ABSTRACT

Bacterial pathogens persist in restraining public health around the globe. We need to identify the pathogenic factors in these bacteria’s / pathogens, which in-turn will aid us to discover novel drugs and better our understanding of the particular disease at the genomic level. With the rapid growth and generation of complete genomic sequence in this post genomic age, it enhances our chances for a computational comparative analysis and studies from just a protein sequence. Here, we analysed the 12 genomes of Yersenia Spp. bacteria to find out the similarity in the genomic and pathogeneic Island. Proteins present in nine genomes were also analysed so that we can develop a drug that can act on the specific common targets present in the nine species of these bacteria’s. Our research focus was on the development of the algorithm to find the functionality related gene clusters in the genome. Our main interest was to predict the localized gene clusters within the given genomes was successfully done with the developed algorithms.