

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

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**

