

# 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 across the globe.*

**Research Domain:** Clinical Genomics/Microbial Study

**Research Focus:** Metagenomics Research

**Research Topic:** Functional Insights into Microbial Genes Associated with Stomach Ulcer Formation and Progression: A Metagenomics Approach.

**Research Aim:** To identify and characterize specific microbial genes associated with stomach ulcer formation and progression in human hosts, providing insights into potential therapeutic targets and contributing to a deeper understanding of the host-microbiome interactions in gastric health and pathology.

**Research Objectives:**

- Investigate the metagenomic composition of the human stomach microbiome to identify and catalog microbial genes that exhibit a significant association with the initiation and progression of stomach ulcers.
- Characterize the functional roles and mechanisms of action of the identified microbial genes, elucidating their impact on host physiology and the development of ulcerative pathology.
- Explore the potential therapeutic implications by evaluating the feasibility of targeting specific microbial genes as novel interventions for stomach ulcer prevention or treatment, aiming to contribute to the advancement of precision medicine strategies in managing gastric health.

## 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 human stomach 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 stomach ulcer development.
- **Understanding Host-Microbiome Interactions:** Gain a deep understanding of the intricate interactions between microbial genes and host factors in the context of stomach ulcer 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 stomach ulcers, 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 stomach ulcers 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	
<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 for ( <b>STOMACH LCER</b> )	<b>WEEK 2</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 patients with stomach ulcer and those without stomach ulcer as control.		
	<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>Deliverable:</b> (Materials and Methods)
	<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:</b> <b>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)
	<p><b>Plasflow Analysis:</b> Prediction of Plasmid, Chromosomal and Unclassified Sequences</p> <ul style="list-style-type: none"> <li>• File Merging on usegalaxy</li> <li>• Plasflow Analysis on usegalaxy</li> </ul>	
<b>Microbial drug resistance and mechanisms of adaptation within the context of stomach ulcer formation and progression</b>	<p><b>Resistome Profile Study on individual samples and plasflow files:</b> Conducting a resistome profile study on individual samples and control groups, examining antibiotic resistance genes within microbial communities in the context of the stomach ulcer microenvironment to discern how they might impact the effectiveness of ulcer treatments involving antibiotics..</p>	<b>WEEK 4</b>
	<b>Write Up 4:</b> Resistome Profiling Analysis	<b>Deliverable:</b> (Materials and Methods)
	<p><b>Statistical Analysis:</b></p> <ul style="list-style-type: none"> <li>• <b>Figure 2:</b> Heatmap of antibiotic resistance genes (ARG) types between stomach ulcer and non-stomach ulcer samples (Antibiotic Class)</li> <li>• <b>Figure 3:</b> Prevalence of AMR genes across stomach ulcer and non-stomach ulcer 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>	<p><b>Virulome Profile Study:</b> 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 stomach ulcer microenvironment, thus contributing to the effort of solving public health challenges associated with gastric pathology.</p> <p><b>Plasmid/Prophages prediction:</b></p> <p><b>Mobilome Analysis:</b> Identifying mobile genetic elements to reveal potential mechanisms for the spread of virulence and resistance genes.</p>	<b>WEEK 5</b>
	<b>Write Up 5:</b> Virulome Profile Analysis, Mobilome, Plasmid and Prophages	<b>Deliverable:</b> (Materials and Methods)
	<p><b>Statistical Analysis:</b></p> <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>Discovering markers with robust correlations, highlighting their potential significance within the context of stomach ulcer pathology.</b>	<b>Biomarker Identification and Correlation in the Context of Stomach Ulcer:</b> <ul style="list-style-type: none"> <li>Uncovering specific gene markers that are strongly associated with pathogenicity, offering insights for comprehensive gastric health in patients.</li> </ul>	<b>WEEK 6</b>
	<b>Pathway and Network Analysis:</b> <ul style="list-style-type: none"> <li>Predicting potential pathways associated with the contribution of specific virulence genes to environmental challenges within the gastric microenvironment.</li> <li>Analyzing enriched biological pathways linked to identified virulence markers in the context of stomach ulcers.</li> <li>Constructing microbial interaction networks, considering the presence of AMR genes, virulence genes, and MGEs, aiming to understand collaborative dynamics specific to the stomach ulcer environment.</li> </ul>	
	<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: Taxonomic Profiling of Stomach Ulcer Metagenomes</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)	
<b>RESEARCH PROJECT OUTLINE FOR PUBLICATION</b>		
<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>