



Application Deadline: 29th FEB, 2024.

INT'L VIRTUAL RESEARCH FELLOWSHIP ON ADVANCED GENOMICS AND BIOINFORMATICS

Dive into Advance Genomics and Bioinformatics Research, and Transform Your Findings into Publishable Papers within 3 - 5 Months

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 Microbiome Research

Research Focus: Human Metagenomics Research

Research Case Study: *Stomach Alcher, Colon Cancer, Gut, Diabetes, etc.*

Research Topic: *To be crafted by the participant*

Research Aim: *To be crafted by the participant*

Research Objectives: *To be crafted by the participant*

LEARNING OBJECTIVES

- **Mastering Metagenomic Techniques:** Develop proficiency in laboratory techniques for metagenomic analysis, including DNA extraction, sequencing, and quality control, to accurately and comprehensively assess the microbial gene content within the disease microbiome.
- **Bioinformatics Proficiency:** Acquire advanced skills in bioinformatics tools and methodologies for analyzing large-scale metagenomic data, focusing on the identification, annotation, and functional analysis of microbial genes associated with disease development.
- **Understanding Host-Microbiome Interactions:** Gain a deep understanding of the intricate interactions between microbial genes and host factors in the context of the disease formation, incorporating knowledge from microbiology and gastroenterology to interpret the biological significance of identified genes.
- **Clinical Relevance and Innovative Applications:** Apply knowledge gained from comparative metagenomic profiling to formulate evidence-based recommendations for targeted intervention strategies by designing experiments to validate the functional roles of specific microbial genes implicated in disease, with an emphasis on assessing their potential as therapeutic targets for clinical applications.

- **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 disease using the metagenomics approach.

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.)	WEEK 1
	Introduction to software tools and their installation, web servers, and pipeline tools (Practical), Basic Linux Command Line Interface	
	Genomics Data and its Analysis using cutting-edge tools (Practical DNA, RNA and Protein samples)	
Specialized Classes	Introduction to Metagenomics for a case study	WEEK 2
	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		
Data Retrieval and Processing	Data Retrieval: Obtain publicly available metagenomic sequencing data from patients with a disease and those without the disease as control.	Deliverable: (Materials and Methods)
	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.	
	Quality Control: Assess data quality, perform trimming, and filter out low-quality reads to ensure reliable results.	
	Write Up 1: Reads Processing and Genome Assembly	
Comprehensive Metagenome Analysis	Functional Annotation: Gene prediction, Protein features, Specialty features, and Chromosomal properties, among others.	
	Write Up 2: Functional Annotation	Deliverable: (Materials and Methods)
	Table 2: Construction of Chromosomal Genome Properties: CDS, Genes, RNA, Hypothetical Protein, Functional Protein, Go assignments, PGfam, Cripsr, etc.	Deliverable: (Results)
	Functional Genome Categorization: The use of the Rastk tool kit to perform comparative subsystem categorization of all MEG samples	WEEK 3
	Write Up 3: Subsystem Functional Categorization	Deliverable: (Materials and Methods)
	Figure 1: Subsystem Functional Categorizations	Deliverable: (Results)
	Plasflow Analysis: Prediction of Plasmid, Chromosomal and Unclassified Sequences <ul style="list-style-type: none"> • File Merging on usegalaxy • Plasflow Analysis on usegalaxy 	
Microbial drug resistance and	Resistome Profile Study on individual samples and plasflow files: Conducting a resistome profile study on individual samples	WEEK 4

mechanisms of adaptation within the context of the Disease formation and progression	and control groups, examining antibiotic resistance genes within microbial communities in the context of the disease microenvironment to discern how they might impact the effectiveness of the disease treatments involving antibiotics..	
	Write Up 4: Resistome Profiling Analysis	Deliverable: (Materials and Methods)
	Statistical Analysis: <ul style="list-style-type: none"> • Figure 2: Heatmap of antibiotic resistance genes (ARG) types between diseased and non-diseased samples (Antibiotic Class) • Figure 3: Prevalence of AMR genes across diseased and non-diseased metagenomics samples • Figure 4: Percentage distribution of ARG resistance mechanism • Figure 5: Relative distribution of AMR genes in antibiotics • Table 3: Shared resistance genes and their putative functions • Table 4: ARG, RM, ATB and their putative functions 	Deliverable: (Results)
Genomic Exploration of Bacterial Virulome Mechanisms	Virulome Profile Study: To identify virulence genes and evaluate their presence, and abundance and to gain insights into how these virulence genes may impact microbial virulence within the disease microenvironment, thus contributing to the effort of solving public health challenges associated with gastric pathology. Plasmid/Prophages prediction: Mobilome Analysis: Identifying mobile genetic elements to reveal potential mechanisms for the spread of virulence and resistance genes.	WEEK 5
	Write Up 5: Virulome Profile Analysis, Mobilome, Plasmid and Prophages	Deliverable: (Materials and Methods)
	Statistical Analysis: <ul style="list-style-type: none"> • Figure 6: Comparing the abundance of virulence genes • Table 5: Shared specific encoding of VR and AMR and their putative functions • Table 6: Predicting pathogenicity • Figure 7: Expression level of MGEs 	Deliverable: (Results)
Discovering markers with robust correlations, highlighting their potential significance within the context of disease pathology.	Biomarker Identification and Correlation in the Context of disease: <ul style="list-style-type: none"> • Uncovering specific gene markers that are strongly associated with pathogenicity, offering insights for comprehensive gastric health in patients. 	WEEK 6
	Pathway and Network Analysis: <ul style="list-style-type: none"> • Predicting potential pathways associated with the contribution of specific virulence genes to environmental challenges within the diseased microenvironment. 	

	<ul style="list-style-type: none"> Analyzing enriched biological pathways linked to identified virulence markers in the context of the disease Constructing microbial interaction networks, considering the presence of AMR genes, virulence genes, and MGEs, aiming to understand collaborative dynamics specific to the diseased environment. 	
	Write Up 6: Pathway (Panther) and Network Analysis	Deliverable: (Materials and Methods)
	Statistical Analysis: <ul style="list-style-type: none"> Table 7: Table of gene and putative functional proteins Figure 8: Comparative charts of biological processes in the pathway Figure 9: Network result 	Deliverable: (Results)
Insights into Microbiota: Taxonomic Profiling of Metagenomes Collected from the Diseased/non-diseased Patients	Taxonomic Analysis: Analyze the composition and interactions of microbiota, shedding light on broader implications for public health assessments.	WEEK 7
	Write Up 7: Taxonomic Analysis	Deliverable: (Materials and Methods)
	Figure 10: Taxonomic Classification: The use of Kraken to compare the sequences with the reference database and assign taxonomic labels (e.g., species, genus, family, etc.) to each sequence Table 8: Abundance Calculation: Compile the relative abundance values for each taxonomic group across all samples (comparative analysis). Figure 11: Differential Abundance Analysis (if applicable): To identify taxonomic groups that are significantly differentially abundant. Figure 12: Others including alpha diversity etc.	Deliverable: (Results)
RESEARCH PROJECT OUTLINE FOR PUBLICATION		
Research Outline	Aims and Objectives	
	Abstract	
	Introduction	To be done between
	Materials and Methods	WEEK 8
	Results	WEEK 9 and 10
	Discussion	WEEK 11
	Conclusion	
	Abstract and References	
Round Up	Certification and Recommendation Letter	

	Follow-up and Publication	WEEK 12 UPWARDS

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