

2 Postdoc positions – Machine Learning and Automation in Synthetic Biology

We are seeking outstanding candidates for two postdoctoral positions in Computational Synthetic Biology. The successful candidates will take part of a 4-year European project funded by H2020 and a pre-competitive project funded by the French government at the MICALIS Institute (Jouy-en-Josas, near Paris, France).

MICALIS (INRA & AgroParisTech) is a research unit of more than 350 researchers developing multidisciplinary approaches and promoting microbial systems biology towards the development of synthetic biology applications for health and biotechnology. Within MICALIS, the recruiting research team (<http://www.jfaulon.com>) specializes in developing whole-cell and cell-free synthetic biology for pathway and biosensor engineering to produce biologically active molecules and detect disease biomarkers.

Position 1

The recruited postdoc is expected to develop: (i) state-of-the-art supervised machine learning tools to predict activities of engineered metabolic pathways, (ii) generative models to design nucleotide sequences for optimization of specific enzymatic activities, and (iii) a reinforcement / active learning pipeline to propose novel pathway sequences for synthesis and experimental characterization. These tasks will be performed using training sets built from experimental data obtained by the host laboratory from large combinatorial pathway libraries. The postdoc will also benefit from several years of experience this research team has in developing machine learning for synthetic biology [1].

Position 2

The recruited postdoc will be responsible for developing scientific workflows for automation of in-house computational retrosynthesis methods [2] to: (i) design retrosynthetic metabolic networks in standard formats including SBOL and SBML, (ii) rank pathways within networks and use the ranking to control retrosynthetic network size, (iii) plug top-ranked pathways into constraint-based models to perform strain engineering, and (iv) determine a list of genes to be up- or down-regulated to optimize pathway productivity in the strain of interest.

Both positions will require interactions with molecular biologists. The recruited postdocs will closely collaborate with an IT research engineer and wet lab scientists in the team.

Expected start dates range from June to October, 2018.

Applicants' profiles

- Applicants should have a Ph.D. in computational chemistry, computational biology, maths, or computer science, with working knowledge of biology.
- Essential qualifications include excellent programming skills in languages such as Python, Java, and C++, as well as scientific software (R or Matlab).
- Ability to write high-quality research manuscripts, strong collaborative skills, and excellent communication skills in English are required.
- For Position 1, experience with machine learning open source tools is a prerequisite.
- For Position 2, experience with scientific workflow systems and familiarity with relational databases are desirable.

To Apply

Applicants should send a detailed curriculum vitae, a letter of intent explaining their motivations for the chosen position, and contact details of two referees to: jean-loup.faulon@inra.fr.

References

- [1] Mellor J, *et al.* Semi-supervised Gaussian Process for automated enzyme search. *ACS Synthetic Biology*, 5(6): 518-528, 2016, see also <http://www.jfaulon.com/machine-learning-methods-for-biotechnology-applications/>.
- [2] Delépine B, *et al.* RetroPath2.0: A retrosynthesis workflow for metabolic engineers. *Metabolic Engineering*, 45: 158-170, 2018.