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Titolo: Multiscale developments of the Cellular Potts Model applied to cell motion,
aggregation and scatter

Abstract

Multiscale problems are ubiquitous and fundamental in all biological 11 phenomena, which naturally emerge from the complex interaction between processes happening at various levels. Such a network of organization is often too intricate to be studied only with experimental techniques, which therefore need an increasing collaboration with applied mathematics. In last decades, a wide range of computational approaches have been developed to deal with biological problems, depending on the particular spatio-temporal scale of interest. However, most of them fall in two categories: continuous and discrete models, of which one of the most used is the Cellular Potts. The CPM is a cell-level, lattice-based, flexible technique, able to accurately identify and describe the phenomenological mechanisms involved in a biological process. In this thesis, we first give a brief overview of its biophysical bases and we discuss its main merits and limitations. We then turn to propose some innovative extensions, focusing on ways to integrate and interface the basic cell-level CPM with continuous approaches accurately modeling microscopic subcellular dynamics. The aim is to create a hybrid environment that is able to deal with the typical multiscale organization of biological development, where the behavior of the simulated individuals is realistically driven by the constant interplay and flux of information between the different scales, and not decided by quite strong a priori assumptions, that are commonly used in published CPM works. The proposed computational approach wants to be a framework for model building rather than a specific biological model: its flexibility is in fact tested and provided with several sample applications, that show a qualitative and quantitative agreement with the relative experimental data. We conclude the work by discussing further possible developments of the method.

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