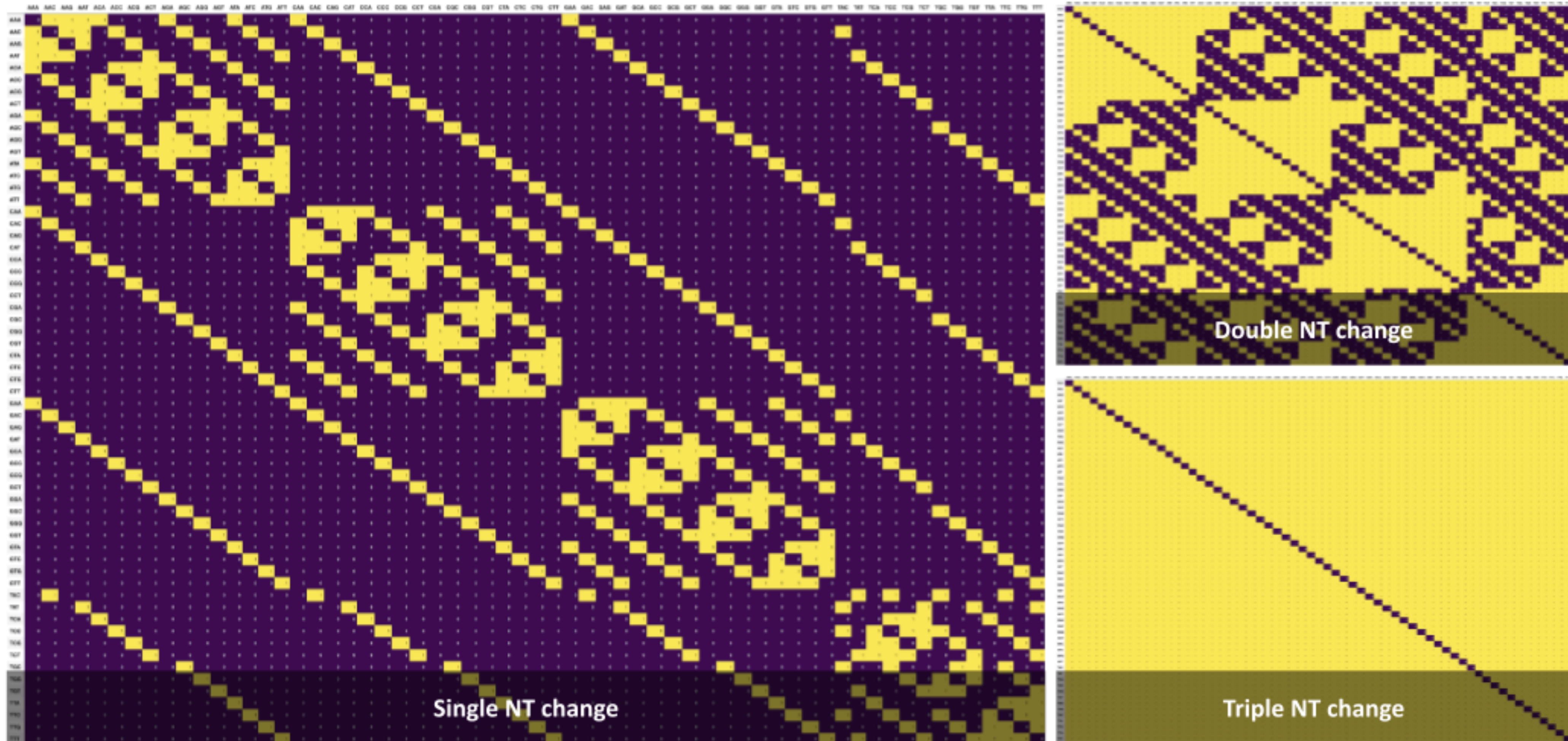


# Illuminating the darkness in molecular evolution



# 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