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BACTOSOM; A novel tool for Comparative Bacterial Proteomics

Recently, comparing bacteria have become very essential in many areas in biology and biotechnology such as taxonomic classification; understanding disease mechanism (pathogenic vs. non pathogenic); designing differential diagnostic tools; developing novel vaccines, and exploring the functions of uncharacterized proteins.

In this work, we propose a novel bioinformatics tool, called BACTOOM that provides a way for comparing bacterial proteomics. This tool is realized by considering the primary structure of the proteins of the bacteria and measuring their distances from a given reference (*Mycoplasma genitalium* protein sequence). BACTOSOM is a high-throughput comparison and mapping tool for bacterial proteomes that will provide a new way of visualizing the result of the comparison process using Self Organizing Map (SOM).

A straightforward solution for comparing bacteria would be performed by applying sequence alignments to the bacteria. But this solution is very slow and provides a poor way of representing the result of the comparison, which makes it very difficult for the researchers to discover the similarity and differences between various species of bacteria. On the other hand, the currently existing approaches such as Gene-Atlas and Blast-Atlas are limited and they only consider gene information.

BACTOSOM takes protein information rather than gene information into consideration and provides a two dimensional colored map of nodes to visualize the difference and the similarity between two or more whole proteomes using many different visualization methods such as P-matrix, following the lines, minimum spanning tree, U-matrix and others. Each node in the map contained a set of proteins that share similarities. Based on the visualization methods, the researcher can discover the common functions of different bacteria, the number of proteins similar to each other, as well as global similarities between different bacteria.

In order to verify BACTOSOM results, a group of bacterial proteins and their corresponding clusters were collected from Protein Clusters Database-NCBI to build a set of hypothetical bacteria by selecting a given number of proteins from different clusters and constructing several virtual proteomes. BACTOSM showed a high accuracy in assigning the different proteins in their corresponding functional clusters that were obtained from Protein Clusters Database.