

## Post-doctoral position (Research engineer level)

Laboratoire de Biométrie et Biologie Evolutive, Centre International de Recherche en Infectiologie,  
Université de Lyon

Duration: 12 months (starting January 1<sup>st</sup> 2018). Possibility of extension depending on the quality of the applicant and her/his eligibility to funding opportunities (Skłodowska Curie Grants, EMBO, FRM, ANR,...).

Funded by the Labex Ecofect [Eco-evolutionary dynamics of infectious diseases](#)

Approximate monthly salary: 1900€ (net income)

Supervision : Samuel Venner, Xavier Charpentier

Collaboration : Dominique Pontier, Maria-Halima Laaberki, David Fouchet, Vincent Miele

### Project: mathematical modeling of antibiotic resistance propagation within bacterial communities

Antibiotic resistance is a global concern that hampers the control of infectious diseases and increases the cost of health care. New mechanisms of antibiotic resistance regularly emerge and some spread globally, yet our understanding of this phenomenon is limited. A leading contributing factor to the spread of antibiotic resistance is horizontal gene transfer (HGT) of mobile genetic elements (MGE) through which pathogens can acquire antibiotic resistance genes (ARG) from other bacteria.

The MGE carrying ARG (AR-MGE) can be considered as entities competing to exploit bacteria, considered here as their limiting resource. We formulate the hypothesis that the AR-MGE should harbor selfish intrinsic properties (hereafter called “selfish competing traits”) aiming at maximizing their propagation in this context of competition between AR-MGE. A potential major competing trait of AR-MGE corresponds to their ability to alter the rate of acquisition of other competing MGE. In this way, AR-MGE could increase their own chances of invasion and/or persistence in bacterial communities in specific ecological contexts. In addition, we hypothesize that under massive and persistent antibiotic treatment, competing traits could drastically accelerate the process of adapted AR-MGE invasion and spread within bacterial communities. This could profoundly influence interactions between bacterial species, and can lead to community instability, and even dysbiosis in the case of microbiota.

The selected candidate will build on an existing Individual Based Model (IBM) to study the dynamics of spread of ARG (invasion, spread, extinction) within bacterial populations or communities. The developed model will be grounded in the framework of the Selfish Gene theory. We will particularly focus on the dynamics of AR-MGE, assumed here to be not only entities that can confer resistance to the recipient bacteria but also entities that seek to maximize their persistence and spread in bacterial communities considering competition with other AR-MGE variants. The model's parameters and predictions will be compared to experimental data on a specific bacterial organism categorized by the WHO as a priority organism for the development of new therapeutic strategies. The model may then be extended to study of more complex bacterial communities (microbiota).

**Sought profile :** Strong knowledge in programming (C++ or other); The candidate should hold a PhD degree in community ecology, evolution and/or eco-epidemiology.

**How to apply:** send a resumé, a cover letter including three references to Samuel Venner ([samuel.venner@univ-lyon1.fr](mailto:samuel.venner@univ-lyon1.fr)) and Xavier Charpentier ([xavier.charpentier@univ-lyon1.fr](mailto:xavier.charpentier@univ-lyon1.fr)).