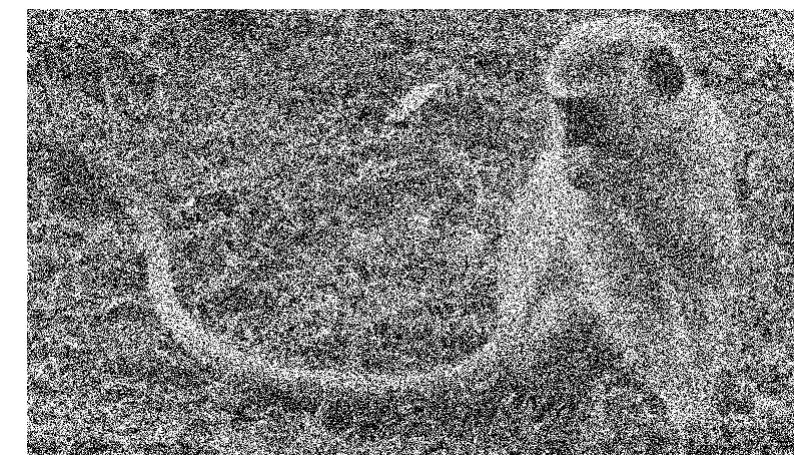
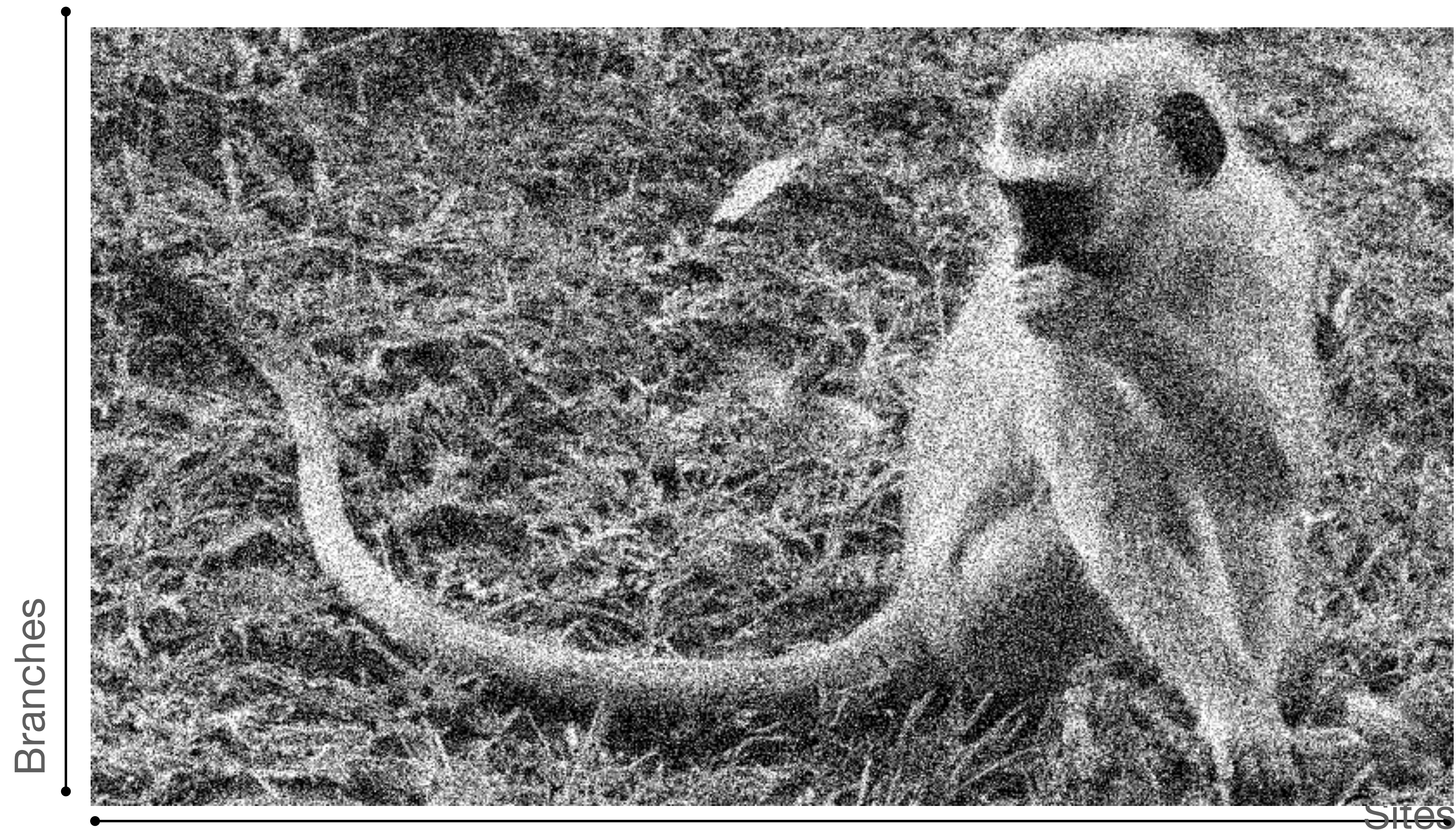


Gene-wide selection (mean dN/dS)

- **Simple**
 - single rate parameter
 - relatively compute-light
- **Very robust to local variation**
- **Sample size ~ 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