

Bioinformatics Software developer

About MetaboHUB

MetaboHUB (MTH) is the national French metabolomics and fluxomics infrastructure. Launched in 2013, MTH is a leading international infrastructure serving more than 700 scientists worldwide. MetaboHUB gathers 6 **regional facilities** including more than **80 permanent staffs**, **16 NMRs**, **68 MS**, **robotic and computational platforms**. MTH aims at pushing forward the field to develop metabolomics, lipidomics and fluxomics from single cell to population. **Your contribution will serve a broad range of researchers** in the fields of biotechnologies, Human health, nutrition and plant science. **Joining MTH, you will be involved in cutting edge research within a highly skilled and motivated consortium.**

The mission

Metabolomics studies generate heterogeneous data that are difficult to integrate and interpret. Within the MetaboHUB national infrastructure, the objective of this position is to develop a reusable tool for integrating, querying and contextualizing data produced in metabolomics studies. Based on the FORVM knowledge graphs, the tool will connect metabolomics data with phenotypic data, biological concepts, molecule–disease–phenotype associations and relevant scientific publications.

The successful candidate will join the PFEM and work alongside bioinformaticians, computer engineers and metabolomics experts. The project will combine Python software development, REST APIs, knowledge graphs, biological data integration, DevOps and Galaxy workflows.

About MTH-Clermont Ferrand

The PFEM (**metabolism exploration platform**) is a metabolomic platform, recognized as a national and international leader in metabolomics applied to **nutrition and health**. PFEM principal research interest concerns the development of MS-based analytical methods and bioinformatics tools for a better characterization of metabolic deviations associated with development of chronic metabolic diseases and the study of nutrition and health relationships:

- Metabolic profiling using multiplatform approaches in biofluids and tissues.
- Development of analytical strategies for biomarker identification using ultra high-resolution MS and bioinformatics tools.
- Development of models and tools to increase knowledge extraction from high throughput data.
- Development of tools, databases and information systems based on big data and web semantic technologies to store data and mining existing knowledge.

Key Responsibilities

The successful candidate will be responsible for:

- Formalising user requirements and designing use cases;
- Developing microservices and REST APIs in Python;
- Integrating resources from the FORVM knowledge graph;
- Setting up automated tests and CI/CD pipelines;
- Documenting, testing and maintaining the software;
- Participating in code reviews and Git-based development;
- Developing a Galaxy wrapper;
- Contributing to the reproducibility and roll-out of the tool within MetaboHUB.



Profile

A background in computer science, bioinformatics, computational biology or a related field is expected (Master level)
Initial experience in Python development, API design or software automation.



Skills

Programming (Python)
Forge (Gitlab, Github)
Database management
English mandatory



Informations

CDD -Engineer
12 months contract
Salary range (gross salary): 2245-2815 euros/month
Depending on experience
Place of work: St Genes Champanelle (63) France
Trips: Rennes, Toulouse
Starting from: 2027 January 1st

How to apply ?

The application should contain the following attachments:

- a motivation letter reasoning your interest for a specific research project described on our webpage (max. one page)
- a full CV (max. two pages) including contact details of two references

Application deadline: 2026 October 30th

Contacts

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More information

www.metabohub.fr