Cloud Genomics

Cloud Genomics as a Service (GaaS) provides cloud-based platforms and infrastructure tailored for genomic data storage, analysis, & management. These services enable researchers, clinicians, & companies to perform complex genomic analyses without the need for substantial in-house computational resources.

Biological Data Analysis

Biological Data Analysis as a Service (BDAaaS) refers to cloud-based platforms and services that provide tools, infrastructure, and support for analyzing biological data. These platforms enable researchers and organizations to perform complex bioinformatics and computational biology tasks without the need to invest in and maintain their own computational resources

Bioinformatics and IOT

Combining bioinformatics and the Internet of Things (IoT) can lead to innovative solutions for healthcare, agriculture, environmental monitoring etc. Bioinformatics involves the analysis & interpretation of biological data, while IoT refers to the network of interconnected devices that collect & exchange data. When integrated, they can enable real-time monitoring, analysis, & decision-making in various fields.

SERVICES We Offer :-

- Metagenomic Analysis
- SNP/SV/CNV Discovery
- Differential Gene Expression Analysis
- Comparative Genome Analysis
- Transcriptome de novo Assembly
- Variant Annotation
- Whole Genome de novo Assembly
- Machine Learning
- Artificial Intelligence in Bioinformatics
- Biological Data Analysis
- Cloud Genomics
- Bioinformatics and IOT

BIOINFORMATICS SERVICES

We undertake contact research and services in the area of bioinformatics. Feel free to contact us.

Celebrating Innovations

Vasishth Genomics Research Lab Pvt Ltd

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Metagenomic Analysis

Metagenomic analysis is a powerful approach to study the collective genomic content of microbial communities directly from environmental samples, without the need for culturing individual species. This method allows researchers to investigate the diversity, function, and dynamics of microbial ecosystems.

Comparative Genome Analysis

Comparative Genome Analysis (CGA) is a powerful approach in genomics used to compare the genomic features of different organisms, strains, or individuals to identify similarities and differences. This analysis can provide insights into evolutionary relationships, functional genomics, and the genetic basis of phenotypic differences.

Whole Genome de novo Assembly

Whole genome de novo assembly is the process of reconstructing a genome from sequencing reads without the use of a reference genome. This approach is essential for studying organisms with no available reference genome or for discovering novel genomic sequences

SNP/SV/CNV Discovery

Single Nucleotide Polymorphisms (SNPs), Structural Variants (SVs), and Copy Number Variants (CNVs) are different types of genetic variations that can be discovered using high-throughput sequencing data.

Transcriptome de novo Assembly

De novo transcriptome assembly is the process of reconstructing the transcriptome from RNA sequencing (RNA-seq) data without a reference genome. This approach is crucial for studying non-model organisms or in cases where the reference genome is incomplete or unavailable.

Machine Learning

Machine Learning as a Service (MLaaS) refers to cloud-based platforms that provide machine learning tools and infrastructure as a service. These platforms enable users to develop, train, and deploy machine learning models without needing to manage the underlying hardware or software infrastructure.

Differential Gene Expression Analysis

Differential Gene Expression Analysis (DGEA) a critical method in genomics used to identify differences in gene expression levels between different conditions, such as diseased vs. healthy tissues, treated vs. untreated samples, or different developmental stages.

Variant Annotation

Variant annotation involves interpreting the biological significance of genetic variants identified in a genome, exome, or transcriptome. This process helps in understanding the potential impact of variants on genes and proteins, and their association with diseases or traits.

Artificial Intelligence in Bioinformatics

Bioinformatics and Genomics are two very related areas of computational systems biology, in which AI can exercise its full potential. Compared to conventional computational approaches, AI offers an advanced toolbox that better facilitates problem-solving in the fields.