

Comparative Genome Analysis

Pubrica's Bioinformatics complex procedures are quality-assured to deliver the correct data in the quickest time possible, at a low cost, and with a flexible and configurable workflow. You can learn more about our procedures and bioinformatics services by contacting us directly and communicating with a representative.

Comparative genomics is a discipline of biology that compares the genomes of different organisms, genome sequences of different species, including humans, mice, and many other animals, from bacteria to chimpanzees. Researchers can learn what characterizes various life forms at the molecular level by comparing the sequences of genomes from different organisms. Comparative genomics is also a valuable technique for researching evolutionary changes in organisms. It aids in discovering genes that are conserved or shared across species and genes that give each organism its distinct characteristics.

A simple comparison of genome characteristics such as genome size, number of genes, and the chromosomal number is being used as a starting point for comparative genomic analysis several fully sequenced model organisms data. Aligning homologous DNA from various species allows for the comparison of discrete portions of genomes. On an evolutionary scale, phylogenetic distance measures the degree of separation between two species or their genomes, commonly expressed as the number of accumulated sequence changes, years, or generations. On an evolutionary scale, phylogenetic distance measures the degree of separation between two species or their genomes, commonly expressed as the number of accumulated sequence changes, years, or generations.

Our comprehensive Bioinformatics Tool services

- Proteomics study
- Protein Model interpretation
- Integrated efficacy and safety summaries of target proteins
- Predict active site of the target ligand
- Identified subfamily

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