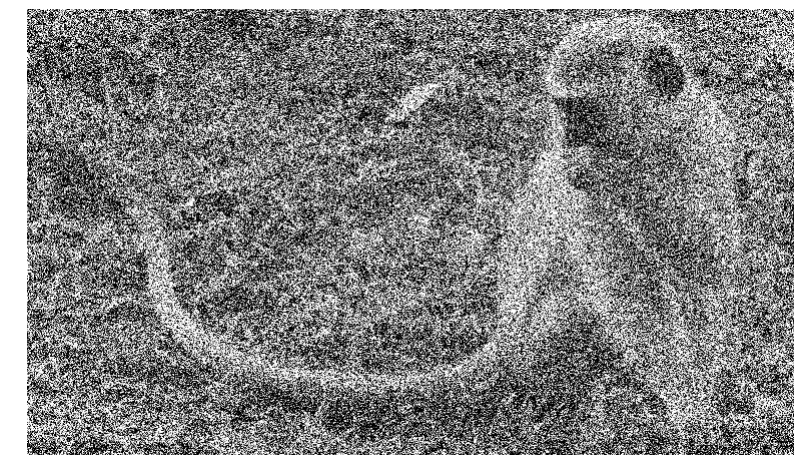
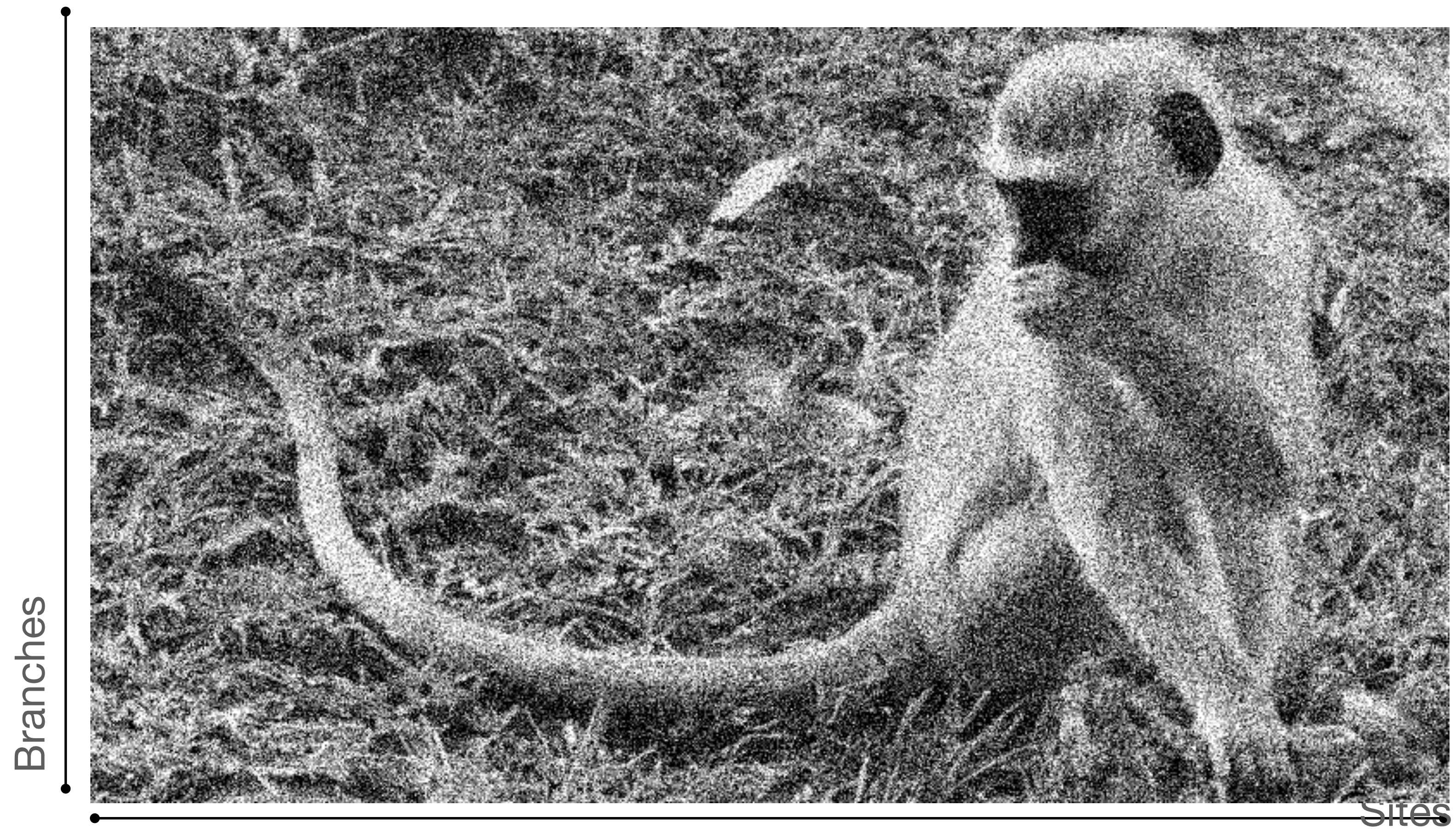


- Simple
 - single rate parameter
 - relatively compute-light
- Very robust to local variation
- Sample size \sim sites x branches
- Very low power
 - most genes are **on average** conserved
- No resolution
 - if selection occurred, how much of the gene was involved, and when did it happen
- Rate variation model is definitely misspecified



Gene-wide selection

random effects over sites and branches [BUSTED]



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 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