DE CIDE

Post-doctoral position proposal

Hosting organization

Organization	INRAE: French National Institute for Agriculture, Food and Environment; Animal Health Division
Research Unit	UMR1300 BIOEPAR (INRAE, Oniris), DYNAMO team
Full Address	Oniris, site de la Chantrerie, rte du Gachet, CS40706, 44307 Nantes, France

Contact persons

Full names	EZANNO Pauline (DR2, HDR) & BEAUNEE Gaël (CRCN)
Positions	Both are full time INRAE permanent researchers
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Research proposal

Title	**Inference algorithms adapted to heterogeneous data sources and stochastic epidemic models**
Starting date	January 2023
Duration	24 months
Salary	Basic gross salary ~2600-3300 €/month (according to experience)
Expected skills	PhD in biostatistics / biomathematics or in ecology / epidemiology with strong quantitative skills Experience in complex system modelling and biological data analyses Significant computational/programming skills (C++, Python, R) Interest in infectious diseases, epidemiology, ecology, interdisciplinary research Strong organizational and written/oral communication skills Be highly motivated towards scientific research
Proposal description	Epidemic mechanistic models are helpful to better understand and anticipate pathogen spread in host populations under contrasted situations, e.g. to prioritize disease control strategies. To reinforce the robustness and precision of model predictions, and thus their usefulness for stakeholders, model parameter values should be inferred on observed data. However, available data sources are heterogeneous (data on host demography and location, epidemiological data, sensor data, etc.). Another challenge is to define model initial conditions according to (if possible real-time) field observations. You will develop an inference algorithm able to tackle such heterogeneous data sources and relevant for stochastic epidemic models. Several options will be considered: simple likelihood-based methods often used in experimental settings but less suitable to heterogeneous field data and stochastic models; Approximate Bayesian Computations (ABC) and its relatives (such as ABC-SMC); the recent approach developed by INRAE, which uses a criterion based on a Monte-Carlo (MC) approximation of a composite likelihood coupled to a numerical optimization algorithm (Nelder-Mead Simplex). These approaches will be compared. The simplest most relevant (and sufficiently generic) one will be used to develop the algorithm which will be used to feed by data specific mechanistic models of the case studies of a H2020 EU project (DECIDE). A first application will concern the spread of the pathogens involved in the bovine respiratory disease (BRD) in young animals. BRD is one of the major enzootic diseases of young cattle in Europe, leading to economic losses, animal welfare issues, and antimicrobial usage. A challenge will be to connect the inference algorithm and/or mechanistic models to warning systems (statistical or machine learning models developed by collaborators) to better define the initial conditions of the mechanistic epidemic models. The inference algorithm will also be connected to our EMULSION software and/or made available as an R package to ease its use by project partners and beyond, for BRD case studies and other enzootic diseases for which similar data exist. Access to data and computing resources needed to complete the project successfully is guaranteed.
How to apply	Please, send to both contact persons: your CV, a cover letter expressing your research experiences and interests, and the names and contact details of two referees. The position is currently available, with flexible starting date in the 1st trimester 2023. Review of applications starts immediately and will stop as soon as the position is fulfilled.