Spectral analysis of a synthetic genetic oscillator

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***Short Abstract* —** **In this work we develop a mathematical model for a synthetic genetic oscillator that has been experimentally build in E. coli using a commercial plasmid well known in molecular biology, the so called pZ expression vector system. The model is numerically simulated using the Gillespie algorithm, in order to take into consideration the biochemical noise; and the results are analyzed using correlation and Fourier techniques, in order to calculate the frequency and strength of the resulted oscillations. The model is validated by comparing its stochastic results with the experimental reports.**

Keywords—**Spectral analysis, biochemical noise, genetic oscillators.**

I. INTRODUCTION

The periodic or cyclic behavior is inherent to almost all high order organisms. All animals have for example the cardiac cycle, circadian cycle, etc. [1] It is not so obvious to find similar periodic behaviors in simpler organisms like yeast or bacteria. Hence, it is always a quite interesting problem to understand what is the function and importance of the periodic biological processes for the low order organisms, when they appear.

On the other hand the biochemical noise has a really strong influence in the periodic behavior. It produces great variations in the period of the oscillations, for example, or it can even kill the oscillations at all [2].

We study a simple biochemical oscillator that has been experimentally implemented in vivo and *silico* by Stricker et al.[3].

II. METHODS

We develop a mathematical model for a synthetic genetic oscillator that has been experimentally build in E. coli using a commercial plasmid well known in molecular biology, the so called pZ expression vector system [4]. We pay special attention to the estimation of all the model parameters from reported experimental data and to the calculation of the resonance frequency of the model, in order to compare the calculated results against the experimental observations. We construct our model as a set of chemical reactions involved in the transcription, translation, and self-control of the LacI repressor. Later we analyze this set of chemical reactions following the classical deterministic and stochastic procedures. That is, we construct a deterministic model of ordinary differential equations with delay in translation of mRNA, using the Law of Mass Action, and we also simulated (at least one hundred thousand times) the set of chemical reactions using the Gillespie algorithm, the latter is done in order to take into consideration the biochemical noise [5]. Finally, we validate our model by calculating the resonance frequencies using Fourier techniques and by comparing the results against those observed experimentally.

III. RESULTS

We carried out deterministic simulations of the set of chemical reactions, on this way we obtained oscillatory behavior but only when the delay was higher than 5 minutes, which is not a real delay in translation process. Furthermore, the period oscillation was not consistent with experimental results. As consequence of this, we implemented a stochastic simulation algorithm with the set of chemical reaction and we calculated the spectrum of stochastic trajectories of chemical species through Fourier techniques in order to calculate the resonance frequency and period oscillation, observing consistency with experimental results.

We found that it is necessary to take account the biochemical noise to observe the resonance frequency reported on experimental data without to make an adjusting of parameters of its experimental value.

IV. CONCLUSION

It is necessary to take account the biochemical noise in this model to observe the period oscillation reported experimentally.

References

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