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

Substitution types
                          Synonymous                        Non-synonymous                  To a stop codon
              Transitions Transversions Total | Transitions Transversions Total |    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.