

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

NG86 example

Mean		Site 1	Site 2	Site 3	Site 4	Site 5	Site 6
	Seq1	<u>ACA</u>	<u>ATA</u>	<u>ATC</u>	<u>TTT</u>	<u>AAT</u>	<u>CAA</u>
	Syn	1	2 / 3	2 / 3	1 / 3	1 / 3	1 / 3
	NonSyn	2	7 / 3	7 / 3	8 / 3	8 / 3	7 / 3
	Seq2	<u>ACA</u>	<u>ATA</u>	<u>ACC</u>	<u>TTT</u>	<u>AAC</u>	<u>CAA</u>
	Syn	1	2 / 3	1	1 / 3	1 / 3	1 / 3
	NonSyn	2	7 / 3	2	8 / 3	8 / 3	7 / 3
	Syn	1	2 / 3	5 / 6	1 / 3	1 / 3	1 / 3
	NonSyn	2	7 / 3	13 / 6	8 / 3	8 / 3	7 / 3

ES = $3\frac{1}{2}$, **EN** = $14\frac{1}{6}$: under neutrality, we expect the ratio of non-synonymous to synonymous substitutions of **EN/ES** ~ 4.05