Gene-wide selection

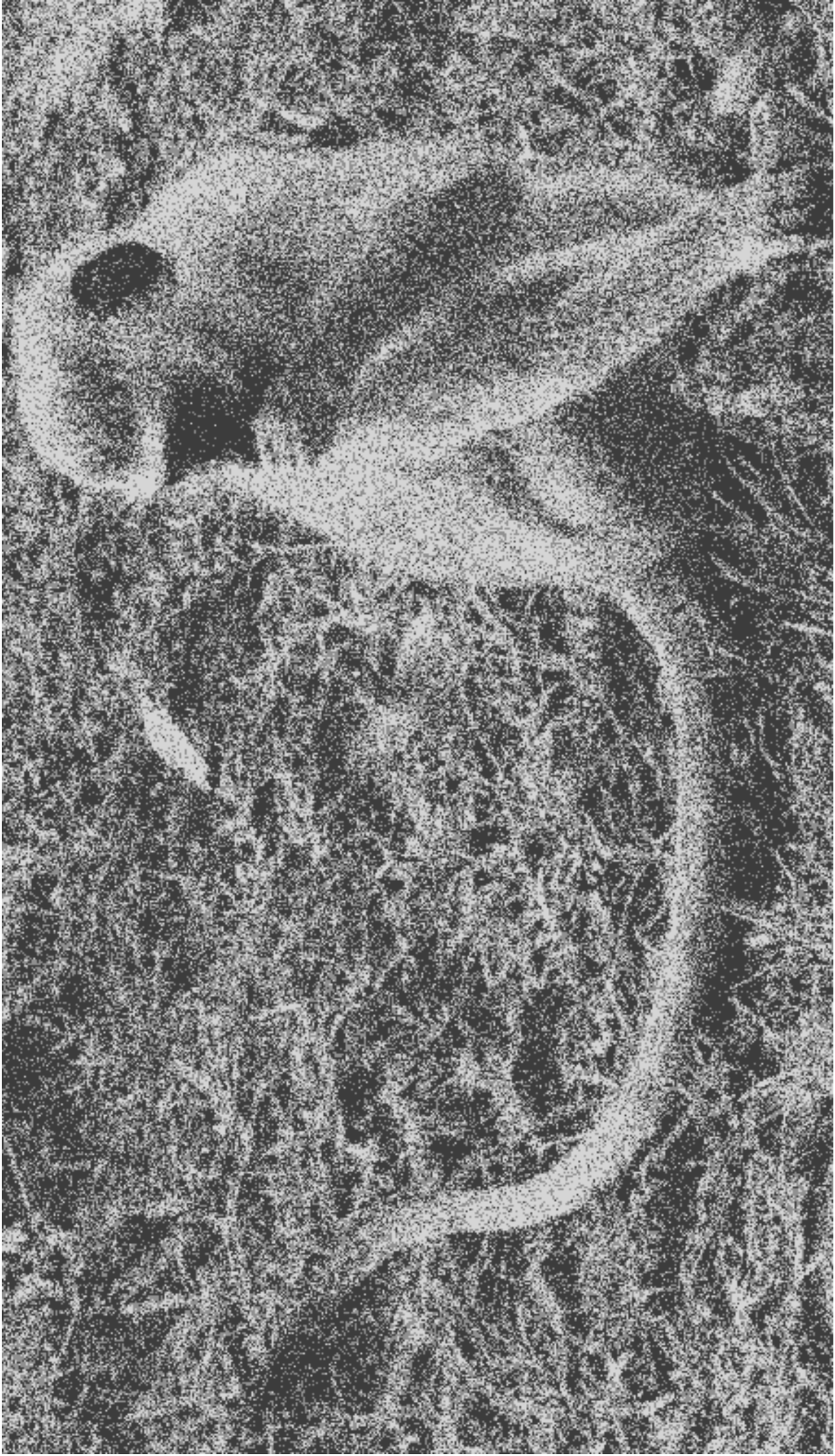
random effects over sites and branches [BUSTED]


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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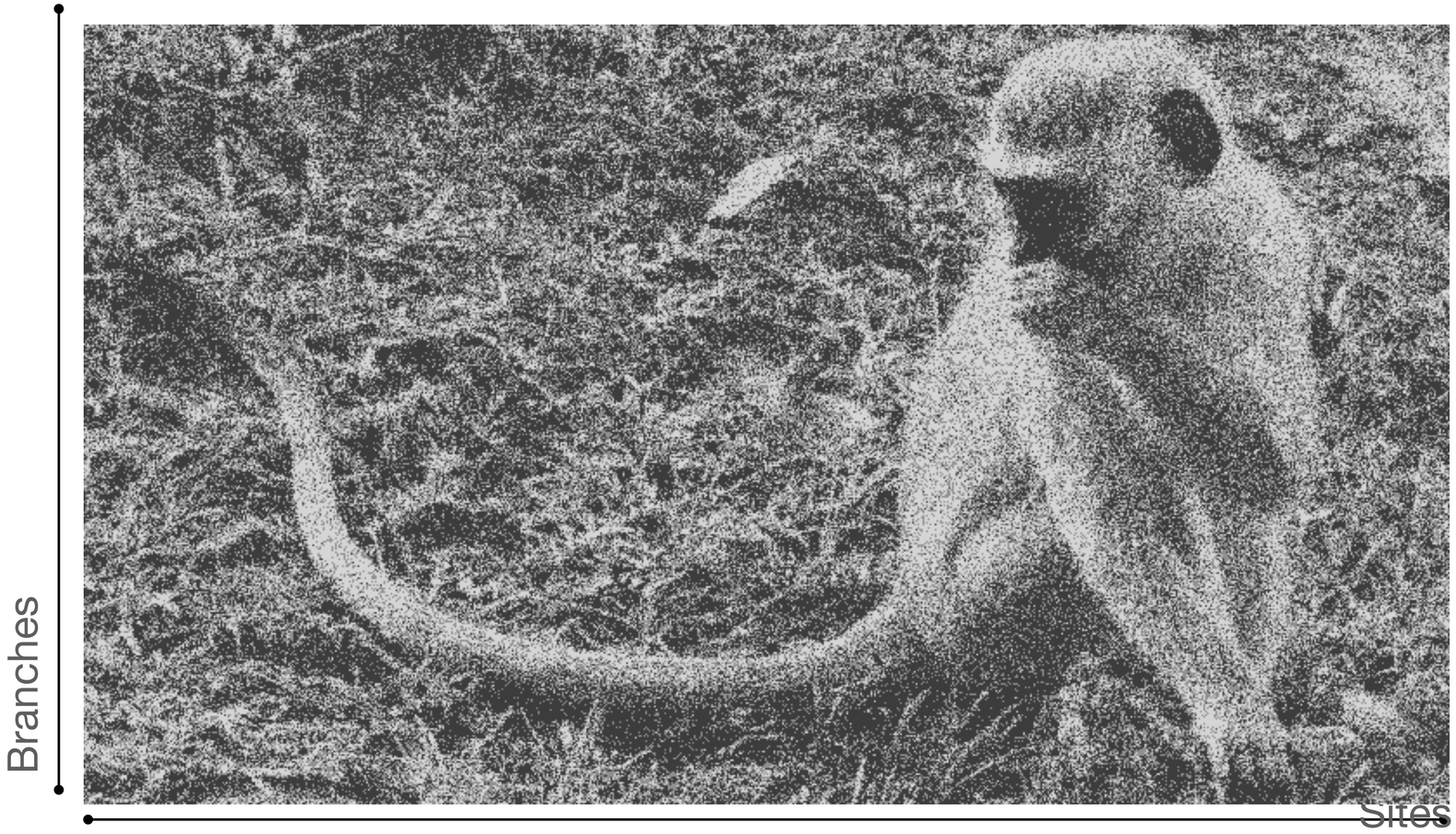

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Figure 1. Empirical Bayes Factors for ω>1 at a particular branch and site (only tested branches are included).