Stochastic models of genetic circuits

by

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Submitted to the Department of Physics in partial fulfillment of the requirements for the degree of

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Supervisor: Juan Manuel Pedraza Leal

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Abstract

All living beings store their genetic information in the DNA and use similar basic mechanisms to read it and, according to its information, build their structure and develop their functions. Nevertheless, the information codified on the DNA is not the only aspect that makes an organism what it is. Genes interact between them and with environmental signals through a complex network of gene regulation that determines which genes are read at a particular moment and the intensity of their activity. This makes possible, for instance, to differentiate between our muscle cells and our neurons, cells that in spite of having the same genetic material, are very different in form and function. Since gene expression is mediated by chemical reactions, which at microscopic levels are random collisions of individual molecules of the reactants, gene expression and regulation is subjected to noise. A cell also regulates the expression of many genes according to the environment, which may change randomly. In response to these important sources of noise, living beings have developed their regulatory networks to work properly under its presence. This work explores the models that have been done on the last years related to stochasticity in gene expression, the insights they have given to us into the principles of biology and the design of synthetic biological circuits.

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