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GENOMAC ONLINE RESEARCH SCHOLARSHIP ON GENOMICS AND BIOINFORMATICS

From Real-life Research Projects to Publishable Papers in 3 - 9 Months
Without Previous Research Experience in Bioinformatics

*We envision inspiring and empowering life scientists to leverage **GENOMICS AND BIOINFORMATICS** to tackle critical challenges, drive innovation, and promote sustainable progress globally.*

Research Domain: Human Genomics
Research Focus: Cancer Genomics (Leukemia)
Research Topic: The Impact of Non-Synonymous SNPs on Protein Function and Disease Susceptibility in Leukemia: A Comparative Human Genomic Analysis
Research Aim: Explore the impact of non-synonymous SNPs within protein-coding genes on leukemia susceptibility and progression, and concurrently, identify biomarkers for potential use in target-based therapeutics.
Research Objectives:

- Examine the genetic variations associated with leukemia susceptibility, focusing on non-synonymous SNPs within protein-coding genes.
- Identify and validate biomarkers linked to leukemia progression, with the goal of informing the development of targeted therapeutic interventions.

LEARNING OBJECTIVES

1. **Genomic Exploration of Leukemia Susceptibility:** Gain hands-on expertise in genomics to investigate the molecular mechanisms contributing to leukemia susceptibility, with a focus on understanding the impact of non-synonymous SNPs within protein-coding genes.

- **Biomarker Identification and Characterization:** Develop practical skills in bioinformatics and advanced genomic analysis techniques to identify and characterize biomarkers associated with leukemia. This exposure contributes valuable insights into disease progression and potential therapeutic targets, fostering proficiency in cutting-edge technologies.
- **Integration of Genomic and Clinical Data**: Enhance proficiency in integrating genomic data with clinical information, fostering a holistic approach to unraveling the genetic landscape of leukemia.

This objective ensures that researchers can translate genomics findings into clinically relevant insights, bridging the gap between laboratory discoveries and patient outcomes.

- **Craft Research Papers for Publication:** Learn how to synthesize and present your findings coherently, culminating in the preparation of research papers suitable for publication, contributing to the broader understanding of the evolution and dissemination of infectious diseases.

EXPECTATIONS WHILE UNDERTAKING THIS INTERNSHIP PROGRAM:

- **Knowledge of Genomics and Bioinformatics:** Develop a solid foundation in genomics and bioinformatics, including an understanding of key concepts, methodologies, and technologies used in the program
- **Proficiency in Data Analysis:** Gain proficiency in analyzing genomic data using bioinformatics tools and software. This includes skills in data preprocessing, quality control, data visualization, and statistical analysis.
- **Research Skills:** Acquire research skills necessary for conducting genomics and bioinformatics studies. This includes formulating research questions, designing experiments, collecting and analyzing data, and interpreting research findings.
- **Critical Thinking and Problem-Solving:** Develop critical thinking skills to analyze complex genomic and bioinformatics problems and propose creative solutions. You would be able to evaluate scientific literature, identify research gaps, and contribute to the advancement of knowledge in the field.
- **Computational Skills:** Gain proficiency in software and applications commonly used in bioinformatics, such as Geneious software, web servers etc. to analyze genomics data and interpret results
- **Communication Skills:** You would be able to effectively communicate your research findings and scientific concepts to both technical and non-technical audiences. This includes writing scientific reports, presenting research orally, and participating in scientific discussions and collaborations.
- **Collaboration and Teamwork:** Be able to develop skills in collaborating with peers and professionals in multidisciplinary research teams. This includes effective communication, teamwork, and the ability to contribute constructively to group projects.
- **Professional Development:** You would be able to develop a professional mindset, including skills in time management, organization, and project management. They should also be aware of current trends and advancements in genomics and bioinformatics, and actively seek opportunities for professional growth and development.
- **Publication and Dissemination:** Contribute to the scientific community by publishing their research findings in peer-reviewed journals

PROGRAM OUTLINE AND SCHEDULE

CLASSES	TOPICS/FOCUS	SCHEDULE & DELIVERABLES
General Classes	Overview of genomics, bioinformatics, and their applications in various fields	
	Understanding the central dogma of molecular biology	
	Introduction to genomics technologies and data generation	
	Data formats in Genomics and Bioinformatics (Practical)	
	Internet tools and Databases (Practical on data retrieval, Blast etc.)	
	Introduction to software tools and their installation, web servers, and pipeline tools (Practical), Basic Linux Command Line Interface	**WEEK 1**
	Genomics Data and its Analysis using cutting-edge tools (Practical DNA, RNA and Protein samples)	
Specialized Classes	Introduction to Cancer Genomics **(Leukemia)**	
	The experimental application of each of these in your field of study	
	Problem identification relative to the above area in the healthcare, industrial, and other life science research space	
	The use of critical thinking and problem-solving tools to design a hypothesis in solving identified problems	
PRACTICAL SESSIONS		**WEEK 2**
Data Acquisition and Preprocessing	**Collection of DNA Data:** Collect genomic datasets containing genetic information on leukemia in patients, including SNP data and clinical outcomes. **(For both Reference and Query)**	
	Table 1: Construction of General Sequence Properties: via data table based on genome information which includes accession number, raw data size, sources, geographical regions platform, genome type, layout, file types, etc.	**Deliverable:** (Materials and Methods)
	Quality Control: Assess data quality, perform trimming, and filter out low-quality reads to ensure reliable results. **Genome Assembly:** Assemble the genomes of leukemia patients' samples using reference-guided or de novo assembly methods.	
	Write Up 1: Reads Processing and Genome Assembly	
DNA Sequence Alignment	**Mapping to Reference:** Aligning Reads to Reference Sample	
Genome Annotation	**Write Up 2:** Mapping to Reference	**Deliverable:** (Materials and Methods)
	Table 2: Construction of Chromosomal Genome Properties: CDS, Genes, RNA, Hypothetical Protein, Functional Protein, Go assignments, etc.	**Deliverable:** (Results)
	Functional Genome Categorization:	**WEEK 3**
	Variant Calling Analysis: Call variants (SNPs and INDELs) by comparing sequenced reads to the reference genome i.e.,	

Comprehensive Genome Analysis	performing variant analysis to identify variants specific to identify relevant SNP-associated variations in leukemia patients **Effect Prediction and Functional Analysis:** Annotate SNP variants to determine their genomic location, potential functional effects, and allele frequencies (i.e., focus on variants affecting protein-coding genes, regulatory elements, and non-coding RNAs).	**WEEK 4**
	Write Up 3: Variant Calling Analysis, Effect Prediction and Functional Analysis	**Deliverable:** (Materials and Methods)
	• **Table 3:** Construction of SNPs or Indels • **Figure 1:** Mapping View • **Figure 2:** Variant Calling View	**Deliverable:** (Results)
	Comparative Variant Analysis: • Compare the identified variants between samples treated and untreated • Identify unique and shared variants, as well as those specific to each sample	**WEEK 5**
	Statistical Analysis: • **Table 4:** General information on all predicted SNPs • **Table 5:** Identify unique and shared variants, as well as those specific to each sample	**Deliverable:** (Results)
Identification of Genetic Markers	**Variant Annotation and Functional Prediction:** • Annotate identified variants using databases and tools to predict their functional impact on genes and regulatory regions. • Classify variants based on their effect types (e.g., nonsynonymous, synonymous, regulatory region). **Differential Analysis and Functional Enrichment:** • Execute statistical analyses to identify variants significantly enriched or depleted within protein-coding genes in the leukemia samples. • Conduct functional enrichment analyses to unveil enriched gene ontology (GO) terms and biological pathways relevant to the adaptive processes associated with leukemia progression.	**WEEK 6**
	Write Up 6: Variant Annotation, Functional Prediction and Functional Enrichment	**Deliverable:** (Materials and Methods)
	Statistical Analysis: • **Table 6:** Annotated SNPs and their functions • **Figure 3:** Percentage abundance of all SNPs covering nonsynonymous, synonymous, and regulatory regions. • **Figure 4:** Ratio of SNPs with effect on protein or functional genes	**Deliverable:** (Results)

	• **Figure 5:** Classification of variants based on their effect types • **Figure 6:** Significantly enriched or depleted variants in both sample subtypes • **Figure 7:** Pathway enrichment analysis	
Comparative Genome Analysis	**Phylogenomic Analysis:** **Molecular Characterization and Alignment:** • Use bioinformatics software for multiple sequence alignment of genes affected by variants. • Analyze aligned sequences for conserved motifs, domains, and potential structural changes.	**WEEK 7**

RESEARCH PROJECT OUTLINE FOR PUBLICATION

Research Outline Round Up	Introduction	**WEEK 6 -7**
	Materials and Methods	**WEEK 8**
	Results	**WEEK 9 & 10**
	Discussion	**WEEK 11**
	Conclusion	**WEEK 12**
	References	**WEEK 13**
	Certification and Recommendation Letter	
	Follow up and Publication	
Round Up		