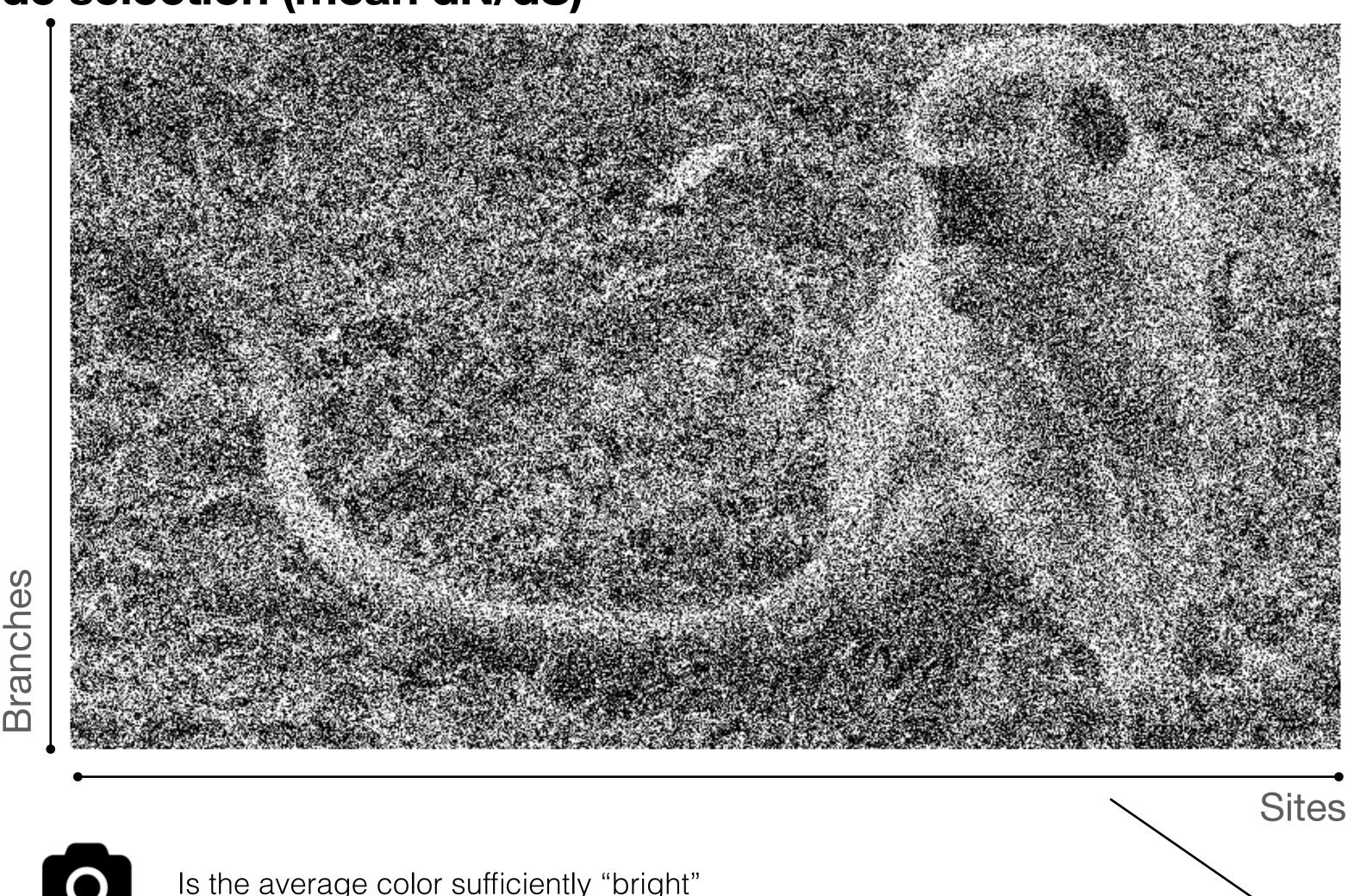
- High local variability
- Stable global (monkey) and local (head, tail) patterns, easily discernible

- ♣ Desired resolution (branch-site) is not attainable
- ♣ Global (and some local) patterns should be inferable and testable
- ♣ Statistical inference draws power from sample (and effect) size, need to aggregate data to gain power

## Gene-wide selection (mean dN/dS)





Is the average color sufficiently "bright"



Is there evidence that **gene-wide dN/dS > 1?** Aggregate data over the entire alignment, by inferring a single dN/dS parameter from all sites and branches