

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)

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

Negative Selection

$dS > dN$ or $\omega < 1$

Neutral Evolution

$dS \approx dN$ or $\omega \approx 1$