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Modeling dual-scale epidemic dynamics on complex networks with reaction diffusion processes

Key words: Worldwide trade networks, Foodborne diseases, Scale-free networks, Mean-field analysis

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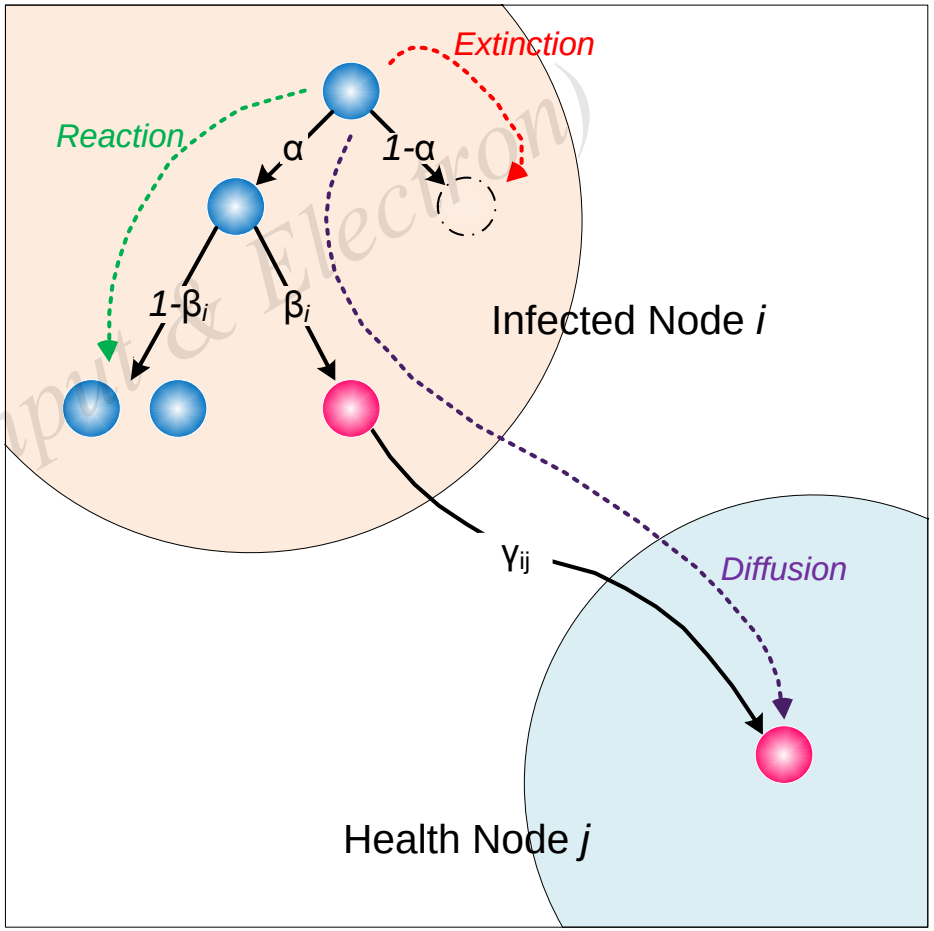
Motivation

- **Severe foodborne diseases:** Recent outbreak of severe foodborne diseases in Europe and the United States poses a new challenge to the existing analysis approaches.
- **Disadvantages of existing methods:** (1) The classical epidemic models cannot handle indirect interactions between humans and vectors; (2) The mechanisms are completely different between proliferation within nodes and diffusion among networks.
- **Our method is aimed to:** (1) adopt reaction-diffusion processes to model complex epidemic dynamics, (2) model both intra-proliferation and inter-diffusion dynamics, and (3) evaluate the importance of countries in worldwide epidemics.

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Framework of our method

Illustration of the model:



The mathematical solution of the average number of outgoing pathogens:

$$D = \varepsilon + h'(1)\cdot\varepsilon + h'(h(1))\cdot\varepsilon + \cdots$$
$$= \varepsilon(1 + h'(1) + (h'(1))^2 + \cdots)$$
$$= \frac{\varepsilon}{1 - h'(1)} = \frac{\alpha - \alpha(1-\beta_i)}{1 - s\alpha(1-\beta_i)},$$

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Summary

- **Motivation:** Design an effective model for analyzing dual-scale epidemic processes.
- **Methodology:** We adopt reaction-diffusion processes to model both intra-proliferation and inter-diffusion dynamics, and provide a mathematical solution to the model with mean-field analysis.
- **Performance:** Simulations performed on real data sets from FAO showed the effectiveness of our model.

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