

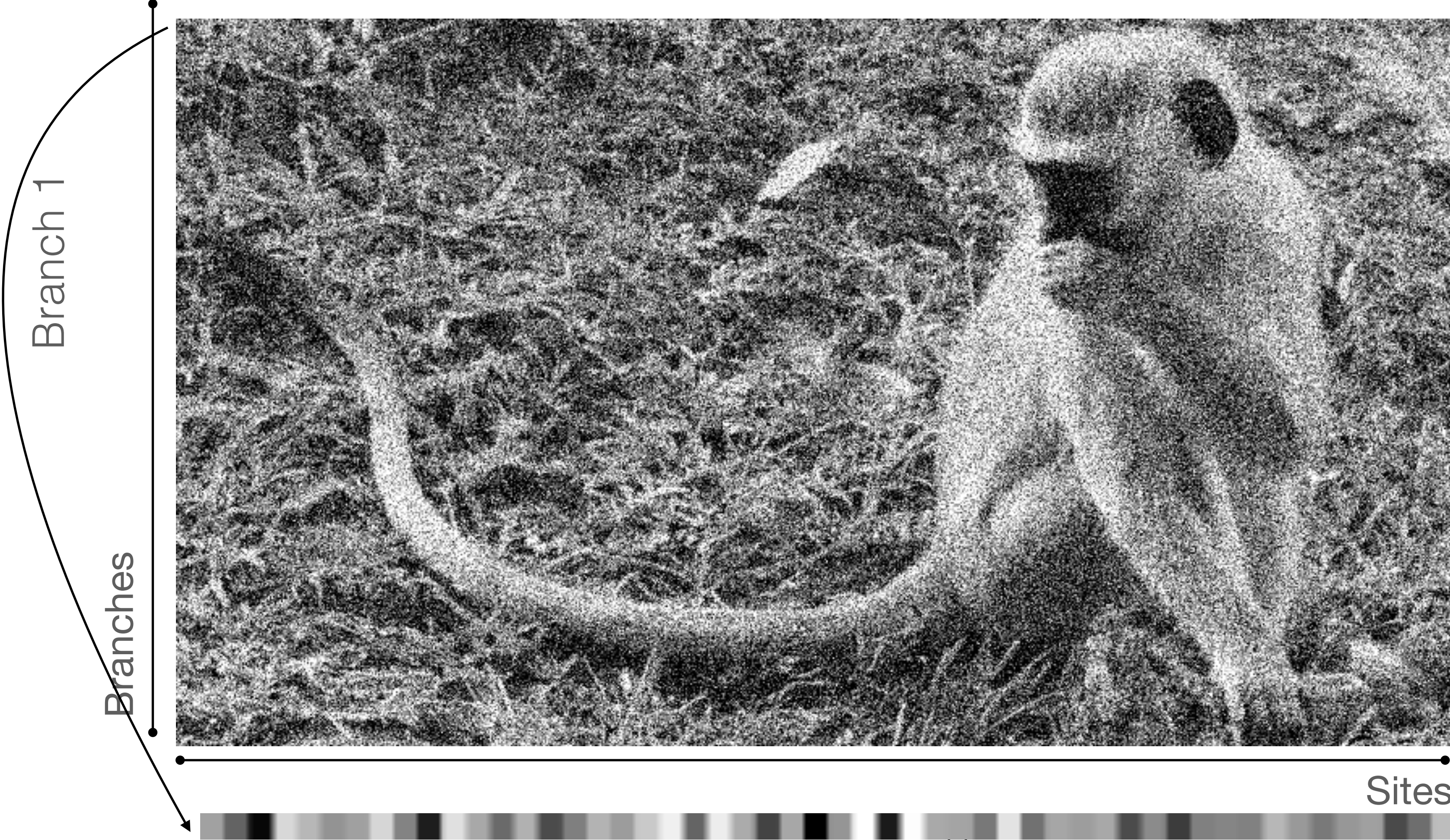
Substitution models in the BUSTED framework

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.

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.