

Title: Microbial comparative genome for in-silico DNA marker extraction

Name: Ali Najafi, Reza Ranjbar, Nadia Jahande

Molecular Biology Research Center, Baqiyatallah University of medical Science, Tehran,
IRAN

Next-generation sequencing (NGS) technologies have developed progressively in microbial genomic research and clinical applications. Also, genetic fingerprinting has been used in molecular epidemiologic studies. Therefore, it is essential that a connection or a link is established between them for discovering DNA marker in whole genome for using in molecular epidemiology and bacterial diagnosis. Bioinformatics and comparative genome analysis tools lead to further and deeper understanding of genomic variation in the bacterial species. Bacterial comparative genome analyses can be used for evolutionary process, structure and function annotations, and importantly in unique DNA marker extraction. These unique probes are suitable for high-throughput diagnostic method such as microarray. Finally, setting up a procedure for comparative analysis will be useful for a wide range of microbial researches and clinical applications.

Biography

Ali Najafi is a Bioinformaticist. He completed masters in Molecular Biology and did PhD in Bioinformatics and systems biology at the age of 34 years from Tehran University, Tehran, Iran. At present, he is a researcher in Molecular Biology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran. His research areas are: microarray data analysis, bioinformatics software development, network and pathway reconstruction, and computational complex disease modeling. To date, he has published more than 30 scientific papers.