

Bayesian approach to parameter identification of pattern formation models

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Abstract

Pattern formation in biological tissues plays an important role in the development of living organisms. Since the classical work of Alan Turing, a pre-eminent way of modelling has been through reaction-diffusion mechanisms. More recently, alternative models have been proposed, that link dynamics of diffusing molecular signals with tissue mechanics. In many experimental situations, only the limiting, stationary regime of the pattern formation process is observable, without knowledge of the transient behaviour or the initial state. The unstable nature of the underlying dynamics in all alternative models seriously complicates model and parameter identification, since small changes in the initial condition lead to distinct stationary patterns. To overcome this problem, the initial state of the model can be randomised. In the latter case, fixed values of the model parameters correspond to a family of patterns rather than a fixed stationary solution, and standard approaches to compare pattern data directly with model outputs, e.g., in the least squares sense, are not suitable. We approach this problem with a statistical approach for parameter identification using pattern data, the so-called Correlation Integral Likelihood (CIL) method, and test the proposed technique using different classes of pattern formation models.