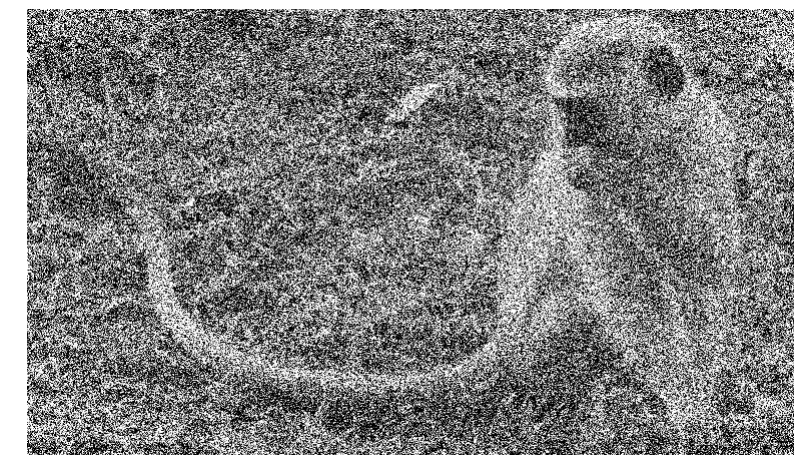- Simple

  - 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]

Branches

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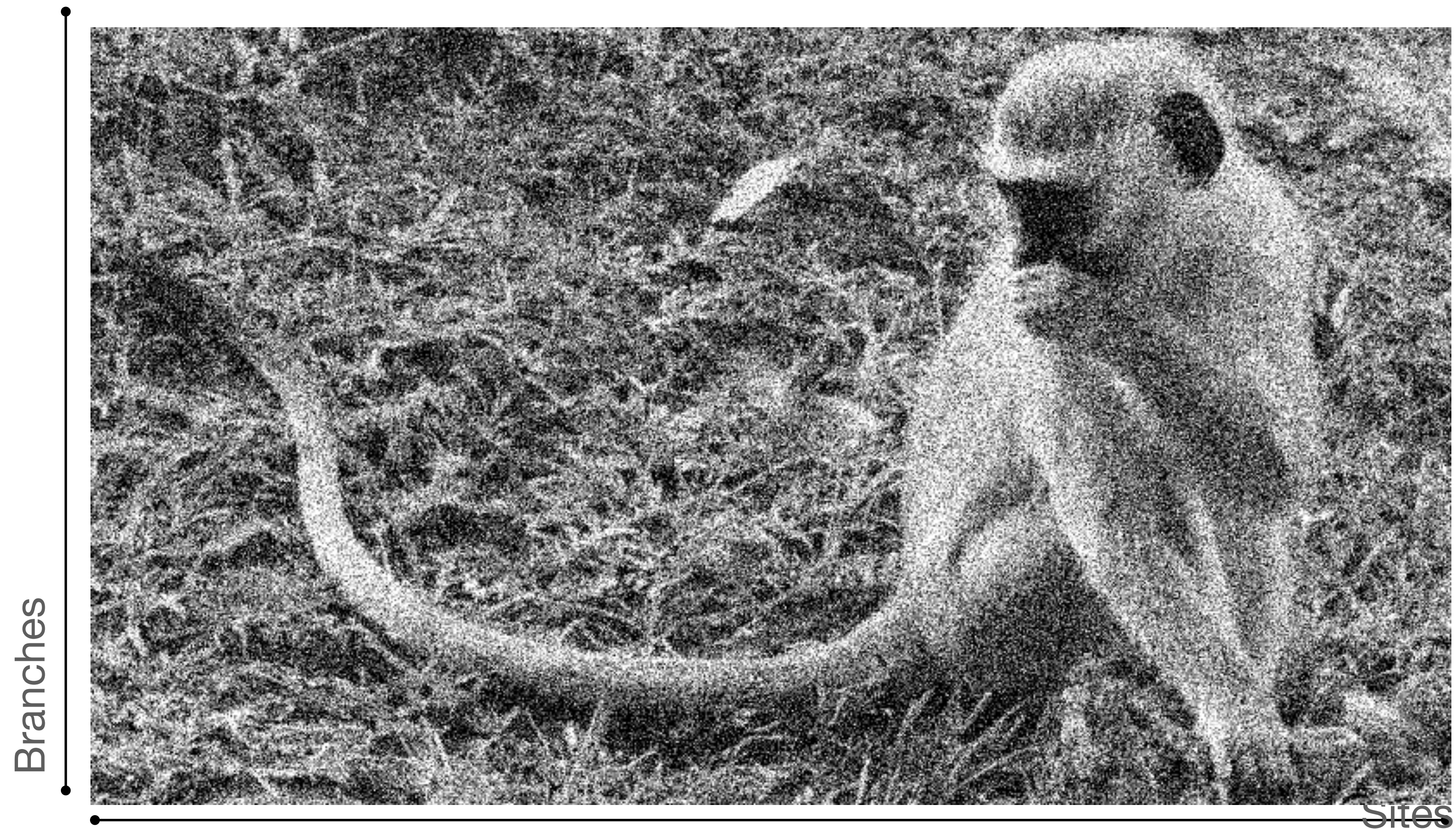
📷 Is there enough **image area** that is sufficiently bright; allow each pixel to be one of K (=3) colors, chosen adaptively, e.g. to minimize perceptual differences

🌲 [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