Gene-wide selection (mean dN/dS)

Branches

Sites

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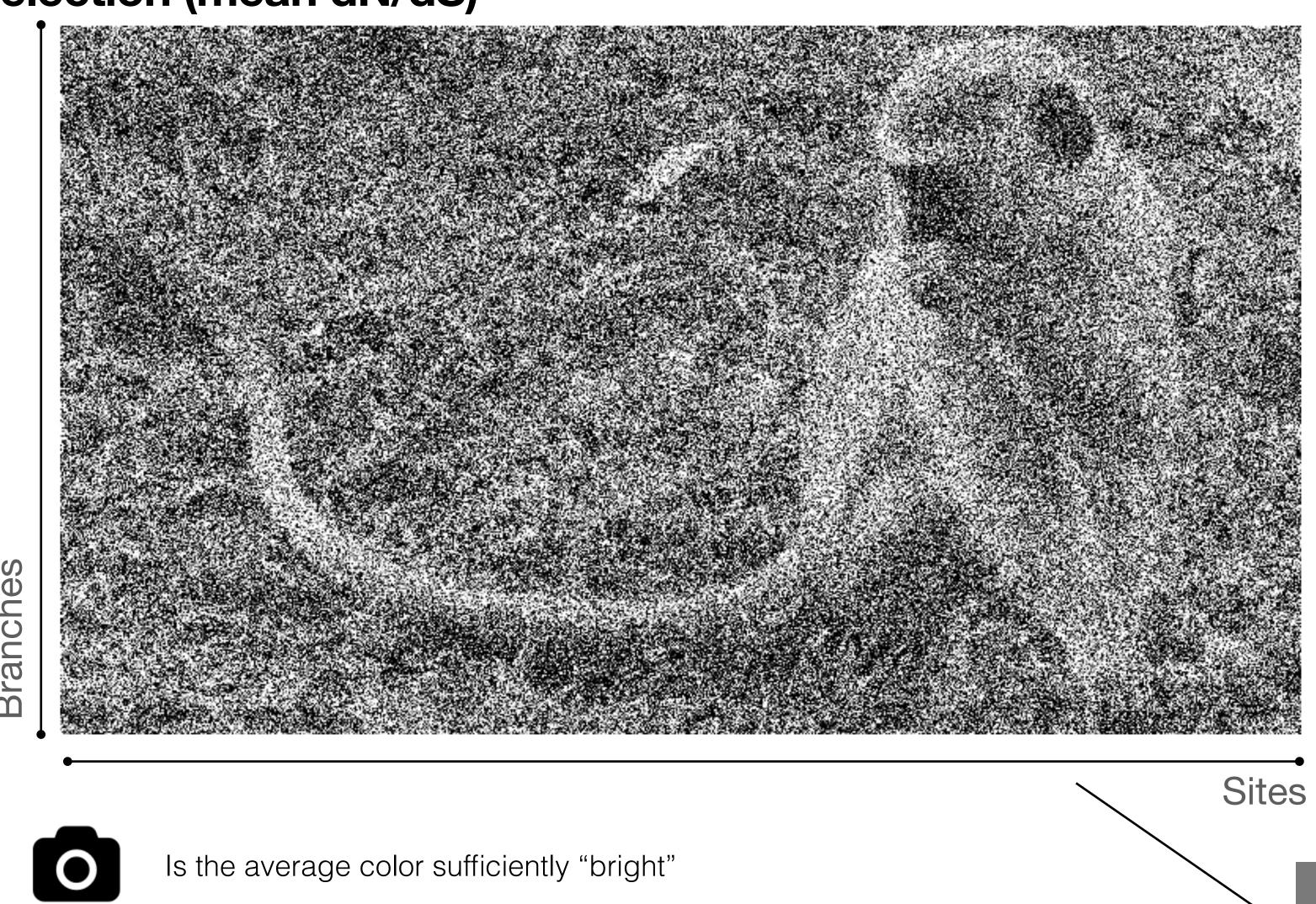
🌲 Is there evidence that **gene-wide dN/dS > 1?** Aggregate data over the entire alignment, by inferring a single dN/dS parameter from all sites and branches

- Simple

  - single rate parameter

  - relatively compute-light

- Very robust to local variation

- Sample size ~ 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