

# A New Approach to Pair Approximation Method for Spatial Model in Ecology

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*Abstract:* - A mathematical model using either mean-field approximation or pair approximation has both advantage and limitation. Mean-field approximation is suitable for describing behaviors of a large system; however, it neglects the scale of individual interaction. On the other hand, pair approximation is suitable for studying local interaction especially singles and pairs; however, the mathematical formulas are still limited. Thus, choosing the right model for the right purpose is recommended. The objective of this paper is to develop the techniques of pair approximation by using probability averaged value based on probability distribution; for example, multinomial distribution and Poisson distribution. These extended formulas are suitable for a model composed of individuals whose event rates are additionally affected by their nearby neighbor. Finally, we apply these tools to a simple SIS epidemic model.

*Key-Words:* - Multinomial distribution, Poisson distribution, Pair approximation, Spatial interaction, Lattice model, Ecology, Epidemiology.

## 1 Introduction

Ecology, derived from Greek, is the study dealing with the interaction ships between organisms and their environment, including the interaction between each other [1]. Mathematical theories have been contributed successfully to all fields of ecology. Among them, population dynamics has the longest history. The population of each species is usually described by concentration that varies in space and time. The real-world phenomenon concerning with the surprising time scales are studied in [2]-[5]. However, in this paper, we mainly focus on spatial model. In the early models, interactions were based on the mass-action law. In other word, the spatial interaction neither exists nor plays an important role. Consequently, the model is typically represented by ordinary differential equations or mean-field model.

In recent years, the effect of spatial structure is frequently taken into account in many ecological interactions such as predation, resource competition, parasitism, and epidemics [6]. Together with sufficient accumulation of mathematical knowledge, new mathematical methods are crystallized. Pair-wise model was first used to explain population dynamics by Matsuda et al. [7] in 1992. His model is composed of an ordinary differential equation where the global and the local densities are the state variables. In this paper, we call his method the

ordinary pair approximation (OPA). Since then, the Japanese researchers have continuously published theoretical results and applications in biological phenomena [8]-[14]. On the other side of the world, Rand, however, establishes a slightly different approach [15]. He derives master equations where the number of sites, the number of pairs, the number of triples, and the number of the paths greater than three are the state variables. Obviously, there is an infinite hierarchy of equations. Thus the truncation of higher order terms is really in need. That is a reason why a moment closure approximation has been developed. Then correlation equations are finally obtained. Pair approximation, the first order of moment closure approximation, has a vast potential for applications because the interactions among each other is usually considered. It has provided an attractive framework for studying epidemiology [16]-[20], ecology [21]-[23], and evolution [24], [25].

In order to contribute theoretical results precisely and understandably, we introduce some notations, definitions, and concepts required throughout this paper in section 2. In section 3, we provide the formulation of pair approximation by using new approach (NPA). Here, the results is the extended version of [26]. Next we apply the NPA to a simple SIS model in section 4. Finally, we discuss the results and draw conclusion.

## 2 Preliminaries

In this section we introduce some useful notations, definitions, and concepts required for this work.

### 2.1 Notations and Definitions

Under a given configuration  $\underline{\sigma} = (\sigma_k)$  where  $k \in \{x, e\}$ , the following notations are defined.

- $\sigma_x$  means the state of the site or the individual  $x$ ,
- $\sigma_e$  means the state of the pair or the edge  $e$ ,
- $\sigma_x = i$  means that the state of the individual  $x$  is  $i$ ,
- $\sigma_e = ij$  means that one end of the edge  $e$  is in state  $i$ ,  $e_i$ , while the other is in state  $j$ ,  $e_j$ ,
- $[i], [ij], [ijk]$  are the number of sites, edges, and triples in state  $i$ ,  $ij$ , and  $ijk$ , respectively,
- $[l]_{l:m}$  means the number of site  $x$  which are in state  $l$  and have  $Q_x(l) = m$ ,
- $Q_x(i)$  is the number of neighbors of the sites  $x$  which are in state  $i$ ,
- $Q_x$  is the number of neighbors of the sites  $x$ ,
- $Q_{e_j}(i)$  is the number of neighbors of the sites  $e_j$  which are in state  $i$ ,
- $\langle Z_x \rangle_{\sigma_x=i}$  is the average of quantity  $Z_x$  over all individuals  $x$  which are in state  $i$ ,
- $\langle Z_{e_i} \rangle_{\sigma_e=ij}$  is the average of quantity  $Z_{e_i}$  over all edges  $e$  which are in state  $ij$ ,
- $\langle Q_x(i) \rangle_{\sigma_x=j}$  is the average value of the number of  $i$ -state neighbors of a  $j$ -state site,
- $\langle Q_x(i) \rangle_{l:m}$  means the average of quantities  $Q_x(i)$  over subsets of the population when  $Q_x(l) = m$ ,
- $\langle Q_{e_j}(i) \rangle_{\sigma_e=jk}$  is the average value of the number of  $i$ -state neighbors of a  $j$ -state site in a  $jk$ -state edge,
- $Q$  is the average number of neighbors,
- $N$  is the total population size,
- $q_i$  equals  $[i]/N$ , and
- $q_{ij}$  equals  $[ij]/Q[j]$ .

In this framework, space is represented by a network of sites. Each site can either be occupied by an individual or remains as an empty site that is still available for an individual to occupy. Two sites are neighbors when they regularly interact with each other. Joining these two neighboring sites performs an edge or pair. A line is used for this interaction. The sites, edges, and states are visualized in Fig. 1.

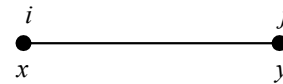


Fig. 1  $\sigma_x = i, \sigma_y = j, \sigma_e = ij$ .

In addition, the order of singleton, pair, and triple is one, two, and three, respectively. We also show how to count singleton, pair, and triples in Fig. 2. There are 11 sites, representing state  $I$  6 sites and state  $S$  5 sites. More importantly, the counting direction is considered.

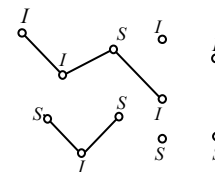


Fig. 2  $[I] = 6, [S] = 5, [IS] = [SI] = 5, [II] = 2, [SIS] = 2$ .

This idea also applies to quadruple and so on.

### 2.2 Master and Correlation Equations

Let  $f$  be a real-valued function of the state of the network at time  $t$ , which can be approximated as continuous. The equation  $f$  is derived by summing over all events in the population which affect  $f$  and the total change produced by those events is

$$\frac{df}{dt} = \sum_{\varepsilon \in \text{events}} r(\varepsilon) \Delta f_{\varepsilon}$$

where  $r(\varepsilon)$  is the rate of event  $\varepsilon$  and  $\Delta f_{\varepsilon}$  is the change produced in  $f$  by event  $\varepsilon$ . It is called the master equation.

Our correlations are microcorrelations which can be measured on the scale of the interactions of individuals. After approximating higher order terms in master equations, we obtain a system of ordinary differential equation which composed of density of lower order terms, known as correlation equations. Moreover, the approximation technique is called the moment closure approximation. For instant, pair approximation, the first order of moment closure

approximation, truncates triples and higher order terms as functions of singletons and pairs only.

### 2.3 Probability Distribution

Through out this paper, we focus only on two well-known probability distributions that are multinomial distribution and Poisson distribution.

#### 2.3.1 Multinomial Distribution

The multinomial distribution is an extension of the binomial distribution. In general, a population is supposed to contains items of  $k$  different types with  $k \geq 2$ , and the proportion of items in the population that are of type  $i$  is  $p_i$  when  $i=1, \dots, k$ . It is also assumed that  $p_i > 0$  for  $i=1, \dots, k$  and  $\sum_{i=1}^k p_i = 1$ . Let  $M_i$  denote the number of selected items that are of type  $i$  when  $i=1, \dots, k$ .

If  $M = (M_1, \dots, M_k)$  has a multinomial distribution together with parameters  $n$  and  $p = (p_1, \dots, p_k)$ , then the following probability can be calculated by using this formula

$$\Pr(M_1 = m_1, \dots, M_k = m_k) = \binom{n}{m_1, \dots, m_k} p_1^{m_1} \dots p_k^{m_k}$$

where

$$\binom{n}{m_1, \dots, m_k} = \frac{n!}{m_1! \dots m_k!}.$$

Moreover,  $E(M_i) = np_i$  and  $Var(M_i) = np_i(1 - p_i)$  for  $i=1, \dots, k$ .

#### 2.3.2 Poisson Distribution

It is said that  $P$  has a Poisson distribution with parameter  $\lambda$  where  $\lambda > 0$  if  $P$  has a discrete distribution with probability function

$$f(m) = \Pr(P = m) = \begin{cases} \frac{e^{-\lambda} \lambda^m}{m!} & ; m = 0, 1, \dots \\ 0 & ; \text{otherwise} \end{cases}$$

In fact the value of both mean and variance is  $\lambda$ .

## 3 Formulation of Pair Approximation

In general, a population network can be constructed over a regular  $d$ -dimensional lattice model whose site can be occupied by an individual carrying only one of many different states. An unoccupied or empty site, sometimes, is considered. Each site also interacts with other nearby sites.

In our system, there are  $n$  individuals carrying  $k$  different types of population with  $k \geq 2$ . Each of them has  $Q$  neighbors. The following symbols can be noticed through out this paper. For  $i=1, \dots, k$ ,  $M_i$ ,

$m_i$ , and  $p_i$  mean each type of the population, the number of each type, and the proportion of each type in the population, respectively.

Before contributing theoretical results, we need to set up three useful assumptions. The first two assumptions imply that  $Q_{e_i}(k)$  and  $Q_{e_j}(k)$  are independent when  $\sigma e = ij$  while the last one implies that the space average and the probabilistic average are identical.

**Assumption 1** For all  $k$ ,  $Q_x(k)$  and  $Q_y(k)$  are independent when  $x \neq y$  because there is no triangle and no multiple connections.

#### Assumption 2

$$\Pr(Q_{e_i}(k) = q) = \Pr(Q_x(k) = q | Q_x(j) \geq 1).$$

#### Assumption 3 (Large $N$ hypothesis)

Where the total system size  $N$  is large ( $N \rightarrow \infty$ ), we can identify the configuration averages  $\langle Z_x \rangle_{\sigma x=i}$  and  $\langle Z_e \rangle_{\sigma e=ij}$ , respectively with the  $P$ -expectations  $E_P(Z_x)$  and  $E_{P_i}(Z_{e_i})$ .

Consequently, we can present a new way to approximate some special higher order terms that the OPA cannot do in the following theorems.

**Assumption 4** Assume that  $Q_x \equiv Q$  is independent of  $x$  and  $Q_x(i)$  with  $\sigma x = j$  is multinomially distributed with parameters  $Q$  and  $p_i$  where  $p_i = q_{i|j}$ .

**Theorem 1**  $\langle Q_x(i) \rangle_{\sigma x=j} = \frac{[ij]}{[j]}$ .

#### Theorem 2

$$\langle Q_x(i_1) Q_x(i_2) \rangle_{\sigma x=j} = \begin{cases} Q q_{i_1|j} + \frac{Q!}{(Q-2)!} q_{i_1|j}^2 & ; i_1 = i_2 \\ \frac{Q!}{(Q-2)!} q_{i_1|j} q_{i_2|j} & ; i_1 \neq i_2 \end{cases}$$

**Theorem 3**  $\langle Q_{e_j}(l) \rangle_{\sigma e=ij} = \begin{cases} (Q-1) q_{l|j} & ; l \neq i \\ (Q-1) q_{l|j} + 1 & ; l = i \end{cases}$ .

#### Theorem 4

$$\langle Q_{e_j}(l_1) Q_{e_j}(l_2) \rangle_{\sigma e=ij} = \begin{cases} (Q-1) q_{l_1|j} + \frac{(Q-1)!}{(Q-3)!} q_{l_1|j}^2 & ; l_1 = l_2 \\ \frac{(Q-1)!}{(Q-3)!} q_{l_1|j} q_{l_2|j} & ; l_1 \neq l_2 \end{cases}$$

These theorems have already been proved in [25], [26]. According to this approach, we now can create more formulas for pair approximation by changing probability distribution from multinomial distribution to Poisson distribution. Before more new theoretical results can be obtained, we have to neglect Assumption 4 and consider the following assumptions instead.

**Assumption 5** Assume that  $Q_x(i)$  with  $\sigma x = j$  is Poisson distributed with parameter  $\lambda = \frac{[ij]}{[j]}$  or Poisson( $\lambda$ ).

Thus,  $\Pr(Q_x(i) = m | \sigma x = j) = \frac{e^{-\lambda} \lambda^m}{m!}$  for  $m = 0, 1, \dots$

The following lemma is a consequence of this assumption.

**Lemma 1**, Assume that  $Q_x(i)$  and  $Q_x(l)$  with  $\sigma x = j$  are following Poisson( $\lambda$ ) and Poisson( $\mu$ ), respectively where  $\lambda = \frac{[ij]}{[j]}$ ,  $\mu = \frac{[lj]}{[j]}$ , and  $l \neq i$ .

Therefore,

$$\Pr(Q_x(i) = n | Q_x(l) = m, \sigma x = j) = \frac{e^{-\lambda} \lambda^n}{n!} \text{ for } n = 0, 1, \dots$$

**Proof**

$$\begin{aligned} & \Pr(Q_x(i) = n | Q_x(l) = m, \sigma x = j) \\ &= \frac{\Pr(Q_x(i) = n, Q_x(l) = m | \sigma x = j)}{\Pr(Q_x(l) = m | \sigma x = j)} \\ &= \frac{\Pr(Q_x(i) = n | \sigma x = j) \Pr(Q_x(l) = m | \sigma x = j)}{\Pr(Q_x(l) = m | \sigma x = j)} \\ &= \Pr(Q_x(i) = n | \sigma x = j) \\ &= \frac{e^{-\lambda} \lambda^n}{n!} \end{aligned}$$

This lemma provides the formula to calculate the conditional probability.

**Lemma 2** Assume that  $Q_x(i)$  with  $\sigma x = j$  is following Poisson( $\lambda$ ) where  $\lambda = \frac{[ij]}{[j]}$ . Thus

$$[l]_{i:m} = \frac{e^{-\lambda} \lambda^m}{m!} [l].$$

**Proof**

$$\begin{aligned} [l]_{i:m} &= \text{count of } \{x : Q_x(i) = m, \sigma x = l\} \\ &= \Pr(Q_x(i) = m | \sigma x = l) [l] \\ &= \frac{e^{-\lambda} \lambda^m}{m!} [l] \end{aligned}$$

**Lemma 3** Assume that  $Q_x(i_1), Q_x(i_2), \dots, Q_x(i_k)$  with  $\sigma x = j$  are following Poisson( $\lambda_1$ ), Poisson( $\lambda_2$ ), ..., Poisson( $\lambda_k$ ), respectively where  $\lambda_n = \frac{[i_n j]}{[j]}$  for  $n = 1, \dots, k$ . Then

$$[l]_{i_1:m_1, \dots, i_k:m_k} = \frac{\lambda_1^{m_1} \lambda_2^{m_2} \dots \lambda_k^{m_k}}{m_1! m_2! \dots m_k!} e^{-(\lambda_1 + \lambda_2 + \dots + \lambda_k)} [l].$$

**Proof**

$$\begin{aligned} & [l]_{i_1:m_1, \dots, i_k:m_k} \\ &= \text{count of } \{x : Q_x(i_1) = m_1, \dots, Q_x(i_k) = m_k, \sigma x = l\} \\ &= \Pr(Q_x(i_1) = m_1, \dots, Q_x(i_k) = m_k | \sigma x = l) [l] \\ &= \frac{\lambda_1^{m_1} \lambda_2^{m_2} \dots \lambda_k^{m_k}}{m_1! m_2! \dots m_k!} e^{-(\lambda_1 + \lambda_2 + \dots + \lambda_k)} [l] \end{aligned}$$

This lemma is an extension of the previous lemma. These lemmas provide the formula to calculate the following probability.

**Lemma 4** Assume that  $Q_x(i)$  and  $Q_x(l)$  with  $\sigma x = j$  are following Poisson( $\lambda$ ) and Poisson( $\mu$ ), respectively, where  $\lambda = \frac{[ij]}{[j]}$  and  $\mu = \frac{[lj]}{[j]}$ . Therefore,

$$\Pr(Q_{e_j}(l) = m | \sigma e = ij) = \begin{cases} \frac{e^{-\mu} \mu^m}{m!} & ; l \neq i \\ \frac{e^{-\mu} \mu^{m-1}}{(m-1)!} & ; l = i \end{cases}$$

**Proof**

$$\Pr(Q_{e_j}(l) = m | \sigma e = ij) = \frac{[j]_{l:m} \langle Q_x(i) \rangle_{l:m}}{[j] \langle Q_x(i) \rangle_{\sigma x = j}}$$

In case that  $l \neq i$ ,

$$\begin{aligned} & \Pr(Q_{e_j}(l) = m | \sigma e = ij) \\ &= \frac{[j]_{l:m} \sum_{k=1}^{\infty} k \Pr(Q_x(i) = k | Q_x(l) = m, \sigma x = j)}{[j] \sum_{k=1}^{\infty} k \Pr(Q_x(i) = k | \sigma x = j)} \\ &= \frac{e^{-\mu} \mu^m}{m!} \end{aligned}$$

In case that  $l = i$ ,

$$\begin{aligned} & \Pr(Q_{e_j}(l) = m | \sigma e = ij) \\ &= \frac{[j]_{l:m} m}{[j] \sum_{k=1}^{\infty} k \Pr(Q_x(l) = k | \sigma x = j)} \\ &= \frac{e^{-\mu} \mu^{m-1}}{(m-1)!} \end{aligned}$$

**Lemma 5** Assume that  $Q_x(l_1)$  and  $Q_x(l_2)$  with  $\sigma x = j$  are following Poisson( $\mu_1$ ) and Poisson( $\mu_2$ ), respectively where  $\mu_1 = \frac{[l_1 j]}{[j]}$  and  $\mu_2 = \frac{[l_2 j]}{[j]}$ . Thus,

$\Pr(Q_{e_j}(l_1) = m, Q_{e_j}(l_2) = n | \sigma e = ij)$  equals one of the following values:

1. 0 when  $l_1 = l_2$  but  $m \neq n$ .
2.  $\Pr(Q_{e_j}(l_1) = m | \sigma e = ij)$  when  $l_1 = l_2$  and  $m = n$ .
3.  $\frac{e^{-(\mu_1 + \mu_2)} \mu_1^{m-1} \mu_2^n}{(m-1)! n!}$  when  $l_1 \neq l_2$  and  $l_1 = i$ .  
For the case  $l_2 = i$ , swapping  $m$  and  $n$ .
4.  $\frac{e^{-(\mu_1 + \mu_2)} \mu_1^m \mu_2^n}{m! n!}$  when  $l_1 \neq l_2$  and both state  $l_1$  and  $l_2$  are not as same as state  $i$ .

**Proof**

(1-2) obviously follow from the probability definition.

(3-4) is similar to the previous lemma.

**Lemma 6** Assume that the state  $l_1, \dots, l_k$  are different and  $Q_x(l_1), \dots, Q_x(l_k)$  with  $\sigma x = j$  are following Poisson( $\mu_1$ ), ..., Poisson( $\mu_k$ ), respectively where  $\mu_n = \frac{[l_n j]}{[j]}$  for  $n = 1, \dots, k$ . Therefore, the probability

$\Pr(Q_{e_j}(l_1) = m_1, \dots, Q_{e_j}(l_k) = m_k | \sigma e = ij)$  equals one of the following values:

1.  $\frac{e^{-(\mu_1 + \dots + \mu_k)} \mu_1^{m_1} \dots \mu_k^{m_k}}{m_1! \dots m_k!}$  when none of state  $l_1, \dots, l_k$  equal  $i$ .
2.  $\frac{e^{-(\mu_1 + \dots + \mu_k)} \mu_1^{m_1} \dots \mu_r^{m_r-1} \dots \mu_k^{m_k}}{m_1! \dots (m_r - 1)! \dots m_k!}$  when  $l_r = i$ .

**Proof**

By mathematical induction.

The following two theorems are concerned with calculating averages.

**Theorem 5** Assume that  $Q_x(l)$  with  $\sigma x = j$  is following Poisson( $\mu$ ) where  $\mu = \frac{[l j]}{[j]}$ . Then

$$\langle Q_{e_j}(l) \rangle_{\sigma e = ij} = \begin{cases} \mu & ; l \neq i \\ \mu + 1 & ; l = i \end{cases}$$

**Proof**

$$\langle Q_{e_j}(l) \rangle_{\sigma e = ij} = \sum_{k=1}^{\infty} k \Pr(Q_{e_j}(l) = k | \sigma e = ij)$$

If  $l \neq i$ , using Lemma 4 and Taylor series expansion

$$\langle Q_{e_j}(l) \rangle_{\sigma e = ij} = \mu.$$

If  $l = i$ , using Lemma 4 and the fact that

$$\sum_{k=1}^{\infty} \frac{k}{(k-1)!} \mu^{k-1} = \mu e^{\mu} + e^{\mu},$$

$$\langle Q_{e_j}(l) \rangle_{\sigma e = ij} = \mu + 1.$$

**Theorem 6** For both  $l_1$  and  $l_2 \neq i$ , assume that  $Q_x(l_1)$  and  $Q_x(l_2)$  with  $\sigma x = j$  are following Poisson( $\mu_1$ ) and Poisson( $\mu_2$ ), respectively where

$\mu_n = \frac{[l_n j]}{[j]}$ . Consequently,

$$\langle Q_{e_j}(l_1) Q_{e_j}(l_2) \rangle_{\sigma e = ij} = \begin{cases} \mu_1 \mu_2 & ; l_1 \neq l_2 \\ \mu_1 (\mu_1 + 1) & ; l_1 = l_2 \end{cases}$$

**Proof**

$$\begin{aligned} & \langle Q_{e_j}(l_1) Q_{e_j}(l_2) \rangle_{\sigma e = ij} \\ &= \sum_{m=1}^{\infty} \sum_{n=1}^{\infty} mn \Pr(Q_{e_j}(l_1) = m, Q_{e_j}(l_2) = n | \sigma e = ij). \end{aligned}$$

For  $l_1 \neq l_2$ , using Lemma 5 and Taylor series expansion,

$$\langle Q_{e_j}(l_1) Q_{e_j}(l_2) \rangle_{\sigma e = ij} = \mu_1 \mu_2.$$

For  $l_1 = l_2$ , using Lemma 2 and the fact that

$$\sum_{m=1}^{\infty} \frac{m}{(m-1)!} \mu^m = \mu_1 e^{\mu} + \mu_2^2 e^{\mu},$$

$$\langle Q_{e_j}(l_1) Q_{e_j}(l_2) \rangle_{\sigma e = ij} = \mu_1 (\mu_1 + 1).$$

After developing NPA, we need to see how the average calculation works and check its validity. The SIS epidemic model is a relatively simple problem to begin with.

### 4 The SIS Spatial Model

The simple SIS epidemic model is a good example to see the usefulness of NPA. As usual, the simple SIS model can be separated into two possible states, that is,  $S$  (a susceptible individual) and  $I$  (an infective individual). The state of each site and edge can evolve over time according to two major types of events such as infection and recovery. Clearly, infection is an edge event. It changes the state  $\sigma e = SI$  of the edge  $e$  into the state  $\sigma' e = II$  at the rate  $\beta$ . However, recovery is a site event. It changes the state  $\sigma x = I$  of a site  $x$  into the state  $\sigma' x = S$  at the rate  $\delta$ .

Therefore, the master equations can be derived as follows.

$$\begin{aligned} \frac{d[S]}{dt} &= \sum_{\sigma x=I} \delta - \sum_{\sigma e=SI} \beta \\ \frac{d[I]}{dt} &= -\sum_{\sigma x=I} \delta + \sum_{\sigma e=SI} \beta \\ \frac{d[SI]}{dt} &= -\sum_{\sigma x=I} \delta Q_x(S) + \sum_{\sigma e=SI} \beta(Q_{e_s}(S) - Q_{e_s}(I)) \\ &\quad + \sum_{\sigma x=I} \delta Q_x(I) \\ \frac{d[SS]}{dt} &= 2\sum_{\sigma x=I} \delta Q_x(S) - 2\sum_{\sigma e=SI} \beta Q_{e_s}(S) \\ \frac{d[II]}{dt} &= 2\sum_{\sigma e=SI} \beta Q_{e_s}(I) - 2\sum_{\sigma x=I} \delta Q_x(I) \end{aligned}$$

However, the human-to-human transmission of Swine Flu usually occurs by inhalation of infectious droplets and droplet nuclei, and by direct contact, which is facilitated by air and land travel and social gatherings [27]. Therefore, the transmission rate and the recovery rate could vary depending on the surrounding infectious people. In other word, we able to write the infection rate and the recovery rate as  $\beta = b_0 + b_1 Q_{e_s}(I)$  and  $\delta = d_0 - d_1 Q_x(I)$ , respectively where  $b_0, b_1, d_0, d_1$  are constant. Moreover, according to the concept of space average,

$$\sum_{\sigma x=j} Q_x(i) = [j] \langle Q_x(i) \rangle_{\sigma x=j}$$

and

$$\sum_{\sigma e=jk} Q_{e_j}(i) = [jk] \langle Q_{e_j}(i) \rangle_{\sigma e=jk}$$

Consequently, the master equations can be rewritten in the average forms instead of the summation terms as shown below.

$$\begin{aligned} \frac{d[S]}{dt} &= d_0[I] - d_1[I] \langle Q_x(I) \rangle_{\sigma x=I} - b_0[SI] \\ &\quad - b_1[SI] \langle Q_{e_s}(I) \rangle_{\sigma e=SI} \\ \frac{d[SI]}{dt} &= -d_0[I] \langle Q_x(S) \rangle_{\sigma x=I} + d_1[I] \langle Q_x(I) Q_x(S) \rangle_{\sigma x=I} \\ &\quad + b_0[SI] \langle Q_{e_s}(S) \rangle_{\sigma e=SI} + b_1[SI] \langle Q_{e_s}(I) Q_{e_s}(S) \rangle_{\sigma e=SI} \\ &\quad - b_0[SI] \langle Q_{e_s}(I) \rangle_{\sigma e=SI} - b_1[SI] \langle Q_{e_s}(I) Q_{e_s}(I) \rangle_{\sigma e=SI} \\ &\quad + d_0[I] \langle Q_x(I) \rangle_{\sigma x=I} - d_1[I] \langle Q_x(I) Q_x(I) \rangle_{\sigma x=I} \\ \frac{d[SS]}{dt} &= 2d_0[I] \langle Q_x(S) \rangle_{\sigma x=I} - 2d_1[I] \langle Q_x(I) Q_x(S) \rangle_{\sigma x=I} \\ &\quad - 2b_0[SI] \langle Q_{e_s}(S) \rangle_{\sigma e=SI} - 2b_1[SI] \langle Q_{e_s}(I) Q_{e_s}(S) \rangle_{\sigma e=SI} \\ \frac{d[II]}{dt} &= 2b_0[SI] \langle Q_{e_s}(I) \rangle_{\sigma e=SI} + 2b_1[SI] \langle Q_{e_s}(I) Q_{e_s}(I) \rangle_{\sigma e=SI} \\ &\quad - 2d_0[I] \langle Q_x(I) \rangle_{\sigma x=I} + 2d_1[I] \langle Q_x(I) Q_x(I) \rangle_{\sigma x=I} \end{aligned}$$

In order to derive the correlation equations, we need pair approximation method. Particularly, if the

infection rate and the recovery rate are constant, then OPA and NPA are obviously identical. However, OPA has some limitations in the SIS case. Therefore, the following correlation equations are obtained by using NPA.

**Spatial SIS model: version 1**

$$\begin{aligned} \frac{d[S]}{dt} &= d_0[I] - d_1[II] - b_0[SI] - b_1[SI] [(Q-1)q_{IIS} + 1] \\ \frac{d[SI]}{dt} &= -d_0[SI] + d_1[I] \frac{Q!}{(Q-2)!} q_{I/I} q_{S/I} \\ &\quad + b_0[SI] (Q-1)q_{SIS} + b_1[SI] \frac{(Q-1)!}{(Q-3)!} q_{IIS} q_{SIS} \\ &\quad - b_0[SI] [(Q-1)q_{IIS} + 1] \\ &\quad - b_1[SI] \left[ (Q-1)q_{IIS} + \frac{(Q-1)!}{(Q-3)!} q_{IIS}^2 \right] \\ &\quad + d_0[II] - d_1[I] \left( Qq_{I/I} + \frac{Q!}{(Q-2)!} q_{I/I}^2 \right) \\ \frac{d[SS]}{dt} &= 2d_0[SI] - 2d_1[I] \frac{Q!}{(Q-2)!} q_{I/I} q_{S/I} \\ &\quad - 2b_0[SI] (Q-1)q_{SIS} - 2b_1[SI] \frac{(Q-1)!}{(Q-3)!} q_{IIS} q_{SIS} \\ \frac{d[II]}{dt} &= 2b_0[SI] [(Q-1)q_{IIS} + 1] \\ &\quad + 2b_1[SI] \left[ (Q-1)q_{IIS} + \frac{(Q-1)!}{(Q-3)!} q_{IIS}^2 \right] \\ &\quad - 2d_0[II] + 2d_1[I] \left( Qq_{I/I} + \frac{Q!}{(Q-2)!} q_{I/I}^2 \right) \end{aligned}$$

**Spatial SIS model: version 2**

$$\begin{aligned} \frac{d[S]}{dt} &= d_0[I] - d_1[II] - b_0[SI] - b_1[SI] \left( \frac{[SI]}{[S]} + 1 \right) \\ \frac{d[SI]}{dt} &= -d_0[SI] + d_1 \frac{[II][SI]}{[I]} + b_0 \frac{[SI][SS]}{[S]} + d_0[II] \\ &\quad + b_1 \frac{[SI][SI][SS]}{[S][S]} - b_0[SI] \left( \frac{[SI]}{[S]} + 1 \right) \\ &\quad - b_1 \frac{[SI][SI]}{[S]} \left( \frac{[SI]}{[S]} + 1 \right) - d_1[II] \left( \frac{[II]}{[I]} + 1 \right) \\ \frac{d[SS]}{dt} &= 2d_0[SI] - 2d_1 \frac{[II][SI]}{[I]} - 2b_0 \frac{[SI][SS]}{[S]} \\ &\quad - 2b_1 \frac{[SI][SI][SS]}{[S][S]} \\ \frac{d[II]}{dt} &= 2b_0[SI] \left( \frac{[SI]}{[S]} + 1 \right) + 2b_1 \frac{[SI][SI]}{[S]} \left( \frac{[SI]}{[S]} + 1 \right) \\ &\quad - 2d_0[II] + 2d_1[II] \left( \frac{[II]}{[I]} + 1 \right) \end{aligned}$$

Hence, spatial SIS model: version 1 is based on multinomial distribution while spatial SIS model: version 2 is based on Poisson distribution. The following results mainly provide the behaviour of spatial SIS model: version 1. In the similar manner, we finally know the behaviour of spatial SIS model: version 2.

**4.1 Theoretical Results**

Firstly, we neglect spatial structure altogether by ignoring the correlation between neighboring sites on the lattice [12]. Hence the superscript  $M$ , the superscript  $P$ , and the subscript  $e$  symbolize for mean-field approximation, pair approximation, and equilibrium, respectively.

**4.1.1 Mean-field Approximation**

In this case, it implies that the local density ( $q_{ij}$ ) equals the global density ( $q_i$ ). Consequently, we obtain fewer equations. The following equation is the change of infectious people

$$\frac{d[I]}{dt} = -b_1Q(Q-1)[I]^3 + [b_1Q^2 - b_0Q - 2b_1Q + d_1Q][I]^2 + [b_0Q + b_1Q - d_0][I] \tag{1}$$

Case 1  $b_1 = 0$ , the equilibrium points are

$$[I]_{e,1,2}^M = 0, \frac{N(b_0Q - d_0)}{Q(b_0 - d_1)}$$

Case 2  $b_1 \neq 0$ , the equilibrium points are

$$[I]_{e,1,2}^M = 0, \frac{NL \pm N\sqrt{L^2 + 4b_1Q(Q-1)(b_0Q + b_1Q - d_0)}}{2b_1Q(Q-1)}$$

where  $L = -b_0Q + b_1Q(Q-2) + d_1Q$ .

**4.1.2 Pair Approximation**

Instead of neglecting the difference between the local and the global densities. We can also search for the equilibrium in the same manner.

Case 1  $b_1 = 0$ , the equilibrium equations are

$$[S]_e^P = \frac{d_0N(Q-1)}{b_0Q(Q-1) - d_0} - \frac{(b_0Q - d_0)(Q-1)N}{(b_0Q(Q-1) - d_0)b_0}d_1 + O(d_1^2)$$

$$[I]_e^P = \frac{NQ(b_0(Q-1) - d_0)}{b_0Q(Q-1) - d_0} + \frac{(b_0Q - d_0)(Q-1)N}{(b_0Q(Q-1) - d_0)b_0}d_1 + O(d_1^2)$$

$$[SI]_e^P = \frac{d_0NQ(b_0(Q-1) - d_0)}{(b_0Q(Q-1) - d_0)b_0} - \frac{(b_0Q(Q-1) - d_0)(2Q-1)(b_0Q - d_0)N}{(b_0Q(Q-1) - d_0)b_0^2}d_1 + O(d_1^2)$$

$$[SS]_e^P = \frac{d_0^2NQ}{(b_0Q(Q-1) - d_0)b_0} - \frac{(2Q-1)(b_0Q - d_0)d_0N}{(b_0Q(Q-1) - d_0)b_0^2}d_1 + O(d_1^2)$$

$$[II]_e^P = \frac{NQ(b_0Q - d_0)(b_0(Q-1) - d_0)}{(b_0Q(Q-1) - d_0)b_0} + \frac{(2b_0Q(Q-1) - d_0(2Q-1))(b_0Q - d_0)N}{(b_0Q(Q-1) - d_0)b_0^2}d_1 + O(d_1^2) \tag{3}$$

Unluckily, we cannot obtain the explicit form of the equilibrium point when  $b_1 \neq 0$ .

**4.2 Numerical Results**

In this section we mainly investigate the density of infected individuals, defined by  $q_i = [I]/N$ , along the time series. Consequently, we have to modify (1) in subsection 4.1.1 by dividing  $N$  both sides. The upcoming figures indicate the asymptotic behaviour of solutions of the modified equation.

In case that the infection rate and the recovery rate are not affected by the surrounding infectious individuals, that is,  $b_1 = 0, d_1 = 0$ , the solution curves are visualized in Fig. 3 with the fixed parameters  $b_0 = 0.3, d_0 = 0.2$  and the varying parameter  $Q = 1, 2, 4, 8$ . Obviously, the highest solution curve occurs when  $Q = 8$  which means that the more neighbours, the higher density of infected individuals at the equilibrium point.

In case that only the infection rate is affected by the surrounding infectious individuals, that is,  $b_1 \neq 0, d_1 = 0$ , Fig. 4 shows the solution curve when  $b_0 = 0.3, d_0 = 0.2, Q = 4$  are fixed and  $b_1$  is assigned with the following values 0.9, 0.3, 0.05, 0.01. The highest solution curve occurs when  $b_1 = 0.9$  implying that the stronger effect of the surrounding infectious individuals on the infection rate, the higher density of infected individuals at the equilibrium point.

In case that only the recovery rate is affected by the surrounding infectious individuals, that is,  $b_1 = 0, d_1 \neq 0$ , the solution curves are then illustrated in Fig. 5 with the fixed parameters  $b_0 = 0.3, b_1 = 0, d_0 = 0.2, Q = 4$  and the varying parameter  $d_1 = 0.05, 0.04, 0.02, 0$ . The highest solution curve occurs when  $d_1 = 0.05$  referring that the stronger effect of the surrounding infectious individuals on the recovery rate, the higher density of infected individuals at the equilibrium point.

In case that the infection rate and the recovery rate are affected by the surrounding infectious

individuals, that is,  $b_1 \neq 0, d_1 \neq 0$ . Fig. 6 shows the effect of the surrounding infectious individuals. The solution curves are obtained by setting  $b_0 = 0.3$ ,  $b_1 = 0.1$ ,  $d_0 = 0.2$ ,  $d_1 = 0.01$  and  $Q = 8, 4, 2, 1$ . The highest solution curve occurs when  $Q = 8$ .

We, finally, compare numerically the qualitative behaviors of two versions of spatial SIS models for a particular value of each parameter. In Fig. 7, the densities of infected individuals in both spatial SIS models asymptotically tend to different equilibrium points. However, they are quite close to each other. In addition, the greater value of  $Q$ , the closer these two equilibrium points are.

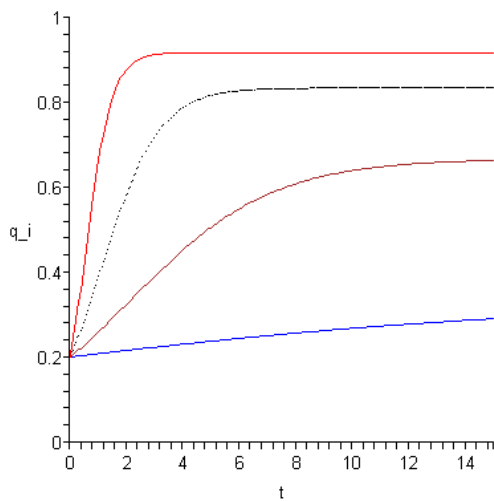


Fig. 3 Time evolution of the density of infected individuals  $q_i$ . Parameters:  $b_0 = 0.3$ ,  $b_1 = 0$ ,  $d_0 = 0.2$ ,  $d_1 = 0$  and  $Q = 8, 4, 2, 1$  (from top to bottom, respectively).

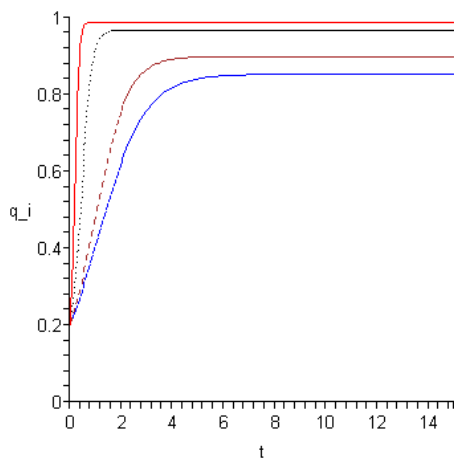


Fig. 4 Time evolution of the density of infected individuals  $q_i$ . Parameters:  $b_0 = 0.3$ ,  $d_0 = 0.2$ ,  $d_1 = 0$ ,  $Q = 4$  and  $b_1 = 0.9, 0.3, 0.05, 0.01$  (from top to bottom respectively).

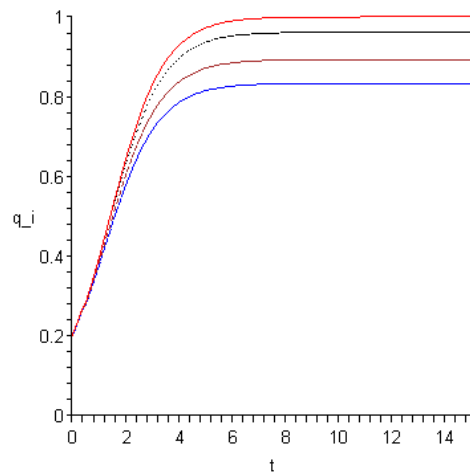


Fig. 5 Time evolution of the density of infected individuals  $q_i$ . Parameters:  $b_0 = 0.3$ ,  $b_1 = 0$ ,  $d_0 = 0.2$ ,  $Q = 4$  and  $d_1 = 0.05, 0.04, 0.02, 0$  (from top to bottom respectively).

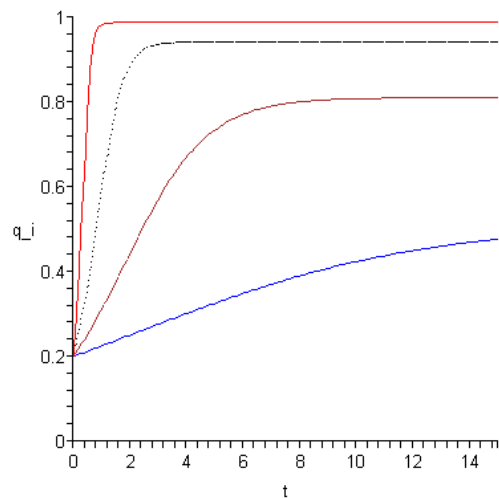


Fig. 6 Time evolution of the density of infected individuals  $q_i$ . Parameters:  $b_0 = 0.3$ ,  $b_1 = 0.1$ ,  $d_0 = 0.2$ ,  $d_1 = 0.01$  and  $Q = 8, 4, 2, 1$  (from top to bottom respectively).

Not only do we focus on equations in subsection 4.1.1, but we also observe the behaviour of system in subsection 4.1.2 by comparing the numbers of infected individuals and links between two infected individuals at the equilibrium point. For example, we could enter the following parameter values  $b_0 = 0.3, d_0 = 0.2, b_1 = 0, d_1 = 0.01, Q = 4, N = 100$  into (2) and (3). After some calculations, we obtain  $[I]_e^p \approx 85$  and  $[II]_e^p \approx 294$ . Obviously,  $[I]_e^p < [II]_e^p$  implying that the infected individuals prefer staying close together or tend to be clumped spatially.



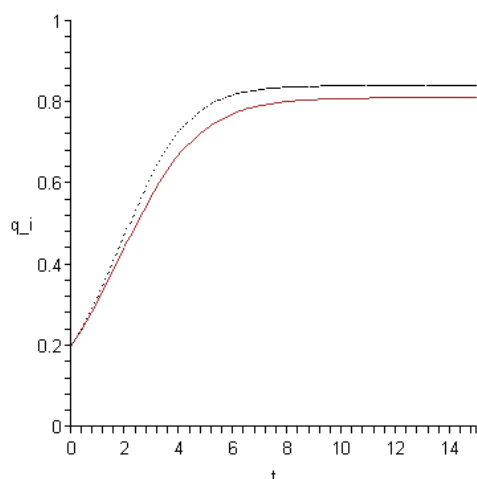


Fig. 7 The time series solution curves of the density of infected individuals  $q_i$ . Parameters:  $b_0 = 0.3$ ,  $b_1 = 0.1$ ,  $d_0 = 0.2$ ,  $d_1 = 0.01$ ,  $Q = 2$ . Poisson distribution (top) and multinomial distribution (bottom).

## 5 Conclusion

Due to the limitation of OPA, we need to find a slightly different path to truncate the special higher order terms. Such a method is using average. We assume that the population size is large; therefore, both space average and probabilistic average are identical. It is the main idea we use to develop pair approximation method. In this paper, multinomial distribution and Poisson distribution are considered. Not only useful for a simple SIS epidemic model, does this given technique (NPA) is also suitable for a model evolving according to the transition rates affecting additionally by neighbors.

Intuitively, people infect flu virus easily from their nearby neighbors. The health organization usually suggests infectious people to have some rest and be away from public places. It implies that if we surrounding with more infectious people, then we have higher chance to infected and/or lower chance to recover as shown in the numerical results.

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