Distributed Computation with Bacteria

Thomas Nowak
Université Paris-Saclay, CNRS, ENS Paris-Saclay, Laboratoire Méthodes Formelles, France
Institut Universitaire de France, France

Abstract

Computing via synthetically engineered bacteria is a vibrant and active field with numerous applications in bio-production, bio-sensing, and medicine. Motivated by the lack of robustness and by resource limitation inside single cells, distributed approaches with communication among bacteria have recently gained in interest. In this talk, we describe the most important distributed approaches to synthetic biology with bacteria and discuss the crucial task of mathematical modeling of these systems. A particular problem is that of population growth happening concurrently, and possibly interfering, with the desired bio-computation. Specifically, we present a fast protocol in systems with continuous population growth for the majority consensus problem and prove that it correctly identifies the initial majority among two inputs with high probability. We also present a fast protocol that correctly computes the NAND of two inputs with high probability. By combining NAND gates with the majority consensus protocol as an amplifier, it is possible to compute arbitrary Boolean functions. The proposed protocols help set the stage for bio-engineered distributed computation that directly addresses continuous stochastic population growth.

Own work presented in this talk is mostly based on joint work with Da-Jung Cho, Matthias Függer, Corbin Hopper, Manish Kushwaha, and Quentin Soubeyran.

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