

# First Joint Meeting Brazil Italy of Mathematics Special Session: Analytical and Numerical Aspects of Modeling Biological Systems

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**Title:** A space-dependent bistable model to understand the gene reading mechanism

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**Abstract:** During embryonic development, the reading of the genetic information produces spatially distributed patterns of proteins. These patterns define precise spatial domains that will later determine the tissue distribution in the adult organism. How the genetic information is read during this process is a fundamental question in biology. Using the fruit fly *Drosophila melanogaster* as the biological model we applied a systems biology strategy combining analytical and numerical approaches with biological experimental data. Our research is focused in understanding the microscopic mechanisms responsible for the establishment of sharp borders between the protein spatial patterns, which are required for establishing the precise spatial domains. We developed a predictive reaction-diffusion model to describe the molecular mechanism of gene regulation(1). Using the Zero Eigenvalue Analysis(2), which establishes a set of sign compatible relations that must be satisfied if the reaction network exhibits multiple stationary states, we shown that the model ODE does exhibit bistability. We used a finite difference method to solve the model PDEs and simulated annealing to determine the model parameters that reproduce the experimental behavior. Our results indicate that space-dependent bistability plays a critical role in the flux of information from the microscopically stored genetic information to the macroscopic organization of cells and tissues.

(1) Lopes, F.J.P., et al. (2008). PLoS Comput. Biol., 4.

(2) Li HY (1998). Zeitschrift fr Naturforschung A. 53: 171-177.