```
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

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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.