

*Thibaut Payen*

[thibaut.payen@nancy.inra.fr](mailto:thibaut.payen@nancy.inra.fr)

Supervisor Francis Martin, INRA

Thibaut Payen's PhD project, aims to develop bioinformatic pipelines to compare genomic sequences including functional genes and identify the various types of polymorphisms (SNPs, CNV, indels) in genomic and metagenomic Illumina datasets. In a pilot experiment, Thibaut Payen is analyzing sequence polymorphism in protein-coding genes in *Tuber melanosporum* genome focusing on genes involved in the symbiotic interactions and the fruiting body development. This information will be used to probe fungal gene diversity in the Illumina-based soil metagenome of the Rollainville truffle ground – a national EcoFINDERS site -- currently in sequencing. The tools developed in this pilot experiment will be used to investigate functional gene polymorphism in Illumina sequences produced from LTO soil metagenomes (pending WP3 budget is available for this task)

*Within the framework of EcoFINDERS WP3, INRA-Nancy (Ecogenomics Lab) is developing bioinformatics pipelines and workflows for processing sequence datasets produced by sequencing of soil microbial DNA from LTOs. The aim is to characterize the microbial genetic and functional diversity in LTO soils via (1) large scale surveys of ribosomal DNA sequences and (2) a targeted approach based on functional gene sequencing and comparative genomics of keystone species. A bioinformatician engineer (J Lengellé), a PhD student (T Payen) and a postdoctoral computational biologist (E Tisserant) are working on the different steps of this WP3 task: analyzing species diversity, identifying functional gene diversity and data.*