Molecular signatures of selection

 The rate of accumulation of synonymous substitutions (dS) can serve as the neutral background evolutionary rate

Because synonymous substitutions do not alter the protein, we often posit that they are neutral

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

number of fixed synonymous mutations proportion of random mutations that are synonymous

number of fixed non-synonymous mutations $dN \sim$ proportion of random mutations that are non-synonymous

What can the denominator proportions depend on?

Molecular signatures of selection

- Because synonymous substitutions do not alter the protein, we often posit that they are neutral
- 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

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

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

Standard codon table architecture

Second letter

		U	С	Α	G	;; }
	U	UUUC } Phe UUC } Leu UUG }	UCU UCC Ser	UAU Tyr UAC Stop UAG Stop	UGU Cys UGC Stop UGA Trp	UCAG
	С	CUU CUC Leu	CCU CCC Pro	CAU } His CAC } GIn CAG }	CGU CGC Arg	U C A G
	Α	AUU Ile AUA Met	ACU ACC Thr	AAU } Asn AAC } Lys AAG } Lys	AGU }Ser AGC }Arg AGA }Arg	U C A G
	G	GUU GUC GUA GUA GUG	GCU GCC GCA GCA GCG	GAU } Asp GAC } Glu GAG } Glu	GGU GGC GGA GGG	U C A G