**Research engineer in bioinformatics and data analysis from microbial metagenomics research using microbial genomic resources**

**(INRA permanent position open in 2017 – application before 16th March)**

**JOB TITLE**

Research engineer in bioinformatics and data analysis

<http://jobs.inra.fr/offers/emploi_perm/concours/ce-it/?campagne=23129&intitule=concours&concours=105069>

**Environment**

The position is open in the “Trees / Microorganisms Interactions” research Unit (INRA / Lorraine University) (<http://mycor.nancy.inra.fr/IAM/?page_id=2000>).

The recruited person will work in collaboration with scientists of the unit and with a permanent bioinformatics engineer from the technical platform in bioinformatics. This person will develop an expertise in microbial metagenomics, and particularly in fungal metagenomics / metatranscriptomics, and he / she will be involved in national (National Research Agency, Meta-omics and Microbial Ecosystems (MEM) meta-program) and international research programs (US Department of Energy Joint Genome Institute; e.g. Metatranscriptomics of Forest Soil Ecosystems).

**CONTEXT AND ACTIVITIES**

The huge microbial richness (bacteria and fungi) in forest soils remains little explored in spite of fundamental or applied research opportunities (understanding of the functioning of ecosystems, analysis of functional diversity, extended phenotype of host plants, forestry management, ecosystem services, bioenergy). The study of this microbial diversity and their trophic and functional interactions requires integrative approaches (“meta-omics”) and powerful analysis and data mining. The use and development of bioinformatics tools for New Generation Sequencing (NGS) data analysis from microbial (prokaryotic and eukaryotic) metagenomic and metatranscriptomic researches will require:

(i) to develop and use appropriate bioinformatics procedures

(ii) to store, search, and compare meta-omic data sets

(iii) to identify the gene networks and associated key functions (indicators) controlling these complex systems.

Finally, in interaction with colleagues of the technical platform, the recruited person will also lead and deploy the hardware and software architecture and its application (installation, assistance, training, evaluation).

**SKILLS AND Personal Qualities**

- PhD in biology, bioinformatics, computer science or Engineer degree from graduate schools or equivalent.

- Professional experience in biology and/or in genomics / metagenomics, ideally applied to microbiology, molecular ecology or plant / microbe physiology. Good knowledge of programming languages and tools for building / managing databases adapted to the analysis of recommended metagenomes.

- One or more proven experiments in (meta) comparative genomics of gene repertoires; Computer processing of sequencing data (HiSeq, MiSeq, PacBio ...); Quantification of fungal gene expression (trimming, mapping, normalization); Differential expression and analysis of co-expression networks.

- Experience in Perl and Python programing, object oriented development, database management (MySQL, PostgreSQL)

- Very good knowledge of UNIX environment

- Fundamentals in biology and biostatistics for data valorisation.

- Good communication skills and autonomy

- Good knowledge of English, spoken and written

- Ensure quality and relevance of analysis and results

- Develop and implement a quality approach

**OPEN INRA COMPETITION**

- Opening date for applications: 14 February 2017

- Submission deadline for application package: 16 March 2017

- Dates of the examinations: May-June 2017

- Starting date for appointments: as from September 2017

- All details: <http://jobs.inra.fr/offers/emploi_perm/concours/ce-it/?campagne=23129&intitule=concours&concours=105069>

**HOST LABORATORY AND contacts**

UMR 1136, Interactions Arbres/Microorganismes (IAM).

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