A Stochastic Spatial Model for Invasive Plants and A General Theory of Monotonicity for Interaction Map Particle Systems

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Joseph Patrick Stover

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As members of the Final Examination Committee, we certify that we have read the dissertation prepared by Joseph Patrick Stover entitled
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and recommend that it be accepted as fulfilling the dissertation requirement for the Degree of Doctor of Philosophy.

_____ Date: 19 May 2008
Joseph C. Watkins

_____ Date: 19 May 2008
Thomas G. Kennedy

_____ Date: 19 May 2008
Jim M. Cushing

Final approval and acceptance of this dissertation is contingent upon the candidate's submission of the final copies of the dissertation to the Graduate College.

I hereby certify that I have read this dissertation prepared under my direction and recommend that it be accepted as fulfilling the dissertation requirement.

_____ Date: 19 May 2008
Dissertation Director: Joseph C. Watkins

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Abstract

Awareness of biological invasions is becoming widespread and several mathematical tools have been used to study this problem. Interacting particle systems, specifically the contact process, have been used to study systems with invasion/infection type dynamics. The Propp-Wilson algorithm is a method for exact sampling from the stationary distribution of an ergodic monotone Markov chain using a method called *coupling from the past*. The contact process is monotone so we can sample exactly from the stationary distribution of a modified finite grid version using the Propp-Wilson algorithm. In order to study an invasion, we would like to include at least 2 species; however, monotonicity is not well defined for contact processes with more than 2 particle types. Here we develop a general theory of monotonicity for interaction map particle systems, which are interacting particle systems with contact process type dynamics. This allows us to create monotone models with any number of particles and to use the Propp-Wilson algorithm for not only sampling from the stationary distribution, but analyzing the path of invasion leading to equilibrium. Virtual particle invasion models that fall into this new theoretical framework, which we develop here, present a wide range of biological dynamics. Computer simulation of the stochastic system and mean field analysis are two powerful tools that we use for analyzing these types of models. Statistics gathered along the path to invasion help us understand the spatial dynamics of this ecological process and what the stationary behavior looks like. This allows us to understand when the invasion is successful or if coexistence occurs and how these depend on the transition rates and interactions within the process.

Chapter 1

Introduction

The motivation for this research is the problem of invasive species. The term *invasive species* has many definitions but is understood here to refer to recently introduced, non-indigenous species capable of proliferation and resulting in significant changes of an ecosystem[5]. It is not known generally what allows a species to be invasive in a particular environment. An area must be within the invader's tolerance limits, and it must fill an available niche or out-compete species existing in the same niche. It may persist in its native environment at a low density, but completely exclude its neighbors in the recipient community[19]. One way to understand the process of invasion is that when habitat is available for a particular species, if it has the ability to acquire resources, it will persist. The notion of habitat availability used here entails everything an organism needs to survive. When a species is introduced into an ecosystem filled with organisms with which it has not co-evolved, the result is often either to not survive at all or to overtake a vast proportion of territory, the latter eventuality may result in a large number of changes to the local ecological community. Some species can however invade and persist at relatively low levels. Problems posed by this issue can be devastation of crops, drastic changes in landscape, and the extinction of native species.

The introduction of grasses from Africa to Southern Arizona for the purpose of grazing cattle and the stabilization of soil due to overgrazing is the main case discussed here. Native grasses tend to grow in smaller patches and as a result leave plenty of open area. This is a situation that does not sustain ranching in the desired manner and has lead to the introduction of foreign species such as *Eragrostis Lehmanniana*,

Lehmann's Lovegrass, and *Pennisetum ciliare*, Buffelgrass. One result is a more dense ground cover that leaves behind more fuel for fires in the dry season[1]. Habitats thus created are preferred less by several native species of insects, birds, and mammals. Some species are found to prefer the new flora however[13, 1, 3]. Lehmann Lovegrass has spread beyond what was previously thought to be its abiotic limits[34, 15].

This work is centered around the creation of models for the purpose of understanding the spatial spread of an introduced plant species. One approach to the problem of understanding invasions is to use a multi-type contact process [8, 29, 22] and simulate it for a long time and then collect data on the near equilibrium state[21]. The first difficulty that arises is that it is not easy to determine exactly when equilibrium is reached or when we are sufficiently close enough. Coupling from the past, CFTP, using the Propp and Wilson algorithm, solves this problem with a Markov Chain that has a unique stationary distribution[31]. Although if the process does not have the property of monotonicity, another issue arises. The CFTP algorithm can take a massive number of simulations (forcing each possible initial configuration to be tested). A major goal of this dissertation is to create a modified version of the multi-type contact process that remains monotone in biologically meaningful situations. Knowing exactly when equilibrium is reached allows one to study transient behavior, the path to invasion.

The effort here is also to develop a general theory of monotonicity for a larger class of models. Several previously studied models fall within this framework. Thus we will know when exact sampling from the stationary distribution can be accomplished. Once the framework is established, an invasion model based on exclusive habitat, where empty sites can only be invaded by one or the other species, will be introduced. We start with an overview of ecological studies on invasion mechanisms and then discuss the example of Lehmann Lovegrass. A brief discussion of some mathematical studies follows and leads into the current work.

1.1 Invasion Ecology

There are many ecological processes that can change in response to species invasions. Community structure can be altered greatly. Competitive dynamics are altered by species–specific effects on ecosystem processes by an invading species that is functionally distinct from dominant native species. This often results in favoring the dominance of the invader and possibly additional exotic species establishment[32]. However, invasions by species whose functional traits are relatively similar to natives can also be successful as well. The Southern Arizona Lovegrass invasion is an example of of this. Here the primary native grasses are Plains Lovegrass and Blue Grama, and the invasive grasses are Boer Lovegrass and Lehmann Lovegrass. These grasses have similar functional traits to the natives, yet the resulting ecological communities are distinct in terms of several measures of species composition and abundance[32, 3]. The main competing views on ecological community structure are that communities are loosely knit together and introducing new species should have relatively little effect on the structure, and the opposing view is that communities are strongly interwoven so that introduced species can result in drastic community wide changes in abundance, composition, and diversity[3].

Invading plants can also change the composition of the microbial community in the soil, and it is less well understood how this affects ecosystem function[2]. Nonnative plant species have the potential to alter species composition, change hydrologic and nutrient cycles, and influence disturbance regimes[15]. In southern Arizona, fire is a major disturbance factor, and the presence of non-native grasses changed the effects of experimental fire on small mammals: differences in species composition of the community of small mammals between burned and unburned areas were greatest when nonnative grasses dominated[25].

Community–wide effects of exotic species have been examined by Simberloff in 1981 and nearly 80% of 854 documented cases showed that an introduced species

has no effect on species in the resident community or on the structure and function of that community. This finding has been used to conclude that communities are only loosely structured assemblages where interactions among species must be weak or unimportant[3]. The grass invasion case in southern Arizona does not fit this conclusion however. Many differences have been identified between stands dominated by native and non-native grasses including species diversity, richness, abundance, and response to disturbance.

1.2 Lehmann Lovegrass

Eragrostis Lehmanniana is a warm season perennial bunchgrass native to South Africa. It grows approximately 1.5 to 2 feet tall. Seeds are small and produced in large quantities. Most fresh seeds are dormant and require 6 to 9 months of afterripening, although laboratory experiments have shown that dry heat treatments scarify the seedcoat and increase the rate of germination. Its ability to displace native species is aided by being able to reseed itself quickly after disturbance[36]. An important factor in southern Arizona is that it leads to an increase in fuel and reappears quickly after fire disturbances[25].

1.2.1 Historical Summary

The introduction of Lehmann Lovegrass into Arizona began in the 1930's and started a transformation of southern Arizona semi-desert grasslands. By 1984, it was the major grass species on 145,000 hectares in southern Arizona[6]. Lehmann Lovegrass was promoted by the government for grazing and topsoil retention and caused decline in local native plant species[1]. Currently Lehmann Lovegrass seed is still available and promoted as a substitute to native grasses.

1.2.2 Santa Rita Experimental Range

The Santa Rita Experimental Range (SRER) consists of 53,159 acres about 35 miles south of Tucson in Pima County, Arizona and was established in 1903 to protect the native rangeland from grazing and to conduct research on problems associated with livestock production. Accumulated information on ecology of the semidesert system at SRER is more complete than for any other tract of comparable size and diversity[27].

Repeat photography at the SRER has occurred intermittently since 1903 at 107 sites distributed throughout the range. Figure 1.1 shows photo station 96 in the year 1926. Figure 1.2 shows photo station 96 in the year 2000. The dominant grass species near this photo station is Lehmann Lovegrass. It is easily discernable in the photo as it almost covers the whole view. In 1988 Lehmann lovegrass (Eragrostis lehmanniana) was the dominant grass over nearly 40% of the range[27].

1.2.3 Predicting the Future Range

In 1986 Cox and Ruyle mapped out the distribution of Lehmann Lovegrass and predicted its future range using abiotic limiting factors. They suggested that it had already reached the limits of its range in many areas. Recently, Lehmann Lovegrass has been found beyond these predicted limits[15, 34]. Due to current land management practices and climate conditions, it is expected to continue its spread[15, 1].

Geiger et al.[15] used scenarios from two general climate models to predict the future spread of Lehmann Lovegrass and compared these predictions to that of Cox and Ruyle. Typically studies have found summer precipitation to be a limiting factor for the invasive grasses spread, but Geiger's study found no meaningful difference between presence and absence due to rainfall. It was however found to increase its upper elevation range compared to that given by Cox and Ruyle. Some areas where it was thought to extend its range to previously were found to be unsuitable under

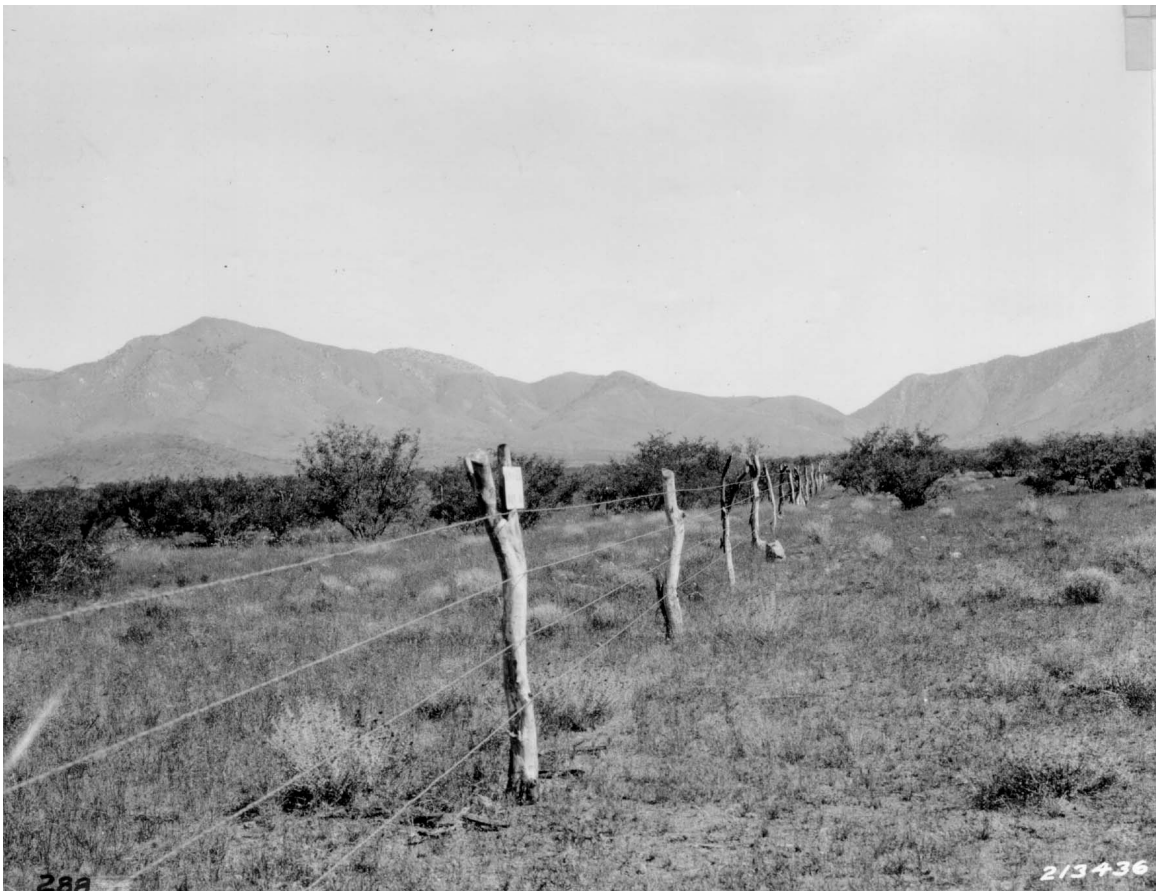


FIGURE 1.1. SRER photo station 96 in 1926.

FIGURE 1.2. SRER photo station 96 in 2000. Lehmann Lovegrass is the dominant grass easily identifiable in the photo.

the predictions given by the climate models.

Predicting the potential distribution of a species is also made more difficult since the limiting factors may be different in the new environment as opposed to that of the invaders native region. Schussman et al collected data from several land management agencies in Arizona and western New Mexico to determine the extent of the spread of Lehmann Lovegrass. They found that it has continued to spread beyond what previous researchers thought would be the limits of its distribution[34].

1.2.4 Ecological Community Effects

In 1986, Bock et al conducted a survey of species abundance in native and exotic stands in southeastern Arizona. Sites dominated by native perennial grasses supported a greater collective variety and abundance of indigenous plants and animals than did areas planted with exotics. Three native species, including one grasshopper, one rodent, and one bird, were found to have greater abundance in stands dominated by Lehmann Lovegrass. Twenty six species, including 10 plants, 5 birds, 3 rodents and 8 grasshoppers, were found more common in stands dominated by native species[3].

Flanders et al studied the effect of non-native grasses(Buffelgrass and Lehmann Lovegrass) on the abundance and species richness of breeding birds, native flora, and arthropods on south Texas rangelands. Arthropod abundance was found to be 60% greater on the native grass site that was sampled. Spiders, beetles, and ants were found to be 42–83% more abundant in the native grass study area than on a buffelgrass site. Grass species richness was greater on native grass sites. This resulted in the exotic grassland being less suitable for breeding birds in general, especially those that foraged near the ground. Bird abundance was found to be 32% greater on sites dominated by native grasses[13].

Non-native grasses also affect the structure of some small mammal populations. Litt observed shifts in age ratios and reproductive activity. The proportion of juveniles

increased and the proportion of reproductively active and pregnant females decreased in areas dominated by nonnative grass. This was purported to indicate a decrease in overall habitat quality in areas dominated by nonnative grass[25].

Litt also studied the changes in insect populations and correlated observations to the abundance of Lehmann Lovegrass. It was found that the number of species and the overall abundance of insects decreased as dominance of nonnative grass increased. Many of these changes correspond to decreases in food sources and imply cascading effects on animal populations as well[25].

In summary, the introduction of Lehmann Lovegrass has significantly altered several aspects of local ecology. This presents an array of management issues and no universal solution to controlling its spread or restoring a more native ecological balance rests in the foreseeable future. Studies continue to document and try to understand the intricacies of these events.

1.3 Mathematical Modeling

Mathematics is playing a more important role in ecology lately. The advent of more computer power enables longer and more complicated simulations for testing various types of model scenarios. Mathematical models have helped with making general predictions, testing hypotheses, forming management practices, and developing statistical tools which can be employed in the field[30].

Spatial effects are becoming increasingly of interest in ecology. Traditionally, ecological models have been based on differential equations leaving out any spatial aspects. While this method of modeling has led to many insights into ecological mechanisms, it is based on the populations being well-mixed and this assumption does not hold in all situations. It is often desirable to include local spatial interactions in order to fit a given situation more appropriately[30, 8].

1.3.1 Spatial Models

Interacting particle systems present a wealth of possibilities for creating models. An interacting particle system consists of a discrete spatial grid where each site is assigned a number representing the type or number of particles sitting there. Particle values represent the different states allowed to exist at each site, for example, a particle value of 1 represents occupation by species 1, and a particle value of 0 represents an empty site. Sites change their values according to a given stochastic interaction rule. The contact process is the basic example used here where births occur at a rate proportional to the number of 1's nearby[23, 8, 24]. Spatial biological models are largely built upon the contact process[33, 8]. For a summary of these types of models and various behaviors, see [8].

Interacting particle systems are often reduced to what are called the mean field equations. This is the well-mixed version of the model where spatial structure is ignored and results in a system of ordinary differential equations. Studying the mean field equations allows a qualitative study of the behavior of the system. Although there may be differences between behavior of spatial and non-spatial versions of the same model[10].

1.3.2 Spatial Effects on Coexistence

The behavior of a model can often change quite significantly when interactions are dependent on the spatial distribution of organisms. Understanding the role that space plays in competitive dynamics is important in the study of biodiversity. Diversity can be much higher in spatially heterogeneous environments[10].

One behavior studied by Leonard and May in [26] showed three species differential equation model where the behavior for a particular parameter region is to spiral out ever more slowly cycling between the points of each species in isolation. Solutions approach each point more closely and take stay nearby for longer periods of time as

time goes on. Durrett and Levin, in [10], showed that this transient behavior is not present when the model is structure spatially. They created an interacting particle system whose mean field equations are those studied by Leonard and May. In the spatial model, each species oscillated between roughly 28% and 36% occupation of the grid.

1.4 Current Work

This dissertation begins with the theory of Markov processes and introduces interacting particle systems. Basic tools such as coupling, monotonicity, mean field analysis, and exact simulation will be discussed. The primary source for the notation and theoretical basis is Liggett's book "Interacting Particle Systems"[23]. Once the mathematical foundation is established, we go on to develop a new framework in which many interacting particle system models fall. This is based on the idea of creating an "interaction map" which defines all transitions allowed in the process. Many Definitions and theorems from Liggett[23] for spin systems will be reformulated to fit the models included in this framework. Then a stochastic spatial model for plant invasions will be presented in which available habitat for the species becomes exclusive in that there are two types of empty sites, each available to only one species and excluding the other.

Chapter 2

Stochastic Processes

A stochastic process is a collection of random variables indexed by some set, $\mathcal{I}$, and in many cases can be reasonably thought of as a temporal sequence of states, usually either discrete time, $\mathbb{N}$, or continuous time, $\mathbb{R}^+$. Here, $\mathcal{I} = \mathbb{R}^+ = [0, \infty)$, is the primary concern. We start with the state space, X, which is a compact metric space in most cases considered here. The path space, $D_X[0, \infty)$, is the space of functions from $[0, \infty)$ to X, which are right continuous with left limits and should be understood as the collection of process realizations. The notation used here usually follows that of Liggett[23], where $\eta_\cdot$, denoted using a dot subscript, represents the sample path with $\eta_0 = \eta$ as the initial state. We will also use $\eta_{\mathbf{t}}$, with a bold $\mathbf{t}$ subscript, from time to time to denote a sample path; so $\eta_{\mathbf{t}} = \eta_\cdot = \{\eta_t; t \in [0, \infty)\}$. If $\eta_\cdot \in D_X[0, \infty)$, then $\eta_\cdot : [0, \infty) \to X$, and $\eta_t \in X$ for each fixed $t \in [0, \infty)$. The notation will be shortened to $D[0, \infty)$ when the state space is understood. It is also necessary to define the evaluation mappings, $\pi_s : [0, \infty) \times D_X[0, \infty) \to X$, such that for any $s \in [0, \infty)$ and $\eta_\cdot \in D_X[0, \infty)$, $\pi_s(\eta_\cdot) = \eta_s$, the state of the process at time s. The σ-algebra $\mathscr{F}$ on $D_X[0, \infty)$ will be the minimal σ-algebra such that all $\{\pi_s\}_{s \in [0,\infty)}$ are measurable, and $\mathscr{F}_t$ is the minimal sigma algebra such that all $\{\pi_s\}_{s \le t}$ are measurable.

It should also be clear that the probability space $(D_X[0, \infty), \mathscr{F}, P)$ is induced by an underlying abstract probability space, $(\Omega, \mathscr{F}_\Omega, P_\Omega)$, where $\eta_\cdot \in D_X[0, \infty)$ is actually a function $\eta_\cdot : \Omega \to D[0, \infty)$, $\{\eta_t(\omega)\}_{t \in [0,\infty)}$ is a particular process realization when ω is fixed. The probability measures on $D_X[0, \infty)$ are defined in terms of P_Ω by $P(A) = P_\Omega\{\omega : \eta_\cdot(\omega) \in A\}$, where $A \subset D_X[0, \infty)$, and the initial state is not fixed in this case.

2.1 Markov Processes

The main types of stochastic processes of concern here will be Markov processes. These particular stochastic processes have a specific memoryless property: given any knowledge of the history of the process, the only thing necessary to know the conditional distribution of future states is the most recent state. This is known as the Markov property and is illustrated by the last condition of Definition 1. In order to use these types of processes to study ecological systems, we must assume that the future state only depends on the current conditions.

Definition 1. A *Markov Process* is a stochastic process described by the collection of probability measures, $\{P^\eta : \eta \in X\}$ on $D[0,\infty)$ satisfy the following properties:

(1) $P^\eta\{\eta_\cdot \in D[0,\infty) : \eta_0 = \eta\} = 1$ for any $\eta \in X$.

(2) The mapping $\eta \to P^\eta(A)$ from X to $[0,1]$ is measurable for every $A \in \mathscr{F}$.

(3) $P^\eta\{\eta_{t+\cdot} \in A|\mathscr{F}_t\} = P^\eta\{\eta_{t+\cdot} \in A|\eta_t\}$ for every $\eta \in X$ and $A \in \mathscr{F}$.

Definition 2. A Markov process is called *time-homogeneous* if (3) in Definition 1 does not depend on t.

$$P^\eta\{\eta_{t+\cdot} \in A|\mathscr{F}_t\} = P^{\eta_t}\{\eta_\cdot \in A\}. \tag{2.1}$$

Modeling a biological process with a time-homogeneous Markov process means we assume a constant environment and constant parameters governing birth and death rates for individual species in the sense that these can only depend on the current state of the system and nothing else. If it is desired to reflect changes in climate, species seasonality, or other non-constant environmental factors, then the prediction of futures states will depend on what time of the season or year we are trying to predict from and not just the state of the system. For example, the conditional distribution of a time-homogenous model of an annual population, $N(t)$, does not

care whether it reaches a certain level early in the year or later. It only matters what the current population size is.

For any initial distribution μ on X, there is a corresponding probability measure on $D[0,\infty)$, P^μ.

$$P^\mu(A) = \int_X P^\eta(A) d\mu(\eta)$$

The distribution P^η is characterized by the initial distribution δ_η, giving mass one to the single state η, $P^\eta = P^{\delta_\eta}$.

$$P^\eta(A) = P\{\eta_\cdot : \eta_\cdot \in A | \pi_0(\eta_\cdot) = \eta\}$$

The expectation for any measurable function, Z, on $D[0,\infty)$, taken with respect to the distribution P^η is

$$E^\eta Z = \int_{D[0,\infty)} Z dP^\eta.$$

Let $C(X)$ be the space of continuous real-valued functions on X, which along with the sup norm $||f|| = \sup_{\eta \in X} |f(\eta)|$, forms a separable Banach space. For $f \in C(X)$, define the expectation

$$S(t)f(\eta) = E^\eta f(\eta_t) = \int_{D[0,\infty)} f(\pi_t(\eta_\cdot)) dP^\eta(\eta_\cdot).$$

This computes the expected value of a function on the state space at a future time, t, given some initial distribution, which is taken to be δ_η here. The linear operators $\{S(t); t \geq 0\}$ are referred to as the *semigroup* for the process.

Definition 3. A stochastic process is called a *Feller process* if $f \in C(X)$ implies $S(t)f \in C(X)$ for each $t \geq 0$.

Definition 4. A Semigroup $\{S(t); t \geq 0\}$ is called a *Feller semigroup* if

(1) $S(0) = I$, the identity

(2) The mapping $t \to S(t)f$ from $[0,\infty)$ to $C(X)$ is right continuous for every $f \in C(X)$.

(3) $S(t+s)f = S(t)S(s)f \ \forall f \in C(X)$ and all $s,t \geq 0$,

(4) $S(t)1 = 1$, the identity on X, $\forall t \geq 0$.

(5) $S(t)f \geq 0$ for all non-negative $f \in C(X)$.

Every Feller semigroup corresponds uniquely to a Markov process[23]. Let $\mathscr{P}$ be the space of probability measures on the state space with the topology of weak convergence: $\lim_{n\to\infty} \mu_n = \mu$ if and only if $\lim_{n\to\infty} \int f d\mu_n = \int f d\mu$ for all $f \in C(X)$. If $\mu \in \mathscr{P}$, then $\mu S(t) \in \mathscr{P}$ is defined by

$$\int_X f(\eta) d(\mu S(t))(\eta) = \int_X S(t) f(\eta) d\mu$$

Given any initial distribution μ, $\mu S(t)$ will be referred to as the distribution of the process at time t. It should be noted that for a Feller Semigroup, the mapping $t \to \mu S(t)$ is right continuous due to the right continuity of $S(t)$.

Definition 5. A distribution $\mu \in \mathscr{P}$ is called *invariant* or *stationary* if $\mu S(t) = \mu$ for all $t \geq 0$. The space of invariant distributions will be denoted $\mathscr{I}$.

Definition 6. A process will be called *ergodic* if there is only one stationary distribution, ν, and $\lim_{t\to\infty} \mu S(t) = \nu$ for any $\mu \in \mathscr{P}$.

Generator Usually we will define a process by giving its infinitesimal generator. There is a one to one correspondence between Markov Semigroups and the infinitesimal generators. The relationship between them is given by the Hille-Yosida theorem.

$$Gf = \lim_{t \searrow 0} \frac{S(t)f - f}{t} \text{ for } f \in C(X) \text{ such that the limit exists.}$$

The infinitesimal generator determines the semigroup via

$$S(t)f = \lim_{n\to\infty} \left(I - \frac{t}{n}G\right)^{-n} f \text{ for } f \in C(X) \text{ and } t \geq 0.$$

A rigorous development of this theory can be found in Liggett[23].

2.2 Coupling and Monotonicity

It is often desired to construct multiple stochastic processes in such a way that the distributions are tied together in some way. This is achieved through a technique known as coupling.

Definition 7. A *coupling* of two stochastic processes $\eta_\cdot$ and $\xi_\cdot$, is a stochastic process $(\tilde{\eta}_\cdot, \tilde{\xi}_\cdot)$ such that marginal distributions of the coupled process are the same as the original processes, $\eta_\cdot \stackrel{D}{=} \tilde{\eta}_\cdot$ and $\xi_\cdot \stackrel{D}{=} \tilde{\xi}_\cdot$.

In other words, a coupling is a construction of multiple processes on a common probability space where the distributions of the original processes are preserved. Joint distributions may be different (and usually are) so that a desired property of the process may be emphasized. The simplest, but possibly most uninteresting, coupling is just two independent identically distributed copies of any stochastic process. We will later see that a useful coupling occurs for interacting particle systems using Poisson point processes. This particular coupling allows multiple initial states to be tested simultaneously. The primary method of coupling of interest here is linked closely to the property called monotonicity.

Definition 8. The state space, X, will be called *partially ordered*, if there exists a binary relation, "$\leq$", such that if η, ξ, and ζ are states in X, then

(1) $\eta \leq \eta$

(2) $\eta \leq \xi$ and $\xi \leq \eta$ implies $\eta = \xi$

(3) $\eta \leq \xi$ and $\xi \leq \zeta$ implies $\eta \leq \zeta$

In most cases considered here, the partial ordering will be an obvious one.

In order to understand what monotonicity means for a Markov process, some more background development is needed. Define the set $\mathscr{M}$ to be the class of functions in $C(X)$ which are monotone in the usual sense that $\eta \leq \xi$ implies $f(\eta) \leq f(\xi)$.

Definition 9. (Definition 2.1 Liggett IPS p.71): If μ_1 and μ_2 are probability measures on X, then we say that $\mu_1 \leq \mu_2$ if $\int f d\mu_1 \leq \int f d\mu_2$ for all $f \in \mathscr{M}$.

Theorem 10. (Theorem 2.2 Liggett IPS p.71): Suppose η_t is a Feller process on X with semigroup $S(t)$. The following two statements are equivalent:

(1) $f \in \mathscr{M}$ implies $S(t)f \in \mathscr{M}$ for all $t \geq 0$

(2) $\mu_1 \leq \mu_2$ implies $\mu_1 S(t) \leq \mu_2 S(t)$ for all $t \geq 0$

So for a Feller semigroup to preserve the ordering of measures, it must also preserve the monotonicity of functions and vice versa. Now we are ready to define what a monotone Feller process is.

Definition 11. (Definition 2.3 Liggett IPS p.72): A Feller process is said to be *monotone* if either of the equivalent conditions of Theorem 10 is satisfied.

If we have a monotone process, it is of interest to find a coupling that demonstrates this property. The following theorem connects ordered marginal distributions, $\mu_1 \leq \mu_2$, via a coupling measure ν. This coupling measure is used to explore the monotonicity of the stochastic process.

Theorem 12. (Theorem 2.4 Liggett IPS p.72): Suppose μ_1 and μ_2 are probability measures on X. A necessary and sufficient condition for $\mu_1 \leq \mu_2$ is that there exist a probability measure ν on $X \times X$ which satisfies

(1) $\nu\{(\eta,\xi) : \eta \in A\} = \mu_1(A)$, and

(2) $\nu\{(\eta,\xi) : \xi \in A\} = \mu_2(A)$, where A is any Borel set in X, and

(3) $\nu\{(\eta,\xi) : \eta \leq \xi\} = 1$

To see the sufficiency of (1), (2), and (3), fix $f \in \mathscr{M}$, and define $g \in C(X \times X)$ by $g(\eta,\xi) = f(\xi) - f(\eta)$. By definition of ν and the monotonicity of f, $E^\nu g \geq 0$.

$$\begin{aligned} 0 \leq \textstyle\int_{X\times X} g(\eta,\xi)d\nu &= \int_{X\times X} f(\xi)d\nu\{(\eta,\xi)\} - \int_{X\times X} f(\eta)d\nu\{(\eta,\xi)\} \\ &= \int_X \int_X f(\xi)d\nu\{(\eta,\xi)|\eta\}d\nu(\eta) - \int_X \int_X f(\eta)d\nu\{(\eta,\xi)|\xi\}d\nu(\xi) \\ &= \int_X \int_X f(\xi)d\nu\{(\eta,\xi)|\eta\}d\mu_1(\eta) - \int_X \int_X f(\eta)d\nu\{(\eta,\xi)|\xi\}d\mu_2(\xi) \\ &= \int_X f(\xi)d\mu_2(\xi) - \int_X f(\eta)d\mu_1(\eta) \end{aligned}$$

This shows that the existence of the measure ν implies that $\mu_1 \leq \mu_2$ since $f \in \mathscr{M}$ implies $\int f d\mu_1 \leq \int f d\mu_2$. For the necessity of the conditions, assume that $\mu_1 \leq \mu_2$, then one can construct the measure ν using the Riesz Representation and Hahn-Banach Theorems. See Liggett for the complete proof[23].

2.3 Sampling from the Stationary Distribution

The question arises concerning how to develop an understanding of the distributions of a process. When an Markov chain is known to have a unique stationary distribution, it is often the case that one wants to sample from this distribution. The stationary distribution is strongly linked to the idea of coupling multiple copies of the chain until they coalesce onto a single state. There are many ways to couple multiple copies of a process together in order to look for this coalescence, but CFTP, *coupling from the past*, is a particularly effective method for analyzing the stationary behavior of

monotone processes. We assume the Markov chain is irreducible, aperiodic, time-homogeneous and has a finite state space. The following development of random transition maps allows computer simulation of the coupled process. Note that in this section, x and y are used to denote states of a Markov chain whereas in the rest of this paper, they represent individual sites within a state usually.

Let S be the finite state space for the Markov chain, X_t, where t is a non-negative integer, with transition matrix $T(x, y)$ and stationary distribution, π. Define the set, $\mathcal{A}$, to be those maps, $\mathbf{f} : S \to S$ who have domain all of S. Each map will be considered a single coupled transition for every single state. Define the probability measure, $P_{\mathcal{A}}$ on $\mathcal{A}$, according to the Markov chain. For any $\mathbf{f} \in \mathcal{A}$,

$$P_{\mathcal{A}}(\mathbf{f}(x) = y) = T(x, y).$$

If we have identically distributed $\{\mathbf{f}_i; i \in \mathbb{Z}\}$, then

$$P_{\mathcal{A}}\{\mathbf{f}_{t_2-1} \circ \mathbf{f}_{t_2-2} \circ \cdots \circ \mathbf{f}_{t_1}(x) = y\} = T^{|t_2-t_1|}(x, y)$$

for any t_1 and $t_2 > t_1$ in $\mathbb{N}$.

The typical way to choose the coupling maps is to index them by a uniform random variable U on $[0, 1]$, so that $\mathbf{f}(\cdot, u) : S \to S$ for any $u \in [0, 1]$. Using the probabilities from the Markov chain, all values of U can each be assigned to a random map, $\mathbf{f}$.

In general, when creating a coupling for a Markov process, we will have all states coupled together in this way, so that the differences in behavior may be looked upon for different initial states. First we start with forward time coupling for coalescence.

2.3.1 Forward Coupling

The problem arising here is that sampling at the *time of first coalescence* is often biased and thus will not give the stationary distribution. We start by selecting a

random map, $\mathbf{f}_1$, from $\mathcal{A}$. This is the first transition for the coupled chain. It is not important that we select a map from the whole set of $\mathcal{A}$, but that we select it out of a subset which allows coalescence of some states and communication of all states. This will be explained later in more detail. Input all states into this map and check if the output state is constant, i.e. check for coalescence of all initial states. If the map, $\mathbf{f}_1$, is not constant, select another map, $\mathbf{f}_2$ and compose the two maps together, keeping the same $\mathbf{f}_1$, and check if $\mathbf{F}_0^2 = \mathbf{f}_2 \circ \mathbf{f}_1$ is constant. We continue this until we have a map, $\mathbf{F}_0^{\tau_f} = \mathbf{f}_{\tau_f} \circ \cdots \circ \mathbf{f}_2 \circ \mathbf{f}_1$ which is constant. Time τ_f is called the forward coalescence time.

It should be apparent that $T^n(x, \cdot)$ is the distribution of $\mathbf{F}_0^n(x)$ for any fixed n, but the following example will show that the forward coalescent distribution, $\mathbf{F}_0^{\tau_f}$, is not necessarily the same as π. The reason is that the process may tend to coalesce on certain states first. (Example 5.1 p.137, Fill 1998) Consider the Markov chain with states $\{0, 1\}$ only. The transition probabilities are that state 0 remains unchanged or becomes state 1 with probability 1/2 each, and the state 1 moves to state 0 deterministically. The stationary distribution of this process is $\pi(0) = 2/3$ and $\pi(1) = 1/3$. The process will always have first coalescence on the 0 state[12]. Coupling from the past however, gets rid of this bias.

2.3.2 Coupling from the Past

So merely checking for coalescence is not enough to declare stationarity. It is still required to run the process for longer to get to the actual stationary distribution. Determining how long to continue after first coalescence is not necessarily an easy task as it is a random time. CFTP however goes beyond this first coalescence in such a way that the stationary distribution is exactly reached. Propp and Wilson devised an algorithm using CFTP, coupling from the past, for sampling exactly from the stationary distribution of an ergodic Markov chain[31].

The Propp-Wilson algorithm chooses a random map, $\mathbf{f}_{-1}$, and for each possible initial state η, we let the state at time -1 be $\eta_{-1} = \eta$ and thus $\eta_0 = \mathbf{f}_{-1}(\eta)$. If the random map, $\mathbf{f}_{-1}$, is not constant, then another map is chosen, $\mathbf{f}_{-2}$. Then we compose the maps together opposite to forward coupling; we put the new map in front of the old one. The two step transition is defined as $\mathbf{F}^0_{-2} = \mathbf{f}_{-1} \circ \mathbf{f}_{-2}$. This two-step transition is then evaluated over every possible initial configuration to see if the output is constant yet. Notice that while $\mathbf{f}_{-1}$ was the first transition originally, $\mathbf{f}_{-2}$ is now the first transition. This algorithm continues adding new steps in front of previous multi-step maps until every initial state gives the same output state. Let τ_p be the number(random) of steps needed for coalescence to occur. The coupling from the past coalescence time, τ_p, is finite with probability 1. It should be noted that the distribution of $\mathbf{F}^0_{-n}$ is the same as $\mathbf{F}^n_0$ for any fixed n, and the distribution of τ_p is the same as τ_f. However, for any x, the distribution of $\mathbf{F}^0_{-\tau_p}$, is that of π. The proof lies in the fact that $\mathbf{F}^0_{-\tau_p}$ and $\mathbf{F}^0_{-\infty}$ have the same distribution, and the latter is exactly π.

Assume that the Markov chain is monotone, has a partially ordered state space, and there are two extremal states, $\bar{0}$ and $\bar{1}$, such that $\bar{0} \leq x \leq \bar{1}$ for any $x \in S$. In this case it is only necessary to check for coalescence from these extremal states as initial input if we use a monotone coupling. We must only choose maps, $\mathbf{f}$, such that given two initial states satisfying $x \leq y$, $\mathbf{f}(x) \leq \mathbf{f}(y)$. The random maps just need to be constructed from a suitable coupling measure. We know this coupling exists by Theorem 12.

This algorithm can be applied to continuous time pure jump Markov processes with finite state spaces as well since states are constant for continuous intervals of time and then jump to another state at exponential rates.

2.4 Interacting Particle Systems

An interacting particle system is a Markov Process whose state space consists of configurations of particles on a discrete grid. The state space for the process is $X = S^{\Lambda}$, where S is a finite set, and $\Lambda \subset \mathbb{Z}^d$, the d-dimensional integer lattice. Usually S will be totally ordered and thus induce a partial ordering on X, $\eta \leq \xi$ if $\eta(x) \leq \xi(x)$ for all $x \in \Lambda$. A particle at an individual site in the grid changes to a different particle type in transitions which occur at exponential rates depending on interactions occurring within the grid. Much work has been done with *spin systems* [23], where only two types of particles are considered, and particle systems with more than two particles have been studied which only allow the particle values to increase or decrease by one, or to swap two particles at different sites [14].

The state space for interacting particle systems will always be assumed to be a metric space. For any two configurations η and ξ, we define the distance between them as

$$d(\eta, \xi) = \sum_x m(x)|\eta(x) - \xi(x)| \tag{2.2}$$

where $m(x)$ is a suitable weight function which allows the sum to converge for any two configurations. An example might be $m(x) = 2^{-|x|_1}$, where $|\cdot|_1$ is the $\mathcal{L}^1$ norm of x.

2.4.1 Generators for Particle Systems

Normally we start with the transition rates and types of interactions and build the infinitesimal generator for the process. The infinitesimal generators for particle systems are constructed on a set of functions which is dense in $C(X)$ so that the closure of is a generator of a Markov semigroup. For $f \in C(X)$ and a grid site, x, define

$$\Delta_f(x) = \sup\{|f(\eta) - f(\xi)| : \eta, \xi \in X, \text{ and } \eta(y) = \xi(y) \text{ for all } y \neq x\}. \tag{2.3}$$

This can be thought of as a measure of the function f's dependence on the coordinate x [23].

$$D(X) = \left\{ f \in C(X) : \sum_x \Delta_f(x) < \infty \right\} \tag{2.4}$$

The set $D(X)$ is a dense subset of $C(X)$. We can also define the set $D_0(X)$ as the set of functions which depend on finitely many coordinates, $f \in D_0(X) \Rightarrow \sum_x \Delta_f(x) = \sum_{|x|<\rho} \Delta_f(x)$ for some $\rho < \infty$. Both $D(X)$ and $D_0(X)$ are suitable cores for defining operators whose closures are defined everywhere on $C(X)$. Once the infinitesimal generator is defined on one of these cores, it is shown to be a Markov pre-generator, and its closure can be shown to have domain all of $C(X)$ and be a Markov generator.

2.4.2 Spin Systems

The state space for a spin system is the configurations of two particle types on a d-dimensional integer lattice, $X = \{a, b\}^{\mathbb{Z}^d}$, where a and b are any arbitrary symbols, usually $\{0, 1\}$ or $\{-1, +1\}$. The primary concern here is the contact process and voter model and so without loss of generality we will use $\{0, 1\}$ for our particle values.

The generator for these processes is defined in terms of flip rates, $c(x, \eta)$, which gives the rate of flipping to value 0 if a 1 is the state at site x and the opposite if 0 is the state at x. For the contact process 0 represents a vacant site, and 1 represents an infected or occupied site. The flip rate is given by

$$c(x, \eta) = \begin{cases} \lambda \displaystyle\sum_{y:|x-y|=1} \eta(y) & \text{if} \quad \eta(x) = 0 \\ 1 & \text{if} \quad \eta(x) = 1 \end{cases} . \tag{2.5}$$

How (2.5) can be understood is that at each site in a configuration of ones and zeros has an exponential clock whose alarm going off depends on what particles occupy the surrounding sites. For example, if $\eta(x) = 1$, then its exponential clock will go off in an amount of time that is exponentially distributed with mean 1, at which time, the

1 will become a 0. Now, if $\eta(x) = 0$, this exponential clock will go off in a time which is exponentially distributed with mean $1/N\lambda$, where N is the number of ones in the nearest neighborhood. Each time the neighborhood changes, the rate of the clock will change.

While for the voter model the flip rate is

$$c(x,\eta) = \begin{cases} \sum_{y:|x-y|=1} p(x,y)\eta(y) & \text{if} \quad \eta(x) = 0 \\ \sum_{y:|x-y|=1} p(x,y)(1-\eta(y)) & \text{if} \quad \eta(x) = 1 \end{cases} \tag{2.6}$$

where $\sum_y p(x,y) = 1$, and 0 and 1 represent the possible opinions of the population. So these are similar, except the voter model works off of a two-way contact interaction between the particles and the contact process only has a one-way influence interaction, and the other direction has a constant rate of flipping.

The generator for a spin system with flip rate $c(x,\eta)$ is defined for $f \in D_0(X)$ as

$$Gf(\eta) = \sum_x c(x,\eta)(f(\eta^x) - f(\eta)). \tag{2.7}$$

where

$$\eta^x(z) = \begin{cases} \eta(z) & \text{if} \quad z \neq x \\ 1-\eta(z) & \text{if} \quad z = x \end{cases} \tag{2.8}$$

The sum (2.7) converges since f only depends on finitely many coordinates and $c(x,\eta)$ is bounded for any η and x.

Contact Process The contact process has two possible stationary distributions, δ_0 and $\bar{\nu}$. Since this process is monotone, we get an ordering on the invariant measures, $\delta_0 \leq \bar{\nu}$. The all 0's state is absorbing since no births can occur. This is represented by δ_0. If the birth rate is high enough though, we may get survival. The upper invariant measure, $\bar{\nu}$, comes from starting with all sites occupied, $\lim_{t\to\infty} \delta_1 S(t) = \bar{\nu}$, where δ_1 is

unit mass on the state with all 1's. We call the contact process ergodic if δ_0 is the only invariant measure, that is $\lim_{t\to\infty} \delta_1 S(t) = \delta_0$.

There is a critical value, λ_c, such that the contact process is ergodic when $\lambda < \lambda_c$. Arriving at exact values for this critical parameter has proven to be extremely difficult. For any dimension, d, the critical value is proven to have the following upper and lower bounds.

$$\frac{1}{2d-1} \leq \lambda_c \leq \frac{2}{d} \tag{2.9}$$

For $d = 1$, the critical parameter has been shown to be close to $\lambda_c \approx 1.6494$[23]. See Liggett for the proof of these statements. When the contact process is ergodic, the only stationary distribution is δ_0, the all 0's state. In order to simulate this process using CFTP it is necessary to fix a source of particle 1 so that all states communicate. On a finite grid this can be a boundary condition or an interior source of particles.

2.4.3 Mean Field Analysis

One of the tools which for understanding the dynamics for an interacting particle system are is mean field analysis. This involves turning our stochastic system into a system of ordinary differential equations. Assuming that the equations are accurately solvable by a typical numerical integrator, we can get an idea on how the fixed points and dynamics change for different parameter values. In order to do this, we start with a finite grid and assume that all sites are neighbors and interact at the same rate which we divide by the number of sites. With the assumption that all sites are independent we let the grid sizes go to infinity while keeping track of the percentages of the grid occupied by each particle type. This gives a system of ODE's.

Define $y_{Ni}(t)$ to be the fraction of sites occupied by particle type i at time t on a grid of size N. The neighborhood mass function is now the constant 1, $\phi(x, y) = 1$, constant across the whole grid, which makes any pair of particles as likely to interact as any other pair. This gets rid of all spatial dependencies and we get the mean field

equations:

$$y_i(t) = \lim_{N\to\infty} y_{Ni}(t) = \lim_{N\to\infty} \frac{n_i(t)}{N}$$

Where $n_i(t)$ = the number of type i at time t and N is the grid size.

For a rigorous theoretical development of diffusion equations and examples for interacting particle systems see DeMasi, Ferrari, and Lebowitz[7] and Durrett and Neuhauser[11].

The mean field equations for the contact process is just the logistic.

$$\frac{d}{dt}f(t) = \lambda f(t)\left(\frac{\lambda - 1}{\lambda} - f(t)\right)$$

The maximum growth rate is given by $r = \lambda - 1$, and the carrying capacity is $K = \frac{\lambda-1}{\lambda}$. So we see that if λ is positive, the species survives in the mean field solution. This does not give a close estimate for the critical value in the stochastic model, but leads us to believe that there is a critical value.

Now we go on to develop the framework of interaction map particle systems and a general theory of monotonicity for models which fall under this framework.

Chapter 3

Interaction Map Particle Systems

Up until now it was only necessary to declare the transition rates in order to define an interacting particle system model. However, when a larger variety of particle types with multiple types of interactions is desired, this is not enough. For example, a given particle value may not be restricted to just increasing or decreasing by 1. For this reason some new terminology is introduced along with a new way to define a particle interaction based model.

An *interaction map particle system* (or IMPS for short) is a type of interacting particle system whose behavior is defined by the interactions allowed to occur between particles. This class will include the contact process and voter model along with many other systems previously studied. The importance of the interaction map does not reveal itself for spin systems. The interactions for a spin system are built into the flip rate. The possible presence of more complicated interactions and transitions when more particles are included is significantly simplified by the interaction map.

First we start with a finite number of totally ordered particle values,

$$\{0, 1, 2, \cdots, n-1\} = \{i\}_{i=0}^{n-1} = S.$$

The state space is $X = S^{\Lambda}$ where $\Lambda \subset \mathbb{Z}^d$, and is a compact metric space. The usual order of integers induces a partial ordering on the state space.

3.1 Particle Interaction Map

The foundation of our approach is the establishment of the specific interactions that are allowed to occur between the particle types. For this the *particle interaction map* is defined.

Definition 13. Given a finite set of totally ordered particle values, S, the map, $\mathscr{J} : S \times S \to S$ is called a particle interaction map if its domain is all of $S \times S$.

This map requires two particles, b and a, as input, and gives the resulting effect on particle a. So $\mathscr{J}(b, a)$ is the resulting influence on particle type a by type b. By convention, b is called the neighboring particle. When particles a and b interact, the interaction has the potential to change particle a only. The domain of $\mathscr{J}$ is partitioned into sets of *up*, *null*, and *down* interactions: $\mathcal{U} = \{(b, a) \in S \times S | \mathscr{J}(b, a) > a\}$, $\mathcal{N} = \{(b, a) \in S \times S | \mathscr{J}(b, a) = a\}$, and $\mathcal{D} = \{(b, a) \in S \times S | \mathscr{J}(b, a) < a\}$. These represent interactions which result in larger, unchanged, and lower particle values respectively. Later on when these particles are distributed over a lattice, what these interactions mean will become more clear.

Figure 3.1 shows the interaction maps for two well studied spin systems.

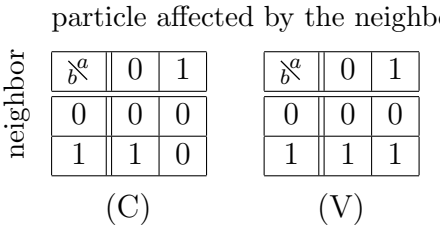


FIGURE 3.1. Interaction Maps for the Contact Process, (C), and Voter model, (V).

Although, there is no need to formulate these processes in terms of the interaction maps since the types of interactions allowed are limited to single possibilities in any case: there is only one possible change for each particle type since there are only

two particle types in total. When we expand to the multi-type contact process, this formulation becomes more useful.

b \ a	0	1	2
0	0	0	0
1	1	0	0
2	2	0	0

FIGURE 3.2. Interaction map formulation for the multi-type contact process

It may at first seem unnatural (except for the 0 particle) for each particle type in the multi-type contact process to interact with a 1 or 2 causing them to become 0's, but this is due to there being constant death rates. When a 1 or 2 is sitting at a site, since the rates for independent exponential random variables sum and the only transition is to become a 0, we get our constant death rates.

Definition 14. The interaction map, $\mathscr{J}$, is called *non-decreasing* on $A \subset S \times S$ if for any two (b_1, a_1) and (b_2, a_2) in A which satisfy $(b_1, a_1) \leq (b_2, a_2)$ (meaning $b_1 \leq b_2$ and $a_1 \leq a_2$), it follows that $\mathscr{J}(b_1, a_1) \leq \mathscr{J}(b_2, a_2)$.

Definition 15. The particle interaction map will be called *attractive* if it satisfies the following conditions:

(1) $\mathscr{J}$ is non-decreasing on $\mathcal{U}$.
(2) $\mathscr{J}$ is non-decreasing on $\mathcal{D}$.
(3) If $(b_1, a_1) \leq (b_2, a_2)$, $(b_1, a_1) \in \mathcal{U}$, and $(b_2, a_2) \in \mathcal{D} \cup \mathcal{N}$, then $\mathscr{J}(b_1, a_1) \leq a_2$.
(4) If $(b_1, a_1) \leq (b_2, a_2)$, $(b_1, a_1) \in \mathcal{U} \cup \mathcal{N}$, and $(b_2, a_2) \in \mathcal{D}$, then $a_1 \leq \mathscr{J}(b_2, a_2)$.

Notice that the last two conditions of Definition 15 can be restated as follows

(3′) If $(b_1, a_1) \in \mathcal{U}$, then $\mathscr{J}(b_1, a_1) \leq \min_a\{a : (b, a) \in \mathcal{D} \cup \mathcal{N}\}$.
(4′) If $(b_2, a_2) \in \mathcal{D}$, then $\max_a\{a : (b, a) \in \mathcal{U} \cup \mathcal{N}\} \leq \mathscr{J}(b_2, a_2)$.

The purpose of this definition is that interactions will preserve the ordering of configurations. It will later be seen to be a requirement for the process to be monotone. The basic idea is that up and down interactions are not allowed to occur simultaneously. If a given interaction between two sites is said to occur for a particular configuration of particles, then looking at the result of that interaction on a configuration above the original one considered should maintain this new, higher, configuration of particles above the other. This picture will become more transparent when the transition rates are introduced and a more detailed description of the process is given.

The first two conditions state that when considering the interaction between two sites, if the particle number is increased or decreased at one of the sites, the result should preserve this order. The third condition states that if a configuration is such that an up transition is possible for a particular site and its neighbor, then the resulting replacement particle cannot be above that for any higher configuration for which the possible transition is null or down. The last condition makes a similar statement. If a configuration allows a down transition for a particular site and its neighbor, then the replacement particle cannot be below that for any lower configuration having the only possible transition as null or up. To check these conditions manually can be a difficult task if there is a large number of particles or a complicated list of interactions. For this reason a computer code is easy to construct and does the job much more efficiently.

Definition 16. Given some interaction map, $\mathscr{J}$, particle value b is said to be *first reachable* by particle value a, if there exists a particle value $\tilde{a}$ such that $\mathscr{J}(\tilde{a}, a) = b$.

Definition 17. Given an interaction map, $\mathscr{J}$, particle b is said to be *accessible* by particle a, if there exist particle values $a_1, a_2, ..., a_n$ such that a_1 is first reachable by a, a_{k+1} is first reachable by a_k for $k = 1, ..., n-1$, and b is first reachable by a_n

Definition 18. Given some interaction map, $\mathscr{J}$, two particle values, a and b, are said to *communicate* if they are both accessible by each other.

Definition 19. The particle interaction map will be called *irreducible* if all particles communicate.

If we have an irreducible interaction map, we would like to build an irreducible process from it. An irreducible interaction map does not guarantee an irreducible process however. Just as with the absorbing all 0's state of the contact process, we may have absorbing states or classes. Irreducibility of the interaction map only guarantees that any particle can eventually be replaced by any other given a proper external configuration of neighboring particles. In the case that absorbtion into a certain state or class does occur. Irreducibility can often be achieved by the inclusion of sources for particles that tend to die out. For example, the contact process restricted to a finite grid can be made irreducible by including a boundary condition with a fixed population of 1's or an interior region of fixed 1's. For the study of invasions, if the invading species can be shown to die out, then the invasion is unsuccessful. In the finite grid model, the probability of extinction is always positive, so we will study a finite grid model later where the invasive species has a constant boundary source.

3.1.1 Constructing Attractive Interaction Maps

To understand the properties of an attractive interaction map is a little difficult from merely reading the definition. The following lemmas should provide more insight. What we want to achieve is a rigorous development of the mathematical structure resulting from Definition 15.

Lemma 20. If $(b, a) \in \mathcal{D}$, for an attractive interaction map $\mathscr{J}$, then for any $b_1 < b$, $(b_1, a) \in \mathcal{D}$ as well. Similarly, if $(b, a) \in \mathcal{U}$, then for any $b_2 > b$, $(b_2, a) \in \mathcal{U}$.

Proof. Assume that $(b, a) \in \mathcal{D}$ and that $(b-1, a) \in \mathcal{U} \cup \mathcal{N}$. By condition (4) in the definition of an attractive interaction map, $\mathscr{J}(b, a) \geq a$. However this is contradictory since it is a strict down transition.

If we assume that $(b, a) \in \mathcal{U}$ and that $(b+1, a) \in \mathcal{D} \cup \mathcal{N}$, then by condition (3) of definition 15 we have $\mathscr{J}(b, a) \leq a$. This again is a contradiction. We have only shown the result for changing the neighbor's particle value by one, but the rest follow by induction. □

Theorem 21. The interaction map $\mathscr{J}$ is attractive if and only if

(1) $\mathscr{J}$ is non-decreasing on $\mathcal{U} \cup \mathcal{N}$ and non-decreasing on $\mathcal{D} \cup \mathcal{N}$,

(2) If $\exists b, a \in S$, such that $(b, a) \in \mathcal{U}$, and $(b, a+1) \in \mathcal{D}$, then $\mathscr{J}(b, a) = a+1$ and $\mathscr{J}(b, a+1) = a$.

Proof. First assume we have an attractive interaction map, $\mathscr{J}$. Take $(b_1, a_1) \leq (b_2, a_2)$ and both are in $\mathcal{U} \cup \mathcal{N}$. Because $\mathscr{J}$ is non-decreasing on $\mathcal{U}$, the only issue is when $(b_1, a_1) \in \mathcal{U}$ and $(b_2, a_2) \in \mathcal{N}$. But due to (3) of definition 15, $\mathscr{J}(b_1, a_1) \leq a_2$. Similarly, if $(b_1, a_1) \in \mathcal{N}$ and $(b_2, a_2) \in \mathcal{D}$, $\mathscr{J}(b_2, a_2) \geq a_1$. Together these prove that (1) in the statement of the theorem holds.

For the second statement of the theorem, note that $a < \mathscr{J}(b, a) \leq a+1$ and $a \leq \mathscr{J}(b, a+1) < a+1$ must be true due to the third and fourth conditions of Definition 15. Then it holds that $\mathscr{J}(b, a) = a+1$ and $\mathscr{J}(b, a+1) = a$.

Now we assume that the statements of the theorem are satisfied and show that the conditions of Definition 15 follow. Beginning with statement (1) of the theorem, the first two conditions of Definition 15 directly follow since $\mathcal{U}$ and $\mathcal{D}$ are subsets of $\mathcal{U} \cup \mathcal{N}$ and $\mathcal{D} \cup \mathcal{N}$ respectively.

Next, take arbitrary $(b_1, a_1) \in \mathcal{U}$ and $(b_2, a_2) \in \mathcal{D} \cup \mathcal{N}$ with $(b_1, a_1) \leq (b_2, a_2)$, and define $\tilde{a} = \max\{a : (b_1, a_1) \leq (b_2, a), a < a_2, (b_2, a) \in \mathcal{U}\}$. By this, it should be clear

that $(b_2, \tilde{a}+1) \in \mathcal{D} \cup \mathcal{N}$ and $\tilde{a}+1 \leq a_2$. Then the next steps follow:

$$\mathscr{J}(b_1, a_1) \leq \mathscr{J}(b_2, \tilde{a}), \text{By (1) of the theorem statement}$$
$$\text{and } \mathscr{J}(b_2, \tilde{a}+1) \leq \tilde{a}+1 \leq a_2.$$

If $(b_2, \tilde{a}+1) \in \mathcal{D}$, then by statement (2) of the theorem, $\mathscr{J}(b_2, \tilde{a}) = \tilde{a}+1$, and $\mathscr{J}(b_2, \tilde{a}+1) = \tilde{a}$. Then $\mathscr{J}(b_1, a_1) \leq \mathscr{J}(b_2, \tilde{a}) = \tilde{a}+1 \leq a_2$ because (b_1, a_1) and $(b_2, \tilde{a})$ are contained in $\mathcal{U}$.

If $(b_2, \tilde{a}+1) \in \mathcal{N}$, then $\mathscr{J}(b_1, a_1) \leq \mathscr{J}(b_2, \tilde{a}+1) = \tilde{a}+1 \leq a_2$ by statement (1) of the theorem since both (b_1, a_1) and $(b_2, \tilde{a}+1)$ are members of $\mathcal{U} \cup \mathcal{N}$.

We conclude that $\mathscr{J}(b_1, a_1) \leq a_2$ satisfying (3) of Definition 15. Now, take arbitrary $(b_1, a_1) \in \mathcal{U} \cup \mathcal{N}$ and $(b_2, a_2) \in \mathcal{D}$ with $(b_1, a_1) \leq (b_2, a_2)$, and define $\tilde{a} = \min\{a : (b_1, a) \leq (b_2, a_2), a_1 < a, (b_1, a) \in \mathcal{D}\}$. By this, it should be clear that $(b_1, \tilde{a}-1) \in \mathcal{U} \cup \mathcal{N}$ and $a_1 \leq \tilde{a}-1$. The following inequalities then hold:

$$\mathscr{J}(b_1, a_1) \leq \mathscr{J}(b_1, \tilde{a}-1), \text{By (1) of the theorem statement}$$
$$\text{and } a_1 \leq \tilde{a}-1 \leq \mathscr{J}(b_1, \tilde{a}-1).$$

If $(b_1, \tilde{a}-1) \in \mathcal{U}$, then by statement (2) of the theorem, $\mathscr{J}(b_1, \tilde{a}) = \tilde{a}-1$, and $\mathscr{J}(b_1, \tilde{a}-1) = \tilde{a}$. Then $a_1 \leq \tilde{a}-1 = \mathscr{J}(b_1, \tilde{a}) \leq \mathscr{J}(b_2, a_2)$ because $(b_1, \tilde{a})$ and (b_2, a_2) are are contained in $\mathcal{D}$.

If $(b_1, \tilde{a}-1) \in \mathcal{N}$, then $a_1 \leq \tilde{a}-1 = \mathscr{J}(b_1, \tilde{a}-1) \leq \mathscr{J}(b_2, a_2)$ by statement (1) of the theorem since both $(b_1, \tilde{a}-1)$ and (b_2, a_2) are members of $\mathcal{D} \cup \mathcal{N}$.

We conclude that $a_2 \leq \tilde{a}-1 \leq \mathscr{J}(b_2, a_2)$ satisfying (4) of Definition 15. This proves that the definition of attractive is equivalent to the statements given by Lemma 21. □

Theorem 21 gives us a more intuitive picture of what an attractive interaction

map actually looks like. When going directly from the set $\mathcal{U}$ to $\mathcal{D}$ horizontally(in terms of the table formats given), there is exactly a decrease of one. This can be seen in Figure 3.3 below. In example (a) $\mathscr{J}(2,1) = 2$, an up transition, and $\mathscr{J}(2,2) = 1$, a down transition, so we can see that this satisfies Theorem 21.

Lemma 22. If $\mathscr{J}$ is an attractive interaction map, $a_1 < a_2$, and for some particle, b, $\mathscr{J}(b,a_1) > \mathscr{J}(b,a_2)$, then $(b,a_1) \in \mathcal{U}$ and $(b,a_2) \in \mathcal{D}$.

Proof. If $(b,a_1) \in \mathcal{D} \cup \mathcal{N}$, then the interaction map cannot be defined for a_2. If $a_2 \in \mathcal{D} \cup \mathcal{N}$, there is a problem because the attractive interaction map is non-decreasing on $\mathcal{D} \cup \mathcal{N}$ and $a_1 < a_2$ would mean that $\mathscr{J}(b,a_1) \leq \mathscr{J}(b,a_2)$. We also find that (b,a_2) is not a member of $\mathcal{U}$ since we get the inequality $a_2 > a_1 \geq \mathscr{J}(b,a_1) > \mathscr{J}(b,a_2)$ by the statement of the lemma when assuming $(b,a_1) \in \mathcal{D} \cup \mathcal{N}$. From this we see that $\mathscr{J}(b,a_2) > a_2$ as well if $(b,a_2) \in \mathcal{U}$. So $(b,a_1) \in \mathcal{U}$ is the only possibility. Now (b,a_2) must be a member of $\mathcal{D}$ because $\mathscr{J}$ is non-decreasing on $\mathcal{U} \cup \mathcal{N}$, and $a_1 < a_2$ would have to give $\mathscr{J}(b,a_1) \leq \mathscr{J}(b,a_2)$ which is contrary to the assumption of the lemma. □

Lemma 23. If $\mathscr{J}$ is an attractive interaction map, $(b,a_1) \in \mathcal{U} \cup \mathcal{N}$, $(b,a_2) \in \mathcal{D} \cup \mathcal{N}$, and $a_1 < a_2$, and $\mathscr{J}(b,a_1) > \mathscr{J}(b,a_2)$, then define $\tilde{a} = \mathscr{J}(b,a_1)$ and the following equations hold:

$$\text{For } a \in [a_1..\tilde{a}-1],\ \mathscr{J}(b,a) = \tilde{a} \tag{3.1a}$$

$$\text{For } a \in [\tilde{a}..a_2],\ \mathscr{J}(b,a) = \tilde{a} - 1 \tag{3.1b}$$

Proof. By lemma 22, $(b,a_1) \in \mathcal{U}$ and $(b,a_2) \in \mathcal{D}$. Combining this with the fact that this interaction map is attractive we also have, by properties (3) and (4) of definition 15, $\mathscr{J}(b,a_1) \leq a_2$ and $a_1 \leq \mathscr{J}(b,a_2)$. Choose an arbitrary $a \in [a_1..\tilde{a}-1]$. If $(b,a) \in \mathcal{D} \cup \mathcal{N}$, then $a_1 < \tilde{a} = \mathscr{J}(b,a_1) \leq a \leq \tilde{a} - 1$ which is contradictory

so $(b,a) \in \mathcal{U}$. Now take $a \in [\tilde{a}..a_2]$. Suppose $(b,a) \in \mathcal{U} \cup \mathcal{N}$. This would give $a_2 \geq \tilde{a} = \mathscr{J}(b,a_1) \geq a > \tilde{a} - 1$ which is a contradiction as well, so $(b,a) \in \mathcal{D}$.

For $a \in [a_1..\tilde{a}-1]$, $\tilde{a} = \mathscr{J}(b,a_1) \leq \mathscr{J}(b,a) \leq \tilde{a}$ because $\tilde{a} \in \mathcal{D}$, so $\mathscr{J}(b,a) = \tilde{a}$. For $a \in [\tilde{a}..a_2]$, $\tilde{a} - 1 \leq \mathscr{J}(b,a) \leq \mathscr{J}(b,a_2) < \mathscr{J}(b,a_1) = \tilde{a}$ because $\tilde{a} - 1 \in \mathcal{U}$, so $\mathscr{J}(b,a) = \tilde{a} - 1$. This completes the proof. □

In other words, if the conditions for this lemma are satisfied, then the interaction map is a step function from one value to the other across the interval $[a_1..a_2]$ for fixed b.

Theorem 24. The interaction map $\mathscr{J}$ is attractive if and only if given any $(b,a) \in S \times S$, $\mathscr{J}(b,a) \leq \mathscr{J}(b+1,a)$ and only one of the following is satisfied:

(1) $\mathscr{J}(b,a) \leq \mathscr{J}(b,a+1)$.

(2) $\mathscr{J}(b,a) = a+1$ and $\mathscr{J}(b,a+1) = a$.

Option (2) above holds if and only if $(b,a) \in \mathcal{U}$ and $(b,a+1) \in \mathcal{D}$

The picture developed here is that an attractive interaction map is step-wise non-decreasing on all sets $S \times \{a\}$. It is step-wise non-decreasing on all sets $\{b\} \times S$ except for required decreases by exactly one on when we go directly from $\mathcal{U}$ to $\mathcal{D}$ from particle pairs (b,a) to $(b,a+1)$, and on this jump, the value the map, $\mathscr{J}$, takes must go from $a+1$ to a.

The interaction map of the multi-type contact process, Figure 3.2, is not attractive because $\mathscr{J}(2,0) = 2 > \min_a\{a : (2,a) \in \mathcal{N} \cup \mathcal{D}\} = 1$. There are several ways to modify this interaction map into one which is attractive. First it seems that we would want to keep the births onto empty sites unchanged. But this means that $\mathscr{J}(2,1) = 2$ is necessary, which amounts to the invasive species seeing the native as non-different from and empty site. This then also forces the requirement that $\mathscr{J}(2,2) = 1$ or 2. It seems more natural to choose the latter, which would eliminate the crowding affect on

the invader, although the first choice could also be reasonable, saying that when the invasive is too densely populated, it is easier for the native to come back in. Figure 3.3 gives these attractive versions of the multi-type contact process interaction map.

$\overset{a}{b}$	0	1	2
0	0	0	0
1	1	0	0
2	2	2	1

(a) Species 1 reinvades by a 2–2 interaction

$\overset{a}{b}$	0	1	2
0	0	0	0
1	1	0	0
2	2	2	2

(b) Species 2 immune to 2–2 interaction.

FIGURE 3.3. Attractive interaction map modifications to the multi-type contact process

3.2 Transition Rates

The transitions for these particle models have been split into two varieties. An *up* transition will be one where the interaction results in a larger particle value, a transition will be called *down* when the interaction results in a smaller particle value. The functions $r_u(\eta, x, y)$ and $r_d(\eta, x, y)$ will denote these transition rates respectively.

$$r_u(\eta, x, y) = \sum_{a \in S, b \in \mathcal{U}_a} \lambda_{ba} \phi(x, y) I_{\{(b,a)\}}(\eta(y), \eta(x)) \tag{3.2a}$$

$$r_d(\eta, x, y) = \sum_{a \in S, b \in \mathcal{D}_a} \lambda_{ba} \phi(x, y) I_{\{(b,a)\}}(\eta(y), \eta(x)) \tag{3.2b}$$

The summation is over the sets $\mathcal{U}_a = \{b \in S : \mathscr{J}(b, a) > a\}$ and $\mathcal{D}_a = \{b \in S : \mathscr{J}(b, a) < a\}$, which split the particles into those causing up and down transitions respectively. Null interactions are not accounted for here since a null transition does not change any state, thus their rates need no consideration.

We require that $\sum_y \phi(x, y) < \infty$ (or maybe need $\phi(x, y) = 0$ for $|x - y| > \rho$

for some $\rho < \infty$, or $\sum_y p(x,y) = 1$, where $p(x,y) = \phi(x,y)/\sum_y \phi(x,y))$ for any x, and typically $\max \phi = 1$, so that λ_{ba} will be the maximum transition rate for a particular interaction, and ϕ will be referred to as the *neighborhood mass function* since it defines how the strength of the interaction depends on a particular neighbor(or the probability that a particular neighbor is chosen to interact with suing $p(x,y)$).

The parameter λ_{ba}, is the rate parameter controlling the interaction that particle type $a \xrightarrow{b} \mathscr{J}(b,a)$ due to the presence of a particle of type b in its neighborhood. If $\lambda_{ba} \equiv 0$ for some a and b, then by convention, we put $(b,a) \in \mathcal{N}$, choosing $\mathscr{J}(b,a) = a$, for the process. This is so that all interactions will either have non-identically zero rates or be of the null variety.

The total transition rate will be denoted $r(\eta,x,y) = r_u(\eta,x,y) + r_d(\eta,x,y)$. This combining of up and down rates is appropriate since r_u and r_d can not be simultaneously nonzero for any given configuration due to the nature of the interaction map; an interaction is strictly either up, down, or null.

Example: For the nearest neighbor contact process, the transition rates are

$$\begin{aligned} r_u(\eta,x,y) &= \lambda_{10}\phi(x,y)I_{\{(1,0)\}}(\eta(y),\eta(x)) \\ r_d(\eta,x,y) &= \delta\phi(x,y)I_{\{(0,1)\}}(\eta(y),\eta(x)) + \delta\phi(x,y)I_{\{(1,1)\}}(\eta(y),\eta(x)) \\ &= \delta\phi(x,y)I_{\{1\}}(\eta(x)) \end{aligned}$$

where

$$\phi(x,y) = \begin{cases} 1 & \text{if } |x-y| = 1 \\ 0 & \text{otherwise} \end{cases} \tag{3.4}$$

There is a difference here that should be taken note of. The contact process is usually stated with a constant death rate of 1. In the current IMPS formulation, this amounts to $\delta = 1/4$ since we sum over the whole neighbor hood to get the total rate of death for particle type 1. If we let $\delta = 1$ in this formulation, then we are essentially rescaling time and would need to take note of how this changes the critical value for

λ_{10}, which is usually just denoted by λ or β. Once again, this formulation may seem more complicated for a spin system, although consistent with, but later on it will become clear that it is appropriate for more complex systems.

The usual way to define the transitions for a process like this is to define f_b as the fraction of neighbors of particle type b for a finite neighborhood of size N. Assuming that $\phi(x, y) = 1/N$ on this neighborhood and is zero elsewhere gives the transition and rate shown in (3.5).

$$\begin{array}{cc} \text{Transition} & \text{Rate} \\ a \to c & \displaystyle\sum_{b:\mathscr{J}(b,a)=c} \lambda_{ba} f_b. \end{array} \tag{3.5}$$

This list should contain all transitions allowed by the model. The interaction map formulation is consistent with this due to the additivity of exponential rates.

Definition 25. The generator for an IMPS is the closure in $C(X)$ of the operator defined on $D(X)$, by

$$Gf(\eta) = \sum_{x,y} r(\eta, x, y)(f(\eta^{xy}) - f(\eta)) \tag{3.6}$$

The state η^{xy} represents the state η with the site x changed according to its interaction with the site y:

$$\eta^{xy}(z) = \begin{cases} \eta(z) & \text{if} \quad z \neq x \\ \mathscr{J}(\eta(y), \eta(x)) & \text{if} \quad z = x \end{cases}. \tag{3.7}$$

This notation is similar to what has been used before to denote a two particle jump or swap but differs in that it is only a change at a single site[23, 14]. The process is said to have *finite range* rates if the interactions occur over a finite neighborhood only,

meaning that there exists a $\rho < \infty$ such that $\phi(x, y) = 0$ for $|x - y| > \rho$. It should be noted also that these rates are assumed to be bounded, $\sup_x \sum_y r(\eta, x, y) < \infty$. This holds true since

$$\sup_x \sum_y r(\eta, x, y) = \sup_x \sum_y \lambda_{\eta(y)\eta(x)} \phi(x, y) \leq \max_{x,y} \phi(x, y) \cdot \max_{a,b} \lambda_{ba}.$$

This is obvious now since the λ_{ba}'s are only numbers and ϕ is bounded.

3.3 Stationary Distributions

Conjecture 1. Assume we have an IMPS with an irreducible interaction map and state space $X = S^\Lambda$, where Λ has a finite number of sites. Then there exist subsets of Λ, $\{A_k; k = 1, ..., m\}$ and particle values $\{a_k; k = 1, ..., m\}$ such that the process restricted to the state space $\tilde{X} \subset S^\Lambda$ is irreducible and ergodic. Where $\eta \in \tilde{X}$ means that $\eta(x) = a_k$ when $x \in A_k$ for all $k = 1, ..., m$.

An example of this restriction of the state space is fixing boundary conditions on a finite grid. Another example is the inclusion of source areas of particles that will not appear in the process if they are not there initially. For example, a plant needs to be initially present to spread seeds and increase its geographical range. If this plant has the ability to survive and remain present in the stationary states of the given environmental conditions, then automatically two stationary distributions will be present. One is when the plant is initially absent and the other when it is initially present in a sufficient density. The finite grid contact process will always have the absorbing all 0's state, but if any source of 1's is fixed on a finite grid process then there is a positive probability that the all 0's state will reach any other state in finite time.

Another approach that is not explored here is to allow spontaneous births of 1's for the contact process. Normally for ecological models, a species will not appear if it

is absent, so allowing spontaneous births allows it to always appear. When included at low rates, this is thought of as rare long range dispersal events. To include these event, the inclusion of multiple interaction maps is necessary and is briefly discussed at the end of this chapter.

3.4 Coupling

Suppose we have two IMPS, $\eta_{\mathbf{t}}$ and $\xi_{\mathbf{t}}$, with transition rates $r_1(\eta, x, y)$ and $r_2(\xi, x, y)$ respectively, with $r_i(\cdot, x, y) = r_{iu}(\cdot, x, y) + r_{id}(\cdot, x, y)$. The coupling to follow is essentially the same as the Vasershtein coupling[37] given for spin systems, also known as the basic coupling[23]. The main desire is that the processes evolve together in such a way that keeps them closely related and each process adheres to the correct marginal rate. The coupled process, $(\eta_{\mathbf{t}}, \xi_{\mathbf{t}})$, will be a Feller process whose state space is $X \times X$.

The coupled process evolves according to the following rates:

$$(\eta, \xi) \to \begin{cases} (\eta^{xy}, \xi^{xy}) & \text{at rate} \quad \tilde{r}(\eta, \xi, x, y) \\ (\eta, \xi^{xy}) & \text{at rate} \quad r_2(\xi, x, y) - \tilde{r}(\eta, \xi, x, y) \\ (\eta^{xy}, \xi) & \text{at rate} \quad r_1(\eta, x, y) - \tilde{r}(\eta, \xi, x, y) \end{cases} . \tag{3.8}$$

With $\tilde{r}(\eta, \xi, x, y) = \min(r_{1u}(\eta, x, y), r_{2u}(\xi, x, y)) + \min(r_{1d}(\eta, x, y), r_{2d}(\xi, x, y))$. So the generator for coupled processes is defined for $f \in C(X \times X)$, the space of continuous functions on $X \times X$, by

$$\tilde{G}f(\eta, \xi) = \sum_{x,y} (r_1(\eta, x, y) - \tilde{r}(\eta, \xi, x, y))(f(\eta^{xy}, \xi) - f(\eta, \xi)) \tag{3.9a}$$

$$+ \sum_{x,y} (r_2(\xi, x, y) - \tilde{r}(\eta, \xi, x, y))(f(\eta, \xi^{xy}) - f(\eta, \xi)) \tag{3.9b}$$

$$+ \sum_{x,y} \tilde{r}(\eta, \xi, x, y)(f(\eta^{xy}, \xi^{xy}) - f(\eta, \xi)) \tag{3.9c}$$

The generator can also be simplified into the following form:

$$\begin{aligned}\tilde{G}f(\eta,\xi) = & \sum_{x,y\in x+N(\rho)} (r_1(\eta,x,y)(f(\eta^{xy},\xi)-f(\eta,\xi)) \\ & +\sum_{x,y} (r_2(\xi,x,y)(f(\eta,\xi^{xy})-f(\eta,\xi)) \\ & +\sum_{x,y} \tilde{r}(\eta,\xi,x,y)(f(\eta^{xy},\xi^{xy})-f(\eta^{xy},\xi)-f(\eta,\xi^{xy})+f(\eta,\xi))\end{aligned}$$

Lemma 26. (Extension of Lemma 1.2 from Liggett IPS p.125) Suppose that $f \in D(X \times X)$ and $g \in D(X)$.

(1) If $f(\eta,\xi) = g(\eta)$, then $\tilde{G}f(\eta,\xi) = G_1 g(\eta)$, and

(2) If $f(\eta,\xi) = g(\xi)$, then $\tilde{G}f(\eta,\xi) = G_2 g(\xi)$,

Where G_1 and G_2 are the generators corresponding to the rates r_1 and r_2 respectively.

Proof. If $f(\eta,\xi) = g(\eta)$, then

$$\begin{aligned}\tilde{G}f(\eta,\xi) = & \sum_{x,y} r_1(\eta,x,y)(f(\eta^{xy},\xi)-f(\eta,\xi)) \\ & +\sum_{x,y} r_2(\xi,x,y)(f(\eta,\xi^{xy})-f(\eta,\xi)) \\ & +\sum_{x,y} \tilde{r}(\eta,\xi,x,y)(f(\eta^{xy},\xi^{xy})-f(\eta^{xy},\xi)-f(\eta,\xi^{xy})+f(\eta,\xi)) \\ = & \sum_{x,y} (r_1(\eta,x,y)(g(\eta^{xy})-g(\eta)) \\ & +\sum_{x,y} (r_2(\xi,x,y)(g(\eta)-g(\eta)) \\ & +\sum_{x,y} \tilde{r}(\eta,\xi,x,y)(g(\eta^{xy})-g(\eta^{xy})-g(\eta)+g(\eta)) \\ = & \sum_{x,y} (r_1(\eta,x,y)(g(\eta^{xy})-g(\eta)) \\ = & \; G_1 g(\eta)\end{aligned}$$

This proves the first part and the second part also follows in a similar way. □

Theorem 27. (Extension of Theorem 1.3 from Liggett IPS p126) The closure of $\tilde{G}$ in $C(X \times X)$ is the generator of a Markov semigroup $\tilde{S}(t)$ on $C(X \times X)$. Given $g \in C(X)$, if $f(\eta, \xi) = g(\eta)$, then $\tilde{S}(t)f(\eta, \xi) = S_1(t)g(\eta)$, and if $f(\eta, \xi) = g(\xi)$, then $\tilde{S}(t)f(\eta, \xi) = S_2(t)g(\xi)$, where $S_i(t)$ is the semigroup with generator G_i. In particular, if (η_t, ξ_t) is a Feller process with semigroup $\tilde{S}(t)$, then η_t and ξ_t are separately Markovian with semigroups $S_1(t)$ and $S_2(t)$ respectively.

The proof of Theorem 27 is almost identical to that in Liggett. The only difference is the form of the rate functions. Now we are ready to prove that an attractive interaction map preserves an ordering almost surely on two processes coupling together as described above when the transition rates satisfy certain restrictions.

Theorem 28. (Extension of Theorem 1.5 from Liggett IPS p127) Define the closed set $K = \{(\eta, \xi) \in X \times X : \eta \leq \xi\}$. Suppose that the interaction map is attractive and thus satisfies

(1) $\mathscr{J}$ is non-decreasing on $\mathcal{U}$

(2) $\mathscr{J}$ is non-decreasing on $\mathcal{D}$

(3) If $b_1 \leq b_2$, $a_1 \leq a_2$, $(b_1, a_1) \in \mathcal{U}$, and $(b_2, a_2) \in \mathcal{D} \cup \mathcal{N}$, then $\mathscr{J}(b_1, a_1) \leq a_2$

(4) If $b_1 \leq b_2$, $a_1 \leq a_2$, $(b_1, a_1) \in \mathcal{U} \cup \mathcal{N}$, and $(b_2, a_2) \in \mathcal{D}$, then $a_1 \leq \mathscr{J}(b_2, a_2)$

Furthermore suppose that whenever $\eta \leq \xi$,

$$r_{1u}(\eta, x, y) \leq r_{2u}(\xi, x, y) \quad \text{when} \quad \eta^{xy}(x) > \xi(x), \tag{3.10a}$$

$$r_{1d}(\eta, x, y) \geq r_{2d}(\xi, x, y) \quad \text{when} \quad \xi^{xy}(x) < \eta(x). \tag{3.10b}$$

Then for all $(\eta, \xi) \in K$ and $t \geq 0$,

$$P^{(\eta,\xi)}[(\eta_t, \xi_t) \in K] = 1. \tag{3.11}$$

Proof. Define $\mathscr{A} \subset C(X \times X)$ to be the subset of functions which are non-negative everywhere and 0 on K. Since $\mathscr{R}(I - \lambda\tilde{G}) = C(X \times X)$ (Prop. 2.8 p.15 Liggett IPS), there exists $h \in \mathscr{D}(\tilde{G})$ such that $(I - \lambda\tilde{G})h = f$ for each $f \in \mathscr{A}$ and $\lambda \geq 0$. Fix $f \in \mathscr{A}$, and define h by $h - \lambda\tilde{G}h = f$. Because K is compact, there exists an $(\eta, \xi) \in K$ where h achieves its maximum. The following cases will show that the generator applied to $h(\eta, \xi)$ is strictly non-positive.

Case 1 If $\xi(x) < \eta^{xy}(x)$, then $r_{1u}(\eta, x, y) \leq r_{2u}(\xi, x, y)$ by (3.10a). Since

$$\tilde{r}(\eta, \xi, x, y) = \min(r_{1u}(\eta, x, y), r_{2u}(\xi, x, y)),$$

we get $r_1(\eta, x, y) - \tilde{r}(\eta, \xi, x, y) = 0$. So the problem transition, $(\eta, \xi) \to (\eta^{xy}, \xi)$, occurs at rate zero by (3.8). The term (3.9a) disappears from the generator and all that is left are transitions which remain in the set K. Because (η, ξ) is where h achieves its maximum, the remaining terms of the generator, (3.9b) and (3.9c) are non-positive.

Case 2 If $\xi^{xy}(x) < \eta(x)$, $r_{1d}(\eta, x, y) \geq r_{2d}(\xi, x, y)$ by (3.10b). Then $r_2(\eta, x, y) - \tilde{r}(\eta, \xi, x, y) = 0$ since r_2 is the minimum here leading to $(\eta, \xi) \to (\eta, \xi^{xy})$ at rate zero. Once again, similar to the above calculation, the term (3.9b) is now zero. The remaining terms are non-positive since h achieves its maximum at (η, ξ).

Case 3 If $\xi(x) < \xi^{xy}(x)$ and $\eta(x) < \eta^{xy}(x)$, then $\eta^{xy}(x) \leq \xi^{xy}(x)$ by the first attractive interaction map property. Assuming that $\xi(x) < \eta^{xy}(x)$ would put us back in case 1 and we are done. If we assume that $\eta^{xy}(x) \leq \xi(x)$, then there are no problem transitions meaning that every possible coupled transition in (3.8) remains in the set K. Once again since (η, ξ) is where h attains its maximum, the generator remains non-positive in this case.

Case 4 If $\xi^{xy}(x) < \xi(x)$ and $\eta^{xy}(x) < \eta(x)$, then $\eta^{xy}(x) \leq \xi^{xy}(x)$ by the second attractive interaction map property. If $\xi^{xy}(x) < \eta(x)$, then we are back in case 2, otherwise all transitions keep us in K and the generator is non-positive.

Case 5 If $\eta(x) < \eta^{xy}(x)$ and $\xi^{xy}(x) \leq \xi(x)$, then $\eta^{xy}(x) \leq \xi(x)$ by the third attractive interaction map property. So $\tilde{r}(\eta, \xi, x, y) = 0$ since the minimum up transition rate is 0 as is the minimum down transition rate. This gives $(\eta, \xi) \to (\eta^{xy}, \xi^{xy})$ at rate zero. The remaining transitions keep us in K.

Case 6 If $\eta(x) \leq \eta^{xy}(x)$ and $\xi^{xy}(x) < \xi(x)$, then $\eta(x) \leq \xi^{xy}(x)$ by the fourth attractive interaction map property. So $\tilde{r}(\eta, \xi, x, y) = 0$ since the minimum up transition rate is 0 as is the minimum down transition rate. This gives and $(\eta, \xi) \to (\eta^{xy}, \xi^{xy})$ at rate zero once again remaining in K for the final case.

This shows that for all possible cases, $\lambda\tilde{G}h(\eta, \xi) \leq 0$ so that $h(\eta, \xi) \leq h(\eta, \xi) - \lambda\tilde{G}h(\eta, \xi) = f(\eta, \xi) = 0$. Since $\min_{(\zeta_1,\zeta_2)\in X\times X} h(\zeta_1, \zeta_2) \geq \min_{(\zeta_1,\zeta_2)\in X\times X} f(\zeta_1, \zeta_2)$ (Prop. 2.8 p.15 with Def. 2.1 p.12 Liggett IPS), we see that $h = 0$ on K, concluding that $h \in \mathscr{A}$. Since $(I - \lambda\tilde{G})^{-1}$ maps $\mathscr{A}$ to itself, so does $\tilde{S}(t)$ (Hille Yoshida Thm). Since this is true for any $f \in \mathscr{A}$, when $(\eta, \xi) \in K$, $P^{(\eta,\xi)}[(\eta_t, \xi_t) \in K] = 1$ for any t. □

With the assumptions of Theorem 28, if μ_1 and μ_2 are probability measures on X with $\mu_1 \leq \mu_2$, then $S(t)\mu_1 \leq S(t)\mu_2$ by Corollary 1.7 in Liggett IPS. This will be useful in the next section for proving the equivalence of monotonicity and attractiveness.

3.5 Monotonicity and Attractiveness

Monotonicity for this type of process requires restrictions on the interaction map in addition to restrictions on the transitions rates.

Definition 29. An IMPS will be called *attractive* if it has an attractive particle interaction map and given $\eta \leq \xi$, the transition rates satisfy:

$$r_u(\eta, x, y) \leq r_u(\xi, x, y) \quad \text{when} \quad \mathscr{J}(\eta(y), \eta(x)) > \xi(x), \tag{3.12a}$$

$$r_d(\eta, x, y) \geq r_d(\xi, x, y) \quad \text{when} \quad \mathscr{J}(\xi(y), \xi(x)) < \eta(x). \tag{3.12b}$$

Definition 29 is similar to the definition of attraction for spin systems given by Liggett[23]. The importance of the interaction map does not reveal itself for spin systems though, since the interactions are built into the flip rate. Separating the transitions rates from the interactions simplifies the system here.

To understand what the inequalities of Definition 29 mean, consider two ordered configurations, $\eta \leq \xi$. In the event that η could possibly jump above ξ at the site x, the latter must have a faster up transition rate(and be going to the same or a higher particle value). When the upper could possibly jump below the lower configuration, the latter must have a larger down transition rate. These definitions together will guarantee monotonicity for the process, and the next step is to show that they are indeed necessary.

Theorem 30. (Extension of Theorem 2.2 from Liggett IPS p.134): An IMPS is monotone if and only if it is attractive.

Proof. Assuming the process is attractive and given two arbitrary and ordered initial distributions on X, $\mu_1 \leq \mu_2$, we will show that $\mu_1 S(t) \leq \mu_2 S(t)$ which is equivalent to monotonicity of the process by Definition 11. For the coupled process (3.8), we are assured the existence of the initial distribution, ν on $X \times X$, according to Theorem 12. Since $\tilde{S}(t)$ is the semigroup of the coupled process, we know $\nu\tilde{S}(t)(\{(\eta, \xi) : \eta \leq \xi\}) = 1$ by Theorem 28. The marginal distributions of $\nu\tilde{S}(t)$ are $\mu_1 S(t)$ and $\mu_2 S(t)$

which proves that $\mu_1 S(t) \leq \mu_2 S(t)$ by Theorem 12, completing the proof that the attractive process is monotone.

Assuming that the process is monotone we must prove that it is attractive. Choose an x and b such that $\eta(x) \leq \xi(x) < b$. This will be used to prove conditions on up transitions. If no such b exists, there is no problem, as $\eta(x)$ cannot jump above $\xi(x)$. Similarly if there is a b such that $b \leq \eta(x) \leq \xi(x)$, then this fact can be used to show something about down transitions.

Start by defining the monotone function $f_{bx}(\eta) = I_{[b..n]}(\eta(x))$, the indicator on all particle values bigger than or equal to b, assuming that n is the maximum particle number. Applying the semigroup to this function, $S(t)f_{bx}$, again gives a monotone function for any $t \in [0, \infty)$ since the process is monotone. Note that in the cases we are considering, b is chosen so that $f_{bx}(\eta) = f_{bx}(\xi)$. This leads to the following calculation.

The generator and semigroup are related by:

$$Gf(\eta) = \sum_x \sum_y r(\eta, x, y)(f(\eta^{xy}) - f(\eta)) = \lim_{t \searrow 0} \frac{S(t)f(\eta) - f(\eta)}{t}$$

For the monotone function $f_{b\tilde{x}}(\eta)$, we don't need to sum over x since it is fixed at $\tilde{x}$ giving:

$$Gf_{b\tilde{x}}(\eta) = \sum_y r(\eta, \tilde{x}, y)(f_{b\tilde{x}}(\eta^{\tilde{x}y}) - f_{b\tilde{x}}(\eta)) = \lim_{t \searrow 0} \frac{S(t)f_{b\tilde{x}}(\eta) - f_{b\tilde{x}}(\eta)}{t}$$

Now that $\tilde{x}$ is fixed, we will drop the tildes. Because $f_{bx}(\eta) = f_{bx}(\xi)$, we get an inequality from the fact that $f_{bx}(\cdot)$ is monotone:

$$S(t)f_{b\tilde{x}}(\eta) \leq S(t)f_{b\tilde{x}}(\xi)$$

implies

$$\frac{S(t)f_{b\tilde{x}}(\eta) - f_{b\tilde{x}}(\eta)}{t} \leq \frac{S(t)f_{b\tilde{x}}(\xi) - f_{b\tilde{x}}(\xi)}{t}$$

which leads to

$$Gf_{bx}(\eta) \leq \lim_{t \searrow 0} \frac{S(t)f_{bx}(\xi) - f_{bx}(\xi)}{t} = \sum_{y \in N(x)} r(\xi, x, y)(f_{bx}(\xi^{xy}) - f_{bx}(\xi)) = Gf_{bx}(\xi)$$

So we get:

$$\sum_{y \in N(x)} r(\eta, x, y)(f_{bx}(\eta^{xy}) - f_{bx}(\eta)) \leq \sum_{y \in N(x)} r(\xi, x, y)(f_{bx}(\xi^{xy}) - f_{bx}(\xi)) \tag{3.13}$$

Which gives the total rate that η goes up into the set $[b, n]$ is less than or equal to the total rate that ξ goes up into the set $[b..n]$, and the total rate that $\eta(x)$ leaves the set $[b..n]$ (by going down) is greater than or equal to the total rate that $\xi(x)$ does the same.

Then, due to the type of rate function, $r(\eta, x, y) = \lambda_{\eta(y),\eta(x)}(x)\phi(x, y)$, (3.13) becomes

$$\sum_{y} \lambda_{\eta(y),\eta(x)}(x)\phi(x, y)(f_{bx}(\eta^{xy}) - f_{bx}(\eta)) \leq \sum_{y} \lambda_{\xi(y),\xi(x)}(x)\phi(x, y)(f_{bx}(\xi^{xy}) - f_{bx}(\xi)) \tag{3.14}$$

If we choose a particular neighbor of interest, say $\tilde{y}$ and make $\eta(y) = \eta(\tilde{y})$ and $\xi(y) = \xi(\tilde{y})$ for all $y \neq x$, (3.14) becomes

$$\lambda_{\eta(\tilde{y}),\eta(x)}(x) \sum_{y} \phi(x, y)(f_{bx}(\eta^{x\tilde{y}}) - f_{bx}(\eta)) \leq \lambda_{\xi(\tilde{y}),\xi(x)}(x) \sum_{y} \phi(x, y)(f_{bx}(\xi^{x\tilde{y}}) - f_{bx}(\xi)) \tag{3.15}$$

and then $\sum_y \phi(x, y)$ cancels out from both sides.

$$\lambda_{\eta(\tilde{y}),\eta(x)}(x)(f_{bx}(\eta^{x\tilde{y}}) - f_{bx}(\eta)) \leq \lambda_{\xi(\tilde{y}),\xi(x)}(x)(f_{bx}(\xi^{x\tilde{y}}) - f_{bx}(\xi))$$

then changing $\tilde{y}$ back into y since this did not depend on exactly which neighbor was singled out:

$$\lambda_{\eta(y),\eta(x)}(x)(f_{bx}(\eta^{xy}) - f_{bx}(\eta)) \leq \lambda_{\xi(y),\xi(x)}(x)(f_{bx}(\xi^{xy}) - f_{bx}(\xi)) \tag{3.16}$$

The following inferences come from looking at the possibilities for (3.16).

(i) If $\eta(x) \leq \xi(x) < b$, then

  (a) $\eta^{xy}(x) \geq b \Rightarrow \xi^{xy}(x) \geq b$

  (b) $\xi^{xy}(x) < b \Rightarrow \eta^{xy}(x) < b$

(ii) If $b \leq \eta(x) \leq \xi(x)$, then

  (a) $\xi^{xy}(x) < b \Rightarrow \eta^{xy}(x) < b$

  (b) $\eta^{xy}(x) \geq b \Rightarrow \xi^{xy}(x) \geq b$

Letting $b = \xi(x) + 1$ in inference (i,a), we see that when $\eta^{xy}(x) > \xi(x)$, (3.16) becomes $\lambda_{\eta(y),\eta(x)}(x) \leq \lambda_{\xi(y),\xi(x)}(x)$ which is our first rate restriction. For the second rate restriction, let $b = \eta(x)$ in inference (ii,a), we see that when $\eta(x) > \xi^{xy}(x)$, (3.16) becomes $\lambda_{\eta(y),\eta(x)}(x) \geq \lambda_{\xi(y),\xi(x)}(x)$ finishing the rate restrictions for being an attractive process.

These inferences are true for any b, thus if both states are looking at possible up transitions, $\eta(x) < \eta^{xy}(x)$ and $\xi(x) < \xi^{xy}(x)$, then $\xi^{xy}(x) < \eta^{xy}(x)$ is not possible since we can let $b = \eta^{xy}(x)$ which violates both inferences under (i). Similarly if both states are looking at possible down transitions, $\eta^{xy}(x) < \eta(x)$ and $\xi^{xy}(x) < \xi(x)$, then $\xi^{xy}(x) < \eta^{xy}(x)$ is not possible since we can let $b = \xi^{xy}(x) + 1$ which violates both inferences under (ii). These give us the first two requirements for the interaction map to be attractive.

Assume that $\eta(x) < \eta^{xy}(x)$ and $\xi^{xy}(x) \leq \xi(x)$, and let $b = \xi(x) + 1$. Then inference (i,b) is only satisfied if $\eta^{xy}(x) < b$. If $\eta(x) \leq \eta^{xy}(x)$ and $\xi^{xy}(x) < \xi(x)$, then

letting $b = \eta(x)$. Inference (ii,b) is now only satisfied if $b \leq \xi^{xy}(x)$. Now the last two attractive interaction map requirements are met. □

The proof of Theorem 30 is somewhat more involved than the case for spin systems. This is because more complicated transitions are allowed which amount to "jump overs". Now this result applies to any interaction map particle system. The limitation should be noted that the neighborhood mass function must be the same for all species of particle for a given site. But spatial and temporal variations can be included and do not affect this result.

3.5.1 Reordering the Particles

If one develops a model which either does not have an attractive interaction map, or the rate restrictions which allow this model to be attractive are not desirable, a re-ordering of the particle values may give attractive model with more desirable rate restrictions. Biologically, the ordering of the particles may not necessarily have a meaning, it is purely a mathematical construction for the purpose of having a monotone model along with the benefit of using CFTP.

Interestingly enough, the multi-type contact process can be made attractive with a re-ordering. The main issue to resolve is that the interaction map is not attractive in this case, but making the permutation $\{0, 1, 2\} \to \{1, 0, 2\}$ in the sense that now $1 < 0 < 2$ our map is now attractive. To abate confusion on such a funny ordering of integers, we label particle 0 as one species of plant(species 0 to avoid confusion), particle 1 as an empty site, and particle 2 remains species 2. The rates are still the same: empty sites become species i at rate β_i and species i dies at constant rate δ_i. This information is summarized in Figure 3.4.

This model now has an attractive interaction map and no rate restrictions. The intuition is usually to let 0 represent an empty site, but in this case it is beneficial to go against this standard by allowing us to label one species as "0" and the other as

$\overset{a}{b}$	0	1	2
0	δ_0	β_0	δ_2
1	δ_0	$\emptyset$	δ_2
2	δ_0	β_2	δ_2

$\overset{a}{b}$	0	1	2
0	1	0	1
1	1	1	1
2	1	2	1

FIGURE 3.4. Reordering of the multi-type contact process for attractiveness.

"2" with the empty site being represented by the particle value of 1. A nice aspect of this reordering is that it doesn't require any special reconsideration for simulation of CFTP. The original "non-monotone" version of the process can be used, we just have to consider $\bar{1}$ and $\bar{2}$ as our extremal states in the original multi-type contact process when using CFTP. Special consideration does need to be taken on the point process couplings used; they need to be chosen properly in order to maintain the partial ordering. The particle die out still needs to be considered on the finite grid of course which would entail fixing a source for each species or an optional rare long range dispersal term, γ. This however requires an additional interaction map and will be discussed in a later section.

3.6 A Universal and Graphical Coupling

Now we define a coupling of these processes constructed by way of Poisson point processes. This graphical representation was first introduced by Harris[17, 18] and subsequently developed by others[23, 14, 24]. This method is extremely useful since it allows multiple copies of the process to be constructed simultaneously.

For each site, x, and every y such that $\phi(x, y) > 0$, let U_{xy} and D_{xy} be two independent, identically distributed Poisson point processes on $(0, \infty) \times (0, \infty)$ with intensity equal to two-dimensional Lebesgue measure. Assume that our rates have

an upper bound, c. For each x, define $\mathfrak{T}_x = \{T_{x,1} < T_{x,2} < ...\}$ by $T_{x,0} = 0$ and

$$T_{x,n} = \inf\{t > T_{x,n-1} : (v,t) \in \bigcup_y U_{xy} \cup D_{xy} \text{ for some } v \leq c\}$$

which will represent the times at which transitions could possibly occur at the site x. This is a projection of a union of independent Poisson point processes, and the intensity measure of points in $\mathfrak{T}_x$ is $2c\#N(x,\rho)$ where $N(x,\rho) = \{y : |x-y| \leq \rho \text{ and } \phi(x,y) > 0\}$, so $\mathfrak{T}_x$ is also a Poisson point process.

The graphical representation is created on a grid $\Lambda \times [0,\infty)$. At each point, t, in $\mathfrak{T}_x$, if $\exists u, y$ such that $(u,t) \in U_{xy}$ draw an arrow from y pointing to x with an open circle at x. If $\exists u, y$ such that $(u,t) \in D_{xy}$ draw an arrow from y pointing to x with a closed circle at x. Write the u values next to the tip of each arrow. Figure 3.5 give a possible realization of the graphical representation of this coupling for a one dimensional index set and rates bound above by $c = 3$.

These point processes are used to evolve the interaction map particle system. First assume we are given an initial state, η and that the rates are bounded above by c.

Theorem 31. The path $\eta_{\mathbf{t}}$ is constructed according to the following rules is the interaction map particle system with interaction map $\mathscr{J}$, and generator given by Definition 25.

(1) Up transition rule: The particle at site, x, is replaced by the particle given by

$$\mathscr{J}(\eta_{t-}(y), \eta_{t-}(x))$$

at time $t \in \mathfrak{T}_x$ if there exists a u such that $(u,t) \in U_{xy}$, with

$$\mathscr{J}(\eta_{t-}(y), \eta_{t-}(x)) > \eta_{t-}(x),$$

and $u \leq r_u(\eta_{t-}, x, y)$.

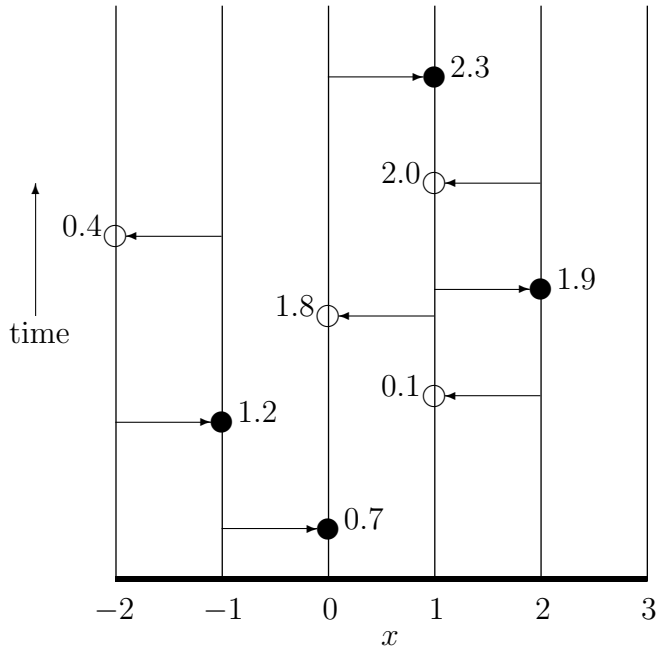


FIGURE 3.5. A realization of the graphical representation of the point process coupling. All points with $u \geq 3$ have been left out. Closed and open circles represent possible down and up transition points respectively.

(2) Down transition rule: The particle at site, x, is replaced by the particle given by

$$\mathscr{J}\left(\eta_{t-}(y), \eta_{t-}(x)\right)$$

at time $t \in \mathfrak{T}_x$, if there exists a u such that $(u,t) \in D_{xy}$, with

$$\mathscr{J}\left(\eta_{t-}(y), \eta_{t-}(x)\right) < \eta_{t-}(x),$$

and $u \leq r_d(\eta_{t-}, x, y)$.

The construction of these Poisson point processes and Theorem 31 is based upon Chapter 32 of Fristedt and Gray; see [14] for a rigorous proof. This is the basis for an accurate method of simulating these types of processes.

Theorem 32. The graphical construction in Theorem 31 is monotone in the sense

that it maintains the partial order of an attractive IMPS.

Proof. This is proven by the fact that all up transitions preserve the order as do down transitions. The only time the partial ordering can be broken would be if up and down transitions which cross each other are allowed by the same point process, this is not the case here. □

So for any attractive interaction map particle system, it is easy to construct a monotone coupling. There are many possibilities that can be used as well. It is not always necessary to used U_{xy} and D_{xy}. Transitions can br grouped into point processes according to any criteria, they just can't be grouped together in such a way that allows an up transition for one configuration and a down transition for another if these two transitions break the ordering.

3.7 Multiple Interaction Maps

It may be the case that more complicated interactions are desired such as allowing a certain transition to have a constant rate parameter in addition to depending on the neighborhood composition. As mentioned earlier, rare long range dispersal events may be desired to induce irreducibility. Take for example the "grass, bushes, trees" model[8]. The transitions and rates are summarized in the typical way below.

Transition	Rate
$0 \to 1$	$\beta_1 f_1$
$0 \to 2$	$\beta_2 f_2$
$1 \to 0$	δ_1
$1 \to 2$	$\beta_2 f_2$
$2 \to 0$	δ_2

This is a standard multi-type contact process except for the fact that 2's can be born onto sites occupied by 1's. In order to make this model attractive it needs two

things. First we must reorder the particles as we did for the multi-type contact process, then we must introduce an extra point process for the births of trees. The basic interaction map, $\mathscr{J}_1$, and transition rates are given by Figure 3.6. This interaction map is the basic multi-type contact process map with births for species 2 removed and is attractive with no rate restrictions. Now we just need to account for this extra birth event. This amounts to including the extra interaction map, $\mathscr{J}_2$, given by Figure 3.7, and this map is attractive as well. There are only two actual transitions occurring

$\overset{a}{b}$	0	1	2
0	δ_1	β_1	δ_2
1	δ_1	$\emptyset$	δ_2
2	δ_1	$\emptyset$	δ_2

$\overset{a}{b}$	0	1	2
0	1	0	1
1	1	1	1
2	1	1	1

FIGURE 3.6. Grass–bushes–trees initial rate parameters and interaction map, $\mathscr{J}_1$.

$\overset{a}{b}$	0	1	2
0	$\emptyset$	$\emptyset$	$\emptyset$
1	$\emptyset$	$\emptyset$	$\emptyset$
2	β_2	β_2	$\emptyset$

$\overset{a}{b}$	0	1	2
0	0	1	2
1	0	1	2
2	2	2	2

FIGURE 3.7. Extra rate parameters and interaction map, $\mathscr{J}_2$, for the birth of trees.

in this map, the births of species 2. This is not a unique formulation, deaths could be distributed among both interaction maps and still maintain attractiveness. When simulating this process we need three Poisson Point Processes: U = up transitions for basic multi-type contact process excluding species 2 births, D = down transitions for multi-type contact process, and B = birth events for species 2. Using this method allows the process to be attractive with no rate restrictions.

It may seem cumbersome to think of the process this way. The idea is that you can have any arbitrary number of interaction maps. If each map is attractive, then a collection of rate restrictions allows the model to be monotone. Each map just

needs to have distinct up and down point processes associated with it in the universal coupling.

Formulating a process with multiple interaction maps my actually relax some parameter restrictions for monotonicity. The equivalency of attractiveness and monotonicity will not be developed here, but a sufficiency condition is given.

Theorem 33. Monotonicity Sufficiency Condition: Assume we have an interaction map particle system with multiple interaction maps, $\mathscr{J}_1, \mathscr{J}_2, ..., \mathscr{J}_n$, such that no two interaction maps have any non-null transitions in common. If each interaction map and the rate parameters associated with it are attractive, then $\{U_1, D_1, U_2, D_2, ..., U_n, D_n\}$, is a monotone coupling for the process. Where U_i and D_i are the point processes for the up and down transitions for interaction map $\mathscr{J}_i$ respectively.

Proof. Each point process preserves the partial ordering of the state space, thus we have a monotone coupling, and therefore the process is monotone. □

This allows us to have interactions between two particle types give non-unique results. In other words, two particle types can interact with the resulting transition chosen from several possibilities. Only a sufficiency condition is given because assuming monotonicity and using the same methods as in Theorem 30 gives inequalities involving sums of parameters rather than individual parameters. This may allow relax the requirement that each individual map and its parameters be attractive. The grass–bushes–trees model in Figures 3.6 and 3.7 is attractive with no rate parameter restrictions according to this theorem.

The multi-type contact process with spontaneous births is formulated as usual, but with the inclusion of 2 extra point processes. One would represent spontaneous births for species 0, B_0, and the other for species 2, B_2. These extra point processes are formulated exactly as described above in the universal coupling. Two rates γ_0 and γ_2

represent the constant rates of spontaneous births for species 0 and 2 respectively. The same formulation of the graphical coupling applies here; if a point in B_i is encountered, then a 1 is allowed to become an i if $u \leq \gamma_i$. This process is still monotone with no parameter restrictions since the interaction maps of these spontaneous transitions are attractive and there are no "overjumps" to consider. The interactions maps and rates are given in Figures 3.8 and 3.9. It may be thought that this formulation is unnecessarily awkward, but it is consistent with the theory presented here.

$\overset{a}{b}$	0	1	2
0	$\emptyset$	γ_0	$\emptyset$
1	$\emptyset$	γ_0	$\emptyset$
2	$\emptyset$	γ_0	$\emptyset$

$\overset{a}{b}$	0	1	2
0	0	0	2
1	0	0	2
2	0	0	2

FIGURE 3.8. Extra rates and interactions for spontaneous births of species 0.

$\overset{a}{b}$	0	1	2
0	$\emptyset$	γ_2	$\emptyset$
1	$\emptyset$	γ_2	$\emptyset$
2	$\emptyset$	γ_2	$\emptyset$

$\overset{a}{b}$	0	1	2
0	0	2	2
1	0	2	2
2	0	2	2

FIGURE 3.9. Extra rates and interactions for spontaneous births of species 2.

Now that we understand monotonicity for a large class of contact process like interacting particle system models with any finite number of particles we can create invasion models and use the universal coupling and CFTP to look at the path to invasion equilibrium.

Chapter 4

Plant Invasion Models

We now have a theoretical framework for a large class of models with contact–type interactions that allows us to test for monotonicity. If a monotone invasion model fits within this framework, we can look at the path up to and including the stationary distribution. In order to get a sense of how this process works, here is a rough guide:

(1) Choose the particles and what they represent ecologically.

(2) Define the interactions between them. Having some flexibility here by considering several possible ways that particles may interact is helpful in creating a monotone process.

(3) Check if the map is attractive.

(4) If the interaction map(s) is(are) attractive, check for rate restrictions that give attractive transition rates.

(5) If the model is not attractive, often, it can be made so by reordering the particles or changing some of the interactions, if there is any flexibility in the model.

We start with defining invasion models that use the concept of virtual particles.

4.1 Virtual Particle Plant Invasion Models

For the basic plant invasion model we need two species: the native and the introduced species. The basic idea for the model is that a site is viewed as either available or unavailable for colonization. A site may be unavailable to a species because it is currently occupied or because it is vacant but not suitable for propagation. Following this line of thought, we define four particle types in the model. For each species

included in the model, there are two particle types: one represents a vacant but available site for colonization only by that species (in essence virtual occupation due to exclusion of the other species) and the other represents actual occupation by the plant. This helps to understand the allowed transitions.

This model falls within the framework of interaction map particle systems as follows. The process is constructed as two separate contact processes that communicate according to a voter model–like rule. First, we change the particle denominations for the state space in order to differentiate between species and particle types. The new state space is $X = \{1-, 1+, 2-, 2+\}^{\mathbb{Z}^2}$. Particle values ending in '$-$' are considered virtual, while those with '$+$' are considered actual. The first ordering to be considered on the particle values is $1- < 1+ < 2- < 2+$. This gives rise to a partial order on the state space: for any $\eta, \xi \in X$, $\eta \leq \xi$ when $\eta(x) \leq \xi(x)$ for all $x \in \mathbb{Z}^2$. This ordering is identical to $0 < 1 < 2 < 3$, and for simulation purposes is programmed that way. It should be noted that the ordering on the particles does not necessarily need to be related to the biology in any particular way. This is a mathematical construction that allows us to consider the monotonicity of the model for the purpose of using monotone CFTP.

It should be clear now that virtual states are empty but 'species-biased' in a manner of speaking. The dynamics of these empty sites, how they communicate, is outlined in the interaction map and transition rates for the process. These 'virtual dynamics' should be thought of as habitat dynamics, where $1-$ is available habitat for species 1 and $2-$ is available habitat for species 2. This is similar to a host pathogen relationship, where each pathogen exclusively occupies a single host type. A host pathogen model has been studied extensively by Durrett, Lanchier, and Neuhauser[22, 9].

The interaction map for this model is shown in Figure 4.1. This interaction map can be seen to be attractive since it is non-decreasing everywhere except at two places, and where it does decrease, it is exactly by one particle value and satisfies the

necessary jump conditions. This happens only when going from a down transition to an up transition: $\mathscr{J}(2+,2-) = 2+ > 2- = \mathscr{J}(2+,2+)$ and $\mathscr{J}(1+,1-) = 1+ > 1- = \mathscr{J}(1+,1+)$. From this calculation and Theorem 21, it follows that this is an attractive interaction map. These transitions should be understood according to the

$\overset{a}{b}$	$1-$	$1+$	$2-$	$2+$
$1-$	$1-$	$1-$	$1-$	$1-$
$1+$	$1+$	$1-$	$1-$	$1-$
$2-$	$2-$	$2-$	$2-$	$2-$
$2+$	$2-$	$2-$	$2+$	$2-$

FIGURE 4.1. Interaction map formulation for the virtual particle invasion model

interpretation in the first paragraph above. If a site is virtually occupied by species i ($i-$), it sees any nearby species j, virtual or actual, purely as species j, and an interaction will cause the site to become virtually occupied by species j. This is represented in the interaction map as $\mathscr{J}(j\pm, i-) = j-$, $j \neq i$. If a site is actually occupied by species i ($i+$), it sees any nearby species j, virtual or actual, again, purely as species j, and the interaction causes the site to become virtually occupied by species j. This is represented in the interaction map as $\mathscr{J}(j\pm, i+) = j-$, $j \neq i$. This is our voter model type interaction. If you disregard the sites as virtual or actual and purely look at them as ones and twos, it will be similar to a voter model If we look at the interaction between the plus and minus versions of a single species, it is exactly a contact process. The virtual species will become actual at a rate proportional to the number of actual plants around it, and actual plants die at a constant rate.

There are six transition parameters included in the model: β_i, δ_i, and ν_{ij} for $i = 1, 2$ and $j \neq i$. The eight allowed transitions and rate parameters are summarized in Table 4.1 along with the ecological meaning of each. The labeling of "up" or "down" is determined by the ordering defined on the particle values.

The transition rate constants are summarized in Figure 4.2.

Transition	Rate	Up or Down	Ecological Description
$1- \to 1+$	β_1	up	birth of species 1
$2- \to 2+$	β_2	up	birth of species 2
$1+ \to 1-$	δ_1	down	death of species 1, leaving species 1 habitat
$1+ \to 2-$	δ_1	up	death of species 1, leaving species 2 habitat
$2+ \to 1-$	δ_2	down	death of species 2, leaving species 1 habitat
$2+ \to 2-$	δ_2	down	death of species 2, leaving species 2 habitat
$1- \to 2-$	ν_{12}	up	habitat becomes available to species 2
$2- \to 1-$	ν_{21}	down	habitat becomes available to species 1

TABLE 4.1. Transitions for the virtual particle model and the ecological meaning of each.

$\overset{a}{\underset{b}{\diagdown}}$	$1-$	$1+$	$2-$	$2+$
$1-$	$\emptyset$	δ_1	ν_{21}	δ_2
$1+$	β_1	δ_1	ν_{21}	δ_2
$2-$	ν_{12}	δ_1	$\emptyset$	δ_2
$2+$	ν_{12}	δ_1	β_2	δ_2

FIGURE 4.2. Table of transition rate parameters for the invasion model.

Figure 4.2 gives the transition rate parameters for the model. For example, a neighboring $1+$ interacts with a $1-$ at rate proportional β_1 resulting in the possible transition of $1- \xrightarrow{1+} \mathscr{J}(1+, 1-) = 1+$, species 1 taking over an available site. Assume that we have a $1+$ occupying a site, x, and that there is a $2-$ occupying a neighboring site, y. Then these two particles will interact at rate $\delta_1 \phi(x, y)$, where $\phi(x, y)$, the neighborhood mass function, is defined as in the previous chapter, in such a way that the result of the interaction would be to kill the species 1 plant at site x leaving behind a $2-$ at x hence preparing it for the possible occupation by species 2. The $\emptyset$ symbol is placed where a *null* interaction exists. Null interactions are not assigned rates since there is no transition which will result in a change of state. If two $2-$'s are to interact, neither site will change its particle number leading to the conclusion that transition rates for null interactions are unnecessary to define.

So the total transition rate at site x for state η is as follows:

The birth rate is

$$b_i(\eta, x) = \beta_i \sum_y I_{\{i+\}}(\eta(y))\phi(x, y)$$

which gives the rate at which $i- \to i+$, the death rate

$$d_{ij}(\eta, x) = \delta_i \sum_y I_{\{j-,j+\}}(\eta(y))\phi(x, y)$$

being the rate at which $i+ \to j-$, and virtual rate

$$v_{ij}(\eta, x) = \nu_{ij} \sum_y I_{\{j-,j+\}}(\eta(y))\phi(x, y), j \neq i$$

being the rate at which $i- \to j-$.

For the sake of clarity the way these transitions and rates would typically be stated follows. Let f_i be the fraction of sites occupied by species i in some finite neighborhood, and define $\phi(x, y) = \frac{1}{N} I_{\{|x-y| \leq \rho\}}$ where N is the number of sites in the neighborhood $\{|x - y| \leq \rho\}$. The typical summary of transitions and rates is given below.

Transition	Rate
$1- \to 1+$	$\beta_1 f_{1+}$
$2- \to 2+$	$\beta_2 f_{2+}$
$1+ \to 1-$	$\delta_1(f_{1-} + f_{1+})$
$1+ \to 2-$	$\delta_1(f_{2-} + f_{2+})$
$2+ \to 1-$	$\delta_2(f_{1-} + f_{1+})$
$2+ \to 2-$	$\delta_2(f_{2-} + f_{2+})$
$1- \to 2-$	$\nu_{12}(f_{2-} + f_{2+})$
$2- \to 1-$	$\nu_{21}(f_{1-} + f_{1+})$

The complete interaction map formulation is given by Figure 4.3.

Each species acts as a contact process in absence of the other, we can examine the critical values for the parameters. If $4\delta_1 = 1$, then the critical birth parameter

δ^a	1−	1+	2−	2+
1−	$\emptyset$	δ_1	ν_{21}	δ_2
1+	β_1	δ_1	ν_{21}	δ_2
2−	ν_{12}	δ_1	$\emptyset$	δ_2
2+	ν_{12}	δ_1	β_2	δ_2

δ^a	1−	1+	2−	2+
1−	1−	1−	1−	1−
1+	1+	1−	1−	1−
2−	2−	2−	2−	2−
2+	2−	2−	2+	2−

FIGURE 4.3. Complete interaction map formulation of the virtual particle invasion model.

satisfies, $1/3 \leq \beta_{1c} \leq 1/2$. Due to the additivity of exponential rates, we can say for sure that the species 1 contact process is subcritical when $\beta_1 < 4/3\delta_1$.

Determining attractiveness depends on the specific model (how many particle types and rate parameters there are), and can be tedious. This is done easily numerically however. The following proposition shows how this is done analytically for the virtual particle invasion model.

Proposition 34. The four particle invasion model described by Figure 4.3 is monotone when the parameters satisfy the following conditions:

(1) $\beta_1 \leq \nu_{12} \leq \delta_1$

(2) $\delta_2 \leq \nu_{21} \leq \delta_1$

Proof. The first thing to show is that the interaction map is attractive. Once the interaction map is established as attractive, then the parameter inequalities above will be shown to give the necessary rate restrictions.

From figure 4.4, it can be seen that $\mathscr{J}$ is non-decreasing on $\mathcal{U}$, highlighted in green, and it is non-decreasing on $\mathcal{D}$, highlighted in red, as well. So the first two conditions of the definition of attractiveness are satisfied. The third and fourth conditions can also be seen as satisfied by $\mathscr{J}(1+,1-) = 1+ = \min_a\{a : (1+,a) \in \mathcal{D}\}$ and $\mathscr{J}(2+,2-) = 2+ = \min_a\{a : (2+,a) \in \mathcal{D}\}$. So our interaction map is indeed attractive since this satisfies Theorem 21.

b \ a	1−	1+	2−	2+
1−	1−	1−	1−	1−
1+	1+	1−	1−	1−
2−	2−	2−	2−	2−
2+	2−	2−	2+	2−

FIGURE 4.4. The interaction map for the invasion model with up transitions(dots) and down transitions(lines).

In order to prove that the rate restrictions are satisfied, there are several cases that must be explored.

Case 1 Looking at $\mathscr{J}(b,a)$ when $a = 1-$ (the first column), we can see that these are possibilities where a lower configuration can jump above a higher one. The transitions below are listed in increasing order from top to bottom.

b	a	$\mathscr{J}(b,a)$	rate parameter
1+	1−	1+	β_1
2−	1−	2−	ν_{12}
2+	1−	2−	ν_{12}

(4.1)

In each configuration in the above array, we see that if η falls into one case, and ξ falls into a case above it, we will have $\eta^{xy}(x) > \xi(x)$. In order to maintain the necessary rate restrictions for attractiveness, we must have $\beta_1 \leq \nu_{12}$.

Case 2 Looking at $\mathscr{J}(b,a)$ when b is 2− or 2+(the 3$^{\text{rd}}$ and 4$^{\text{th}}$ rows), we can see that these are possibilities where a lower configuration can jump above a higher one

as well. The transitions below are again listed in increasing order from top to bottom.

b	a	$\mathscr{J}(b,a)$	rate parameter
$2-$	$1-$	$2-$	ν_{12}
$2-$	$1+$	$2-$	δ_1
$2+$	$1-$	$2-$	ν_{12}
$2+$	$1+$	$2-$	δ_1

(4.2)

In each configuration in the above array, we see that if η falls into one case, and ξ falls into a case above it, $\eta^{xy}(x) > \xi(x)$ will result. In order to maintain the necessary rate restrictions for attractiveness, we must have $\nu_{12} \leq \delta_1$.

Case 3 Looking at $\mathscr{J}(b,a)$ when b is $1-$ or $1+$(the 1^{st} and 2^{nd} rows), we can see that these are possibilities where a lower configuration can jump above a higher one as well. The transitions below are again listed in increasing order from top to bottom.

b	a	$\mathscr{J}(b,a)$	rate parameter
$1-$	$1+$	$1-$	δ_1
$1-$	$2-$	$1-$	ν_{21}
$1-$	$2+$	$1-$	δ_2
$1+$	$1+$	$1-$	δ_1
$1+$	$2-$	$1-$	ν_{21}
$1+$	$2+$	$1-$	δ_2

(4.3)

In each configuration in the above array, we see that if η falls into one case, and ξ falls into a case above it, $\xi^{xy}(x) < \eta(x)$ will result. In order to maintain the necessary rate restrictions for attractiveness, we must have $\delta_2 \leq \nu_{21} \leq \delta_1$. The other possible configurations which exhibit this possibility of jumping above or below do not produce any further difficulties since considering them shows that they have the

same rate parameters in each instance. This completes the proof that in order for the particle model to be attractive, the outlined parameter restrictions are necessary. □

In order for the virtual particle model to be attractive, the species 1 contact process, when there are only 1−'s and 1+'s occupying the grid, must already be subcritical, $\beta_1 \leq \delta_1$. This is actually well below subcritical for the 2D process.

4.1.1 Reordering the Particles

Here is an equivalent formulation of the virtual particle model with a reordering of the particle values: $1+ < 1- < 2- < 2+$. The interactions and rate parameters are kept intact. The new formulation is given in Figure 4.5.

$\eta(a)$ \ $\eta(b)$	$1+$	$1-$	$2-$	$2+$
$1+$	δ_1	β_1	ν_{21}	δ_2
$1-$	δ_1	$\emptyset$	ν_{21}	δ_2
$2-$	δ_1	ν_{12}	$\emptyset$	δ_2
$2+$	δ_1	ν_{12}	β_2	δ_2

$\eta(a)$ \ $\eta(b)$	$1+$	$1-$	$2-$	$2+$
$1+$	$1-$	$1+$	$1-$	$1-$
$1-$	$1-$	$1-$	$1-$	$1-$
$2-$	$2-$	$2-$	$2-$	$2-$
$2+$	$2-$	$2-$	$2+$	$2-$

FIGURE 4.5. Equivalent formulation of the virtual particle invasion model.

The new up/down labeling for the transitions are given below. The biological interpretation does not change and there is no difference in the simulation methods except that what we label as the lower extremal state changes to $\overline{1+}$.

Transition	Rate	Label
$1- \to 1+$	β_1	down
$2- \to 2+$	β_2	up
$1+ \to 1-$	δ_1	up
$1+ \to 2-$	δ_1	up
$2+ \to 1-$	δ_2	down
$2+ \to 2-$	δ_2	down
$1- \to 2-$	ν_{12}	up
$2- \to 1-$	ν_{21}	down

Proposition 35. The interaction map particle system given by Figure 4.5 is attractive when

(1) $\delta_1 \leq \nu_{12}$

(2) $\delta_2 \leq \nu_{21}$

Proof. The easiest way to understand these rate restrictions is to look where possible "jump overs" can occur. There are only two places where we have this being an issue due to different rate parameters. One involves the transitions $2+ \to 1-$ and $2- \to 1-$. If a $2+$ "jumps below" a $2-$ in this way, then the $2-$ must jump as low or lower and at an equal or faster rate in order to maintain monotonicity. This give rate restriction (2). A similar line of reasoning when comparing the transitions $1+ \to 2-$ and $1- \to 2-$ will lead to condition (1) above. □

The restrictions on parameters in this version of the virtual particle model are much more relaxed than the previous one. They certainly occupy two overlapping sets in the parameter space and thus can be used to sample from the stationary distributions for different parameter values.

There are 2 other re-orderings which result in monotone particle systems. If we allow $1+ < 1- < 2+ < 2-$, then we get the restrictions $\beta_2 \leq \nu_{21} \leq \delta_2$ and $\delta_1 \leq \nu_{12} \leq \delta_2$, and if we assume $1- < 1+ < 2+ < 2-$, then the rate parameter restrictions for monotonicity are $\delta_1 = \delta_2 = \delta$, $\nu_{12} \leq \delta$, and $\nu_{21} \leq \delta$. This leads to the following summarization:

Proposition 36. The virtual particle model with interactions and rate parameters given by Figure 4.5 is monotone under the following four cases involving different particle orderings:

(1) $1- < 1+ < 2- < 2+$

  (a) $\beta_1 \leq \nu_{12} \leq \delta_1$

(b) $\delta_2 \leq \nu_{21} \leq \delta_1$

(2) $1+ < 1- < 2+ < 2-$

(a) $\beta_2 \leq \nu_{21} \leq \delta_2$

(b) $\delta_1 \leq \nu_{12} \leq \delta_2$

(3) $1+ < 1- < 2- < 2+$

(a) $\delta_1 \leq \nu_{12}$

(b) $\delta_2 \leq \nu_{21}$

(4) $1- < 1+ < 2+ < 2-$

(a) $\delta_1 = \delta_2 = \delta$

(b) $\beta_1 \leq \nu_{12} \leq \delta$

(c) $\beta_2 \leq \nu_{21} \leq \delta$

To prove Proposition 36, we write out the interaction map and check that it satisfies the conditions of Theorem 24, and then check when the transition rate map satisfies Definition 29. Then we have monotonicity by Theorem 30.

Where ever $\mathscr{J}(b, a_1) > a_2$ for any $a_1 < a_2$, we get the rate parameter restriction $\lambda_{ba_1} \leq \lambda_{ba_2}$, and where ever $a_1 > \mathscr{J}(b, a_2)$ for any $a_1 < a_2$, we get the rate parameter restriction $\lambda_{ba_1} \geq \lambda_{ba_2}$. Finally, where ever $\mathscr{J}(b_1, a) > a$, it must be true that $\lambda_{b_1 a} \leq \lambda_{b_2 a}$ for any $b_2 \geq b_1$, and where ever $\mathscr{J}(b_2, a) < a$, it must be true that $\lambda_{b_1 a} \geq \lambda_{b_2 a}$ for any $b_1 \leq b_2$. In each case the model is exactly the same except that attractiveness is given by different sets of parameter values. This allows us to use CFTP in a wide variety of cases. In each case, we have different extremal states. One thing to notice is that the extremal states are the states which communicate the slowest. For example look at case (4) above. Particles $1-$ and $2-$ communicate with the slowest rates thus making $\overline{1-}$ and $\overline{2-}$ our extremal states; when those coalesce, everything else will as well.

4.2 Qualitative Dynamics

The possible stationary dynamics of this model can be summarized by:

(1) $1-$ Absorbing state

(2) $2-$ Absorbing state

(3) $\{1-, 2-\}$ Habitat voter model

(4) $\{1-, 1+\}$ Species 1 contact process

(5) $\{2-, 2+\}$ Species 2 contact process

(6) $\{1-, 1+, 2-\}$ Species 1 contact process with some unsuitable habitat

(7) $\{2-, 2+, 1-\}$ Species 2 contact process with some unsuitable habitat

(8) $\{1-, 1+, 2-, 2+\}$ Coexistence

There will always be the empty absorbing states, but they may be unstable. If $\beta_1/4\delta_1 > \lambda_c$, the critical value for the 2-dimensional contact process with death rate 1, then the species 1 contact process is supercritical and the $1-$ absorbing state is unstable. What this means is that in the absence of species 2, species 1 survives. A similar statement can be made about species 2 in the absence of species 1. The habitat voter model dynamics are determined by comparing ν_{12} and ν_{21}. If ν_{ij} is the larger of the two, then particle $i-$ loses.

When the species 1 contact process survives, it may be such that it can still survive with the introduction of some unsuitable habitat, $2-$. A similar statement can be said about species 2. And finally, we could also possibly have coexistence. We begin by analyzing the mean field equations.

4.2.1 Mean Field Equations

The first step in analyzing our model is to observe the behavior of the mean field equations. This allows some insight into how the qualitative behavior of the spatial stochastic model. The mean field differential equations are given in (4.4). We are

allowed to reduce our system to three dimensions since $\sum_i \frac{d}{dt} y_i = 0$ when we sum over all particle values, $\{1-, 1+, 2-, 2+\}$. So we exclude particle type $1-$ knowing that $y_{1-} = 1 - y_{1+} - y_{2-} - y_{2+}$. So our solutions are restricted to the pyramid in $\mathbb{R}^3$, bounded by $y_{1+} + y_{2-} + y_{2+} = 1$ and the 3 coordinate planes. One thing to note about this model is that there is a certain symmetry about switching the labels 1 and 2. So whenever an argument is made about species 1, a similar statement about species 2 can often be made by switching the labels 1 and 2. This should become apparent in the linear stability analysis of fixed points below.

The fractional population sizes, y_i should be understood to be dimensionless and thus the parameters will have units $\frac{1}{\text{time}}$. This can be understood by the fact that they are connected to exponential random variable whose expected values are inversely proportional to the parameters and represent the mean time between particle transitions. The timescale of the dynamics of the system are entirely set by the parameters. Normally a parameter is fixed at 1 and this sets the timescale for the model.

$$\begin{aligned}
\frac{d}{dt} y_{1+} =& y_{1+}(\beta_1(1 - y_{1+} - y_{2-} - y_{2+}) - \delta_1), \\
\frac{d}{dt} y_{2-} =& (\delta_1 y_{1+} + \delta_2 y_{2+})(y_{2-} + y_{2+}) - \nu_{21} y_{2-}(1 - y_{2-} - y_{2+}) \\
& + \nu_{12}(1 - y_{1+} - y_{2-} - y_{2+})(y_{2+} + y_{2-}) - \beta_2 y_{2+} y_{2-}, \\
\frac{d}{dt} y_{2+} =& y_{2+}(\beta_2 y_{2-} - \delta_2)
\end{aligned} \tag{4.4}$$

Invariant Subspaces The first thing to notice from these equations is that there are a few invariant subspaces.

(1) $1+$ axis

(2) $2-$ axis

(3) $\{1+, 2-\}$ plane

(4) $1 - y_{2+}$ diagonal

(5) $\{2-, 2+\}$ plane

The first on the list correspond to the species 1 contact process in isolation, if some unsuitable habitat is included, $2-$, then we get the third item on the list. The second invariant subspace listed represents the habitat voter model, when there are no '+' particle types, this is the $2-$ axis. The last two invariant subspaces on the list are the species 2 contact process in absence of species 1, and then with some unsuitable habitat included respectively.

Absorbing $\overline{1-}$ State There is a fixed point for the system in which only particle type $1-$ is present. This fixed point does not depend on the parameters of the system, however its local stability does.

$$\begin{aligned} &\text{Fixed Point: } [0, 0, 0] \\ &\text{Eigenvalues: } [\beta_1 - \delta_1, -\nu_{21} + \nu_{12}, -\delta_2] \end{aligned} \tag{4.5}$$

In order for this point to be stable, the species 1 contact process must be subcritical and the virtual dynamics must be biased towards $1-$. For the mean field, this is equivalent to $\beta_1 < \delta_1$ and $\nu_{21} > \nu_{12}$. Although these are not the same inequalities we get for the stochastic system, it still gives us an idea on the behavior we expect to get. Otherwise it is a saddle. The eigenvectors for this fixed point are given by

The eigenvectors are given by

$$\begin{bmatrix} 1 \\ 0 \\ 0 \end{bmatrix}, \quad \begin{bmatrix} 0 \\ 1 \\ 0 \end{bmatrix}, \quad \begin{bmatrix} 0 \\ \nu_{12} \\ \nu_{21} - \nu_{12} - \delta_2 \end{bmatrix}. \tag{4.6}$$

From this we can see that the first two column vectors lie on the axes and the stability of these linearized eigenspaces is determined by the parameter choices. The eigenvalue, $-\delta_2$, has an eigenvector which lies in the $\{2-, 2+\}$ plane. This is al-

ways a stable eigenspace since we are only considering positive parameter values, but whether or not it intersects the pyramid depends on the parameters. In the case that $\nu_{12} > \nu_{21}$, the eigenvector lies outside of the pyramid and thus for the purposes of this model only has two relevant eigenvectors

Absorbing $\overline{2-}$ State This fixed point also is always present, with stability dependent on the parameters.

$$\begin{aligned} &\text{Fixed Point: } [0, 1, 0] \\ &\text{Eigenvalues: } [\nu_{21} - \nu_{12}, -\delta_1, \beta_2 - \delta_2] \end{aligned} \tag{4.7}$$

This is similar to the $1-$ absorbing state except that the inequalities for stability are $\nu_{21} < \nu_{12}$, and $\beta_2 < \delta_2$. The cases where these absorbing states are stable are not the main interest here however. We would like both species to persist on their own and then look at the possible interactions between the two.

The eigenvectors for this fixed point are given by

$$\begin{bmatrix} 0 \\ -1 \\ 1 \end{bmatrix}, \quad \begin{bmatrix} 0 \\ 1 \\ 0 \end{bmatrix}, \quad \begin{bmatrix} \nu_{21} - \nu_{12} + \delta_1 \\ \delta_1 - \nu_{12} \\ 0 \end{bmatrix}. \tag{4.8}$$

From this we can see that when $\nu_{12} - \nu_{21} - \delta_1 > \delta_1 - \nu_{12}$ the eigenvector corresponding to eigenvalue $-\delta_1$ lies outside the pyramid.

Since the difference $\nu_{21} - \nu_{12}$ appears in both eigenspaces, we see that the $2-$ axis becomes a global center manifold when $\nu_{12} = \nu_{21}$ otherwise we have either a structurally stable connection between some combination of a saddle, a stable node and an unstable node between these two 'absorbing' states. This is apparent because the $2-$ axis is an invariant subspace and is always included as an eigenvector for these two fixed points. No perturbation of parameters will changes this, although as the

parameters are varied we will surely have variations in stability.

Species 1 Contact Process

$$\begin{aligned} &\text{Fixed Point:} \quad \left[\frac{\beta_1 - \delta_1}{\beta_1}, 0, 0\right] \\ &\text{Eigenvalues:} \quad \left[-\delta_2, -\beta_1 + \delta_1, -\frac{\delta_1^2 - \nu_{12}\delta_1 - \delta_1\beta_1 + \beta_1\nu_{21}}{\beta_1}\right] \end{aligned} \tag{4.9}$$

This fixed point is stable when $\beta_1 > \delta_1$ and $\delta_1 - \nu_{12} - \beta_1 + \frac{\beta_1}{\delta_1}\nu_{21} > 0$. Otherwise it is a saddle since the 1+ axis will always be the stable manifold.

Species 2 Contact Process

$$\begin{aligned} &\text{Fixed Point:} \quad \left[0, \frac{\delta_2}{\beta_2}, \frac{\beta_2 - \delta_2}{\beta_2}\right] \\ &\text{Eigenvalues:} \quad \left[-\delta_1, -\beta_2 + \delta_2, -\frac{\delta_2^2 - \nu_{21}\delta_2 - \delta_2\beta_2 + \beta_2\nu_{12}}{\beta_2}\right] \end{aligned} \tag{4.10}$$

This fixed point is stable when $\beta_2 > \delta_2$ and $\delta_2 - \nu_{21} - \beta_2 + \frac{\beta_2}{\delta_2}\nu_{12} > 0$, otherwise it is a saddle since the diagonal, $y_{2+} = 1 - y_{2-}$ with $y_{1+} = 0$, is the stable manifold.

Species 1 contact process with some unsuitable habitat In this case the analytical eigenvalues are too complex to display.

$$\text{Fixed Point:} \quad \left[\frac{\delta_1(-\nu_{21} + \nu_{12})}{\beta_1(-\delta_1 + \nu_{21})}, \frac{(\delta_1^2 - \nu_{12}\delta_1 - \delta_1\beta_1 + \beta_1\nu_{21})}{\beta_1(-\delta_1 + \nu_{21})}, 0\right] \tag{4.11}$$

This point merges with the Species 1 contact process point when

$$\beta_1 = \frac{\delta_1(\nu_{12} - \delta_1)}{(\nu_{21} - \delta_1)} \tag{4.12}$$

Species 2 contact process with some unsuitable habitat In this case the analytical eigenvalues are too complex to display.

$$\text{Fixed Point: } \left[0, \frac{\delta_2}{\beta_2}, \frac{\delta_2(\nu_{12}-\nu_{21})}{\beta_2(\nu_{12}-\delta_2)}\right] \tag{4.13}$$

This point merges with the Species 1 contact process point when

$$\beta_2 = \frac{\delta_2(\nu_{21}-\delta_2)}{(\nu_{12}-\delta_2)} \tag{4.14}$$

Possible Coexistence In this case the eigenvalues and eigenvectors involve complex roots.

This merges with the "$1\pm, 2-$" fixed point when

$$\nu_{21} = \frac{(-\delta_1\beta_2 + \nu_{12}\beta_2 - \beta_1\delta_2 + \beta_1\beta_2)\delta_1}{(\beta_2-\delta_2)\beta_1} \tag{4.15}$$

This merges with the "$2\pm, 1-$" fixed point when

$$\nu_{12} = \frac{(-\delta_2\beta_1 + \nu_{21}\beta_1 - \beta_2\delta_1 + \beta_2\beta_1)\delta_2}{(\beta_1-\delta_1)\beta_2} \tag{4.16}$$

The pyramid region of phase space for this model can be summarized in Figure 4.6.

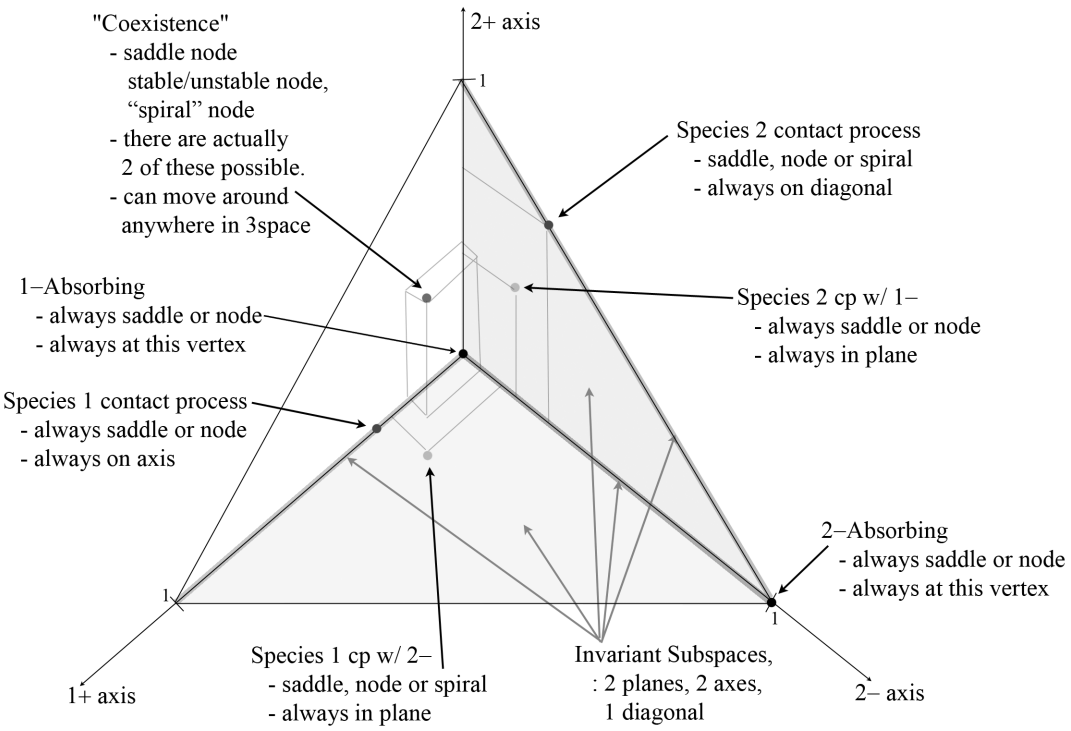


FIGURE 4.6. Phase space summary for the virtual particle model.

4.3 Analysis of an Invasion Path

Due to the presence of the absorbing states where the whole grid is filled completely with $1-$'s or $2-$'s we included boundary conditions which eliminate these absorbing states. For the purpose of studying an invasion, we set a fixed source of the introduced species, $2+$, on the left boundary and a fixed source of the native species, $1+$, on the right boundary. This satisfies Proposition 1, and we now have an ergodic process on the finite grid which allows the use of CFTP.

To approximate a plant invasion, we start with parameters that give the native species a low stationary density. The native landscape will be approximated by a contact process with death rate 1 and birth rate 0.46. These rates are in the standard contact process formulation and translated to the interaction map formulation we get $\delta_1 = 0.25$ and $\beta_1 = 0.46$. The reason is that our interactions are now defined per

individual in the neighborhood and the desire is that our death rates add to 1 over the nearest particle neighborhood, $|x - y| = 1$.

In order to understand the path of an invasion, it is necessary to analyze the spatial structures which appear. When a species is present, we would like to quantify its spatial pattern. Is it uniformly distributed or significantly clumped together. The *distance index of dispersion*, I_d, is a measure of spatial pattern and was devised by Johnson and Zimmer (1985) [20]. Given a sample of n points with distances x_i from the i^{th} point to the nearest object, the dispersion index is the ratio of the sum of the squares of the squared distances to the square of the sum of the squared distances.

$$I_d = (n+1)\frac{\sum_{i=1}^{n}(x_i^2)^2}{\left(\sum_{i=1}^{n} x_i^2\right)^2} \tag{4.17}$$

For random patterns, $I_d \approx 2$; for uniform patterns, $I_d < 2$, and for clumped patterns, $I_d > 2$. An intuitive understanding of the dispersion index is the following example of bugs distributed on leaves: A random pattern is where each leaf has the same probability of having a bug, a uniform pattern is when each leaf has the same number of bugs, and a clumped pattern is where a few leaves have lots of bugs while most leaves have none[35].

In addition to describing the spatial pattern, we would like to know how thick a species grows. To measure thickness, we randomly select n sites occupied by a species and find the distance x_i to the nearest site occupied by something other than that species. Each x_i is raised to the power 1.2 and then the average is taken.

$$I_t = \frac{1}{n}\sum_{i=1}^{n} x_i^{1.2} \tag{4.18}$$

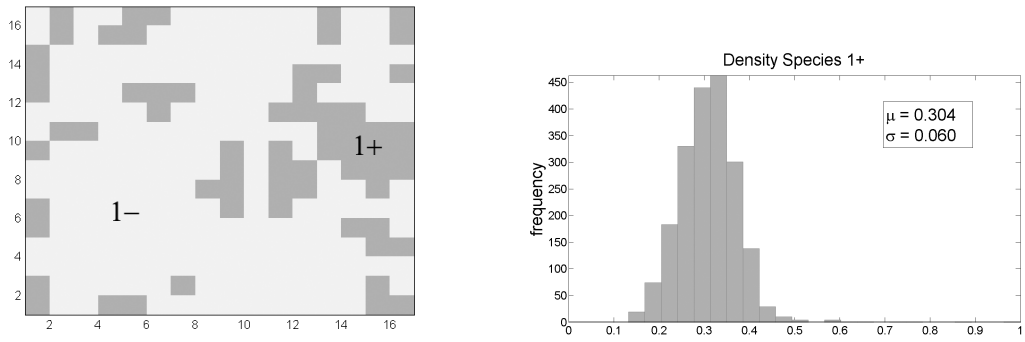
The reason for using a power of 1.2 is to add some bias towards the larger distances.

If we look at a square of 9 sites, only 1 site will get a distance of 2, the desire is for this single 2 to carry more weight in determining the thickness measure. The presence of any occupied site would get a thickness index of 1 automatically, so we define $I_t = 1$ if no sites are occupied. This power was chosen so that the maximum difference between birth and death rates to be considered here gives $I_t \approx 3$ for the stationary distribution of a contact process.

In order to use a virtual particle model, we choose the formulation in Figure 4.5 so that our system can retain monotonicity with our chosen parameters for species 1.

4.3.1 The Underlying Contact Processes

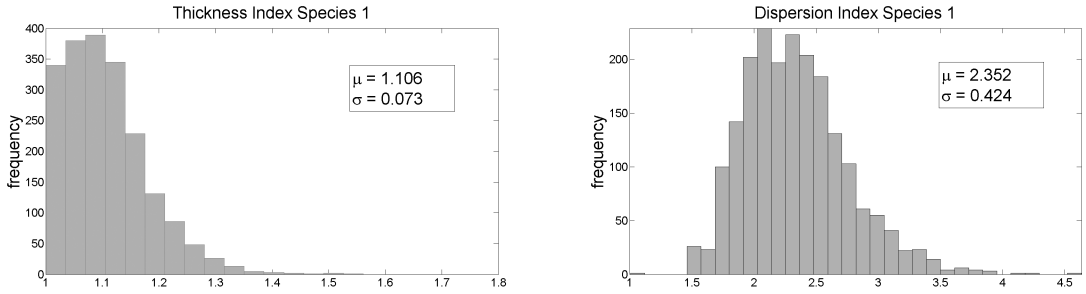
Figure 4.7(a) gives the stationary distribution for species 1 on a 16×16 grid. Species 1 occupies about 30% of the grid, with a mean thickness index of 1.1, and a mean dispersion index of 2.35. The introduced species to be considered will be assumed to have a higher birth rate and a higher death rate as well. The parameters $\beta_2 = 1.2$ and $\delta_2 = 0.4$ will be used initially. The species 2 contact process stationary behavior is illustrated by Figure 4.9(a).



(a) (b)

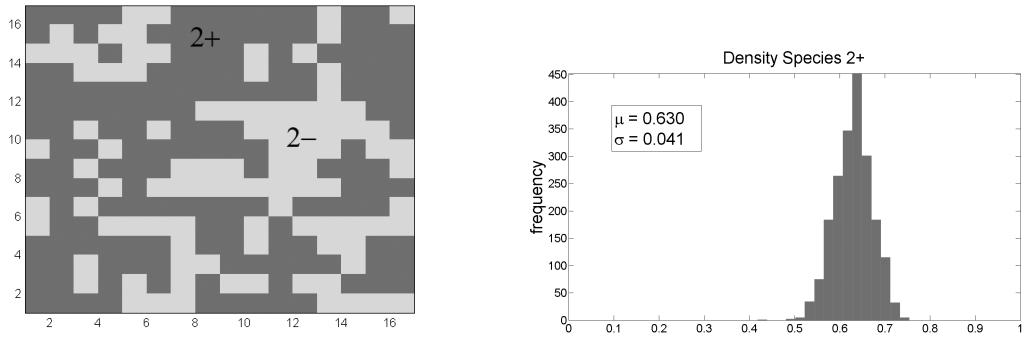
FIGURE 4.7. Stationary spatial grid(a) and density histogram(b) for species 1.

Now in order to set these 2 processes on the same grid, we let the virtual states communicate according to ν_{12} and ν_{21}. The first case considered will be $\nu_{12} = 1.0$



(a) (b)

FIGURE 4.8. Histograms for the stationary thickness index(a) Dispersion Index(b) statistics for species 1.



(a) (b)

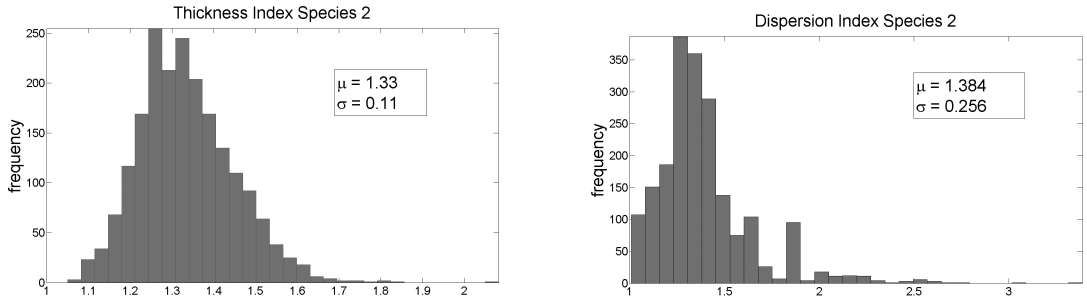
FIGURE 4.9. Stationary spatial grid(a) and density histogram(b) for species 2.

and $\nu_{21} = 1.02$. We will consider species 2 as the introduced one and since this one survives at a higher density, we will let its habitat disappear at a slightly higher rate. These virtual transition parameters is where a lot of flexibility lies in the model.

4.3.2 Mean Field Analysis

To summarize the above, the parameter values under current consideration are

$$\beta_1 = 0.46, \beta_2 = 1.2, \delta_1 = 0.25, \delta_2 = 0.4, \nu_{12} = 1.0, \nu_{21} = 1.02 \tag{4.19}$$



(a) (b)

FIGURE 4.10. Histograms for the stationary thickness index(a) Dispersion Index(b) statistics for species 2.

So we have 2 surviving contact processes. The mean field equations are:

$$\begin{aligned}
\frac{d}{dt}y_{1+} =& y_{1+}(0.46(1 - y_{1+} - y_{2-} - y_{2+}) - 0.25), \\
\frac{d}{dt}y_{2-} =& (0.25y_{1+} + 0.4y_{2+})(y_{2-} + y_{2+}) - y_{2-}(1 - y_{2-} - y_{2+}) \\
& + 1.02(1 - y_{1+} - y_{2-} - y_{2+})(y_{2+} + y_{2-}) - 1.2y_{2+}y_{2-}, \\
\frac{d}{dt}y_{2+} =& y_{2+}(1.2y_{2-} - 0.4)
\end{aligned} \tag{4.20}$$

Fixed Points: The system of ODE's in (4.20) has six fixed points of interest. There are others, but we are only concerned with the region $0 \leq y_{1+} + y_{2-} + y_{2+} \leq 1$ with $y_i \geq 0$ for each particle type. Figure 4.11 lists the fixed points for our chosen parameters. The coordinate for particle type $1-$ has been included by subtracting all other coordinates from 1. This gives us an idea on how we expect the stochastic model to behave qualitatively.

4.3.3 Stochastic Simulation

We start by using the Propp-Wilson algorithm to reach the stationary distribution then using the coupling realization generated to run from specific initial conditions. We are interested in what happens if species 1 is initially stationary with species 2

Fixed Point	Interpretation	Type
$[0, 0, 0]$	Absorbing $1-$	Saddle
$[0, 1, 0]$	Absorbing $2-$	Saddle
$[0, 0.33, 0.01]$	Species 2 CP w/ $1-$	Saddle
$[0, 0.33, 0.67]$	Species 2 CP	Stable Node
$[0.543, 0, 0]$	Species 1 CP	Stable Node
$[0.543, 0.333, 0.061]$	Coexistence	Saddle

FIGURE 4.11. Fixed points(approximate) for the invasion model and their interpretations.

absent and then species 2 is introduced with a constant source boundary. Figure 4.12 gives the percentage of sites occupied by each particle type. Up until about

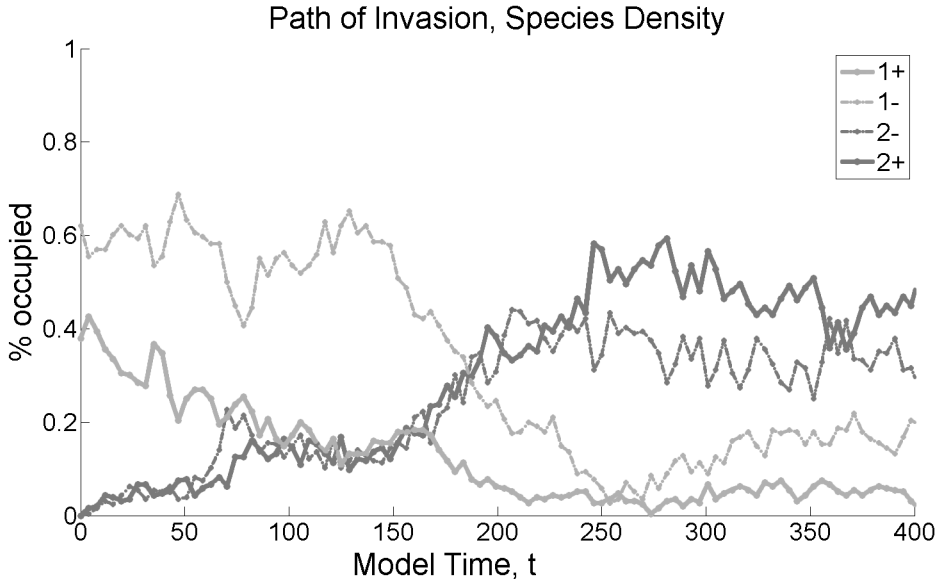


FIGURE 4.12. Species density along the path of invasion.

$t = 150$, the native species 1 dies out while species 2 slowly moves in, at which point particle type $1-$, species 1 habitat, begins to quickly disappear. The invader reaches its equilibrium density which is not far below its basal contact process level of 63%.

We can see the pattern change within the landscape during the invasion. When species 1 is stationary by itself it is just above the threshold for being considered

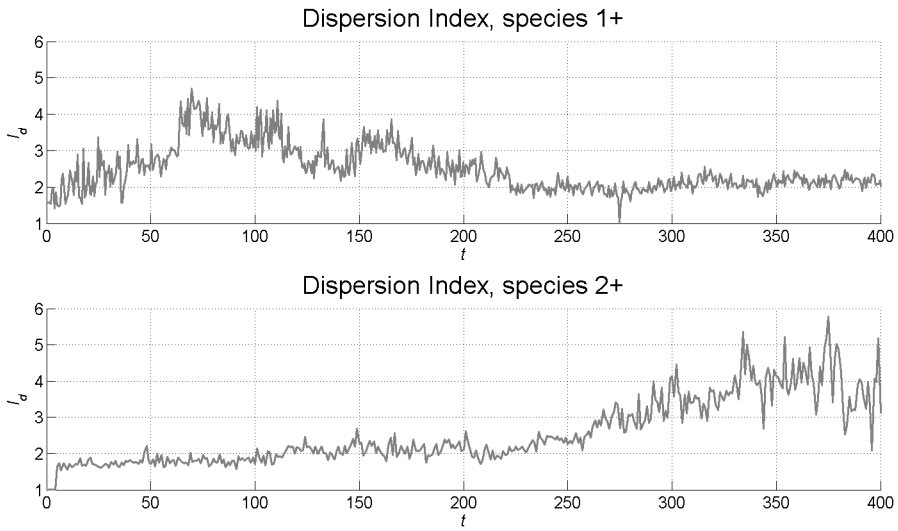


FIGURE 4.13. Index of dispersion along the path of invasion.

clumpy. Species 2 pushes in with an almost uniform wave front which causes species 1 to clump together even more. In the end, it is apparent that the presence to the species 1 source boundary makes the species to dispersion index indicate a thick clumped pattern while species 1 is hardly present with a uniform thickness of 1 on average.

Stationary Distribution Once the Propp-Wilson algorithm has given a sample from the stationary distribution, we can continue past this sample to get the actual stationary behavior of the system. Figures 4.15(a) through 4.18(b) display the stationary behavior of the model. These figures are histograms for 1200 samples from the stationary distribution. These samples were taken by going randomly chosen amounts of time past the sample given by PW.

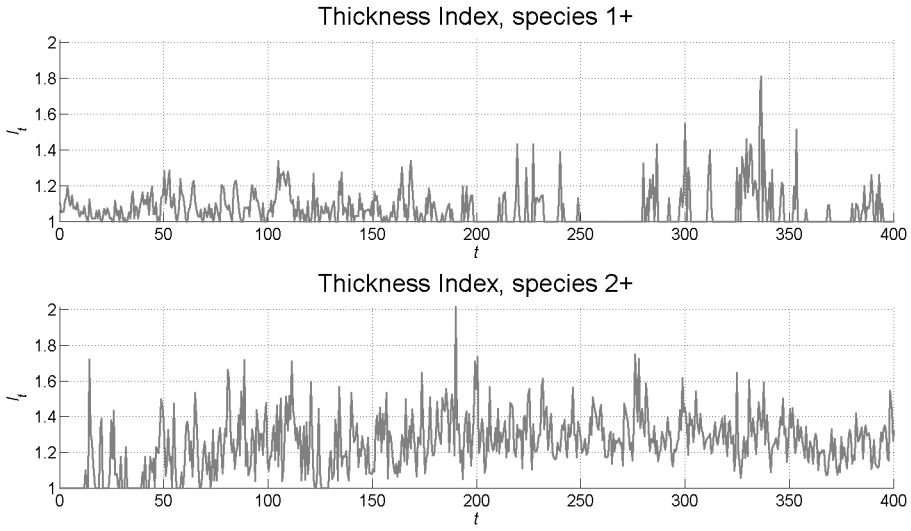
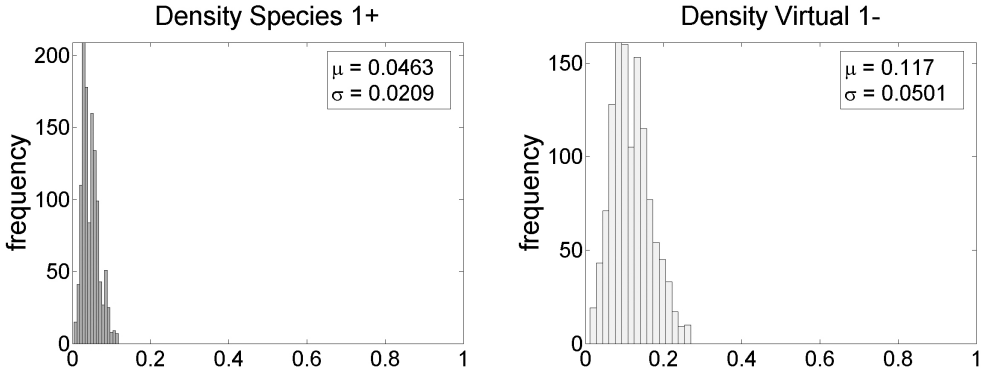
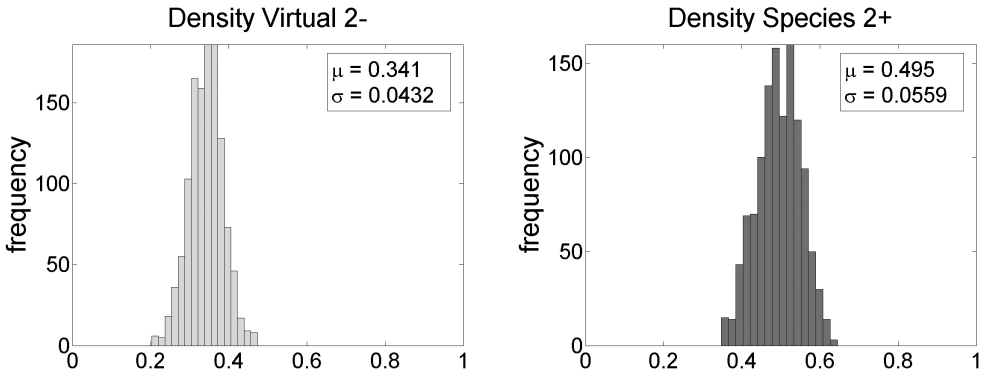


FIGURE 4.14. Thickness index along the path of invasion.



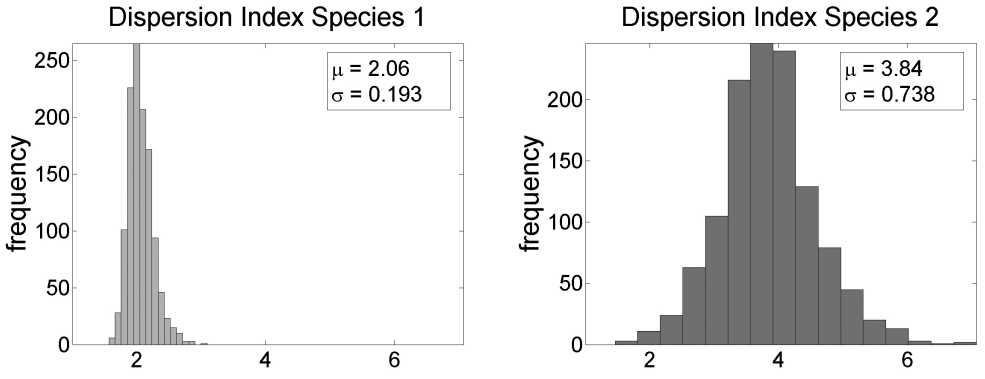
(a) (b)

FIGURE 4.15. Histograms for stationary density (a) 1+ (b) 1−.



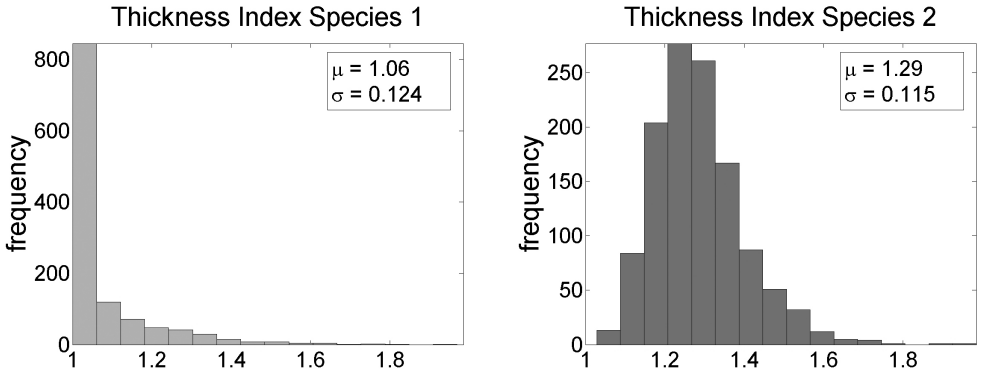
(a) (b)

FIGURE 4.16. Histograms for stationary density (a) 2− (b) 2+.



(a) (b)

FIGURE 4.17. Histograms for stationary dispersion index (a) 1+ (b) 2+.



(a) (b)

FIGURE 4.18. Histograms for stationary thickness index (a) 1+ (b) 2+.

4.3.4 Virtual Parameter Dependence

We have some freedom in setting the virtual transition rates. Since species 2 survives at a higher density, we may expect it to be a little more fit in the sense that its habitat can be the loser of the voter interaction and yet it still persists. Figure 4.19 shows that the is a critical parameter value just below $\nu_{21} = 1.2$ where we have a transition to specie 1 winning. The exact value is difficult to find with high accuracy however.

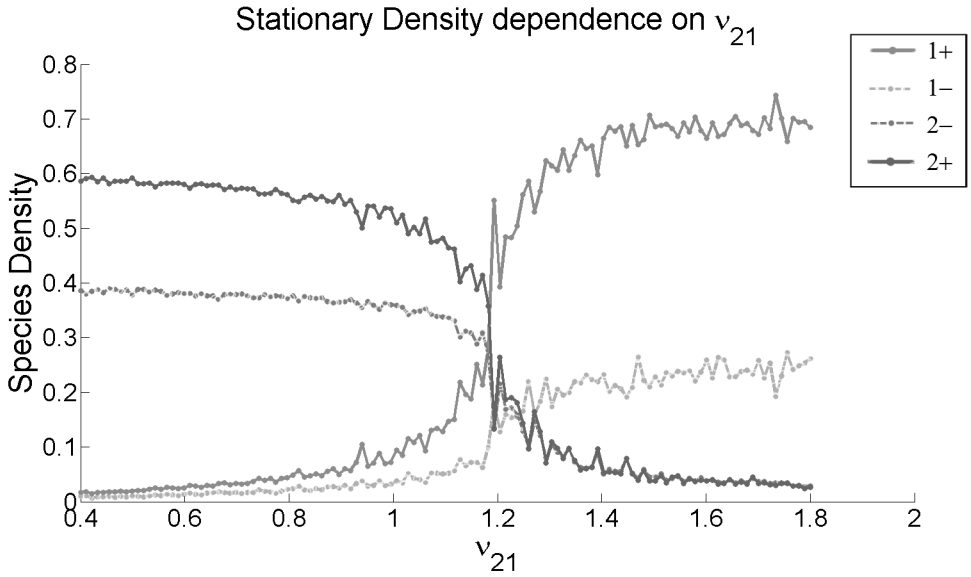


FIGURE 4.19. Dependence of stationary density on virtual rate ν_{21}.

In the infinite grid model, without the boundary conditions, this leads us to suspect that our space of invariant distributions changes as we vary the parameter, ν_{21}. After examining Figure 4.19, it may be natural to conjecture the following for the infinite model.

Conjecture 2. For the virtual particle model where the species 1 and 2 contact processes are both supercritical, with ν_{12} fixed, there exists 3 critical values, $\nu_{c_1} \leq \nu_{c_2} \leq \nu_{c_3}$ such that starting with infinitely many 1+'s and infinitely 2+'s

(1) $\nu_{21} < \nu_{c_1} \Rightarrow$ Species 1+ dies.

(2) $\nu_{c_1} < \nu_{21} < \nu_{c_2} \Rightarrow$ Coexistence, but species 2+ dominant.

(3) $\nu_{c_2} < \nu_{21} < \nu_{c_3} \Rightarrow$ Coexistence, but species 1+ dominant.

(4) $\nu_{c_3} < \nu_{21} \Rightarrow$ Species 2+ dies.

This conjecture illustrates the underlying dependence of the habitat dynamics for the survival of a species. The success of an invasion depends partly on the availability of habitat

4.3.5 Concluding Remarks on Invasion

In the event that a native species survives at a lower density than an introduced species whether or not the invasion is successful depends on the availability of habitat to the invading species. The virtual particle dynamics in the invasion allow us to keep track of the habitat in the ecosystem. When the habitat necessary for the introduced species to persist is lost at a high enough rate, the invasion cannot occur. Numerical findings lead us to believe that when two supercritical contact processes communicate using these voter model like virtual particle dynamics, whether or not we have extinction of ones species or coexistence depends on the "habitat dynamics".

Chapter 5

Future Work

There are limitless avenues to explore within the framework developed here. Particle systems have a wide range of applications and where monotone models can be developed, the stationary behavior can be known exactly. Expanding our understanding of monotonicity is the bedrock of much of the work here, if we can expand this understanding to an even larger class of models, then the methods here will be even more powerful. Developing methods of sampling from non-monotone models will expand the methods of analysis for these models as well. When the dual process is understood, ergodic theorems will be within reach for the virtual particle model. These are the foremost areas to to study currently.

Multiple Interaction Types. The IMPS framework is currently limited to *one way* interactions in which a single particle can be changed by its neighbors. The inclusion of jumps and k-cycle type interactions may be desirable in order to broaden the scope of the theory to include exclusion process type interactions.

$$\begin{aligned} a_1 &\to \mathscr{J}_1(a_2, a_1) \\ a_2 &\to \mathscr{J}_1(a_3, a_2) \\ &\vdots \\ a_k &\to \mathscr{J}_1(a_1, a_k) \end{aligned}$$

Where $\mathscr{J}_1$ could possibly be a new interaction map defined specifically for these types of shuffling interactions.

Including multi-neighbor interactions would also be of interest. In the Ising model,

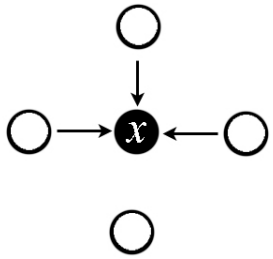


FIGURE 5.1. Multiple neighbors affect x simultaneously

a particle can be thought to interact with the neighborhood rather than any specific neighbor. This type of interaction cannot exactly be accommodated in the current formulation.

The current formulation is also limited to each interaction being over the same neighborhood for any given site. Extending this framework to models which allow different dispersal distances for particles also increases the reach of the theory.

Models previously explored. Many different interacting particle systems have been explored in the past. One particular example would be that of bacteria and colicin. Bacteria may produce toxic substances that kill or inhibit the growth of competing bacteria[8]. The rates for this model are

$$\begin{array}{llllll} 0 \to 1 & \text{at rate} & \beta_1 f_1 & 1 \to 0 & \text{at rate} & \delta_1 \\ 0 \to 2 & \text{at rate} & \beta_2 f_2 & 2 \to 0 & \text{at rate} & \beta_2 + \gamma f_1 \end{array}$$

Where f_i is the fraction of sites occupied by particle i in a given neighborhood. This is a variation on the multi-type contact process and so could easily be adapted to the interaction map framework. This is merely one example where the work presented here could make advances.

The virtual particle model discussed here is similar to the host pathogen model studied by Durrett, Lanchier and Neuhauser[22, 9]. If the methods here can be applied to that model, then maybe more results may be obtained.

Duality. Over the past 30 years, coupling and duality have proven to be the two most useful tools for studying interacting particle systems[16]. Developing ergodic theorems for the multi-type contact process relies heavily on duality arguments[29]. The virtual particle model presented here is essentially a modified version of the multi-type contact process. We would also like to prove that in the limit as the virtual particle dynamics become fast, the model converges to the multi-type contact process. If we can develop an understanding of the dual process for various parameter regions, then we should be able to understand the ergodic behavior. The theory of monotonicity developed here should also prove useful here. For monotone versions of the model, we get ordered extremal invariant distributions.

Non-Monotone Coalescence Non-monotone parameter values seem to exhibit extremely interesting behavior as well. Using methods of Fill, Machida, Murdoch, and Rosenthal[12, 28], Kendall and Cai[21, 4], and Propp and Wilson[31]. Coupling from the past could possibly be extended to non-monotone models. Understanding any partial-monotone structures that exist for the process will help make the algorithms more efficient. For example in several interesting cases of the virtual particle model presented here, the coupling can be made totally monotone except for a few of the transitions. There may be tricks that allow us to get around this.

Appendix A

Computer Code

The computer code used for simulations is given below.

A.1 Propp-Wilson Simulation Code

```
%%%%%%%%%%%%%%%%%%%%%%%%%%
%
% Joseph Stover
% PM program for Invasive Species
%
% PM = +/-
% State Space={1-,1+,2-,2+}^L = {0,1,2,3}^L
%
% 5/6/2008
%
% This is CFTP (Propp-Wilson).
%
%  This program generates and saves coupling maps as binary data.
%  and runs a monotone IMPS from the chosen extremal states
%
%
%%%%%%%%%%%%%%%%%%%%%%%%%%

b1=params_(1); %birth 1- -> 1+
b2=params_(2); %birth 2- -> 2+
d1=params_(3); %death 1+ -> 1-/2-
d2=params_(4); %death 2+ -> 1-/2-
v1=params_(5); %virtual 1- -> 2-
v2=params_(6); %virtual 2- -> 1-

percent1p=inits_(1);
percent1m=inits_(2);
percent2m=inits_(3);
percent2p=inits_(4);

%%%%%%%%%%%%%%%%%%%%%%%%%%
% Propp-Wilson Path
%%%%%%%%%%%%%%%%%%%%%%%%%%

for nn=nn_startValue:maxSteps/pwMult;
    if nn>nn_endValue;
        skipGenU_sw=0;
    end
    if skipGenU_sw==0;
        % Generate transition
        yPick1=(-1).^round(rand(pwMult,1));
        yPick2=(-1).^round(rand(pwMult,1));
        chooseVec=round(rand(pwMult,1));
```

```
    U=zeros(pwMult,6);
    U(:,1)=ceil(rand(pwMult,1)*(Space)); %x1
    U(:,2)=ceil(rand(pwMult,1)*(Space))+1; %x2
    U(:,3)=chooseVec.*(mod(mod(U(:,1)+yPick1,Space)-1,Space)+1)+(1-chooseVec).*U(:,1); %y1
    U(:,4)=chooseVec.*U(:,2)+(1-chooseVec).*(U(:,2)+yPick2); %y2
    U(:,5)=rand(pwMult,1)*maxRate;%/nbhdSize; %max(max(up(1,:)),max(down(1,:)));
    U(:,6)=round(rand(pwMult,1));

    % save transition U
    % save x and y
    popfileName1=sprintf(strcat(folderNameU,'/binUxy_%0.5g_%0.5g'),Space,nn);
    fid=fopen(popfileName1,'w');
    fwrite(fid,U(1:pwMult,1:4),'ubit8');
    fclose(fid);
    % save u-value
    popfileName2=sprintf(strcat(folderNameU,'/binUu_%0.5g_%0.5g'),Space,nn);
    fid=fopen(popfileName2,'w');
    fwrite(fid,U(1:pwMult,5),'float64');
    fclose(fid);
    % save b/d declaration
    popfileName3=sprintf(strcat(folderNameU,'/binUbd_%0.5g_%0.5g'),Space,nn);
    fid=fopen(popfileName3,'w');
    fwrite(fid,U(1:pwMult,6),'ubit1');
    fclose(fid);
end

if nn/popSimMult-round(nn/popSimMult)==0; %run pop sim:
    if rand_Int==0;
        % Generate initial maximal populations
        %all 0's (1-'s)
        Population(1:Space,1,1)=BCleft;
        Population(1:Space,2:Space+1,1)=extLower*ones(Space,Space);
        Population(1:Space,Space+2,1)=BCright;
        %all 3's (2+'s)
        Population(1:Space,1,2)=BCleft;
        Population(1:Space,2:Space+1,2)=extUpper*ones(Space,Space);
        Population(1:Space,Space+2,2)=BCright;
    elseif rand_Int==1;
        % random populations
        %1
        Population(1:Space,1,1)=BCleft;
        Population(1:Space,2:Space+1,1)=round(3*rand(Space,Space));
        Population(1:Space,Space+2,1)=BCright;
        %2
        Population(1:Space,1,2)=BCleft;
        Population(1:Space,2:Space+1,2)=round(3*rand(Space,Space));
        Population(1:Space,Space+2,2)=BCright;
    elseif rand_Int==2;
        for i=1:2;
            for xx=1:Space;
                for yy=2:Space+1;
                    chooseParticle=rand;
                    if chooseParticle<=percent1p;
                        Population(xx,yy,i)=0;
                    elseif chooseParticle>percent1p & chooseParticle<=percent1m+percent1p;
                        Population(xx,yy,i)=1;
                    elseif chooseParticle>percent1m+percent1p & chooseParticle<=percent1m
                                +percent1p+percent2m;
                        Population(xx,yy,i)=2;
                    else Population(xx,yy,i)=3;
                    end;
                end;
```

```
        end;
        Population(1:Space,1,i)=BCleft;
        Population(1:Space,Space+2,i)=BCright;
    end;
end %elseif rand_Int==4;

%add the edges for plotting:
Population(Space+1,1:Space+2,1:2)=0;
Population(1:Space+1,Space+3,1:2)=0;

% run the program PW
for ii=1:nn;
    %previous transitions:
    U=[reshape(fread(fopen(sprintf(strcat(folderNameU,...
            '/binUxy_%0.5g_%0.5g'),Space,nn-ii+1),'r'),'ubit8'),pwMult,4),...
        fread(fopen(sprintf(strcat(folderNameU,...
            '/binUu_%0.5g_%0.5g'),Space,nn-ii+1),'r'),'float64'),...
        fread(fopen(sprintf(strcat(folderNameU,...
            '/binUbd_%0.5g_%0.5g'),Space,nn-ii+1),'r'),pwMult,'ubit1')];
    fclose('all');

    for t=1:pwMult;
        if U(pwMult-t+1,5)<=maxRate;
            PopulationNew=Population;

            x1=U(pwMult-t+1,1);
            x2=U(pwMult-t+1,2);

            y1=U(pwMult-t+1,3);
            y2=U(pwMult-t+1,4);

            uVal=U(pwMult-t+1,5);%*max([up(1,:),down(1,:)]);
            phiVal=phiVal_; %1/nbhdSize;%phi(x1,x2,y1,y2);

            for i=1:2; %256;
                x_Particle=Population(x1,x2,i);
                y_Particle=Population(y1,y2,i);
                if U(pwMult-t+1,6)==1;
                    if x_Particle==0;
                        if y_Particle>=0 & y_Particle<=1 & uVal<=d1*phiVal;
                            PopulationNew(x1,x2,i)=1;
                        elseif y_Particle>=2 & uVal<=d1*phiVal;
                            PopulationNew(x1,x2,i)=2;
                        end
                    elseif x_Particle==1;
                        if y_Particle>=2 & uVal<=v1*phiVal;
                            PopulationNew(x1,x2,i)=2;
                        end
                    elseif x_Particle==2;
                        if y_Particle==3 & uVal<=b2*phiVal;
                            PopulationNew(x1,x2,i)=3;
                        end
                    end
                elseif U(pwMult-t+1,6)==0;
                    if x_Particle==1;
                        if y_Particle==0 & uVal<=b1*phiVal;
                            PopulationNew(x1,x2,i)=0;
                        end
                    elseif x_Particle==2;
                        if y_Particle<=1 & uVal<=v2*phiVal;
                            PopulationNew(x1,x2,i)=1;
                        end
```

```
                            elseif x_Particle==3;
                                if y_Particle<=1 & uVal<=d2*phiVal;
                                    PopulationNew(x1,x2,i)=1;
                                elseif y_Particle>=2 & uVal<=d2*phiVal;
                                    PopulationNew(x1,x2,i)=2;
                                end
                            end
                        end
                    end
                    Population=PopulationNew;
                end
            end % for t=1:pwMult;

            NumDifferent=(Space+1)*(Space+3)-sum(sum(Population(:,:,1)==Population(:,:,2)));

        end %ii

        if Population(:,:,1)==Population(:,:,2); % check for coalescence
            break;
        end %gen new transitions

    end % if nn multiple of popsim
end %for nn=1:maxSteps/pwMult;

nn_endValue=nn; %where the program terminated
```

A.2 Code for Forward Simulation

```
%%%%%%%%%%%%%%%%%%%%%%%%%
%
% Joseph Stover
% PM program for Invasive Species
%
% PM = +/-
% State Space={1-,1+,2-,2+}^L = {0,1,2,3}^L
%
% 5/6/2008
%
% Run this from "invRun.m"
% This is forward time.
%
% This program inputs different initial conditions
%    and runs along the CFTP generated coupling
%    to get a path to stationarity.
%
%%%%%%%%%%%%%%%%%%%%%%%%%

b1=params_(1); %birth 1- -> 1+
b2=params_(2); %birth 2- -> 2+
d1=params_(3); %death 1+ -> 1-/2-
d2=params_(4); %death 2+ -> 1-/2-
v1=params_(5); %virtual 1- -> 2-
v2=params_(6); %virtual 2- -> 1-

percent1p=inits_(1);
percent1m=inits_(2);
percent2m=inits_(3);
percent2p=inits_(4);
```

```
% counter variables:
Dcount=1;
Dcount2=1;
pc=1;

%%%%%%%%%%%%%%%%%%%%%%%%%
% Initial Populations
%%%%%%%%%%%%%%%%%%%%%%%%%

if rand_Int==0;
    % Generate initial maximal populations
    %all 0's (1-'s)
    Population(1:Space,1,1)=BCleft;
    Population(1:Space,2:Space+1,1)=extLower*ones(Space,Space);
    Population(1:Space,Space+2,1)=BCright;
    %all 3's (2+'s)
    Population(1:Space,1,2)=BCleft;
    Population(1:Space,2:Space+1,2)=extUpper*ones(Space,Space);
    Population(1:Space,Space+2,2)=BCright;
elseif rand_Int==1;
    % random populations
    %1
    Population(1:Space,1,1)=BCleft;
    Population(1:Space,2:Space+1,1)=round(3*rand(Space,Space));
    Population(1:Space,Space+2,1)=BCright;
    %2
    Population(1:Space,1,2)=BCleft;
    Population(1:Space,2:Space+1,2)=round(3*rand(Space,Space));
    Population(1:Space,Space+2,2)=BCright;
elseif rand_Int==2;
    for i=1:2;
        for xx=1:Space;
            for yy=2:Space+1;
                chooseParticle=rand;
                if chooseParticle<=percent1p;
                    Population(xx,yy,i)=0;
                elseif chooseParticle>percent1p & chooseParticle<=percent1m+percent1p;
                    Population(xx,yy,i)=1;
                elseif chooseParticle>percent1m+percent1p & chooseParticle<=percent1m
                           +percent1p+percent2m;
                    Population(xx,yy,i)=2;
                else Population(xx,yy,i)=3;
                end;
            end;
        end;
        Population(1:Space,1,i)=BCleft;
        Population(1:Space,Space+2,i)=BCright;
    end;
end %elseif rand_Int==4;

%add the edges for plotting:
Population(Space+1,1:Space+2,1:2)=0;
Population(1:Space+1,Space+3,1:2)=0;


%get inital conditions, plotting, saving, etc...
if popCount_sw==1;
    for i=1:2;
        for pt=1:4
            popCount(pc,pt,i)=sum(sum(Population(1:Space,2:Space+1,i)==pt-1))/Space^2;
            pcTvec(pc)=0; %-log(1-rand)/Space^2/(max(up(1,:))+max(down(1,:)));
        end
```

```
    end
end %popCount

if popPlot_sw==1;
    plot_title=sprintf('step=%0.5g, time=%0.5g',0,0);
    subplot(2,1,1), pcolor(Population(:,:,1)), shading('flat'),
    colormap([.2 .8 .2; .8 1 .8; 1 .8 .8; .8 .2 .2]);
    title(plot_title);
    subplot(2,1,2), pcolor(Population(:,:,2)), shading('flat'),
    colormap([.2 .8 .2; .8 1 .8; 1 .8 .8; .8 .2 .2]);
    title(plot_title);
    pause(PlotPause);
end

if binPopSave_sw==1;
    popfileName=strcat(popFileName_);
    fid=fopen(popfileName,'w');
    fwrite(fid,Population(1:Space,2:Space+1,:),'ubit2');
    fclose('all');
end

%dispersion index, sample random sites:
sizevp=size(vp);
xr1=ceil(Space*rand(1,sampleSize));
xr2=ceil(Space*rand(1,sampleSize))+1;
for svp=1:sizevp(2);
    for i=1:2;
        dnrVec=0;
        dnr=0;
        for kk=1:sampleSize;
            mPop=Population(1:Space,2:Space+1,i);
            mPop(xr1(kk),xr2(kk))=vp(svp)-1;
            [m3,n3]=find(mPop(:,:)==vp(svp));
            if isempty(m3)==0;
                dist3=min(abs(xr1(kk)-m3)+abs(xr2(kk)-n3));
                dnrVec(kk)=dist3;
            else
                dist3=1;%min(abs(xr1(kk)-m3)+abs(xr2(kk)-n3));
                dnrVec(kk)=1;
            end
        end
        dispersionIndex(Dcount,svp,i)=(sampleSize+1)*sum(dnrVec(:).^2.^2)./(sum(dnrVec(:).^2)).^2;
    end
end
Dcount=Dcount+1;

%thickness index, sample random sites:
for svp2=1:sizevp(2);
    for i=1:2;
        drtVec=0;
        drt=0;
        [m5_,n5_]=find(Population(1:Space,2:Space+1,i)==vp(svp2));
        if isempty(m5_)==0;
            i5_=ceil(max(size(m5_))*rand(1,max(size(m5_))));
            for kk2=1:min(sampleSize,max(size(m5_)));
                [m5,n5]=find(Population(1:Space,2:Space+1,i)~=vp(svp2));
                if isempty(m5)==0;
                    dist5=min(abs(m5_(i5_(kk2))-m5)+abs(n5_(i5_(kk2))-n5));
                    drtVec(kk2)=dist5;
                else
                    dist5=3;%min(abs(m5_(i5_(kk2))-m5)+abs(n5_(i5_(kk2))-n5));
                    drtVec(kk2)=3;%dist5;
```

```
                end
            end
            thicknessIndex(Dcount2,svp2,i)=min(sum(drtVec.^1.2)/min(sampleSize,max(size(m5_))),3);
        else
            thicknessIndex(Dcount2,svp2,i)=1;%sum(drtVec.^2)/min(sampleSize,max(size(m5_)));
        end
    end
end
Dcount2=Dcount2+1;

%%%

nn=nn_startValue;

%%%%%%%%%%%%%%%%%%%%%%%%%
% Forward Path
%%%%%%%%%%%%%%%%%%%%%%%%%

% run the program Forward
for ii=1:nn;
    %previous transitions:

    U=[reshape(fread(fopen(sprintf(strcat(folderNameU,...
                    '/binUxy_%0.5g_%0.5g'),Space,nn-ii+1),'r'),'ubit8'),pwMult,4),...
        fread(fopen(sprintf(strcat(folderNameU,...
                    '/binUu_%0.5g_%0.5g'),Space,nn-ii+1),'r'),'float64'),...
        fread(fopen(sprintf(strcat(folderNameU,...
                    '/binUbd_%0.5g_%0.5g'),Space,nn-ii+1),'r'),pwMult,'ubit1')];
    fclose('all');

    for t=1:pwMult;
        if U(pwMult-t+1,5)<=maxRate;
            PopulationNew=Population;

            x1=U(pwMult-t+1,1);
            x2=U(pwMult-t+1,2);

            y1=U(pwMult-t+1,3);
            y2=U(pwMult-t+1,4);

            uVal=U(pwMult-t+1,5);%*max([up(1,:),down(1,:)]);
            phiVal=phiVal_; %phi(x1,x2,y1,y2); %1/nbhdSize;

            for i=1:2; %256;
                x_Particle=Population(x1,x2,i);
                y_Particle=Population(y1,y2,i);
                if U(pwMult-t+1,6)==1;
                    if x_Particle==0;
                        if y_Particle>=0 & y_Particle<=1 & uVal<=d1*phiVal;
                            PopulationNew(x1,x2,i)=1;
                        elseif y_Particle>=2 & uVal<=d1*phiVal;
                            PopulationNew(x1,x2,i)=2;
                        end
                    elseif x_Particle==1;
                        if y_Particle>=2 & uVal<=v1*phiVal;
                            PopulationNew(x1,x2,i)=2;
                        end
                    elseif x_Particle==2;
                        if y_Particle==3 & uVal<=b2*phiVal;
                            PopulationNew(x1,x2,i)=3;
                        end
                    end
```

```
    elseif U(pwMult-t+1,6)==0;
        if x_Particle==1;
            if y_Particle==0 & uVal<=b1*phiVal;
                PopulationNew(x1,x2,i)=0;
            end
        elseif x_Particle==2;
            if y_Particle<=1 & uVal<=v2*phiVal;
                PopulationNew(x1,x2,i)=1;
            end
        elseif x_Particle==3;
            if y_Particle<=1 & uVal<=d2*phiVal;
                PopulationNew(x1,x2,i)=1;
            elseif y_Particle>=2 & uVal<=d2*phiVal;
                PopulationNew(x1,x2,i)=2;
            end
        end
    end
end
Population=PopulationNew;

if t/PlotInt-round(t/PlotInt)==0 | [t,ii]==[pwMult,nn];

    if popCount_sw==1;
        for i=1:2;
            for pt=1:4
                popCount(pc+1,pt,i)=
                    sum(sum(Population(1:Space,2:Space+1,i)==pt-1))/Space^2;
                pcTvec(pc+1)=pcTvec(pc)-PlotInt*(1+randn/sqrt(PlotInt))*timeMult;
            end
        end
        pc=pc+1;
    end %popCount

    if popPlot_sw==1;
        plot_title=sprintf('modelStep=%0.5g, modelRealTime=%0.5g',...
                    (ii-1)*pwMult+t,((ii-1)*pwMult+t)*timeMult);
        subplot(2,1,1), pcolor(Population(:,:,1)), shading('flat'),
        colormap([.2 .8 .2; .8 1 .8; 1 .8 .8; .8 .2 .2]);
        title(plot_title);
        subplot(2,1,2), pcolor(Population(:,:,2)), shading('flat'),
        colormap([.2 .8 .2; .8 1 .8; 1 .8 .8; .8 .2 .2]);
        title(plot_title);
        pause(PlotPause);
    end

    if binPopSave_sw==1;
        fid=fopen(popfileName,'a');
        fwrite(fid,Population(1:Space,2:Space+1,:),'ubit2');
        fclose('all');
    end

    %dispersion index, sample random sites:
    sizevp=size(vp);
    xr1=ceil(Space*rand(1,sampleSize));
    xr2=ceil(Space*rand(1,sampleSize))+1;
    for svp=1:sizevp(2);
        for i=1:2;
            dnrVec=0;
            dnr=0;
            for kk=1:sampleSize;
                mPop=Population(1:Space,2:Space+1,i);
                mPop(xr1(kk),xr2(kk))=vp(svp)-1;
```

```
                        [m3,n3]=find(mPop(:,:)==vp(svp));
                        if isempty(m3)==0;
                            dist3=min(abs(xr1(kk)-m3)+abs(xr2(kk)-n3));
                            dnrVec(kk)=dist3;
                            %dnr(xr1(kk),xr2(kk))=dist3;
                        else
                            dist3=1;%min(abs(xr1(kk)-m3)+abs(xr2(kk)-n3));
                            dnrVec(kk)=1;%dist3;
                            %dnr(xr1(kk),xr2(kk))=1;%dist3;
                        end
                    end
                    dispersionIndex(Dcount,svp,i)=
                            (sampleSize+1)*sum(dnrVec(:).^2.^2)./(sum(dnrVec(:).^2)).^2;
                end
            end
            Dcount=Dcount+1;

            %thickness index, sample random sites:
            for svp2=1:sizevp(2);
                for i=1:2;
                    drtVec=0;
                    drt=0;
                    [m5_,n5_]=find(Population(1:Space,2:Space+1,i)==vp(svp2));
                    if isempty(m5_)==0;
                        i5_=ceil(max(size(m5_))*rand(1,max(size(m5_))));
                        for kk2=1:min(sampleSize,max(size(m5_)));
                            [m5,n5]=find(Population(1:Space,2:Space+1,i)~=vp(svp2));
                            if isempty(m5)==0;
                                dist5=min(abs(m5_(i5_(kk2))-m5)+abs(n5_(i5_(kk2))-n5));
                                drtVec(kk2)=dist5;
                            else
                                dist5=3;%min(abs(m5_(i5_(kk2))-m5)+abs(n5_(i5_(kk2))-n5));
                                drtVec(kk2)=3;%dist5;
                            end
                        end
                        thicknessIndex(Dcount2,svp2,i)=
                                min(sum(drtVec.^1.2)/min(sampleSize,max(size(m5_))),3);
                    else
                        thicknessIndex(Dcount2,svp2,i)=1;
                    end
                end
            end
            Dcount2=Dcount2+1;

        end
    end
end % for t=1:pwMult;
end %ii

%%%%%%%%%%%%%%%
%show results:
%%%%%%%%%%%%%%%

if saveStats_sw==1;
    fid=fopen(sprintf(strcat(popFileName_,'dispersionIndexStat')),'w');
    fwrite(fid,dispersionIndex,'float64');
    fclose(fid);

    fid=fopen(sprintf(strcat(popFileName_,'thicknessIndexStat')),'w');
    fwrite(fid,thicknessIndex,'float64');
    fclose(fid);
end
```

```
if popCount_sw==1;
    fid=fopen(sprintf(strcat(popFileName_,'_count')),'w');
    fwrite(fid,popCount,'float64');
    fclose(fid);
end %popCount
```

A.3 Code for Checking an Attractive Interaction Map

```
%%%%%%%%%%%%%%%%%%%%%%%%%
%
% Joseph Stover
% 4/11/2008
%
% requires input map
%
% This program checks to see if an
%    interaction map is attractive.
%
%%%%%%%%%%%%%%%%%%%%%%%%%

%input map here:
testMap=[
1 0 1 1
1 1 2 2
1 1 2 2
2 2 3 2
];


mapUDtest=zeros(3,3);

ParticleNum=4;
nonMonCHK=0;

for i=1:ParticleNum;
    for j=1:ParticleNum;
        if testMap(i,j)<j-1;
            mapUDtest(i,j)=0;
        end
        if testMap(i,j)==j-1;
            mapUDtest(i,j)=1;
        end
        if testMap(i,j)>j-1;
            mapUDtest(i,j)=2;
        end
    end
end

for ii1=1:ParticleNum;
    if nonMonCHK==1; %not attractive
        'b1'
        break;
    end
    for jj1=1:ParticleNum;
        if nonMonCHK==1; %not attractive
            'b2'
            break;
```

```
        end
        for ii2=1:ParticleNum;
            if nonMonCHK==1; %not attractive
                'b3'
                break;
            end
            for jj2=1:ParticleNum;
                if nonMonCHK==1; %not attractive
                    'b4'
                    break;
                end

                %check rules now
                if ii1<=ii2 & jj1<=jj2 %ordered configurations
                    if mapUDtest(ii1,jj1)==mapUDtest(ii2,jj2) & mapUDtest(ii1,jj1)~=1;
                        if testMap(ii1,jj1)>testMap(ii2,jj2); %lower jumps above upper
                            nonMonCHK=1; %not attractive
                            'bCond1'
                            x1=jj1;
                            y1=ii1;
                            x2=jj2;
                            y2=ii2;
                            [y1-1 x1-1]
                            [y2-1 x2-1]
                            break;
                        end
                    elseif mapUDtest(ii1,jj1)==1 | mapUDtest(ii1,jj1)==2; %lower going up or null
                        if mapUDtest(ii2,jj2)==0 | mapUDtest(ii2,jj2)==1; %upper going down or null
                            if testMap(ii1,jj1)>jj2-1 | testMap(ii2,jj2)<jj1-1; %check jumps
                                nonMonCHK=1; %not attractive
                                'bCond2'
                                x1=jj1;
                                y1=ii1;
                                x2=jj2;
                                y2=ii2;
                                [y1-1 x1-1]
                                [y2-1 x2-1]
                                break;
                            end
                        end
                    end
                end %if

            end %for
        end
    end
end %end 4 for loops

if nonMonCHK==0; %map is attractive
    'map is attractive!!!'
end

if nonMonCHK==1;
    jj1=x1;
    ii1=y1;
    jj2=x2;
    ii2=y2;
end
```

Appendix B

Notation Reference

$\mathscr{J}(b,a)$ = Interaction map, outputs the new particle value which replaces a

$[a..b]$ = Integer interval $\{a, a+1, a+2, \cdots, b-1, b\}$

S = Set of particle values, usually $\{0, 1, 2, \ldots, n\}$

$\mathbb{Z}^d$ = d-dimensional integer lattice

$S^{\mathbb{Z}^d}$ = Infinite grid configuration space

x, y, z Usually denote grid sites on the integer lattice

Λ = an index set, usually finite and $\Lambda \subset \mathbb{Z}^d$

S^Λ = subset of configuration space, usually finite grid state space, (if size of Λ is finite)

η, ξ, ζ usually denote configurations of particles

$\eta_t(x)$ = particle at site x at time t with η as the initial configuration($\eta_0 = \eta$)

η_{t-} = configuration up until time t (limit in S^Λ of η_s as $s \nearrow t$)

η^{xy} = the configuration η with the particle at x replaced by the result of its interaction with the particle at y

η^x = the configuration η with the particle at x *flipped*, usually restricted to spin systems

$1\pm$ = the set $\{1-, 1+\}$, so $\mathscr{J}(1\pm, b)$ = the interaction map evaluated at $(1-, b)$ and $(1+, b)$

$\eta_{\mathbf{t}} = \eta_\cdot$ = is a sample path

$\pi_t(\eta_{\mathbf{t}}) = \pi_t(\eta_\cdot) = \eta_t$ is the state at time t

$x \overset{D}{=} y$, x and y have the same distribution

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