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Law of large numbers for the SIR model with random vertex weights on Erdős–Rényi graph

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HIGHLIGHTS

- We study the SIR model with random vertex weights on Erdös–Rényi graph.
- We give the law of large numbers of the model.
- Our result extends classic theory of SIR on the complete graph.
- Our result is consistent with the intuitive mean-field idea.

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ABSTRACT

In this paper we are concerned with the SIR model with random vertex weights on Erdős–Rényi graph $G(n, p)$. The Erdős–Rényi graph $G(n, p)$ is generated from the complete graph C_n with n vertices through independently deleting each edge with probability $(1 - p)$. We assign i. i. d. copies of a positive r. v. ρ on each vertex as the vertex weights. For the SIR model, each vertex is in one of the three states 'susceptible', 'infective' and 'removed'. An infective vertex infects a given susceptible neighbor at rate proportional to the production of the weights of these two vertices. An infective vertex becomes removed at a constant rate. A removed vertex will never be infected again. We assume that at $t = 0$ there is no removed vertex and the number of infective vertices follows a Bernoulli distribution $B(n, \theta)$. Our main result is a law of large numbers of the model. We give two deterministic functions $H_S(\psi_t), H_V(\psi_t)$ for $t \geq 0$ and show that for any $t \geq 0$, $H_S(\psi_t)$ is the limit proportion of susceptible vertices and $H_V(\psi_t)$ is the limit of the mean capability of an infective vertex to infect a given susceptible neighbor at moment t as n grows to infinity.

1. Introduction

In this paper we are concerned with the SIR (Susceptible–Infective–Removed) model with random vertex weights on Erdős–Rényi graph $G(n, p)$. First we introduce some notations. For each integer $n \geq 1$, we denote by A_n the set $\{0, 1, 2, \ldots, n - 1\}$. We consider the n elements in A_n as n vertices and assume that any two vertices are connected by an edge. As a result, we obtain a complete graph with n vertices, which we denote as C_n. Let $p \in (0, 1)$, then we can obtain a random graph G_n through the procedure that each edge on C_n is independently deleted with probability $1-p$, in other words, remained with probability p. The graph G_n with vertices set A_n and edges which are remained is called the Erdős–Rényi graph with parameter $G(n, p)$ (see Chapter 4 of [1]). For any $0 \leq i < j \leq n - 1$, we denote by $i \sim j$ when the edge connecting i and j on C_n is remained during the procedure to generate G_n. That is to say, $i \sim j$ when and only when i is a neighbor of j on the graph G_n.

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Let ρ be a positive random variable such that $P(\rho > 0) > 0$ and $P(0 \leq \rho \leq M_1) = 1$ for some $M_1 < +\infty$ while $\{\rho(i)\}_{0\leq i<+\infty}$ are i.i.d. copies of ρ which are independent of $\{G_n\}_{n\geq 1}$, then the SIR model $\{X_t\}_{t\geq 0}$ on G_n with vertex weights $\{\rho(i)\}_{0\leq i\leq n-1}$ is a continuous-time Markov process with state space $\{0, 1, -1\}^{A_n}$. That is to say, at each moment $t \geq 0$, there is a spin on each vertex on G_n with value taking from $\{0, 1, -1\}$. For each $i \in A_n$ and $t \geq 0$, we denote by $X_t(i)$ the value of the spin on i at moment t, then $\{X_t\}_{t\geq 0}$ evolves according to the following rules. If $X_t(i) = -1$, then i is frozen in state -1 after the moment t. That is to say, $X_s(i) = -1$ for any $s \geq t$. If $X_t(i) = 0$, then

$$P\big(X_{t+\Delta t}(i) = 1\big|X_s, s \leq t\big) = \Big(\frac{\lambda}{n}\sum_{j=0}^{n-1}\rho(i)\rho(j)\mathbf{1}_{\{j\sim i, X_t(j)=1\}}\Big)\Delta t + o(\Delta t)$$

and

$$P\big(X_{t+\Delta t}(i) = 0\big|X_s, s \leq t\big) = 1 - P\big(X_{t+\Delta t}(i) = 1\big|X_s, s \leq t\big) + o(\Delta t)$$

where $\lambda > 0$ is a positive parameter called the infection rate and $\mathbf{1}_A$ is the indicator function of the random event A. If $X_t(i) = 1$, then

$$P\big(X_{t+\Delta t}(i) = -1\big|X_s, s \leq t\big) = \Delta t + o(\Delta t) = 1 - P\big(X_{t+\Delta t}(i) = 1\big|X_s, s \leq t\big) + o(\Delta_t).$$

Note that there exists an unique continuous-time Markov process satisfying the above transition rates functions according to classic probability theory (see Section one of [2]).

Intuitively, $\{X_t\}_{t\geq 0}$ describes the spread of an epidemic on G_n. Vertices in state 0 are susceptible which are healthy and may be infected by the epidemic. Vertices in state 1 are infective that can infect susceptible neighbors. Vertices in state -1 are removed which will never be infected again. An infective vertex waits for an exponential time with rate one to become removed while a susceptible vertex is infected by an infective neighbor at rate proportional to the production of the vertex weights on these two vertices. Note that here we say two vertices are neighbors when the edge connecting them is remained during the procedure to generate G_n.

For any $t \geq 0$, we define

$$S_t = \sum_{j=0}^{n-1}\mathbf{1}_{\{X_t(j)=0\}} \tag{1.1}$$

as the number of susceptible vertices at moment t and

$$V_t = \sum_{j=0}^{n-1}\rho(j)\mathbf{1}_{\{X_t(j)=1\}} \tag{1.2}$$

as the total capability of the infective vertices to infect neighbors at moment t. We write X_t, S_t and V_t as $X_t^{(n)}$, $S_t^{(n)}$ and $V_t^{(n)}$ when we need to point out that process is on G_n. For the moment $t = 0$, we assume that $\{X_0^{(n)}(i)\}_{i=0}^{n-1}$ are i.i.d. such that

$$P(X_0^{(n)}(0) = 1) = \theta = 1 - P(X_0^{(n)}(0) = 0) \tag{1.3}$$

for some $\theta \in [0, 1]$. Under this assumption, we obtain the law of large numbers for $\big(\frac{S_t^{(n)}}{n}, \frac{V_t^{(n)}}{n}\big)$ as n grows to infinity at any moment t. For mathematical details, see the next section.

Readers may wonder what will occur when at $t = 0$ there is only one infective vertex. We study a similar epidemic model under this assumption in [3]. According to a similar analysis with that in [3], it can be shown that if there is only one infective vertex at $t = 0$, then the epidemic 'outbreaks' when and only when $\lambda > \lambda_c = \frac{1}{p\mathrm{E}\rho^2}$ (see the main theorem of [3] for the accurate meaning of 'outbreak'). Actually we think this is an important result but we do not want to repeat in this paper lot of similar calculation with that in [3], so we only give a simple comment here. Readers interested with mathematical details can see [3].

When $\rho = p = 1$, then our model reduces to the classical SIR model on complete graphs. According to the theory of density dependent population model introduced in Section 11 of [4], under assumption (1.3), $(\frac{S_t^{(n)}}{n}, \frac{V_t^{(n)}}{n})$ converges in probability to the solution (s_t, v_t) of the following ODE as $n \to +\infty$.

$$\begin{cases}\frac{d}{dt}s_t = -\lambda s_t v_t, \\ \frac{d}{dt}v_t = \lambda s_t v_t - v_t, \\ s_0 = 1-\theta, \\ v_0 = \theta.\end{cases} \tag{1.4}$$

Our main result given in the next section can be seen as an extension of the above conclusion. Phase transition occurs for ODE (1.4). Conditioned on v_0 is very small, v_t decreases to 0 exponentially when $\lambda < 1$ while increases exponentially at first when $\lambda > 1$. Figs. 1–4 in the Appendix give simulation results for v_t, where $t \in [0, 10]$, $v_0 = 0.001$ and $\lambda = 0.5, 0.99, 1.01, 2$ respectively.