## PhD Position

# Signal Amplification via Engineered Competition in Bacteria

### **Topic profile**

theory/math	
wet-lab	

### Tags

#synthetic biology
#genetic circuits
#bacterial conjugation

### **Supervision**

Matthias Függer

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Thomas Nowak Professor at ENS Paris-Saclay

### Context

In the past few decades, synthetic biology has laid considerable focus on the re-programming of cells as computing machines, e.g., via genetic circuits and molecular control mechanisms. A central problem in this setting is to maintain a consistent state of circuit values among the bacteria. The problem of maintaining a consistent state among agents has been studied in distributed computing for decades in different contexts, e.g., for replicated state machines and mobile networks. Starting from a mathematical computing model, analysis of a system's behavior has led to correctness proofs and performance bounds of proposed solutions, also shedding light on how protocol parameters influence the quality of the outcome [1].

## Research

We use engineered competition to boost the relative population of one bacterial type over another for differential signal amplification. An initial mixed population of 60% bacteria of type Yes and 40%of type No being amplified into a population of, say, 95% of type Yes and 5% of type No makes downstream computations based on these signals less complex and more robust [2]. As such, this form of signal amplification is a relaxed variant of the distributed consensus problem. A simple yet effective algorithm to achieve signal amplification is to introduce the single inter-bacterial reaction Yes + No  $\rightarrow \emptyset$  that removes opposing bacteria. We will implement this mechanism by DNA communication of a genetic circuit part via bacterial conjugation [3]. The always present duplication and death reactions make the mathematical analysis challenging and non-standard. They do, however, actually introduce robustness to noise for our algorithm due to the fact that constant duplication keeps some high-variance stochastic effects caused by low population counts from occurring.

#### We are looking for

Prerequisites are a Master degree in a relevant subject (e.g., biology or computer science). We expect a curious, driven attitude and interest to combine wet-lab and modeling work.

### The team

You will be part of an interdisciplinary research team at Laboratoire Méthodes Formelles in the ENS Paris-Saclay, near Paris, working at the interface between computer science and synthetic biology.

### References

[1] Cho et al. Distrib. Comput.'21. URL

[2] Aoki et al. Nature'19. URL

[3] Marken, Murray. Nature Comm.'23. URL

#### You are interested or would like to join us?

Please mail your questions or, in case you would like to apply, a short statement of interest and a curriculum vitae to Matthias Függer (mfuegger@lmf.cnrs.fr) and Thomas Nowak (thomas@thomasnowak.net). Applications until the end of April 2024 will receive full consideration.

#### https://cellularcomputing.group/