An integrated approach for statistical genome sequence analysis between genetic datasets

---

Abstrak

Genome Sequence Analysis for genetic data
sets 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 geneticdatasets. 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.