Biological Lattice-Gas Cellular Automata

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Biological lattice-gas cellular automata (LGCA) can be viewed as models for collective behaviour emerging from microscopic migration and interaction processes of biological cells. Such LGCA are used to model the interplay of cells with each other and with their heterogeneous environment by describing interactions at a cell-based (microscopic) scale and facilitating both efficient simulation and theoretical analysis of emergent, tissue-scale (macroscopic) parameters [35]. Historically, LGCA have been introduced as models of gas and fluid flows, through implementing simplistic local collisions. Often, the overall macroscopic behaviour of the system can be approximated very well if averages over larger spatial scales are considered [57]. In a biological context, LGCA particles are interpreted as cells and cell migration is modelled by updating cell positions at each time step based on local cell interactions. Local cell interactions are described by problem-specific LGCA transition rules. These transition rules are different from the rules that have been used for modelling fluid flows. LGCA transition rules in models of cell migration, in general, do not assume energy or momentum conservation. Biological LGCA models can be classified as stochastic cellular automata with time-discrete, synchronous updates consisting of stochastic interaction and subsequent deterministic movement steps. The deterministic movement steps are alternated with stochastic interaction steps, in which processes affecting cell number, e.g., birth and death can be implemented. Implementing movement of individuals in traditional synchronous-update cellular automaton models is not straightforward, as one site in a lattice can typically only contain one individual, and consequently movement of individuals can cause collisions when two individuals want to move to the same empty site. In a lattice-gas model this problem is avoided by having separate channels for each direction of movement and imposing an exclusion principle. In addition, rest channels can be added for non-moving cells.

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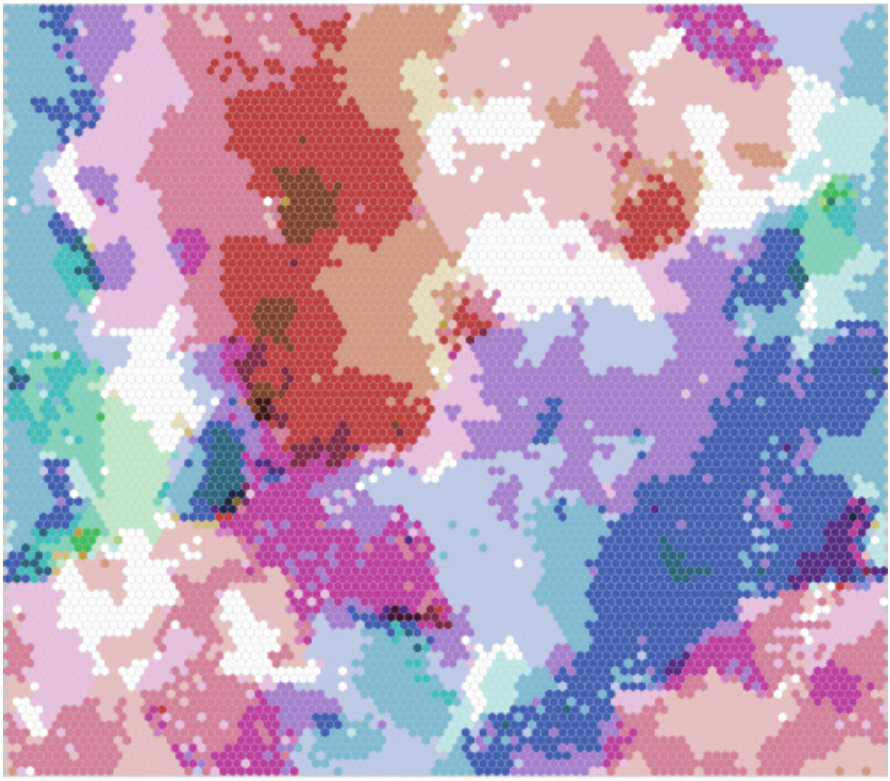
The LGCA idea has led to models for migration of individual cells during spatio-temporal pattern formation in microorganisms, cell cultures and developing organisms. The essential modelling idea is the definition of appropriate transition probabilities characterizing specific cell interactions. In particular, cell motion may be influenced by the interaction of cells with components of their immediate local surrounding through haptotaxis or differential adhesion, interaction with the extracellular matrix, contact guidance, contact inhibition, and processes that involve cellular responses to signals that are propagated over larger distances (e.g. chemotaxis). LGCA models have also been used to study emergent collective behaviour in cell swarming [27], angiogenesis [120] and Turing pattern formation. Furthermore, LGCA models have been suggested for various aspects of tumour growth [124]. In particular, simulations and analysis of appropriate LGCA models permit to characterize different growth and invasion scenarios [74, 73].



Clusters of alignment in a LGCA simulation. ©2015 Andreas Deutsch.
The figure is based on a LGCA that we have introduced as a model for random walkers with biologically motivated interactions favouring local alignment and leading to collective motion or swarming behaviour [27]. The degree of alignment is controlled by a sensitivity parameter, and a dynamical phase transition exhibiting spontaneous breaking of rotational symmetry occurs at a critical parameter value. The model has been analysed using non-equilibrium mean-field theory. Mean-field predictions have been derived that describe the phase transition as a function of sensitivity and density. Different colours encode different cell orientations. The figure indicates formation of alignment clusters.