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A HYBRID APPROACH TO STUDY CELLULAR DIFFERENTIATION PATTERNS

Serena Cristellon[1],
Gianluca Selvaggio[2] and Luca Marchetti*[2]

[1]Università degli Studi di Trento,
Department of Mathematics,
Via Sommarive, 14, Povo (Trento), Italy

[2]Fondazione The Microsoft Research,
University of Trento Centre for Computational and Systems Biology (COSBI),
Piazza Manifattura, 1, Rovereto

serena.cristellon@studenti.unitn.it, selvaggio@cosbi.eu,
marchetti@cosbi.eu (*corresponding author)

During cellular differentiation, from an original group of identical cells, tissues develop salt and pepper patterns, in which adjacent cells reach different fates. A significant role in this pattern formation is played by lateral inhibition; precisely, transmembrane proteins Delta and Notch on different adjacent cells are involved in this process. However, it is not fully understood how global patterns are generated, in tissue, from local cellular interactions, without needing external agents contribution. There are several models which explore how this mechanism works, either with quantitative ODE or Turing like diffusion-reaction equations [1, 2]. Here, our purpose is to introduce a hybrid approach for modeling this phenomenon. In particular, at the intracellular level, we will describe the problem in a continuous way, using ODE models, while for intercellular interactions we will take advantage of a parameter-free approach, adopting the logical formalism. The chosen hybrid strategy integrates different mathematical abstraction levels to describe distinct biological layers and their communications. Thus, it becomes crucial in dealing with problems for which we dont have a detailed knowledge of the processes involved. The hybrid approach herein employed allows us to combine the pros of different modeling techniques by overcoming the lack of quantitative information with a qualitative description that discretizes activation and inhibition processes, thus avoiding complexity.

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