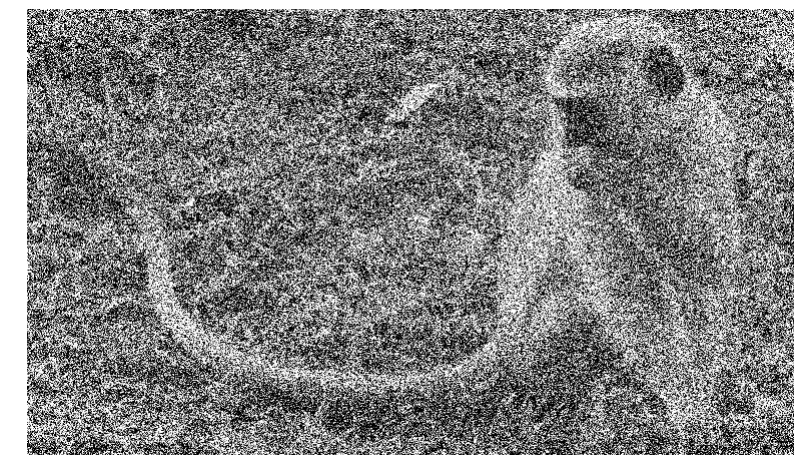


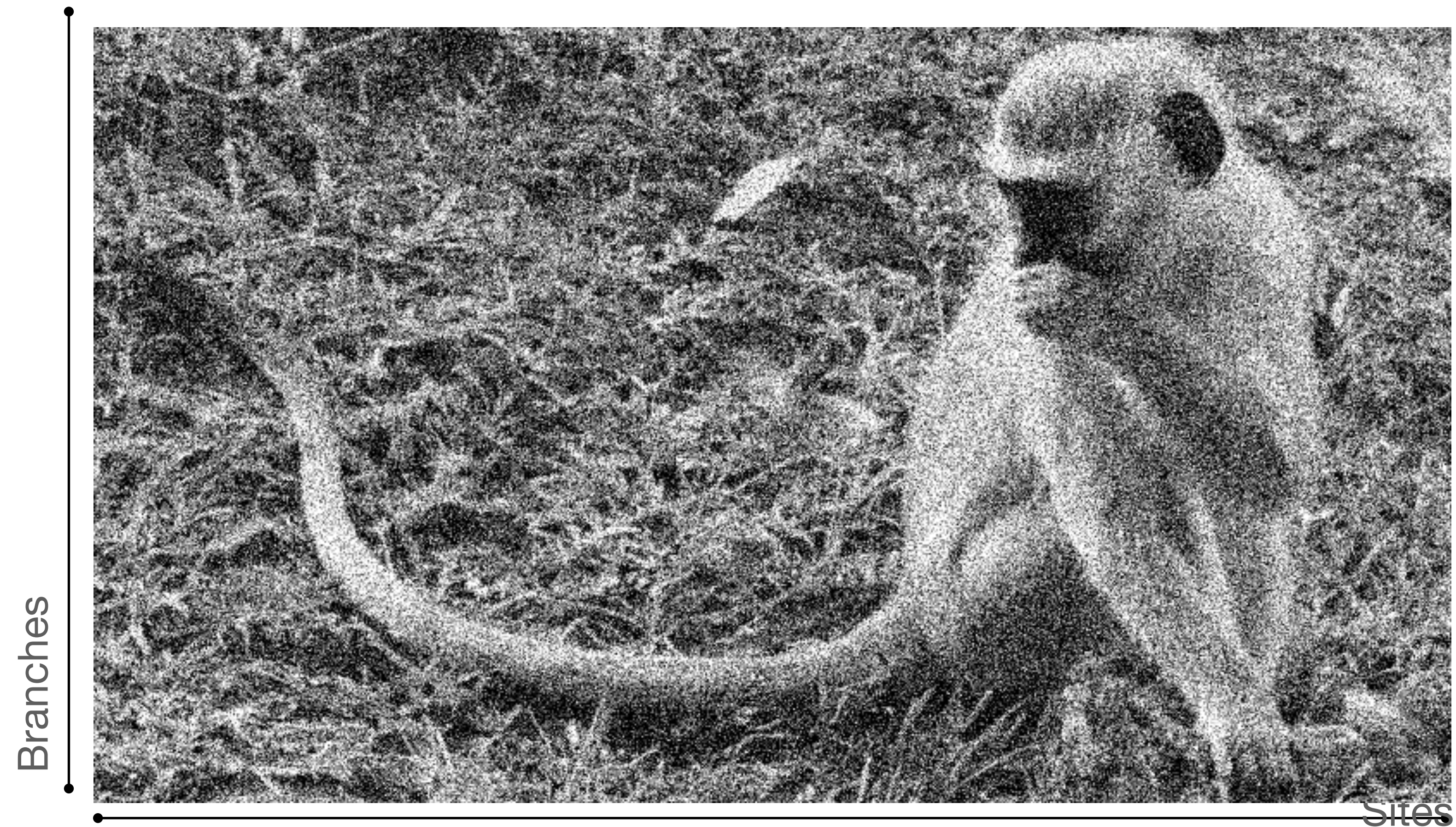
- Simple
  - single rate parameter
  - relatively compute-light
- Very robust to local variation
- Sample size  $\sim$  sites x branches
- Very low power
  - most genes are **on average** conserved
- No resolution
  - if selection occurred, how much of the gene was involved, and when did it happen
-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