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Review

# Pattern transitions in spatial epidemics: Mechanisms and emergent properties

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## Abstract

Infectious diseases are a threat to human health and a hindrance to societal development. Consequently, the spread of diseases in both time and space has been widely studied, revealing the different types of spatial patterns. Transitions between patterns are an emergent property in spatial epidemics that can serve as a potential trend indicator of disease spread. Despite the usefulness of such an indicator, attempts to systematize the topic of pattern transitions have been few and far between. We present a mini-review on pattern transitions in spatial epidemics, describing the types of transitions and their underlying mechanisms. We show that pattern transitions relate to the complexity of spatial epidemics by, for example, being accompanied with phenomena such as coherence resonance and cyclic evolution. The results presented herein provide valuable insights into disease prevention and control, and may even be applicable outside epidemiology, including other branches of medical science, ecology, quantitative finance, and elsewhere. © 2016 Elsevier B.V. All rights reserved.

*Keywords:* Reaction–diffusion equation; Cellular automata; Spatial heterogeneity; Seasonality and noise; Coherence resonance; Cyclic evolution

## 1. Introduction

Despite advances in their prevention and control, infectious diseases are still a threat to human health. In 2009, for example, influenza A(H1N1) outbreak in Mexico and spread throughout the world, ultimately reaching 214 countries and regions, and resulting in about 18,500 deaths [1]. In 2013, a new type of avian influenza, H7N9, appeared in

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Mainland China and subsequently caused considerable economic losses alongside public health risks [2]. In 2014, Ebola virus disease emerged in West Africa and infected more than 10,000 people [3,4]. Another new virus—Middle East Respiratory Syndrome coronavirus (MERS-CoV)—had emerged in 2012 and by mid 2015 caused 1,379 human infections with a death toll of 531 people from 26 countries [5]. A particularly instructive case of MERS-CoV outbreak happened in South Korea where 164 infections and 23 deaths were traced back to an individual traveling from the Middle East. These examples illustrate the dangers associated with infectious diseases and the origins of motivation for modeling their transmission dynamics.

Mathematical models have a long tradition in epidemiology and represent a useful tool for revealing the transmission dynamics of infectious diseases. Starting in 1760, Bernoulli was the first to investigate the effectiveness of smallpox vaccination by means of mathematical techniques [6]. In 1906, Hamer resorted to the law of mass action to find the causes of the repeated outbreaks of measles [7]. In 1911, a Nobel Prize winner Ronald Ross used a differential equation to describe the transmission of malaria between humans and mosquitoes [8]. In 1927, Kermack and McKendrick put forth a mathematical framework for compartmental models in epidemiology [9] that has been in use ever since. At about the same time, Reed and Frost developed a chain binomial model with the recognizable susceptible–infectious–recovered (SIR) structure, but their work remained unpublished until exposed by others [10].

If only temporal (as opposed to spatial) dynamics is considered, the basic reproduction number—defined as “the average number of secondary cases caused by an infectious individual in a completely susceptible population” [11]—is the key quantity for determining the fate of epidemics. When this number is less than unity, a pathogen goes extinct regardless of the initial conditions; otherwise, the pathogen persists and the number of infections increases through time [11–15]. Although studies on the temporal dynamics of diseases proved insightful, observations that pathogens (like substances) diffuse from high to low density regions of space enticed the development of spatially explicit models capable of discerning, for example, disease transmission hotspots. Incorporating space explicitly into epidemiological models revealed that a pathogen may go extinct even if the basic reproduction number is greater than unity [16]. Spatial dynamics occasionally induced chaos [17] and displayed various emergent properties [18]. The overwhelming conclusion was that the role of space in epidemic spread is non-negligible and therefore warrants further study of spatial dynamics in the context of disease transmission.

Spatially explicit models in epidemiology display two properties of interest: traveling wave solutions [19–22] and pattern formation [23–28]. Traveling waves characterize the transition between the different equilibrium states, whereas pattern formation is representative of the distribution of individuals in both time and space. Because we are interested primarily in the distribution and the transmission of infectious diseases in space, this review focuses on spatial patterns, the underlying mechanisms, and related emergent properties.

### 1.1. Epidemiological models without spatial dynamics

A population with an active pathogenic agent is often divided into three compartments. Healthy individuals are susceptible to an infection ( $S$ ), infectious individuals carry and transmit the pathogen regardless of whether they exhibit symptoms ( $I$ ), and recovered individuals remain unaffected by the disease ( $R$ ). These recovered individuals are assumed to either have natural immunity or immunity attained by recuperating from the infection [11–13]. Sometimes individuals lost to the disease are mixed with those who have recovered in which case  $R$  stands for removed. Based on the described compartmentalization, the classical Susceptible–Infectious–Removed (SIR) model without spatial dynamics has the following form:

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI, \\ \frac{dI}{dt} &= \beta SI - \gamma I, \\ \frac{dR}{dt} &= \gamma I,\end{aligned}\tag{1}$$

where  $\beta$  and  $\gamma$  are infection and recovery (removal) rates, respectively. The basic reproductive number of system (1) is  $R_0 = \beta S_0 / \gamma$ , where  $S_0$  is the initial number of susceptible individuals. If  $R_0 < 1$ , the number of infectious individuals is a decreasing function of time and the disease disappears after a while; otherwise, the disease eventually outbreaks.

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