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Mechanisms of pattern formation in biological systems caused by diffusion instability

Pattern formation in living systems including morphogenesis is one of the most challenging problems of theoretical biology. Starting from early seventies a number of models based on the idea of the so-called Turing instability [1] were suggested (one can find some examples in [2]). Turing instability is a type of diffusion instability when one of the eigenvalues of the linearized problem becomes positive in a certain non-zero range of wave vectors. This instability may be responsible for stationary nonhomogeneous pattern formation.

Another type of diffusion instability is the wave instability when a pair of complex conjugate eigenvalues acquires a positive real part in a certain range of wave vectors. Wave instability may be responsible for a lot of spatial-temporal patterns observed both in biological (for example, in bacterial colonies) and in chemical systems (Belousov-Zhabotinsky reaction in microemulsion [3]). While Turing instability can arise in a two-variable reaction-diffusion model, not less than three equations are necessary for the wave instability.

We obtain the conditions for both Turing and wave instabilities in a threevariable reaction diffusion model which follow from linear analysis and formulate qualitative properties of the system for each of the instabilities to occur. While for the Turing bifurcation the system should possess an autocatalytic variable which has a sufficiently small diffusion coefficient compared with the two others (it coincides with the condition for this bifurcation in a two-variable model), the conditions for the wave bifurcation are somewhat different. Autocatalysis is necessary but not sufficient. Namely, the sum of two terms on the main diagonal of the linearization matrix should be positive and the diffusion coefficient of the third variable should be sufficiently large. It is essential that the conditions for these two bifurcations do not contradict and both instabilities can take place simultaneously.

Numerical simulations of the modified Brusselator model support analytic results and demonstrate a variety of spatial-temporal patterns for different regions of the parametric space. Finally we discuss biological systems in which pattern formation may be caused by the above mechanisms.

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