

Computational design of RNA-based oscillatory circuits

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Abstract—the abstract

I. INTRODUCTION

The process of gene expression can be briefly summarised as follows: DNA is read, and a copy of it is made, in the form of an RNA molecule (this is called *transcription*). This RNA molecule (known as messenger RNA, or mRNA) makes its way to a piece of cellular machinery called the Ribosome, which reads it, and makes a protein - which protein is made depends on the DNA sequence originally read (*translation*).

The path from genetic transcription to protein expression is naturally regulated in many ways [?]. This regulation allows a cell to control protein expression, and so cell behaviour, in response to various environmental cues. The natural cell machinery in place to perform this regulation offers rich possibilities for modification, and an important goal within synthetic biology is to understand and manipulate it.

As well as acting as the intermediate between DNA and protein, RNA's play direct and important roles in regulating cell behaviour [1]

- goal of the project - emph on quantitative modelling of biological system and data, getting a quantitative model, finding its parameters.
- Biological background, taken from those 3 papers.
- give structure of the report.

II. RESULTS AND DISCUSSION

A. *Model Derivation*

- introduce the proposed ode model, explain its biology.
- Biological background, taken from those 3 papers.

B. *Parameter Estimation*

- basically the whole project. [1]

III. CONCLUSIONS AND FURTHER WORK

REFERENCES

- [1] F. J. Isaacs, D. J. Dwyer, and J. J. Collins, "RNA synthetic biology." *Nature biotechnology*, vol. 24, no. 5, pp. 545–554, 2006.