

Building Network With Bacterial Genome Comparing 16S Gene

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In this work we build DNA sequence networks for a set of complete bacterial genomes and for isolated 16s genes. A DNA sequence network is an amalgamation of string, entropy and periodicity tools aiming to extract a global measure of relative small DNA sequences. Those measures should be taken over a complete DNA sequence (as a mean) or isolated in small scale (up to 600bp). Our network is formed by a set of vertices (64 triplet possibilities inspired in codon size) and links are established by juxtaposition. Our measure is based in a clustering coefficient and its distance from random-generated DNA sequence. The main objective here is to compare and classify (for some sets of phylogenetic close organisms) results from 16s alone and full genome. In a preliminary approach we were able to draw alternative phylogenetic trees inside those groups that keep a good degree of similarity with other known measures.