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**Nucleotide Mutation and Amino Acid Evolution** JOSE PARRA, BERNARD GERSTMAN, Department of Physics, Florida International University — We have found a set of nucleotide coupling propensities (ncp) that best reproduces the currently observed probability distribution of amino acids found in protein data banks. These ncp represent the biochemical potentials that produce different probabilities for different mutations within a sequence of nucleotides. We have allowed these ncp to act on a random sequence of nucleotides whose codons initially produce a random arrangement of amino acid residues. Interestingly, though the mutating action of the ncp on the chain of nucleotides results in the correct evolution of the probability of appearance of each individual amino acid towards the present distribution, there is however no evolutionary trend in major global characteristics of the amino acid distribution. We present results that show that properties of amino acids that are considered important for protein structure do not evolve on average, such as: hydrophobic/hydrophilic, size, aromatic/non-aromatic, aliphatic/non-aliphatic, helical-preference/beta-strand.

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