

📷 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