Offer #2025-08806

PhD Position F/M RESERVOIR COMPUTING WITH BACTERIA

Contract type : Fixed-term contract

Level of qualifications required : Graduate degree or equivalent

Fonction : PhD Position

About the research centre or Inria department

The Inria center at the University of Bordeaux is one of the nine Inria centers in France and has about twenty research teams.. The Inria centre is a major and recognized player in the field of digital sciences. It is at the heart of a rich R&D and innovation ecosystem: highly innovative SMEs, large industrial groups, competitiveness clusters, research and higher education players, laboratories of excellence, technological research institute...

Context

Project description

In contrast to traditional bottom-up approaches that build biological devices for computation within organisms [1-3], this PhD project proposes a novel top-down strategy . The goal is to leverage bacterial strains in a reservoir computing (RC) framework to solve complex computational tasks.

Engineering bottom-up biological devices is challenging. These devices place a significant metabolic burden on host cells, are difficult to fine-tune, and are prone to noise [4, 5]. The design of such devices often draws inspiration from biological information-processing systems, akin to logic gates, switches, and perceptrons, already found in nature [6, 7]. This raises an intriguing question: instead of constructing devices from the ground up, could natural microorganisms themselves be harnessed for complex computational tasks?

By developing a reservoir computing approach with bacterial strains, this PhD research is expected to highlight the potential of a top-down approach in synthetic biology for biocomputing, with implications for solving complex tasks typically handled by digital systems. The project also aims to set the groundwork for further applications in medical diagnostics and propose avenues for integrating bacterial reservoir computing with emerging technologies, such as neuromorphic computing and engineered living materials.

Supervision

The PhD will be co-supervised by Jean-Loup Faulon (HDR, PR) at INRAe et Xavier HINAUT (HDR, CR) at Inria.

Assignment

Domain

Artificial Intelligence Applied to Biological Data.

Reservoir Computing (RC) is a branch of artificial intelligence that explores the computational capabilities of physical, chemical, and biological systems [8]. Initially developed as an alternative to traditional artificial neural networks, particularly recurrent neural networks (RNNs), RC offers a more efficient training process. There are two main types of RC systems: conventional RC and physical RC.

In a typical conventional RC framework, input data is fed into a reservoir, the states of the reservoir nodes are recorded, and this information is passed to a “readout” layer — usually a simple linear classifier or regressor — which interprets the states to produce the final output. Unlike RNNs with trainable weights, conventional RC uses a reservoir of RNNs with fixed weights, making it faster to train. This makes it well-suited for applications such as time series prediction, dynamic system control, and Internet of Things (IoT) use cases that require fast and efficient processing [9].

In physical RC, the reservoir is replaced by a physical system. The process involves first introducing input data into the physical reservoir, which transforms the data into a high-dimensional dynamic state. These transformed states are then passed to a readout layer, similar to conventional RC. Applications of physical RC include pioneering systems like the liquid state machine for pattern recognition in water [10], developments in chemical RC for classification tasks and solving differential equations [11], and biological RC systems using cultured rat cortical neurons on micropatterned substrates to solve classification tasks [12].

Objectives

This PhD project aims to evaluate the feasibility of using bacterial strains within a reservoir computing (RC) framework and to explore their potential as reservoirs. Like other machine learning methods, RC relies on training data composed of features and labels, with the goal of predicting labels from features. In a bacterial reservoir approach, the problem features are represented by nutrients supplied to the bacteria, and the bacterial responses are measured through phenotypic observations. These measurements are then processed by a standard machine learning regressor or classifier to provide solutions to computational tasks.

Main activities

Concretely, the project will begin (Year 1) by using E. coli as a test strain, trained on media enriched with various metabolites, and recording growth curves for different medium compositions. The computational capabilities of this E. coli-based reservoir will then be compared to classical machine learning techniques such as multiple linear regression (MLR), support vector machines (SVM), and multilayer perceptrons (MLP) across various regression and classification tasks. As illustrated in Figure 2 of the PDF document and in Faulon et al. [13], preliminary results obtained from a dataset of E. coli growth rates with different nutrients (sugars, amino acids, nucleotides) suggest that this approach can be used to classify both linear and nonlinear patterns.

As a practical application, bacterial reservoirs will also be tested (Year 1) for clinical sample classification, using either wild-type or mutant bacterial strains. As shown in Figure 3 of the PDF document, preliminary data suggest that a reservoir based on a mutant E. coli strain can accurately classify COVID-19 sample severity, distinguishing moderate from severe cases based on the strain’s responses.

During the second year, genome-scale metabolic models (GEMs) from different bacterial species or gene knockout (KO) mutants will be explored to design new reservoirs. Growth data will be experimentally collected for the most promising candidates. These species and their associated growth data will then be used to solve standard regression and classification tasks, with additional testing on clinical samples planned for Year 3. Instead of relying on a single species, the multi-species RC system will be composed of a consortium of wild-type or mutant species acting as reservoirs.

For clinical sample testing, the student will have access to prostate cancer and COVID-19 cohorts provided by the university hospitals (CHUs) of Montpellier and Grenoble. Additional samples related to other pathologies may be acquired during the project. Finally, the potential for detecting environmental pollutants (e.g., in water) will also be explored within the multi-species RC framework.

For computer-simulated experiments, the ReservoirPy library [14] — developed by the Inria research team — will be the preferred tool:
https://github.com/reservoirpy/reservoirpy

A version of the project with figures is available at the following link:
https://jfaulon.com/phd-subject-bacterial-reservoir-computer/

Bibliography

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Benefits package

- Subsidized meals
- Partial reimbursement of public transport costs
- Leave: 7 weeks of annual leave + 10 extra days off due to RTT (statutory reduction in working hours) + possibility of exceptional leave (sick children, moving home, etc.)
- Possibility of teleworking partiel and flexible organization of working hours
- Professional equipment available (videoconferencing, loan of computer equipment, etc.)
- Social, cultural and sports events and activities

Remuneration

2200 € grossly / month (before charges and taxes)

General Information

- **Theme/Domain :** Computational Neuroscience and Medicine
  Biologie et santé, Sciences de la vie et de la terre (BAP A)
- **Town/city :** Bordeaux
- **Inria Center :** Centre Inria de l'université de Bordeaux
- **Starting date :** 2025-10-01
- **Duration of contract :** 3 years
- **Deadline to apply :** 2025-04-26

Contacts

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About Inria

Inria is the French national research institute dedicated to digital science and technology. It employs 2,600 people. Its 200 agile project teams, generally run jointly with academic partners, include more than 3,500 scientists and engineers working to meet the challenges of digital technology, often at the interface with other disciplines. The Institute also employs numerous talents in over forty different professions. 900 research support staff contribute to the preparation and development of scientific and entrepreneurial projects that have a worldwide impact.

The keys to success

M2 research in computational biology , bioinformatics, applied mathematics, or another relevant discipline. Passion for programming and machine learning. Experience with Python.

Warning : you must enter your e-mail address in order to save your application to Inria. Applications must be submitted online on the Inria website. Processing of applications sent from other channels is not guaranteed.

Instruction to apply

Thank you to send:

- CV
- Cover letter
- Master marks and ranking
- Support letter(s) if available

Defence Security :
This position is likely to be situated in a restricted area (ZRR), as defined in Decree No. 2011-1425 relating to the protection of national scientific and technical potential (PPST).Authorisation to enter an area is granted by the director of the unit, following a favourable Ministerial decision, as defined in the decree of 3 July 2012 relating to the PPST. An unfavourable Ministerial decision in respect of a position situated in a ZRR would result in the cancellation of the appointment.

Recruitment Policy :
As part of its diversity policy, all Inria positions are accessible to people with disabilities.