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# Turing instability in reaction–diffusion models on complex networks

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## HIGHLIGHTS

- Turing instability in reaction–diffusion models on complex networks was discussed.
- Unstable regions of a constant steady state differed, depending on network topology.
- We obtained some theoretical results on the existence of the unstable region.

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## ABSTRACT

In this paper, the Turing instability in reaction–diffusion models defined on complex networks is studied. Here, we focus on three types of models which generate complex networks, i.e. the Erdős–Rényi, the Watts–Strogatz, and the threshold network models. From analysis of the Laplacian matrices of graphs generated by these models, we numerically reveal that stable and unstable regions of a homogeneous steady state on the parameter space of two diffusion coefficients completely differ, depending on the network architecture. In addition, we theoretically discuss the stable and unstable regions in the cases of regular enhanced ring lattices which include regular circles, and networks generated by the threshold network model when the number of vertices is large enough.



## 1. Introduction

We can observe various types of pattern phenomena in nature. In order to understand the pattern formation mechanisms of such phenomena, mathematical models have been proposed and analyzed from the viewpoint of both numerical and theoretical studies. Among these models, reaction–diffusion systems have attracted many researchers [1]. Though the systems which describe a local interaction and a long-range dispersal between chemical substances or biological species are rather simple, Turing stated that spatially inhomogeneous structures can be formed in a self-organized way under certain conditions [2]. Since then, a lot of studies on the reaction–diffusion systems have been reported. Turing considered the following system of partial differential equations:

$$\begin{aligned} \frac{\partial u}{\partial t} &= d_u \Delta u + f(u, v), \\ \frac{\partial v}{\partial t} &= d_v \Delta v + g(u, v), \end{aligned} \tag{1.1}$$

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where $u = u(t, x)$ and $v = v(t, x)$ indicate concentrations of chemical substances or population densities of biological species at time $t$ at position $x$, $d_u$ and $d_v$ mean respectively diffusion coefficients of $u$ and $v$, and the functions $f(u, v)$ and $g(u, v)$ express a local interaction between $u$ and $v$. In addition, Turing gave the following assumption on the reaction system of ordinary differential equations without diffusion terms

$$\begin{aligned} \frac{du}{dt} &= f(u, v), \\ \frac{dv}{dt} &= g(u, v). \end{aligned} \tag{1.2}$$

**Assumption.** The system (1.2) possesses an equilibrium point $(u, v) = (\overline{u}, \overline{v})$ and it is asymptotically stable.

In this framework, Turing derived a paradox that the equilibrium solution $(u, v) = (\overline{u}, \overline{v})$ in (1.1) with suitable boundary conditions can be destabilized in spite of adding the diffusion terms which possess a smoothing effect of spatial heterogeneity even though the equilibrium point $(u, v) = (\overline{u}, \overline{v})$ is stable in the sense of (1.2). This is well known as the diffusion-induced instability or the Turing instability. As a consequence of the Turing instability, (1.1) exhibits spatially inhomogeneous structures called Turing patterns. Therefore, the Turing instability is regarded as important for the onset of pattern formation on the reaction–diffusion systems.

However, since (1.1) is a system describing a local interaction and a dispersal between $u$ and $v$ on continuous media, it cannot represent an interaction on a spatially discrete environment, such as dynamics of metapopulation, cellular networks of biological morphogenesis and networks of diffusively coupled chemical reactors. Therefore, in order to treat such situations, studies on reaction–diffusion models defined on networks have proceeded [3–15]. So far, the Turing instability arising in reaction–diffusion models defined on networks with a small number of vertices has been investigated [3–6]. Recently, studies on Turing patterns formed on complex networks with a large number of vertices have proceeded [7–15]. In these papers, the differences between the classical Turing patterns on continuous media and network organized Turing patterns, and properties on Turing patterns on complex networks have been shown by numerical simulations, a theory of mean field approximation, and analytical techniques. The authors in Refs. [7–9,14] also discussed the Turing instability on networks with a large number of vertices in a somewhat general framework, which the Turing patterns are based on. (For example, see the Methods section in Ref. [7].) However, they do not mention the influence of network topology on the Turing instability. In other words, it is not clear whether the Turing instability on a complex network occurs or not when the network topology changes. In this study, considering reaction–diffusion models on complex networks with a large number of vertices, we investigate a relation between the Turing instability and network topology with a large number of vertices in detail by using the linear stability analysis. In particular, our interest is how network topology influences the Turing instability. Therefore, we focus on three types of models which generate typical networks, i.e. the Erdős–Rényi, the Watts–Strogatz, and the threshold network models. We emphasize that the Turing instability is an important concept as the onset of self-organized pattern formation. However, thorough studies focusing on the Turing instability in reaction–diffusion models on complex networks with many vertices are very few. Potential applications of reaction–diffusion models on networks were introduced in Refs. [7,9,10,16]. If we regard vertices as cells, the model describes cellular networks of early biological morphogenesis. When vertices are regarded as patchy habitats, it is a model describing population dynamics with an interaction on a patchy environment (ecological metapopulation). In order to understand self-organized phenomena with the network architecture, a theoretical approach using models defined on networks could be needed. As a first step, we discuss the Turing instability on complex networks in this paper.

This paper is organized as follows: in the next section, we formulate reaction–diffusion models defined on complex networks, which we discuss in this paper. Sections 3–5 are devoted to computer-aided analysis of the Turing instability in reaction–diffusion models on networks generated by the Erdős–Rényi, the Watts–Strogatz, and the threshold network models, respectively. We reveal that these analyses derive different results on the Turing instability of a homogeneous steady state, depending on network topology. In Section 6, we give theoretical results on the instability when the number of vertices is large enough. We complete this paper in Section 7, where concluding remarks and future works are listed.

## 2. Formulation of a reaction–diffusion model on a graph

As an analogy of the reaction–diffusion model on continuous media (1.1), we formulate a model on a graph with $N$ vertices. When there is no connection between any vertices, the dynamics on each vertex is described by a local interaction only as follows:

$$\begin{aligned} \frac{du_i}{dt} &= f(u_i, v_i), \\ \frac{dv_i}{dt} &= g(u_i, v_i), \end{aligned} \qquad (i = 1, 2, \ldots, N), \tag{2.1}$$

where a pair $(u_i, v_i) = (u_i(t), v_i(t))$ denotes some quantities on the $i$th vertex, such as population densities of biological species or concentrations of chemical substances. Note that the interaction functions $f$ and $g$ are the same on each vertex. As