



**Molecular signatures of selection**

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- The **rate** of accumulation of synonymous substitutions (**dS**) can serve as the neutral background evolutionary rate
- We can compare the **rate** of accumulation of non-synonymous substitutions (**dN**), which alter the protein sequence, to **dS** and use their ratio to classify the nature of the evolutionary process

$$dS \sim \frac{\text{number of fixed } \textcolor{red}{\text{synonymous}} \text{ mutations}}{\text{proportion of random mutations that are } \textcolor{red}{\text{synonymous}}}$$

$$dN \sim \frac{\text{number of fixed non-synonymous mutations}}{\text{proportion of random mutations that are non-synonymous}}$$



*What can the denominator proportions depend on?*

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# Evolutionary Modes

Positive Selection  
(Diversifying)

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

Negative Selection

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

Neutral Evolution

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