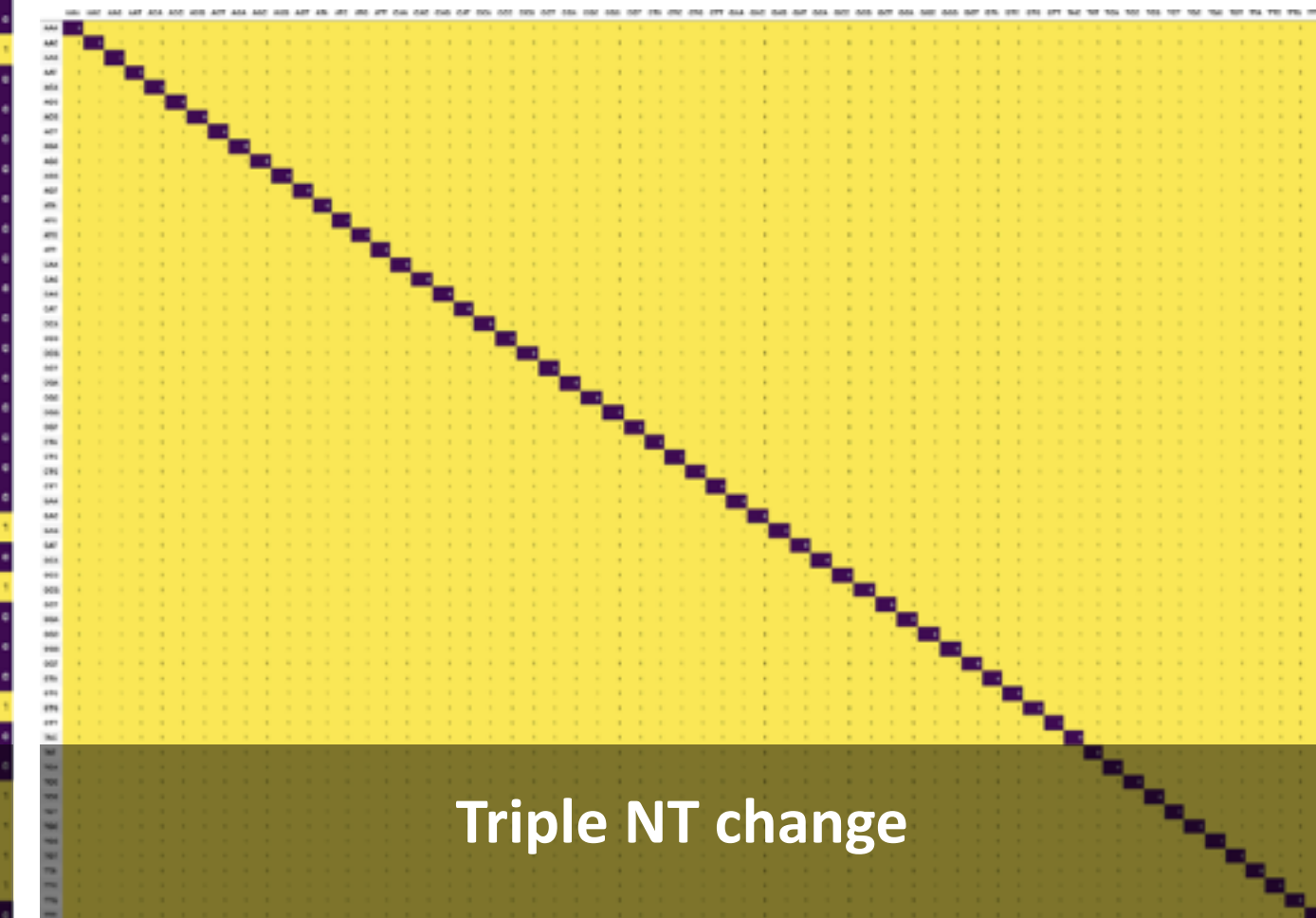
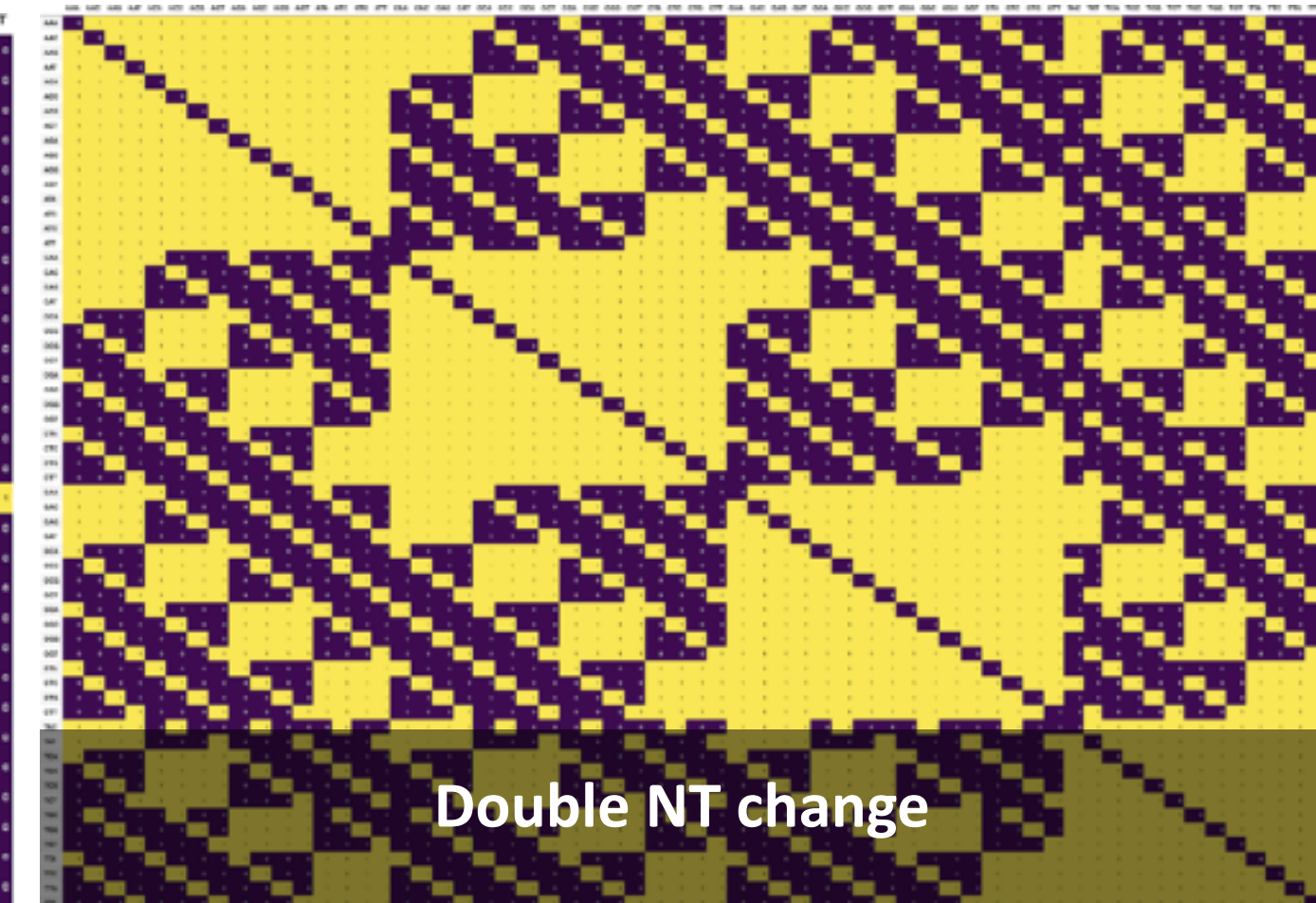
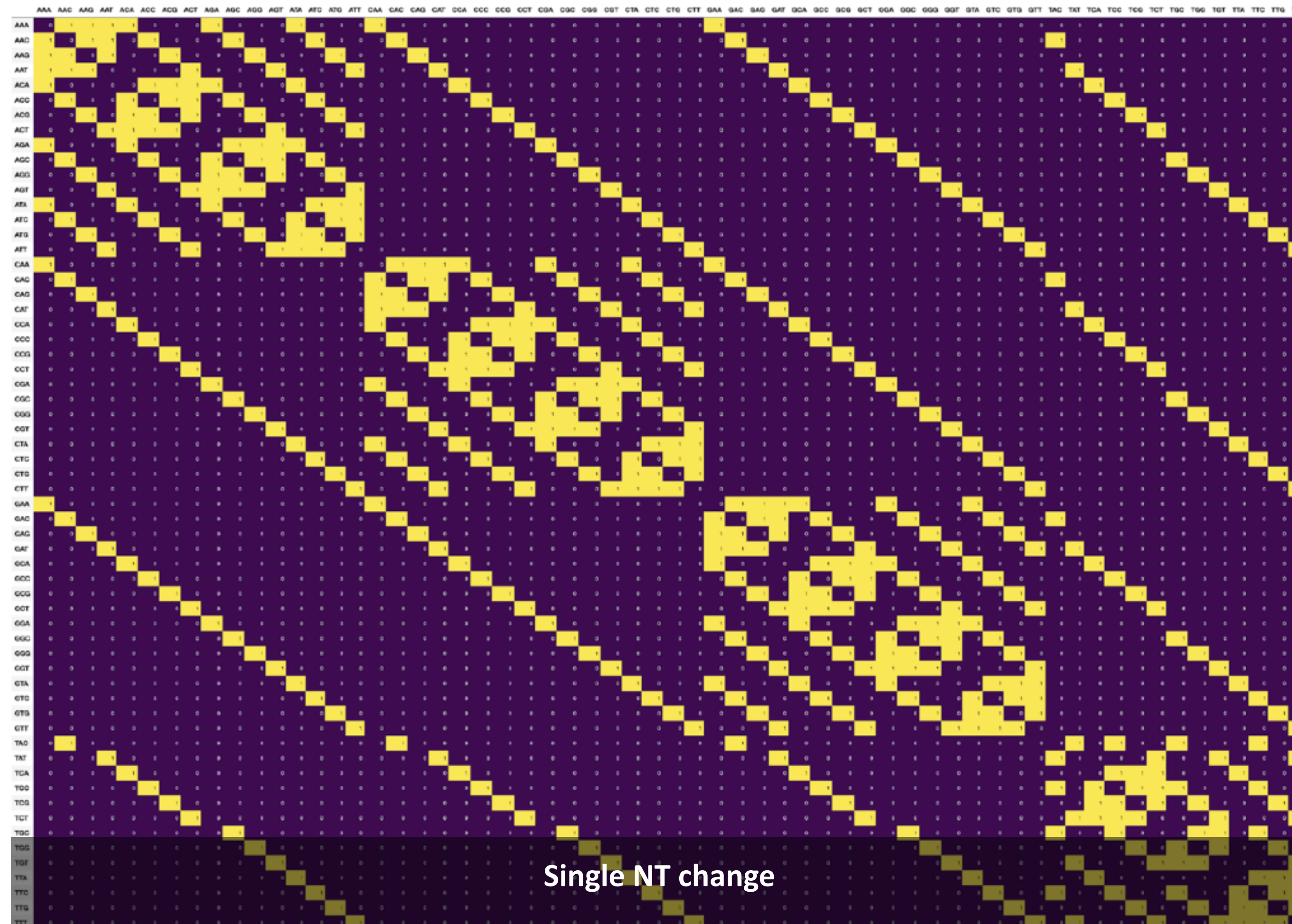


Illuminating the darkness in molecular evolution



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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Mol. Biol. Evol. 3 418--426 (1986)

>5,300 citations