

**Computing synonymous and non-synonymous
sites for GAA (Glutamic Acid)**

8/3 non-synonymous sites (or 7/3 + 1/3 “stop” site)

1/3 synonymous sites

	1	2	3
Start codon:	G	A	A
A	AAA Lysine	*	*
C	CAA Glutamine	GCA Alanine	GAC Aspartic Acid
G	*	GGA Glycine	GAG Glutamic Acid
T	TAA Stop	GTA Valine	GAT Aspartic Acid
Synonymous changes	0	0	1
Non-synonymous changes	3	3	2
Synonymous sites	0	0	1/3
Non-synonymous sites	1	1	2/3

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1/3 synonymous sites

Nei-Gojobori dN/dS estimate (NG86)

- For each codon C we define $ES(C)$ and $EN(C)$ - the numbers of synonymous and non-synonymous *sites* of a codon
 - e.g., $ES(GAA) = 1/3$, $EN(GAA) = 8/3$.
- May also define them as fractions of substitutions that do not lead to stop codons,
 - e.g., $ES(GAA) = 1/3$, $EN(GAA) = 7/3$.
- The sum of ES and EN over all codons in a sequence gives an estimate of expected synonymous and non-synonymous **sites** in a sequence.
- For two sequences (the target of the original method), we average $ES(C)$ and $EN(C)$ at each site.
- EN/ES is thus the ***expected ratio of non-synonymous to synonymous substitutions counts under neutral evolution***

Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions

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>5,300 citations