Call for Applications
Graduate Course: Introduction to Metagenomics and Its Applications
Special Focus: Viral Identification and Discovery

Host Institution: Universidad Mayor de San Andrés

Collaborating Institution: Chan Zuckerberg Biohub, San Francisco. USA

Dates: July 14th – July 25th 2025
Location: UMSA, La Paz Bolivia

General Description

This course offers a comprehensive theoretical framework and hands-on training in metagenomics as a cutting-edge tool for pathogen identification, with a specialized focus on emerging and re-emerging viral diseases. Designed to bridge knowledge gaps and empower local expertise at low-resource settings, the program integrates into the Graduate Program in Biosciences at Universidad Mayor de San Andrés (UMSA) and strengthens regional capacity in pathogen surveillance, diagnostics, and outbreak response.

Course Objectives

By the end of this course, students will be able to:

- Understand core principles of viral metagenomics and its applications in public health.
- Design and implement viral metagenomics studies, including sample preparation and sequencing.
- Analyze metagenomic data using bioinformatics tools for taxonomic classification, genome assembly, and phylogenetic analysis.

Target Audience:

- Students: Undergraduate/graduate students in biology, biochemistry, veterinary medicine, or related fields.
- Professionals: Laboratory specialists, researchers, involved in pathogen detection, genomics, or diagnostics (human/animal health sectors).

Course Structure

1. Foundational Theory (2 Days)

Format: Hybrid (online/in-person)
Audience: All enrolled participants (without restriction)
Content:

- Overview of NGS technologies. Introduction to viral metagenomics: principles, applications, and challenges.
- Epidemiology of emerging viruses: surveillance, outbreak investigation, and public health implications.

Purpose: Ensure all participants—regardless of specialization—share basic introductory knowledge of metagenomics.

2. Practical Training

A. Week 1: Wet-Lab NGS Techniques
Format: In-person (lab-based)
Capacity: 15 participants (selection via application)
Topics:

- Hands-on library preparation for viral metagenomics (e.g., RNA/DNA extraction, amplification).
- Nanopore Sequencing platform: operation, troubleshooting, and quality control.
- Best practices for contamination control and metadata documentation.

B. Week 2: Bioinformatics Pipeline Development
Format: In-person (computer lab)

Capacity: 30 total participants

- 15 returning from Week 1 (continuity cohort).
- 15 new participants (bioinformatics-focused only): (selection via application).

Topics:

- Bioinformatics Pipelines: Hands-on training in viral sequence analysis.
- Viral sequence analysis: read trimming, assembly, and alignment tools.
- Taxonomic classification and viral genome annotation.
- Phylogenetics and visualization.

Key Features

Prerequisites:

- English proficiency (course delivery in English).
- Basic knowledge of biology, genetics, and molecular techniques.

Funding Opportunities:

- Bolivian Applicants (outside La Paz): 2-3 scholarships covering domestic travel + accommodation.
- International Applicants: 3 scholarships for round-trip travel + accommodation.

Priority will be given to applicants demonstrating active engagement in infectious disease research or diagnostics.

Apply online: <u>Submit online application by May 9th, 2025:</u>

Contact: For inquiries,

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