

# Neutral expectation

- A random mutation is **~3 times more likely to be non-synonymous than synonymous**, depending on the variety of factors, such as codon composition, transition/transversion ratios, etc.
- We need to **estimate** the proportion of random mutations that are synonymous, and use it as a reference to compute **dS**.
- In early literature, these quantities were codified as synonymous and non-synonymous “sites” and/or mutational opportunity.
- As a very crude approximation (assuming that third positions ~ synonymous), each codon has 1 synonymous and 2 non-synonymous sites.

# Evolutionary Modes

Positive Selection  
(Diversifying)

$$dS < dN \text{ or } \omega := dN/dS > 1$$

Negative Selection

$$dS > dN \text{ or } \omega < 1$$

Neutral Evolution

$$dS \approx dN \text{ or } \omega \approx 1$$