

# 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





- 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

