# 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]

Branches

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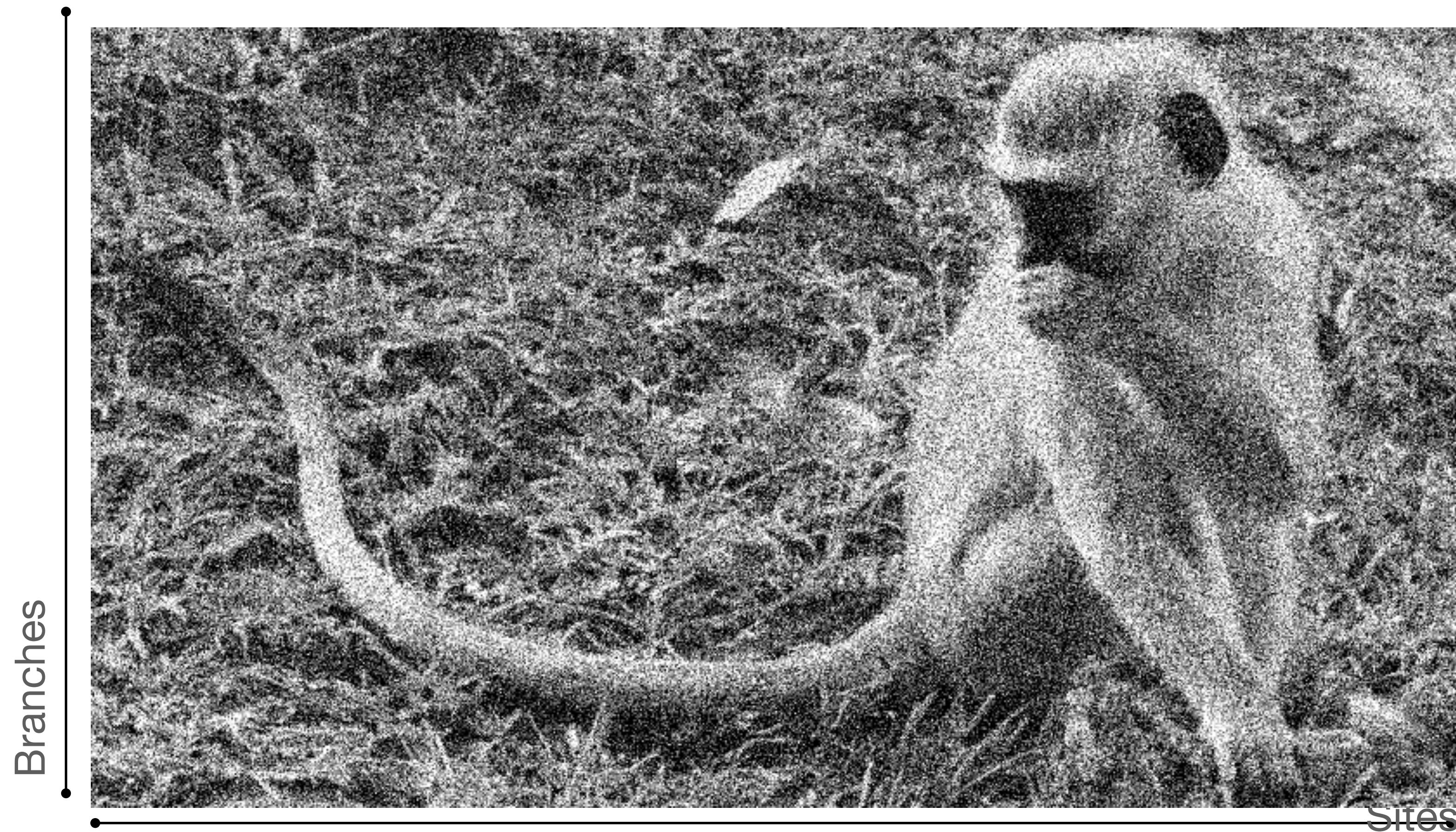
📷 Is there enough **image area** that is sufficiently bright; allow each pixel to be one of K (=3) colors, chosen adaptively, e.g. to minimize perceptual differences

🌲 [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