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Abstrak

ABSTRAK

Genome Sequence Analysis for genetic datasets by using ORF (Open Reading Frames) techniques is an interesting area of research for bioinformatics researchers nowadays. There is a strong research focus on comparative analysis between genetic behaviors and diversity of different species. Contrary to whole genome sequence analysis, scientists are now trying to concentrate specifically on layered analysis to get a better insight of relevancy among genetic datasets. This phenomenon will help to better understand species. An ORF statistical analysis for genetic data-sets of species Chimera Monstrosa and Poly Odontidae is presented. For completion of this analysis, we use a hybrid approach that combines a generic mechanism for statistical analysis with specific approach designed for out performance. At first instance, genetic datasets are refined for better usage at next level. These sets are then passed through layers of filters that perform DNA to Protein translation. Statistical comparison is performed during this translation. This layered architecture helps in better understanding of the degree of similarity and differences in genomic sequences.