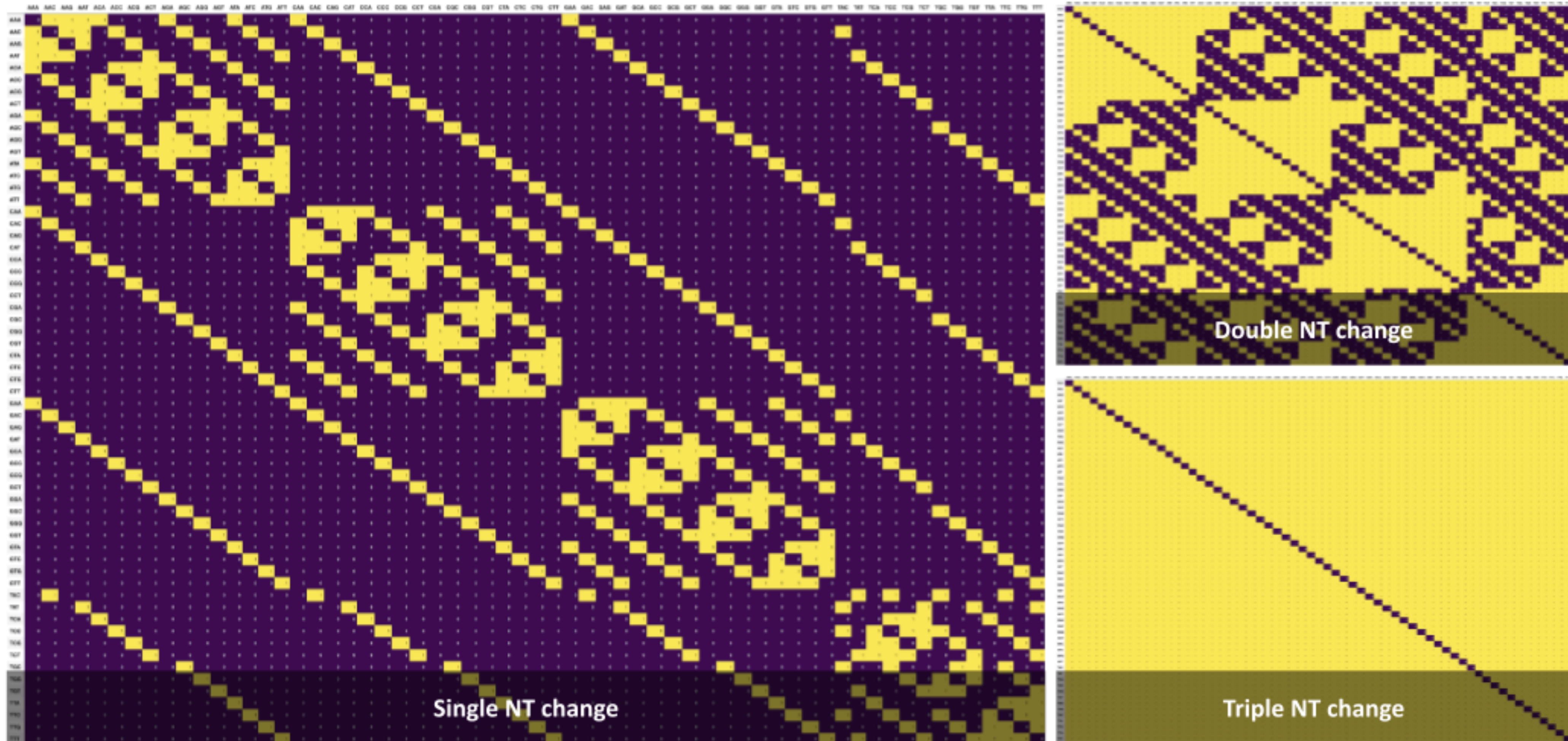


Illuminating the darkness in molecular evolution



Computing the transition probabilities

- In order to recover transition probabilities $\mathbf{T}(t)$ from the rate matrix \mathbf{Q} , one computes the matrix exponential $\mathbf{T}(t) = \exp(\mathbf{Q}t)$, same as with standard nucleotide models, e.g. HKY85 or GTR.
- Because the computational complexity of matrix exponentiation scales as the cube of the matrix dimension, codon based models require roughly $(61/4)^3 \approx 3500$ more operations than nucleotide models.
- This explains why codon probabilistic models were not introduced until the 1990s, even though they are relatively straightforward extensions of 4x4 nucleotide models