

Analysing GC Content of mtDNA Genome through Network

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In this work we use an alternative network approach to describe DNA sequence based in triplet juxtaposition. Due to the complex nature of DNA sequence we use a model of 64 vertices (each DNA triplet possibility) and using as connection the pure juxtaposition in sequence. With this model we are able to measure how tricodons are correlated with a simple clustering coefficient (defined from network theory). Our preliminary analysis results in a measure that take into account GC and 3-bp periodicity bias and shows separation between different classes of organisms without considering only specific isolated gene (as 16S for instance). As a secondary result we show that our measure has a dependence of GC that cannot be explained by randomness itself alone and seems to be a characteristic of mtDNA in a general way.