Postdoctoral Fellow in Genomics and Comparative Genomics

Project: Genome Sequencing, Assembly and Genome-Wide Association Studies in Vector Snails of Trematode Parasites

Context of the project and position overview

Understanding the genetic architecture of host resistance is fundamental to deciphering coevolutionary dynamics, pathogen persistence, and patterns of disease incidence. This project leverages a uniquely natural system: the interaction between the globally significant zoonotic trematode *Fasciola hepatica* and its intermediate and worldwide-invasive snail host *Pseudosuccinea columella*. In this system, naturally occurring snail populations include both highly susceptible and completely resistant phenotypes. Remarkably, resistant snails consistently eliminate the parasite through an immune-mediated response, irrespective of parasite genetic background. Such phenotype invariance strongly suggests a major-effect resistance architecture consistent with a gene-for-gene framework. Crucially, this interaction does not occur in a simple pairwise context: *F. hepatica* exhibits a complex multi-host life cycle, embedding the snail–parasite interaction within a broader host–parasite–host network.

The Postdoctoral Fellow will lead genome sequencing, high-quality genome assembly, comparative genomics between resistant and susceptible lineages, and genome-wide association studies (GWAS). The goal is to identify resistance-associated genomic regions and detect evolutionary signals such as selective sweeps, balancing selection, reduced diversity, or structural variation. Hence, the position offers a unique opportunity to integrate evolutionary theory with high-resolution genomics in a natural, non-model animal system, at the intersection of evolutionary biology, genomics, and immunogenetics, within a collaborative and interdisciplinary research environment.

Research Objectives

- Develop and implement strategies for whole-genome sequencing of non-model species
- Generate high-quality de novo genome assemblies using short- and long-read sequencing technologies
- Perform genome annotation and structural/functional characterization
- Conduct comparative genomic analyses across related species or populations
- Design and implement genome-wide association studies (GWAS) to identify loci associated with phenotypic or adaptive traits
- Integrate genomic, phenotypic, and environmental datasets
- Contribute to the development of reproducible bioinformatics pipelines

Key Responsibilities

- Lead the genomic component of the research project
- High-molecular-weight DNA extraction optimization
- Long-read genome assembly (PacBio HiFi / ONT)
- Genome polishing and quality assessment (BUSCO, QUAST)
- Structural and functional annotation
- Variant discovery (SNPs, indels, SVs)

- Population genomic analyses (FST, demographic inference)
- Mixed-model GWAS accounting for structure
- Workflow development (Snakemake/Nextflow)
- HPC-based pipeline implementation
- Publish results in peer-reviewed journals
- Present findings at international conferences
- Collaborate with experimental and computational team members
- Contribute to project development
- Mentor graduate students when appropriate

Required Qualifications

- PhD in Genomics, Evolutionary Biology, Bioinformatics, Computational Biology, or a closely related field
- Strong background in GWAS
- Proficiency in scripting (e.g., Python, R, Bash)
- Experience with bioinformatics tools for assembly, variant calling, and comparative analyses
- Strong publication record relative to career stage
- Excellent written and oral communication skills in English.
- Experience handling and processing large-scale genomic datasets
- Autonomy, strong work ethic and team-playing

Preferred Skills

- Experience with optimization of long fragment extraction
- Experience with long-read sequencing technologies (PacBio, Oxford Nanopore)
- Experience in genome assembly and annotation
- Familiarity with structural variant detection
- Familiarity with invertebrate organisms is desirable
- Experience in interdisciplinary collaborations
- Strong time-management skills
- Scientific creativity and the ability to structure and develop research directions

Contract Details

- **Institution:** Laboratoire Interactions Hôte – Pathogène – Environnement (UMR 5244), Univ. Montpellier, CNRS, IFREMER, Univ. Perpignan
  Start date: June 1, 2026.
- **Duration:** 2 years (fixed-term contract)
- **Salary:** competitive salary according to institutional and national regulations
- **Application:** CV, cover letter, 3 references to annia.alba-menendez@umontpellier.fr ; deadline: April 15, 2026
- **Constraints:** although the position of mainly bioinformatic analyses, the candidate will be involved in some bench work to optimize the DNA extraction on the given snail species. His/her involvement in assuring the production of biological material (alive snails) might be required, at some point.

Research Environment

The successful candidate will join a dynamic research group working on the ecology and evolution of host–parasite–environment interactions. The position is based in Montpellier, a vibrant scientific hub in Southern France internationally recognized for excellence in ecology and evolutionary biology. The IHPE laboratory provides a collaborative research environment with access to high-performance computing facilities, sequencing platforms, and strong interdisciplinary interactions across research institutions in the Montpellier area.

The thematic line is embedded within the regional scientific project InvaSnail led by Annia Alba and financed by the ExposUM initiative from the Montpellier University.