Abstract

Manal Helal

Dynamic programming algorithms for discovery of antibiotic resistance in microbial genomes

The translation of comparative genomics into clinical decision support tools depends on the quality of sequence alignments. However, currently, used methods of multiple sequence alignments suffer from significant biases and inability to align diverged sequences. The objective of this study was to test and develop a new MSA algorithm suitable for the high-throughput comparative analysis of different microbial genomes. We have used the clinically relevant task of identifying regions that determine resistance to antibiotics to test the new MSA algorithm and to compare its performance with existing methods.