



Company or University and INRAE laboratory: University Orléans (FRANCE), Lab P2e (Physiology, Ecology Environment) and INRAE-EPGV Evry (FRANCE)

Address:

Unité EPGV US1279
CEA - Institut de biologie François Jacob
Site d'Evry - Bat G1
2 rue Gaston Crémieux - 91057 Evry Cedex

Supervisor (to be contacted for applying):

- Last name: MAURY
- First name: Stéphane
- Position: Full professor
- Email: stephane.maury@univ-orleans.fr
(<https://www.univ-orleans.fr/en/p2e/teams/trees-and-responses-hydric-and-environmental-constraints>)

Co-supervisor: Damien Hinsinger, Damien.hinsinger@inrae.fr

Internship title: Integrative multi-Omic analysis for priming potential in a model forest and cultivated tree species: poplar.

Keywords: Data analysis from Epigenomics and Transcriptomics, NGS data analysis (Long reads and WGBS), integrative statistical analysis and modelling

Internship description (½ page à 1 page) :

The P2e laboratory is conducting research into the epigenetics of trees in response to climate change, integrating ecophysiology, biochemistry, genetics and genomics. It works with the sequencing platform EPGV to implement long reads sequencing for transcriptomics and epigenomics analyses.

An M2 internship is proposed to focus on the integrative bioinformatic, and statistical modelling of omics data obtained from the ANR EPITREE (the project explored the impact of epigenetic marks on the adaptation of trees such as poplar).

The intern will first focus on RNAseq data available at EPGV to build an analyse pipeline for long reads RNAseq data (cDNA reads from the Oxford Nanopore Technology – ONT- platform), based on ONT recommendations and tools for gene expression, differential expression, RNA splicing characterisation.

Then, a multi-omics analysis will be performed as implemented in the R package MIXoMICS, using available methylome (WGBS and sequence capture bisulfite), RNAseq and bacteriome NGS data. The newly candidate genes identified will be compared to those already identified using a methylome pipeline implemented at P2e, and the candidate will perform several additional analyses, such as GO enrichment or gene network analyses to extract a biological interpretation in conjunction with the phenotyping data.

Pipeline will be built using standard languages (Snakemake/Nextflow, python, perl, etc) to be implemented on HPC (High Performance Computer) platforms. Statistics and publication-ready graphs production will be performed using R.

Internship will be located at EPGV (Evry) or shared-time EPGV and P2e (Orléans) (to be discussed). His/her detailed interests: genomics, bioinformatics (programming language : Snakemake/Nextflow, python or perl) and bioanalyses (RNAseq, multi-omic analyses), with a strong interest for pipeline development and exploratory analyses.

Allowance: 3800 euros for the 6 months (633 euros per month).