Gene-wide selection
random effects over sites and branches [BUSTED]

Sites

Branches

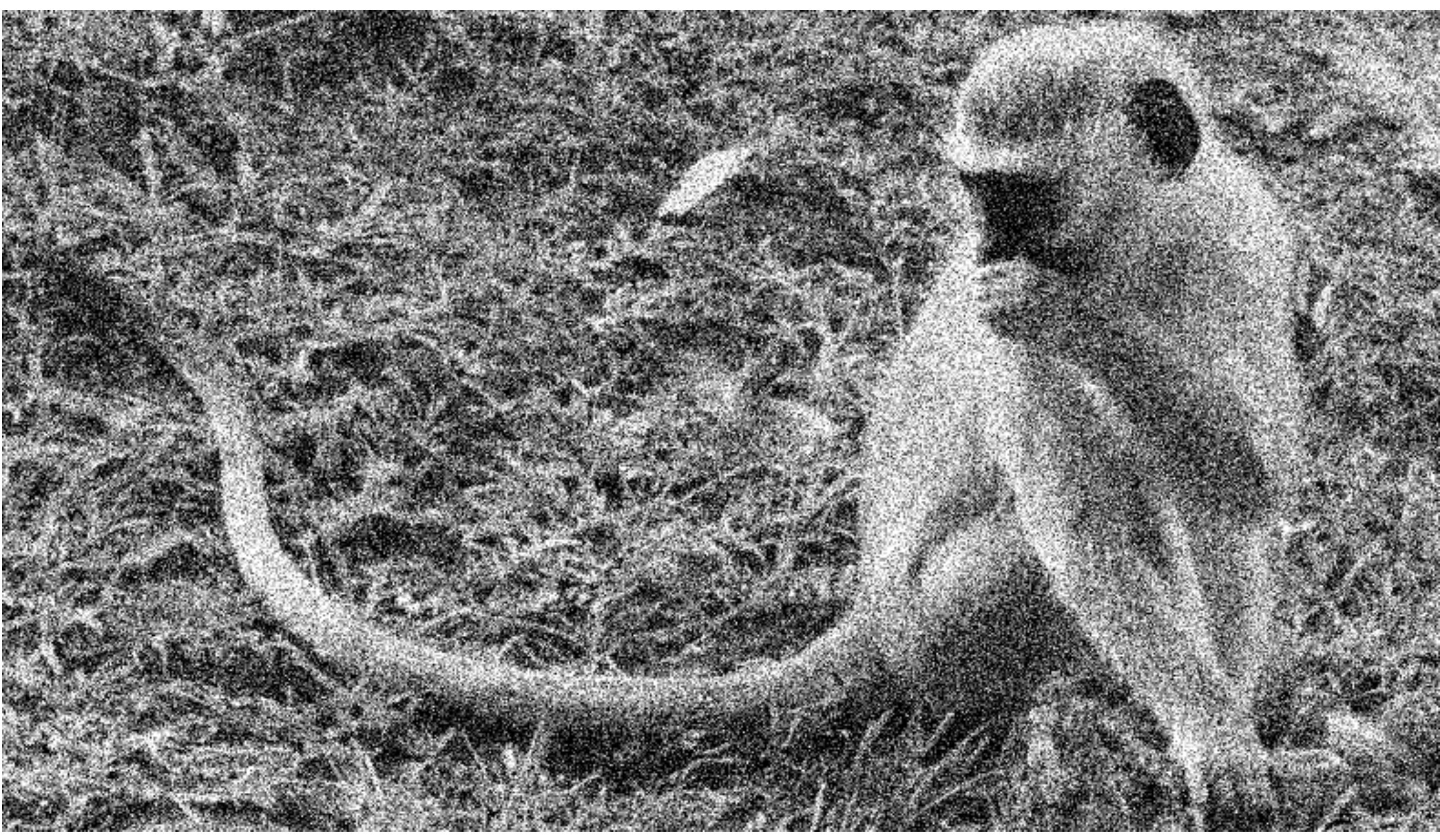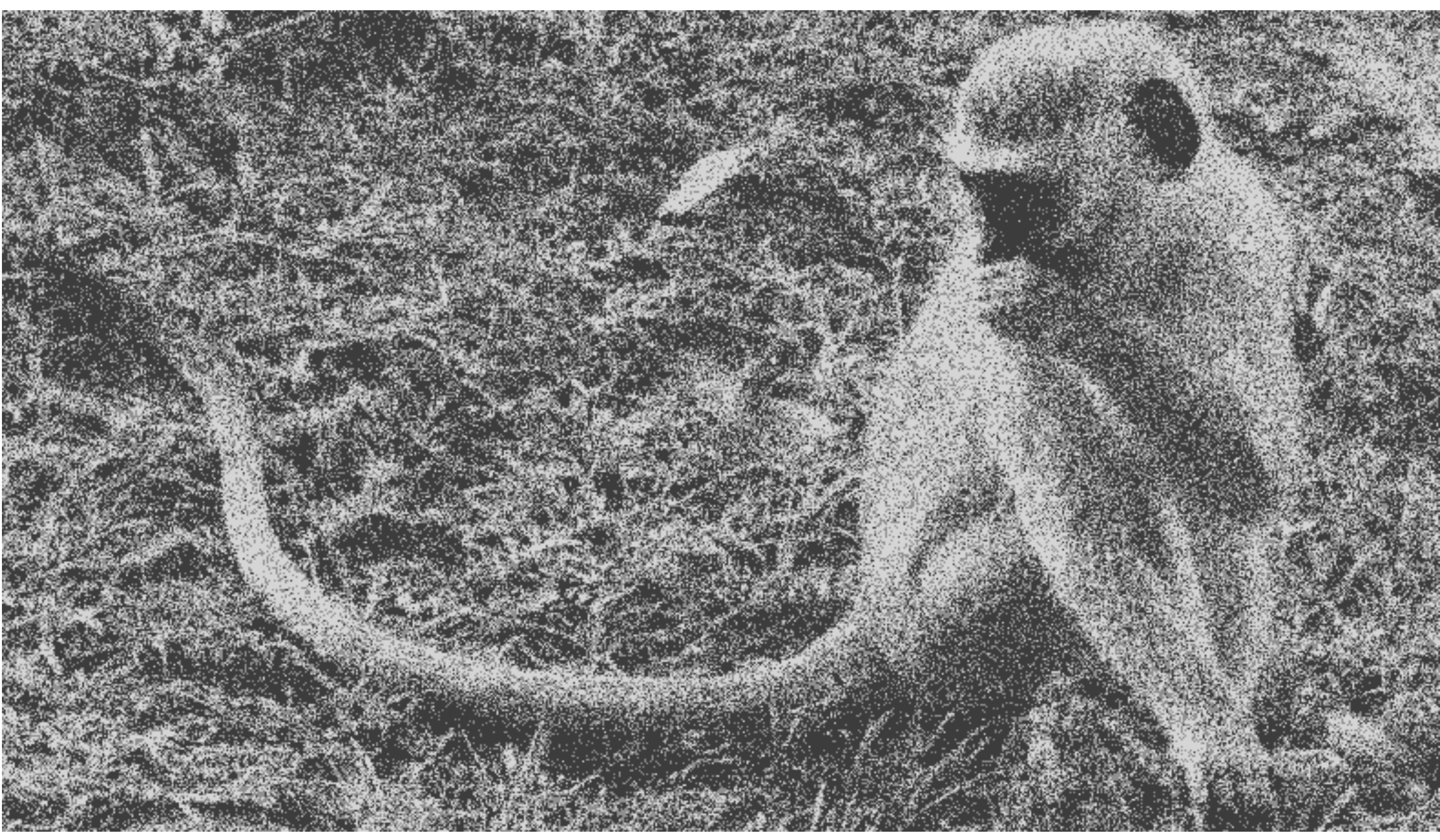Is there enough **image area** that is sufficiently bright; allow each pixel to be one of K (=3) colors, chosen adaptively, e.g. to minimize perceptual differences

[BUSTED]: each branch-site combination is a drawn from a K-bin (dS,dN) distribution. The distribution is estimated from the entire alignment. Tests if dN/dS>1 for some branch/site pairs in the alignment

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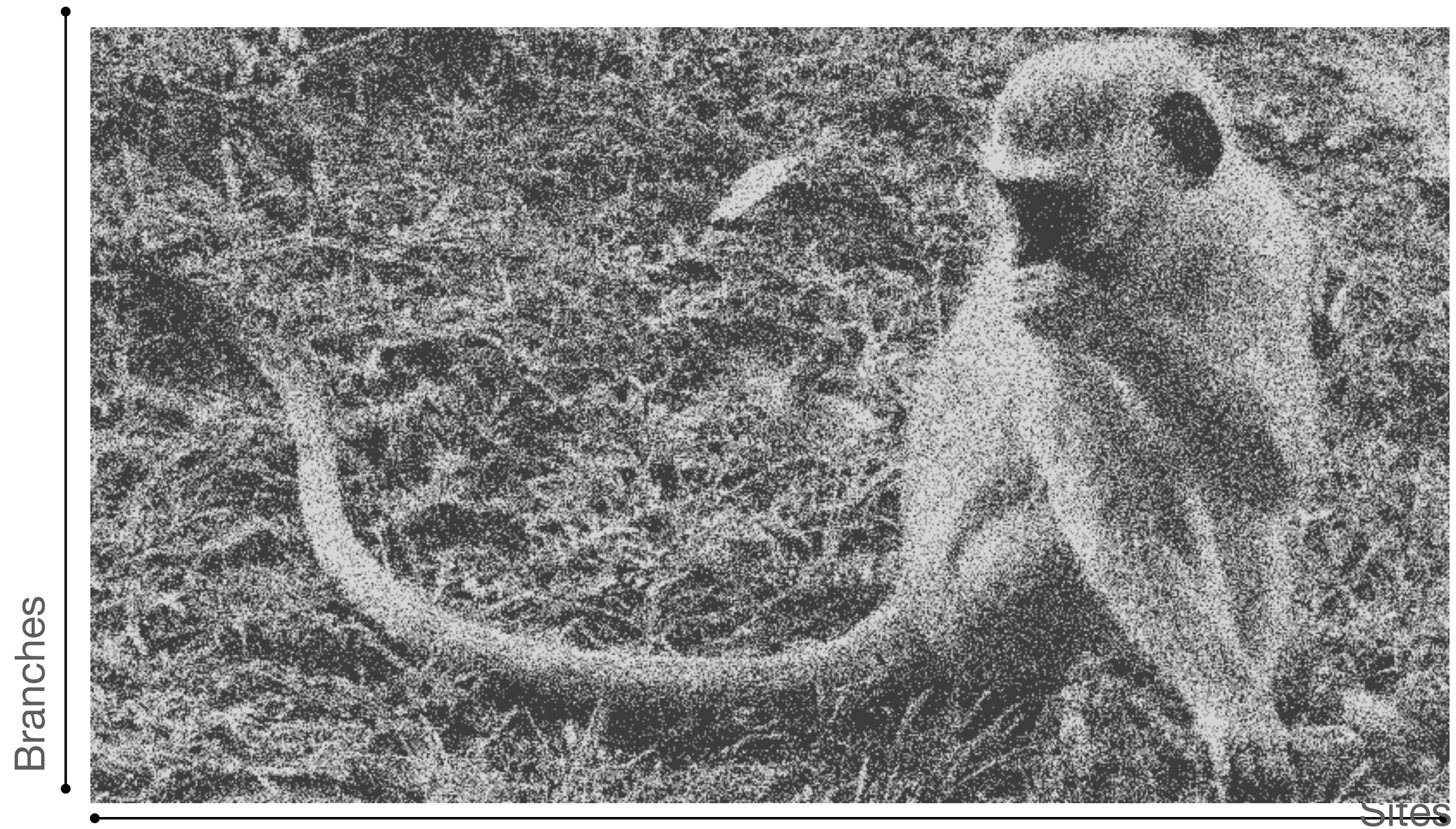[BUSTED]: each branch-site combination is a drawn from a K-bin (dS,dN) distribution. The distribution is estimated from the entire alignment. Tests if dN/dS>1 for some branch/site pairs in the alignment

Gene-wide selection analysis using a branch-site method (BUSTED), HIV-1 *env*

Model fits

Model	*log* L	#. params	AIC$_c$	Branch set	ω_1	ω_2	ω_3	
Unconstrained model	-2040.0	45	4170.9	Test	0.58 (85.37%)	0.73 (12.50%)	93.41 (2.13%)	
Constrained model	-2076.6	44	4242.1	Test	0.00 (29.28%)	1.00 (54.27%)	1.00 (16.45%)	

This table reports a statistical summary of the models fit to the data. Here, **Unconstrained model** refers to the BUSTED alternative model for selection, and **Constrained model** refers to the BUSTED null model for selection.

```
hyphy busted --srv No --alignment HIV-sets.fas --starting-points 5
```

Produces *HIV-sets.fas.BUSTED.json* file
View in http://vision.hyphy.org/BUSTED