

PyEcoLib: a python library for simulating *E. coli* stochastic size dynamics

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Abstract—We synthesized a recent theory in the tool PyEcoLib, a python-based library to simulate bacterial cell size stochastic dynamics. This library can simulate single-cell size trajectories with an arbitrary small sampling period, including stochasticity in variables such as size at the beginning of the experiment, division timing, growth rate, and splitting position. We also explain how to couple these size dynamics to gene expression. The simplicity of use of the tool and the transparency of the underlying models should promote the inclusion of cell-size stochasticity into more complex models of gene expression.

Index Terms—Stochastic Simulation, Open Source Software, cell size.

I. PURPOSE

THE origin of the random fluctuations (noise) of gene products in cells is currently an active research field [1]. Intrinsic sources of this noise include randomness in chemical kinetics, such as random molecule binding and spontaneous degradation. Other sources, also known as extrinsic sources, are only partially understood. They include the activation of the genes by other noisy proteins (transmitted noise) and fluctuations in growth rate and cell division, also described as fluctuations in cell size. These sources have been studied recently through the development of techniques for high-throughput measurements of cell size [2].

Among the mechanisms responsible for the transmission of the cell size fluctuations to gene expression, we can include the random segregation of the low number molecules during division and variability in the reactant concentrations, dilution rates, and division times. However, it is currently not clear how to couple gene expression mechanisms to the stochastic size dynamics because the relation between expression rates and growth is still under study [3]. Some attempts have been made [4], [5] but they consider division as a discrete process. Although they estimate steady distributions, the continuous gene expression dynamics are still unclear.

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We recently proposed a mathematical framework [6] describing division as a Continuous Time Markov Chain easily coupled to gene expression as shown in [7]. Here, we synthesize this framework into an easy-to-use tool by developing PyEcoLib; a python based library that can model the stochastic cell size dynamics. This library reproduces most of the known properties of bacterial division, such as the division strategies [8], bacterial proliferation, the known distributions of division times [2], and the stochastic fluctuations in both growth rate and septal position [9]. The user can incorporate this library into any simulation script to model gene expression, including size and growth effects in bacterial physiology. The library can be found in our repository [10]¹ and can also be installed using the Python Package Index (pip install PyEcoLib).

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¹<https://github.com/SystemsBiologyUniandes/PyEcoLib>