

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

Aminoacid	Codons	Redundancy
Alanine	GC*	4
Cysteine	TGC,TGT	2
Aspartic Acid	GAC,GAT	2
Glutamic Acid	GAA,GAG	2
Phenylalanine	TTC,TTT	2
Glycine	GG*	4
Histidine	CAC,CAT	2
Isoleucine	ATA,ATC,ATT	3
Lysine	AAA,AAG	2
Leucine	CT*,TTA,TTG	6
Methionine	ATG	1
Aspargine	AAC,AAT	2
Proline	CC*	4
Glutamine	CAA,CAG	2
Arginine	AGA,AGG,CG*	6
Serine	AGC,AGT,TC*	6
Threonine	AC*	4
Valine	GT*	4
Tryptophan	TGG	1
Tyrosine	TAC,TAT	2
Stop	TAA,TAG,TGA	3

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

1/3 synonymous sites

Start codon:	G	A	A
Site/Change to	1	2	3
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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Nei-Gojobori dN/dS estimate (NG86)

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

M. Nei and T. Gojobori

Mol. Biol. Evol. **3** 418–426 (1986)

- 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***