

# Codon table architecture

		Second letter				
		U	C	A	G	
First letter	U	UUU } Phe UUC } UUA } Leu UUG }	UCU } UCC } Ser UCA } UCG }	UAU } Tyr UAC } <b>UAA Stop</b> <b>UAG Stop</b>	UGU } Cys UGC } <b>UGA Stop</b> UGG Trp	U C A G
	C	CUU } CUC } Leu CUA } CUG }	CCU } CCC } Pro CCA } CCG }	CAU } His CAC } CAA } Gln CAG }	CGU } CGC } Arg CGA } CGG }	U C A G
	A	AUU } AUC } Ile AUA } <b>AUG Met</b>	ACU } ACC } Thr ACA } ACG }	AAU } Asn AAC } AAA } Lys AAG }	AGU } Ser AGC } AGA } Arg AGG }	U C A G
	G	GUU } GUC } Val GUA } GUG }	GCU } GCC } Ala GCA } GCG }	GAU } Asp GAC } GAA } Glu GAG }	GGU } GGC } Gly GGA } GGG }	U C A G

# 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.