Short Note on Bioinformatics Tool

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Introduction

Modern study of living things/qualities of living things is seen as the generation of huge data sets which require a computer based treatment in order to produce useful information for them and their use is more important in biological research due to irreversible data- oriented trends in field, as metagenomics is form of putting DNA in correct order which DNA sequencing present in particular sample as the researcher are finding novel genes with encoded metagenomes it may get evolved in pharmaceutical industry, bioinformatics tools are for assembly and annotation of sequence data with development of new novel genes.

Keywords

Bioinformatics Tool, Visual Representation, Phylogenetic Analysis, Artificial Intelligence, Neural network, Machine Learning

Description

There are two ways to study micro biomes using high-throughput sequencing- marker-gene studies, whole genome shotgun (WGS) metagenomics.

Marker-gene studies are designed to PCR amplifies particular genomes e.g.: bacteria, archea or fungi, the resulted product are sequenced this is fast and cheap method which isn't used for gene encoded in part of Meta genomes that remained un-sequenced.

Tools used in bioinformatics

Sequencing Technologies for Whole Genome Shotgun Metagenomics: WGS-shotgun-metagenomics is an alternative complementary method metagenomics is application of sequencing technologies for genomic material present in microbiome of present sample. It also provide information about function, structure, organization of genes, novel genes identification and biocatalysts, advances in this sequencing technologies have provided hundreds of gigabases of DNA sequencing at very less cost and provide wide range of enzyme and biocatalyst applications in marketplace and biotechnology, pharmaceutical industry.

Many microbiomes are complex incredibly for these the sequencing technologies have enabled much deeper and second generation sequence have technologies like Illumina and Ion Torrent and third generation have Pac bio and ONT which have longer reads and not widely used as it have high rate of homopolymer.

Metagenomics assembly: DNA sequence fragment of genomes assembly is process of reconstruction in silico original genomes for smaller fragments, de novo assembly software tools uses main paradigms like OLC and de Brujin graph- it can construct graph by constructed without pairwise comparison and its most effective and less expensive than OLC approach.

Phylogenetic binning: Phylogenetic Binning is form of clustering genomes sequence into groups with each separate biological single genome in to group that separate taxon, from which single genome is assemble connecting diverse taxon, LikelyBin is unsupervised statistical binning metagenomics fragments, PHYSCIMM is composition of species presented in public data base.

Protein domain database: Number of large published protein structure/sequence/database is collaboration of twelve databases, INTERPRO integrate information about active sites, protein families and protein activity and functioning. It combines all these characterization of sequence theses are checked for link and original publications. InterProScan is protein function prediction software which gives an input query sequence in multiple data base, when no match then it is passed.

Targeted gene discovery: When there is small amount of protein then no need to go through whole database metagenomics gene, XANDER is a gene targeted assembler uses HMMs for guiding graphs traversal; less compute intensive due to small amount of data is used.

Pathway Databases: It refer to series of action between the biomolecule with particular products, Reactome is curated database with biological pathway and with single reaction in lowest level. Kyoto Encyclopaedia of gene and genomes is phenotypically information for which it consist multiple data base, information about protein, enzyme, genomes diseases and drug pathways; different links are available like NCBI, OMIM, and Uni Prot.

Conclusion

The process of sequencing genomes in all organism require technologies and research into diverse microbiomes tools provide researchers to analyse larger metagenomics data bases and extraction of novel genes, protein, enzyme. It gives characterization of protein functioning and novel enzyme in effective and significant way.