

# Substitution models in the BUSTED framework

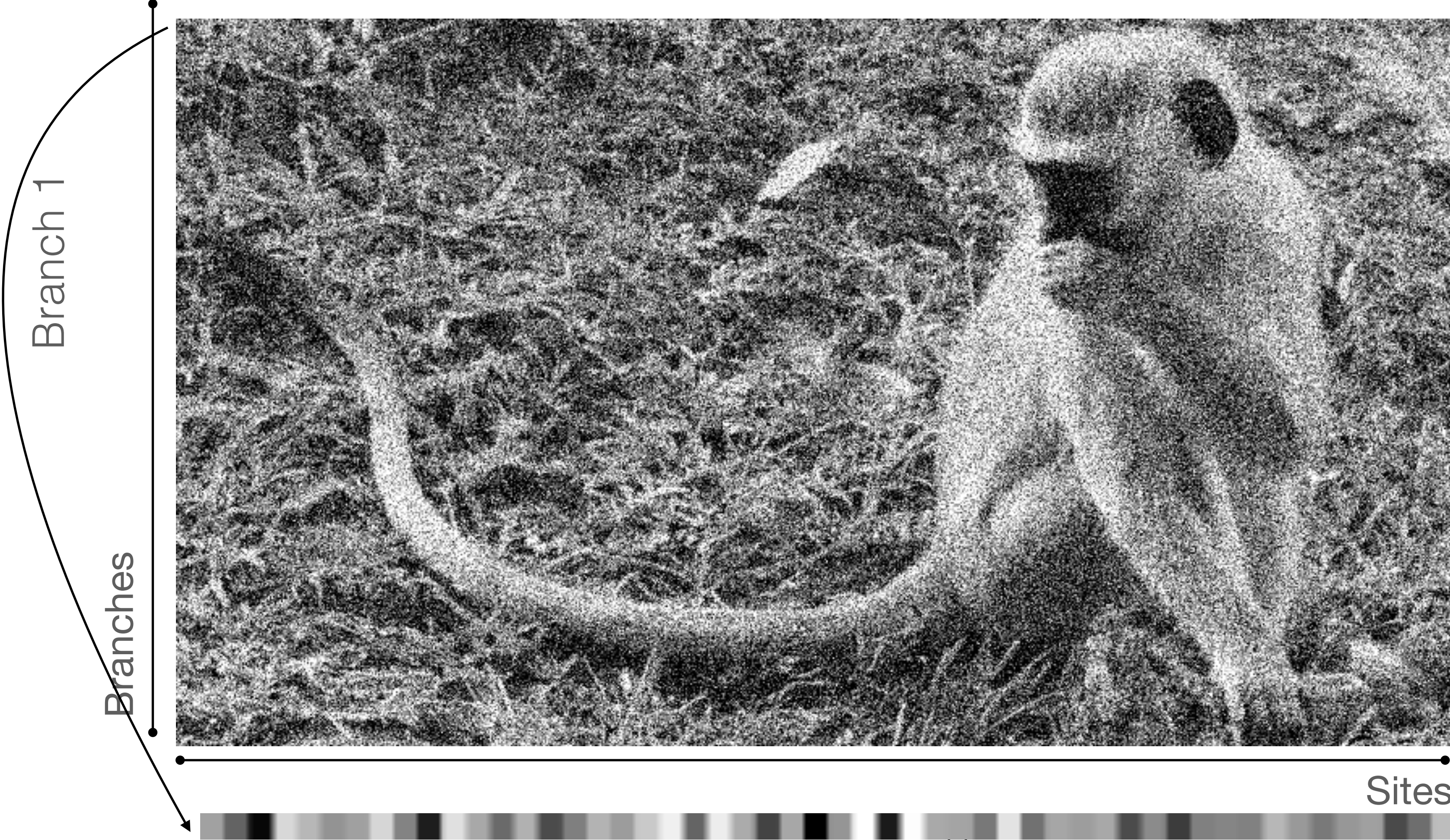
**Table 1.** Substitution Models Considered in this Paper.

Model	Reference	Nonsynonymous Rates	Synonymous Rates	Multinucleotide Substitutions	Number of Parameters
BUSTED	<a href="#">Murrell et al. (2015)</a>	Random effects branch–site modeled by a $K(=3)$ -bin discrete distribution	None	None	$B + 13 + 2 \times K$
+S	<a href="#">Wisotsky et al. (2020)</a>	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	<a href="#">Lucaci et al. (2021)</a>	Random branch–site effects modeled by a $K(=3)$ -bin general discrete distribution	None	Alignment-wide double- ( $\delta$ ) and triple- ( $\psi$ ) 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- ( $\delta$ ) and triple- ( $\psi$ ) 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.



Which branches are under selection? (aBSREL)



For each image **row**, is there a significant proportion of bright pixels, once the column has been reduced to **N** colors only?



[aBSREL]: at a given branch, each site is a draw from an N-bin ( $dN/dS$ ) distribution, which is inferred from all data for the branch. Test if there is a proportion of sites with  $dN/dS > 1$  (LRT). **N** is derived adaptively from the data.