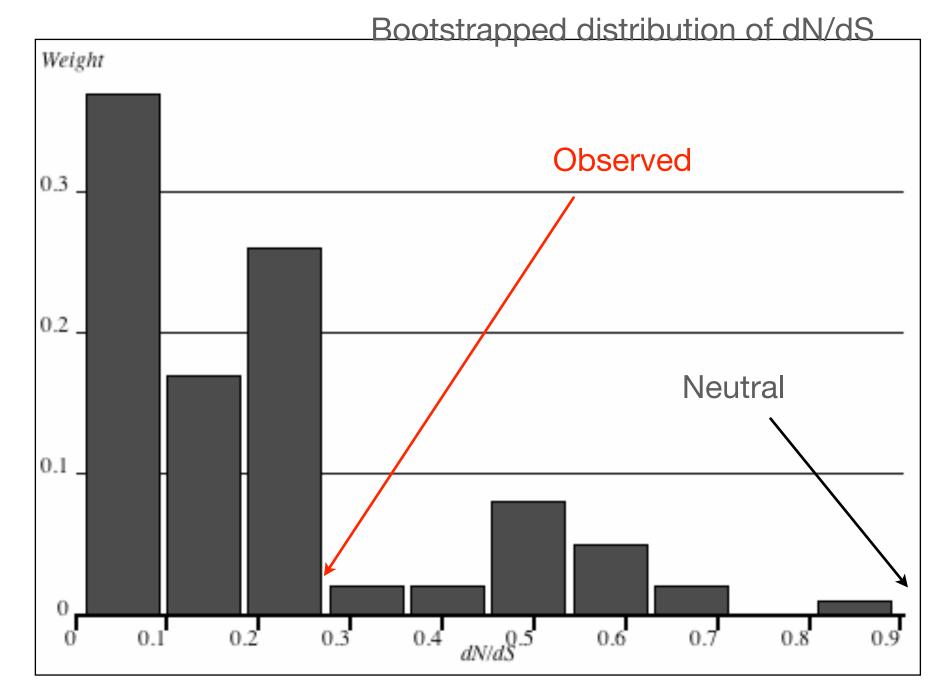
NG86 example

- The observed N/S ratio (1.0) is lower than the expected EN/ES ratio (4.05).
- The ratio of the ratios (N:S)/(EN:ES) yields $dN/dS = 1/4.05 \sim 0.25$.
- This ratio quantifies the *excess* or *paucity* of non-synonymous substitutions and is near dN/dS = 1 for neutrally evolving sequences/sites.
- Because there are fewer non-synonymous substitutions than expected under neutrality, we conclude that most non-synonymous mutations are removed by natural selection, i.e., the sequences are under negative selection
- If there were more non-synonymous substitutions than expected, we would conclude that many non-synonymous mutations are fixed due to natural selection, i.e., the sequences are under positive selection

NG86 example

- How reliable is the inference based on only 6 codons?
- Obtain sampling variance via bootstrap (or by limiting approximations)
- In this case, dN/dS is significantly less than 1.0 (p ~ 0.01)



```
Count = 100
Mean = 0.207385
Median = 0.166687
Variance = 0.0490168
Std.Dev = 0.221397
COV = 1.06757
Sum = 20.7385
Sq. sum = 9.15351
Skewness = 0.266313
Kurtosis = 33.381
Min = 0
2.5% = 0
97.5% = 0.741176
Max = 1
```