Universal genetic code

This genetic code has 61 sense (non-termination) codons

Substitution types

	Synonymous			Non-synonymous			To a stop codon
	Transitions	Transversions	Total	Transitions	Transversions	Total	l Total
1st position:	8	0	8	140	26	166	9
2nd position:	0	0	0	148	28	176	7
3rd position:	58	68	126	2	48	50	7
Total	66	68	134	290	102	392	23

- Approximately 3:1 (392 N : 134 S) ratio when mutations are generated and fixed completely at random
- Non-random distribution over codon positions
 - All second position mutations are non-synonymous
 - Most (but not all) synonymous mutations are confined to the third position

Neutral expectation

- A random mutation is ~3 times more likely to be non-synonymous that synonymous, depending on the variety of factors, such as codon composition, transition/transversion ratios, etc.
- We need to **estimate** the proportion of <u>random</u> 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.