

Postdoctoral fellowship: Metabolic modelling of the rumen microbiome for guiding strategies of methane reduction

Project description. Ruminants play a significant role in human nutrition and food security. Ruminants can harvest nutrients from forage diets rich in fibres and transform them into human-edible products with high-quality proteins. Feed transformation occurs mainly in the rumen through a metabolic cascade of hydrolytic and fermentative reactions carried out by a complex microbial community (rumen microbiota) constituted by hundreds of species that include bacteria, archaea and eukaryotes. During rumen fermentation, methane (CH₄) is produced and eructed by the animal. This CH₄ contributes to 44% of greenhouse gas emissions from the livestock sector.

The postdoc project aims at developing metabolic models of rumen microbiota with capabilities for designing microbial strategies for reducing methane emissions and improving rumen fermentation. It will contribute to fill the existing gap on how to integrate microbial genomic information into rumen fermentation models [1].

The postdoc fellow will be part of the project [H2Rumen](#) funded by the French National Agency for Research (ANR). The specific objectives are

- (i) To obtain metabolic models of the species constituting a rumen microbial mini-consortium.
- (ii) To derive a bag-of-genome model of a complex rumen consortium.
- (iii) To develop a community-scale kinetic models of mini and complex consortia accounting for H₂ transactions and thermodynamic control.

The postdoc fellow will collaborate with [Clémence Frioux](#), [Simon Labarthe](#) and [David James Sherman](#) from the [PLEIADE](#) team (Inria, INRAE, Bordeaux) and with [Rafael Muñoz-Tamayo](#) from the [MoSAR](#) team (INRAE, AgroParisTech, Université Paris-Saclay). The work is organized in two parts. 18 months in PLEIADE to work on the objectives (i,ii) and 14 months at MoSAR to work on the objective (iii).

Genome-scale network reconstructions will be done with state-of-the-art methods and pipelines developed in PLEIADE. Metabolic capabilities of rumen microbial communities will be explored using Metage2Metabo [2]. Kinetic models will be built on the basis of existing models developed at MoSAR [3,4]. Models will be constructed using experimental data produced by our partners at [UMRH](#) and [MoSAR](#).

Background and skills required

- PhD in applied mathematics or computational biology or process engineering.
- Experience in metabolic modelling with willingness to learn dynamic modelling or viceversa. Expertise in dedicated software: Python, R or Scilab/Matlab.
- Experience on modelling the metabolism of microbial ecosystems and/or systems biology is a plus.
- Excellent communications skills, willing to discuss with scientists with different backgrounds.

Contract information

Location: Bordeaux (18 months contract with Inria), Palaiseau (14 months contract with INRAE), France

Start date: October 1st 2025/position immediately available

Salary: 2,788€ to 3,405€ gross/month based on experience

To postulate, apply with your motivation letter, CV and the name of two scientists (references) online on <https://recrutement.inria.fr/public/classic/en/offres/2025-08790> . Only online applications will be considered.

For more information, contact clemence.frioux@inria.fr; simon.labarthe@inrae.fr; david.sherman@inria.fr; Rafael.Munoz-Tamayo@inrae.fr

References

1. Muñoz-Tamayo R, Davoudkhani M, Fakhri I, Robles-Rodriguez CE, Rubino F, Creevey CJ, et al. Review: Towards the next-generation models of the rumen microbiome for enhancing predictive power and guiding sustainable production strategies. *animal*. 2023;17: 100984. doi:10.1016/J.ANIMAL.2023.100984
2. Belcour A, Frioux C, Aite M, Bretaudeau A, Hildebrand F, Siegel A. Metage2metabo, microbiota-scale metabolic complementarity for the identification of key species. *Elife*. 2020;9: e61968. doi:10.7554/eLife.61968

3. Muñoz-Tamayo R, Chagas JC, Ramin M, Krizsan SJ. Modelling the impact of the macroalgae *Asparagopsis taxiformis* on rumen microbial fermentation and methane production. *Peer Community J.* 2021;1: e7. doi:10.24072/PCJOURNAL.11
4. Fakhri I, Got J, Robles-Rodriguez CE, Siegel A, Forano E, Muñoz-Tamayo R. Dynamic genome-based metabolic modeling of the predominant cellulolytic rumen bacterium *Fibrobacter succinogenes* S85. *mSystems.* 2023;8: e01027-22. doi:10.1128/msystems.01027-22