

M2 Internship Proposal 2025

TITLE: Comparative genomics of *Naegleria* species to improve knowledge on *N. fowleri* pathogenesis.

- **Host institution :** Institut Pasteur de la Guadeloupe (IPG)
- **Director of the Institute:** Antoine DES GRAVIERS
- **Coordinator of the Training:** Nina ALLOUCH (Research Engineer in Bioinformatics), Isabel MARCELINO (PhD, HDR)

Context and Research Problem

Members of the *Naegleria* genus belong to the major eukaryotic lineage Heterolobosea. These free-living amoebae (unicellular eukaryotes) are ubiquitous in soils and freshwater habitats, being important predators of bacteria. Of the 47 *Naegleria* species described, *N. fowleri* is the only one being pathogenic to humans, causing a rare but fulminant primary amoebic meningoencephalitis, with 97% mortality. Despite the significant clinical implications of *N. fowleri* and ongoing research on its genome, the genomic mechanisms underlying its pathogenicity remain largely unknown.

During this internship, the student will explore, for the first time, the genome of *Naegleria australiensis* (known to be pathogenic only to animals). For this, Illumina short reads and Nanopore long reads obtained from whole genome sequencing will be used, followed by reads assembly and structural and functional annotation of *N. australiensis* genome. The intern will then perform a comparative analysis between *N. australiensis* and *N. fowleri* genomes to identify key genetic differences that may drive pathogenicity and biology of these *Naegleria* species.

Objectives

1. **Genome Assembly and Annotation:**
Conduct the first complete genome assembly and annotation of *Naegleria australiensis* using established bioinformatics tools previously applied to *Naegleria fowleri* by our team. This process includes quality control, read filtration, assembly, repeat detection, and both structural and functional gene annotation.
2. **Genomic and Comparative Analysis:**
Examine the genomic features of *N. australiensis* to identify potential virulence factors. Perform comparative genomics between *N. australiensis* and *N. fowleri* to investigate genetic variations (SNPs, structural rearrangements, differences in gene functions ...) that may elucidate the distinct pathogenicity and biology of these species.

Expected Outcomes

- A high-quality, annotated genome of *Naegleria australiensis*.
- Identification of key genomic differences between *N. australiensis* and *N. fowleri*, improving our understanding of pathogenicity.
- An optimized bioinformatics pipeline for future *Naegleria* genome projects.
- Contribution to a peer-reviewed publication on the genomic characteristics of *Naegleria australiensis* and its comparison with *N. fowleri*.

Available Resources

- Raw sequencing data from *Naegleria australiensis* isolates in Guadeloupe.
- Access to computational resources, including a cluster and servers at Université des Antilles.
- Guidance from a team of bioinformatician and biologist at the Institut Pasteur de la Guadeloupe.

Candidate Profile

- **Education:** Master's degree (M2) in Bioinformatics or a related field.
- **Skills:** Proficient in Linux and server environments, with familiarity in genome assembly and annotation tools as a plus.
- **Biology:** Strong foundation in biology and genomics.
- **Collaboration:** Excellent communication and writing skills, with ability to work effectively in a research team.

Internship Details

- **Start Date:** Between January-March 2025
- **Duration:** 6 months

This internship offers the opportunity to work on an emerging pathogen using advanced genomic bioinformatics techniques. The candidate will gain hands-on experience in microbial genomics and contribute to the first genomic characterization of *Naegleria australiensis*.

Contact: Send your CV and letter of motivation to nallouch@pasteur-guadeloupe.fr (Nina ALLOUCH).