Project 1

Developing an Integrative Repository for Genetic Variants and Mutational Analysis to Uncover Biomarkers and Therapeutic Targets in Colorectal Cancer

Objectives:

1. To create a centralized and comprehensive repository for storing and managing genetic variants, mutational patterns, SNPs, and other results derived from exome analysis of colorectal cancer datasets.

2. To enable integrative analysis of these genetic features to identify potential biomarkers and therapeutic targets associated with colorectal cancer.

Project 2

Developing an integrative tool for enhanced Quantitative Trait Locus (QTL) analysis using genome sequencing and RNA-seq data.

The tool aims to improve our understanding of complex traits in Mulberry by leveraging advanced algorithms, machine learning, and cloud computing to analyse large datasets and accurately identify QTLs associated with key agricultural traits

Objectives:

1. Integrate Genomic and RNA-seq Data: Develop a platform to integrate genome sequencing and RNA-seq data for QTL analysis, employing advanced algorithms for trait-associated QTL identification.

2. Implement Statistical Methods and Visualization Tools: Employ state-of-the-art statistical methods to enhance QTL mapping accuracy. Create intuitive visualizations and interfaces for data interpretation.

3. Enhance Agricultural Sustainability: Validate the tool with four Mulberry genotypes, aiming to improve economic viability and environmental sustainability through advanced QTL analysis, with potential applications across agricultural genomics.

Project 3:

The project involves the development of a sophisticated tool designed to analyse genome sequences uploaded by individuals to assess their risk and impact of prolonged COVID-19.

Objectives:

1) Develop a Personalized Genomic Analysis Tool for Prolonged COVID-19: Create a user-friendly platform that enables individuals to upload their genome sequences for personalized analysis, identifying genetic variants associated with prolonged COVID-19 and providing actionable insights into potential health impacts and management strategies.

2) Integrate Advanced Computational Techniques for Comprehensive Analysis: Utilize cutting-edge technologies including SNP analysis, population genetics, machine learning, and cloud computing to

deliver precise and scalable genomic analysis, mapping genetic variants to biological pathways and organ systems, and predicting their impact with high accuracy.

Project 4:

Quantum Methods for Predicting Protein Folding in Intrinsically Disordered Regions of using Bayesian Phase Difference Estimation

Intrinsically disordered proteins (IDPs) present a formidable hurdle in traditional protein structure prediction due to their absence of stable conformations. To surmount this challenge, we aim to develop computational models that translate peptide structures into qubit configurations, enabling the design of optimized quantum circuits for phase difference estimation. By doing so, our study aims to elucidate the energy landscapes and folding transitions of IDPs. Benchmarking these quantum methods against error-mitigated Variational Quantum Eigensolver will furnish insights into their efficacy in optimizing ground state energy.

The overall project is on evaluating role of Quantum Bayesian phase difference estimation (BPDE) in peptide folding.

Objectives:

1. Evaluating role of Quantum Bayesian phase difference estimation (BPDE) in peptide folding.
2. Benchmarking of BPDE results with VQE.