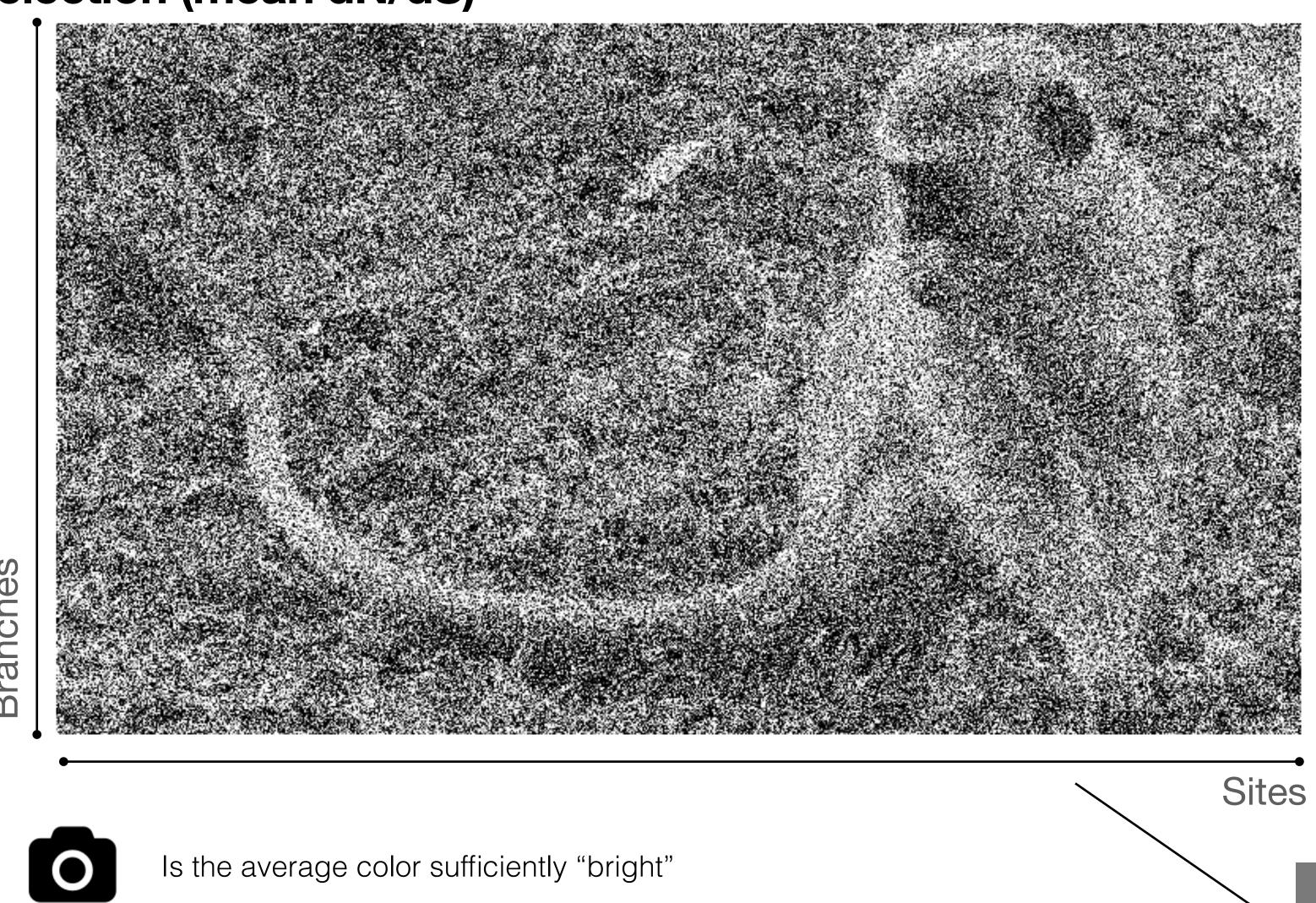
Gene-wide selection (mean dN/dS)





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

- 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

