336034

BUSTED Model-testing application





Available at https://github.com/veg/BUSTED_ModelTest