



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:** Epidemiology and Public Health

**Research Focus:** Metagenomics Research

**Research Case Study:** *Human, Plant, Animal, Water, Soil, Air, Feces 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

- **Metagenomic Analysis Proficiency:** Gain proficiency in metagenomic techniques, including sample collection, DNA extraction, and sequencing methodologies, to effectively analyze microbial functional diversity in polluted water environments.
- **Epidemiological Skills and Expertise:** Acquire a comprehensive understanding of global surveillance strategies for antimicrobial resistance, including the utilization of bioinformatics tools and databases for data interpretation and comparison across diverse geographical regions.
- **Functional Annotation and Mechanistic Insights** Develop skills in functional genomic analysis, focusing on identifying and characterizing antimicrobial resistance mechanisms in major human pathogens through the interpretation of metagenomic data.
- **Clinical Relevance and Innovative Applications:** Apply knowledge gained from comparative metagenomic profiling to formulate evidence-based recommendations for targeted intervention strategies, contributing to the enhancement of public health risk assessment and management practices related to waterborne microbial contaminants.
- **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 public health investigation using the metagenomics approach.

## EXPECTATIONS WHILE UNDERTAKING THIS FELLOWSHIP 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
<b>General Classes</b>	Overview of genomics, bioinformatics, and their applications in various fields	<b>WEEK 1</b>
	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	
	Genomics Data and its Analysis using cutting-edge tools (Practical DNA, RNA and Protein samples)	

<b>Specialized Classes</b>	Introduction to Metagenomics ( <b>Public Health Risk</b> )	
	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	
<b>PRACTICAL SESSIONS</b>		<b>WEEK 2</b>
<b>Data Retrieval and Processing</b>	<b>Data Retrieval:</b> Obtain publicly available metagenomic sequencing data from polluted water sources across geographical regions.	<b>Deliverable:</b> (Materials and Methods)
	<b>Table 1: Construction of General Sequence Properties:</b> via data table based on genome information which includes accession number, raw data size, sources, geographical regions platform, genome type, layout, file types, etc.	
	<b>Quality Control:</b> Assess data quality, perform trimming, and filter out low-quality reads to ensure reliable results.	
	<b>Write Up 1:</b> Reads Processing and Genome Assembly	
<b>Comprehensive Metagenome Analysis</b>	<b>Functional Annotation: Gene prediction, Protein features, Specialty features, and Chromosomal properties, among others.</b>	
	<b>Write Up 2:</b> Functional Annotation	<b>Deliverable:</b> (Materials and Methods)
	<b>Table 2: Construction of Chromosomal Genome Properties: CDS, Genes, RNA, Hypothetical Protein, Functional Protein, Go assignments, PGfam, Cripsr, etc.</b>	<b>Deliverable:</b> (Results)
	<b>Functional Genome Categorization:</b> The use of the Rastk tool kit to perform comparative subsystem categorization of all MEG samples	<b>WEEK 3</b>
	<b>Write Up 3:</b> Subsystem Functional Categorization	<b>Deliverable:</b> (Materials and Methods)
	<b>Figure 1:</b> Subsystem Functional Categorizations	<b>Deliverable:</b> (Results)
	<b>Plasflow Analysis:</b> Prediction of Plasmid, Chromosomal and Unclassified Sequences <ul style="list-style-type: none"> <li>• File Merging on usegalaxy</li> <li>• Plasflow Analysis on usegalaxy</li> </ul>	
<b>Understanding Microbial Drug Resistance Mechanisms in Polluted Water for Public Health Risk Assessment.</b>	<b>Resistome Profile Study on Individual Samples and Plasflow Files:</b> Understanding this sheds light on potential challenges in water treatment approaches. Antibiotic resistance genes and the mechanism of resistance in microbial communities may impact the effectiveness of public health interventions.	<b>WEEK 4</b>
	<b>Write Up 4:</b> Resistome Profiling Analysis	<b>Deliverable:</b> (Materials and Methods)
	<b>Statistical Analysis:</b>	

	<ul style="list-style-type: none"> <li>• <b>Figure 2:</b> Heatmap of antibiotic resistance genes (ARG) types between wastewater metagenomics samples from different regions (Antibiotic Class)</li> <li>• <b>Figure 3:</b> Prevalence of AMR genes across different waste water metagenomics samples</li> <li>• <b>Figure 4:</b> Percentage distribution of ARG resistance mechanism</li> <li>• <b>Figure 5:</b> Relative distribution of AMR genes in antibiotics</li> <li>• <b>Table 3:</b> Shared resistance genes and their putative functions</li> <li>• <b>Table 4:</b> ARG, RM, ATB and their putative functions</li> </ul>	<b>Deliverable:</b> (Results)
<b>Genomic Exploration of Bacterial Virulome Mechanisms</b>	<b>Virulome Profile Study:</b> Detecting virulence genes and assessing their presence and abundance to provide insights into the potential impact on microbial virulence in shaping the wastewater environment and contributing to public health challenges. <b>Plasmid/Prophages prediction:</b> <b>Mobilome Analysis:</b> Identifying mobile genetic elements to reveal potential mechanisms for the spread of virulence and resistance genes.	<b>WEEK 5</b>
	<b>Write Up 5:</b> Virulome Profile Analysis, Mobilome, Plasmid and Prophages	<b>Deliverable:</b> (Materials and Methods)
	<b>Statistical Analysis:</b> <ul style="list-style-type: none"> <li>• <b>Figure 6:</b> Comparing the abundance of virulence genes</li> <li>• <b>Table 5:</b> Shared specific encoding of VR and AMR and their putative functions</li> <li>• <b>Table 6:</b> Predicting pathogenicity</li> <li>• <b>Figure 7:</b> Expression level of MGEs</li> </ul>	<b>Deliverable:</b> (Results)
<b>Uncovering markers with strong correlations, emphasizing their potential significance in public health contexts.</b>	<b>Biomarker Identification and Correlation:</b> <ul style="list-style-type: none"> <li>• Uncover virulence genes strongly correlated with pathogenicity, providing insights for broader public health assessments.</li> <li>• Identify potential virulence markers as indicators of microbial behavior with implications for public health contexts.</li> </ul>	<b>WEEK 6</b>
	<b>Pathway and Network Analysis:</b> <ul style="list-style-type: none"> <li>• Predict potential pathways associated with the contribution of specific virulence genes to environmental challenges.</li> <li>• Analyze enriched biological pathways linked to identified virulence markers, providing insights for broader public health assessments.</li> <li>• Construct microbial interaction networks, considering the presence of AMR genes, virulence genes, and MGEs,</li> </ul>	

	aiming to understand collaborative dynamics within diverse environments."	
	<b>Write Up 6:</b> Pathway (Panther) and Network Analysis	<b>Deliverable:</b> (Materials and Methods)
	<b>Statistical Analysis:</b> <ul style="list-style-type: none"> <li>• <b>Table 7:</b> Table of gene and putative functional proteins</li> <li>• <b>Figure 8:</b> Comparative charts of biological processes in the pathway</li> <li>• <b>Figure 9:</b> Network result</li> </ul>	<b>Deliverable:</b> (Results)
<b>Insights into Microbiota Associated with Environmental Challenges</b>	<b>Taxonomic Analysis:</b> Analyze the composition and interactions of microbiota, shedding light on broader implications for public health assessments.	<b>WEEK 7</b>
	<b>Write Up 7:</b> Taxonomic Analysis	<b>Deliverable:</b> (Materials and Methods)
	<b>Figure 10: Taxonomic Classification:</b> 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 <b>Table 8: Abundance Calculation:</b> Compile the relative abundance values for each taxonomic group across all samples (comparative analysis). <b>Figure 11: Differential Abundance Analysis (if applicable):</b> To identify taxonomic groups that are significantly differentially abundant. <b>Figure 12:</b> Others including alpha diversity etc.	<b>Deliverable:</b> (Results)

## RESEARCH PROJECT OUTLINE FOR PUBLICATION

<b>Research Outline</b>	Aims and Objectives	
	Abstract	
	Introduction	<b>To be done between</b>
	Materials and Methods	<b>WEEK 8</b>
	Results	<b>WEEK 9 and 10</b>
	Discussion	<b>WEEK 11</b>
	Conclusion	
	Abstract and References	
<b>Round Up</b>	Certification and Recommendation Letter	<b>WEEK 12</b>
	Follow-up and Publication	<b>UPWARDS</b>