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Essays in Population Dynamics

DISSERTATION

submitted in partial satisfaction of the requirements  
for the degree of

DOCTOR OF PHILOSOPHY

in Social Science, Mathematical Behavioral Sciences

by

Nikhil Addleman

Dissertation Committee:  
Professor Jean-Paul Carvalho, Chair  
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2021



# TABLE OF CONTENTS

	Page
<b>LIST OF FIGURES</b>	<b>iv</b>
<b>LIST OF TABLES</b>	<b>v</b>
<b>ACKNOWLEDGMENTS</b>	<b>vi</b>
<b>VITA</b>	<b>vii</b>
<b>ABSTRACT OF THE DISSERTATION</b>	<b>viii</b>
<b>1 Introduction</b>	<b>1</b>
1.1 Overview . . . . .	2
1.2 On Modelling . . . . .	6
<b>2 The Ecology of Religious Denominations</b>	<b>12</b>
2.1 Introduction and Background . . . . .	12
2.1.1 Data . . . . .	13
2.1.2 Sampling concerns . . . . .	14
2.2 Statistics: relating religion and ecology . . . . .	15
2.2.1 Diversity Measures . . . . .	15
2.2.2 The Group Abundance Distribution . . . . .	16
2.2.3 Canonical Lognormal Distribution . . . . .	17
2.2.4 Power-law behavior . . . . .	18
2.3 Spatial Statistics . . . . .	21
2.3.1 Spatial Autocorrelation Measures . . . . .	21
2.4 Investigating Theoretical Models . . . . .	25
2.5 Discussion . . . . .	28
<b>3 Chaos in a two-population rock-paper-scissors game</b>	<b>36</b>
3.1 Introduction . . . . .	36
3.1.1 Motivation . . . . .	41
3.2 The Model . . . . .	42
3.2.1 Identifying chaos . . . . .	44
3.2.2 Chaotic subspace . . . . .	45
3.3 Conclusion . . . . .	46

<b>4</b>	<b>Weak Points</b>	<b>51</b>
4.1	Background . . . . .	52
4.1.1	Evolutionary Game Theory . . . . .	52
4.1.2	Network Effects . . . . .	53
4.2	Model & Discussion . . . . .	55
4.3	Results . . . . .	56
<b>5</b>	<b>Concluding Remarks</b>	<b>63</b>
	<b>Bibliography</b>	<b>69</b>

# LIST OF FIGURES

	Page
2.1 Religious Membership ECDF . . . . .	30
2.2 Regional religious ECDFs . . . . .	30
2.3 Robustness check for lognormal hypothesis . . . . .	31
2.4 Religious groups histogram (base 2) . . . . .	31
2.5 Religious groups histogram (base 3) . . . . .	32
2.6 CDF and ECDF comparison . . . . .	32
2.7 Proportion of population belonging to Southern Baptist Convention . . . . .	33
2.8 Log-proportion of population belonging to Southern Baptist Convention . . . . .	33
2.9 Empirical semivariogram of proportion of county population belonging to the Southern Baptist Convention . . . . .	34
2.10 LDS empirical semivariogram . . . . .	34
2.11 Catholic empirical semivariogram . . . . .	35
3.1 Nonchaotic Poincaré section . . . . .	47
3.2 Chaotic Poincaré section . . . . .	48
3.3 Diverging trajectories . . . . .	49
3.4 Chaotic and nonchaotic parameters . . . . .	50
4.1 Location-dependent invadable graph: type $G$ . . . . .	57
4.2 Location-dependent invadable graph: type $L$ . . . . .	59

## LIST OF TABLES

	Page
2.1 $\alpha$ -, $\beta$ -, and $\gamma$ -diversities . . . . .	15
2.2 Moran's $I$ for various denominations . . . . .	23
4.1 Stag Hunt payoff matrix . . . . .	52
4.2 General Stag Hunt payoffs . . . . .	52

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# ABSTRACT OF THE DISSERTATION

Essays in Population Dynamics

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University of California, Irvine, 2021

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Populations comprising humans or agents following simple rules offer a varied landscape of dynamic behaviors and configurations. This dissertation presents three articles that follow an interdisciplinary approach where mathematical and statistical techniques are adapted from the pure mathematics and biology and applied to problems in the social sciences. A novel hypothesis, that American religious populations follow a lognormal distribution is presented and tested, and descriptive spatial statistics are employed to improve descriptions of this religious landscape. The next chapters offer complementary mathematical work in evolutionary dynamics and introduce mathematical models which may be employed on similar empirical problems. An example of a chaotic evolutionary dynamic is presented that is minimal in that it requires only two populations. This result highlights the link between theoretical social science models, evolutionary biology, and physics, and offers a new hypothesis consistent with observed chaotic phenomena in systems with dominance cycles. Chapter 4 considers the role local interaction structures have when a Stag Hunt coordination game is played by a population of best-responding agents. An infinite family of graphs is presented that are susceptible to invasions of the socially suboptimal strategy if the invasion begins on a vertex belonging to a proper subgraph. The projects are unified by a discussion of the philosophical and practical features of mathematical and interdisciplinary approaches to modeling in the social sciences.

# Chapter 1

## Introduction

The past two centuries have seen immense advancement of the mathematical and statistical techniques employed by scientists studying social phenomena. Some of these techniques, such as the specification of game theory as a standalone field by von Neumann [27] were developed to better understand human subjects and later on found use across scientific disciplines. One of game theory's most celebrated descendants is evolutionary game theory, presented in its modern form by Maynard-Smith and Price [49], which traces the opposite path, from its original development by biologists to finding applications in the social sciences. In fact, there is a panoply of examples of mathematical techniques finding their way into social science applications having originated in another field. Lurking behind the activity of interdisciplinary adaptations is a sobering truth: human activity is immensely complex and frequently (perhaps even always) resists attempts at tidy description by simple mathematical and statistical models.

Researchers, rather than being dismayed by the complexities of human interaction, must tackle social scientific questions with the eagerness and excitement that come from recognizing two consequences of the basic intricacy of the subject. First, bluntly, there is still

“low-hanging fruit”. Decades old survey data that has been scrutinized by scores of research teams may still reveal new discoveries when studied from a novel perspective. Adapting techniques from other disciplines is a great tradition among social scientists. At worst, such projects broaden the set of available tools by introducing social scientists to useful techniques from the greater scientific world. There is also the possibility for deep interdisciplinary connections to be uncovered that reveal remarkable connections between disparate subjects. Second, having recognized the complexity of all social puzzles, it is clear that any attempts by political scientists, economists, sociologists, or anyone involved in the mathematical social sciences to present a mathematical model of any phenomenon under their purview requires radical assumptions in its axiomatization. Again, this is not so much a difficulty as an opportunity for researchers. Interrogating assumptions underlying existing models offers the opportunity to develop derived models that are more general, realistic, or simply ones that explore unexpected social behaviors that might be more easily revealed by mathematical tweaking than through empirical study.

## 1.1 Overview

This dissertation presents a selection of research articles in the mathematical social sciences that reveal the truth of the optimism above. Following this introduction is a chapter on “The Ecology of Religious Denominations” which presents some robust, fundamental statistical findings regarding religious demographics in the United States. It presents discoveries made by employing basic statistical techniques commonly used in ecological research on social demographic data. The surprising outcome is that the distribution of religious denomination sizes, in terms of number of adherents, closely resembles the ecological species abundance distribution, that is, the distribution describing the number of individuals belonging to each species in a particular habitat.

This commonality raises the question of why two clearly different phenomena, existing in completely different scientific domains and operating on hugely different time scales, would be empirical analogues. The end of the chapter offers a philosophical discussion of the various possibilities: that there is some deep link between the processes of biological speciation and the formation of new religious denominations, that there is a different sort of statistical commonality inherent in describing the distributions of many things from the same “type”, or that there might more mundane reasons, artifacts of the measurement or categorization process that only become obvious when the same phenomenon seems to appear as the answer to two unrelated questions.

The chapter includes a presentation of spatial statistical results estimating the degree to which religious demographics in one region of the country predict the composition of nearby areas. The purpose of this presentation is twofold. Researchers in religious studies may supplement their study of the historical features that distinguish American religions as more or less evenly distributed across the country with an objective measure of this property. The chapter section also introduces these geospatial statistical tools, which see most of their use outside of social science, in an actively developed software package with functionality on the religious congregations data set.

The next chapter “Chaos in a two-population rock-paper-scissors game” develops a simple evolutionary model featuring chaotic solutions. In essence, the children’s game of rock-paper-scissors (RPS) where players simultaneously reveal one of the three titular symbols, with rock beating scissors, scissors beating paper, and paper beating rock, offers the simplest possible analogy for thinking about problems featuring cyclic dominance. Despite (or perhaps because of) its toy-like simplicity, RPS has become a favorite tool for researchers in theoretical biology, and game theory. In particular evolutionary RPS models may exhibit stable limit cycles: solutions which eternally trace a closed trajectory through space.

The social and biological phenomena studied with evolutionary models may not exhibit any

simple solution, limit cycle or otherwise. If population levels fluctuate wildly, but theory suggests strategic interactions are at play, a researcher might be tempted to attribute the phenomenon's unpredictability to stochastic effects. This is often a reasonable conclusion. It is uncommon for social or biological populations to be isolated from external factors, and it is often the case that something outside the scope of the modelled mechanism drives observations more than those factors theory can predict. A fly buzzing in your room might be driven by some strategic incentives, moving towards fruit, avoiding angry moving bodies, but these hardly help predict its zigzag path.

However, giving a strong impression of randomness, unpredictability can belie the precise deterministic rules governing some systems! Edward Lorenz defines a chaotic system as one that is “not random but looks random” [21]. In such systems, unpredictability stems from sensitivity to where the system starts, but does not depend on chance. Whether chaotic systems can be designed using evolutionary game theory is a natural question to ask given that evolutionary models are almost always specified using the same tools (differential equations, difference equations) as the canonical examples of mathematical chaos.

Chaos as defined by mathematicians is something of a red-herring. There is not a single, concise specification of chaos better than theoretical unpredictability in a deterministic system. The measures and methods of identifying chaos are more fully outlined in Chapter 3, but there is a simple idea that gives its essence. A chaotic dynamical system is one where two starting states may be nearly identical, one is perturbed by a microscopic amount, and yet the two trajectories traced from each starting point diverge from one another exponentially fast. It is estimated that extending the weather forecast by a few days would require ten times better measurements, and doubling the duration of accurate predictions might require a weather station for every square meter of the Earth's surface. This is the sort of chaos developed in Chapter 3, where a simple, precisely defined system with no random component becomes unpredictable in a short span of time even if initial measurements are made millions

of times more precise.

The most famous example of chaos arising in an evolutionary game theory model is a spatial dynamics presented by Nowak and May [30]. This remarkable paper spurred many researchers towards exploring the sometimes beautiful chaotic behavior in deterministic evolutionary systems and the complex behaviors of evolving populations on networks or graphs. See [52] for an engaging overview of evolutionary games on networks. The chaos we are interested in is more pedestrian. Chapter 3 does not offer the stunning visuals derived from lattice-bound populations evolving fighting over territory, but attempts to go in the other direction: revealing chaos in the simplest possible model. There are only two, well-mixed populations and three strategies. By introducing a simple tweak to this well-studied case, making the populations engage in self-play at the same time they compete, all hope of predicting the long-run behavior of the system disappears. Unpredictable behavior in social or biological systems with cyclic dominance need not be evidence of strong stochastic effects, but might just as well indicate one of several minor modifications to the “pure” RPS game.

Chapter 4 focuses on the evolutionary dynamics of populations on networks and so is more in the flavor of “modern” evolutionary game theory, where instead of treating whole populations as a unit which can be represented by a differential equation, diversity among individuals (or their relationships) is represented explicitly. This domain is called agent-based modelling. To represent the structure of the population, who interacts with whom, individual agents are represented as nodes on a network.

The chapter considers a particular kind of coordination game called the stag hunt. Such games feature two equilibria: one is socially optimal—everyone involved gains as much as possible, but all must coordinate to get the big prize. In the other case, the payout is lower, but it is guaranteed regardless of your partner’s behavior. The metaphor that gives the stag hunt its name is a situation where it takes two hunters acting together to catch the stag, but each one can individually bag a hare whatever the other does.

The rich history of social models involving stag hunts is further explored in the first section of Chapter 4. At this point it is enough to assert that lots has been written about stag hunts played on networks, especially attempts to specify which networks can maintain socially optimal, cohesive behavior and under what conditions. The research presented in this chapter continues that tradition. A new class of networks is defined called location-dependent invadable graphs, which lie on the knife's edge between stability and susceptibility to falling into suboptimal situations with everyone hunting hares.

## 1.2 On Modelling

As each chapter includes mathematical or statistical models of social phenomena with varying degrees of empirical justification. It will be useful to include a brief philosophical digression to describe the nature of mathematical models and explore some of the different types employed by social scientists. As was emphasized above, social phenomena are extremely complex, interconnected, and with causally significant features at so many scales, it is so far impossible to produce a model of even the simplest social phenomenon that is at once veridical and useful. What is it then that mathematical social scientists do?

This section presents a brief philosophical discussion of what scientific models are. Its point is not to indulge in a purely academic digression, but should clarify the types of contributions that might be made by mathematical social scientists, especially by this author in writing his dissertation.

We ignore the epistemological debate between scientific realists and positivists, i.e., whether a theoretical model can be real beyond its role as a useful scientific tool. It may be the case that the scientific realist position has some merit regarding some subset of models in physics; it can hardly be relevant to social scientists' idealized models that make no claim to



absolutely representing the real. Tracing the delineations of models from the most natural through more and more idealized or simplified theories, in the first place are those models where one actual physical system is taken to represent another. An example of a model of this type is a miniature scale model of a vehicle in a wind tunnel. Scale models are the simplest of what philosopher Mary Hesse calls material analogies, where comparisons are made between real objects or processes. Material analogies are distinguished from formal analogies, where at least one of the analogues is a mathematical formalism [13] [14].

The most veridical, or “true” models are those physical theories that are so precise they can actually be called representational. Representational models may be falsified, or they may be superseded in a Popperian sense by another theory that makes more extensive or more general claims. Representational models do not take simplifying abstractions for causally relevant features of a phenomenon. They give a veridically precise description of all causal structure and attempt to represent a physical entity or process fully in the language of mathematics. The best examples of representational models come from physics. The theories of relativity are excellent examples of models of this type. One prediction from general relativity is called gravitational redshift, the idea that photons travelling out of a gravity well ought to lose energy, and should have a correspondingly lower frequency. When we think about such theories, the image of a gravity well is on the astronomical scale. We picture something like a photon travelling from the sun to Earth. It is remarkable, then, that general relativity is so precise, and fits so well with the rest of physics that in 1959 Pound and Rebka designed an experiment that confirmed the accuracy of theoretical gravitational redshift predictions at a “human” scale, by emitting photons from the top of a tower into a receiver on the ground, only 20 meters deeper into Earth’s gravity well [36] [12].

On the other hand, a physicist might make predictions assuming the Earth and a satellite are point masses, an economist supposes a market comprises a population of rational, expected utility maximizing agents all capable of making arbitrarily sophisticated computations, or

an ecologist makes predictions from a model where species counts are continuously varying real numbers, ignoring seasonality, weather, and migration, let alone the fact that the counts are inherently discrete.

These models all feature significant idealizations: simplifying distortions of reality that make them conceptually tractable. Such models are appropriately called idealized models, or depending on the severity of simplification, toy models. Some philosophers of science suggest that idealized models are intermediate steps in a scientific program that ultimately converge to the truth [59]. Another point of view gives up the status of progress towards realism and takes a purely pragmatic stance, justifying models that do not claim at all to be explanatory [17] [35].

Idealized models may be wrong for a variety of reasons, ranging from narrow applicability—that is, correctness only in a particular (laboratory) circumstance—through the grossest examples of curve-fitting where a regression might only be a summary of observations, and no claim is made that it captures any structural or causal relationship. Models of the second type are called phenomenological models. Phenomenological models may be effective predictors, but the key point is that their variables need not even be reductive distortions or simplifying abstractions of anything that exists, but are purely mathematical machinery for the purpose of fitting and predicting measurements. A psychologist may explain the relative difficulty of puzzles by appealing to computability theory without having any theoretical reason to believe that some neural structure actually implements a Turing machine. Models of this type are the norm in engineering where relationships are accurately parameterized by an equation or distribution that is entirely empirically derived, with little reference to any underlying theoretical justification.

However, even phenomenological models remain experimentally justified. Mathematicians involved in developing theories, especially in the social and life sciences, may resort to pure theory building without any empirical basis whatsoever. This process, called exploratory

modelling, is an inversion of phenomenological modelling. The internal variables of the model exist, or are at least plausibly justified, but the model does not target any specific empirical phenomenon. Pervasive as exploratory models are, being a standard technique in microeconomics and finding widespread use across the social and life sciences, it is worth spending some time to discuss why they are developed and what such models can achieve.

Several prominent social scientists have endorsed the position that the sort of model we discuss here, the type that makes up the contributions of Chapters 4 and 5 of this dissertation, are simply communication devices. Systems are designed in the precise domain of mathematics and logic to convey, using metaphor, some message or moral about the real world. Certainly this exercise might be useful, in the same way Aesop's fables are useful, but just because their internal logic is precise does not make them any less imaginary. Microeconomist Ariel Rubinstein, in fact, says that the words fable, tale, and model are all synonyms [40]. His point is not to deride the scholarship of his colleagues, but to emphasize models' role as communication devices and tools we use to enrich our imagination. Models, like fables, exist in some liminal space between fantasy and reality, conveying some understanding or clarifying our concepts about the world, without acting as a representation of it in any real, or precisely scientific sense.

Philosophers of science make the same point without daring to conflate scientists and fabulists. The explicit, "fable" can only decorously be used by practitioners who engage in modeling themselves, but Rubinstein is not alone. The prominent economists Thomas Schelling and Roger Myerson have made essentially identical claims about the status of models. Philosophers prefer to call this line of argument the pragmatic justification for the practice of idealized modelling. The pragmatic methodology of modelling lays out several possible outcomes which may justify the practice of modeling. Exploratory models can be the source of new testable hypotheses, they may produce (political/economic, scientific, personal) policy recommendations, and they can suggest the possibility of unexpected outcomes

[17]. To these we should add “how-plausibly”-type explanations. Defining a scientific model can adjust our understanding of a testable phenomenon by producing an alternative explanation that is consistent with the result. Neutral models in genetics, that is, those without any fitness advantage between the types, importantly expand and more precisely delineate the set of outcomes consistent with both natural selection and its absence, and so guide future experimenters and theoreticians towards testing and developing more specific predictions.

Pragmatist philosophers have proposed these sensible justifications for idealizations in science. I would like to add two others, not to justify a particular model, but to explain the scientific and social benefits of mathematical modelling. Applied mathematicians derive great pleasure from the playful systematization of natural phenomena in simple toy models. The best examples of these not only produce some scientific insight, but also feature interesting mathematics. A model can have purely aesthetic qualities which enrich mathematics as a whole. This inevitably draws more theoreticians to consider the problem. Drawn in by the fun of it, dabblers might inadvertently make contributions that are valuable to those studying the original problem. Part of the process of modelling is to present a description in mathematics. This translation by its nature makes (at least one aspect of) the question accessible to non-experts, and so the community researching the topic is allowed to grow. The second point is related. Models, mechanisms, and theories are devised by practitioners in disparate fields. When these models are mathematical and thus comprehensible to outsiders, it becomes possible to recognize when the same problem is being worked out by two communities, and, with luck, adopt wholesale the set of tools and techniques that were developed elsewhere. The cost of too-narrow focus can be decades of lost time. In 1971 Thomas Schelling presented one of the most celebrated social science models in his paper “Dynamic models of segregation”. A a grid of sites is populated by individuals from two types. Individuals look at neighboring sites, those to the North, South, East, and West, and may move if they see that their type is the minority. He observed the formation of “ghettos,” large, homogeneous regions of only one type, without any explicit discrimination [43]. His

result has excited sociologists for fifty years and is an exemplar of idealized models. It is a shame, then, that had a physicist read social science journals or had Schelling dabbled in physics, he could have drawn on decades of work on the mathematically simpler Ising model where the racial metaphor is replaced by magnetism. In fact, the world had to wait for the recent popularization of sociophysics to find out that Schelling's classic model is essentially the same as the well studied low-temperature Ising model with Kawasaki dynamics [25]. The interdisciplinary modelling tradition motivates two chapters in this dissertation. Chapter 2 is an explicit example of discovering cross-discipline analogies, while chapter 3 considers a system that could not have been conceived without the historical interplay between biologists and economists, and more recently, computer scientists, studying evolutionary dynamical systems.

So the pragmatic justification comes in several flavors. Understanding and communication are both cognitive tasks, that is, they feature as human activities and not the reproduction of reality. The view that models must be representational is rejected on the grounds that many useful ones are not. This is not an attack on scientific realism or on the status of theories, but simply the suggestion that theories and models are two pieces of the scientist's toolkit, the first may be representational or explanatory, but the second need only increase our understanding, our ability to communicate, or to introduce and develop the scope of the mathematical tools at scientists' disposal.

# Chapter 2

## The Ecology of Religious Denominations

### 2.1 Introduction and Background

In the United States, religion is abundant, diverse, and substantially important. Although American religious diversity is manifest, the bulk of research on this topic can be divided into attempts to accurately model and describe trends, and the production of data by polls and surveys. This work supplements our understanding of this domain by explicating existing data through the use of ecological metrics.

Particular attention is paid to denomination-level diversity. This refines existing work that characterizes religious diversity according to broad taxonomic categories. Researchers present diversity figures that partition populations into broad religious traditions [18], but choices like distinguishing Catholic and Protestant churches while grouping all Buddhist denominations can distort diversity metrics.

Ecology offers sophisticated tools for characterizing diversity. Diversity indices summarize diversity in a single number, and can clarify how much diversity occurs within and between geographical subunits. It is important that an understanding of the distribution giving rise to a diversity index accompanies the interpretation of the statistic. Macroecology presents the species-abundance distribution (SAD) characterizing the biodiversity of ecological communities. We propose the religious group-abundance distribution (GAD) and note patterns it shares with the apparently unrelated biological statistic.

Spatial statistics are presented on the geographical properties of the American religious landscape. These include spatial autocorrelation measures and semivariogram analysis to reveal how similarities in the religious composition of geographical regions diminishes with distance.

The paper is organized as follows. Section 1 presents a brief overview of the content and ends with a description of the demographic and geographic data sources used. Section 2 presents statistical results including several diversity measures and attempts to characterize the religious GAD. It is argued that the GAD is well approximated by a lognormal distribution that matches a pattern seen in ecology. Section 3 considers spatial phenomena, investigating the similarity between denominations' abundances in neighboring regions.

### **2.1.1 Data**

Religious diversity is investigated by looking at data from the 2010 Religious Congregations and Membership Study downloaded from the Association of Religion Data Archives (theARDA.com). The data include adherent numbers for dozens of religious denominations at the county level. The study is conducted every ten years by contacting a representative from each religious group who reports the number of adherents and congregations belonging to that group in each US county. The study requires some estimation. Membership may be

a stricter category than being an adherent. Some groups report a membership number that only includes adults and so does not match the standardized definition of adherent used in the study [4].

County-level religion data from 2010 is coupled with the Department of Agriculture’s 2013 Rural-Urban Continuum Codes, a categorization of US counties into metropolitan and non-metropolitan by the population of their largest metropolitan areas, and, in the latter case, whether or not they are adjacent to a metropolitan county. The continuum consists of nine classes, three for metropolitan counties and six for nonmetropolitan.

Geographic data is taken from the 2010 US Census gazetteer file. This reference provides information on US counties including population, area, and representative latitude and longitude coordinates.

### **2.1.2 Sampling concerns**

Ecologists have raised concerns about the validity of research favoring the lognormal hypothesis citing potentially confounding sampling issues [10] [23] [7]. In studying religion, the scope of the RCM study avoids many of these. Whereas ecological species counts are invariably skewed by the small number of individuals observed or collected in a field survey, the RCM seeks responses from every religious congregation with members for each county in the US. The presence of very small, or newly formed religious groups not included in the study would distort the presented results. However, the methodological approach of this paper will apply just as well to any new data that attempt to rectify this possible omission, and the qualitative features of the religious group abundance distribution remain for all groups above an intermediate size.



	Richness	Shannon entropy	Simpson diversity
$\gamma$	176.0000	4.0331	0.8466
$\alpha$	59.9443	3.1848	0.7463
$\beta$	116.0557	0.8483	0.1003

Table 2.1:  $\gamma$ -diversity is the total diversity across the US.  $\alpha$ - and  $\beta$ - diversity are the weighted mean diversities within counties, and the diversity between counties, respectively.

## 2.2 Statistics: relating religion and ecology

### 2.2.1 Diversity Measures

Three popular diversity indices used in the social and biological sciences are richness, Shannon entropy, and Simpson diversity. The richness of a region is the number of species present. Shannon entropy (also known as the Shannon diversity index, or the Shannon-Wiener index) describes the unpredictability of a random variable with a given distribution. The Simpson index, or the Herfindahl–Hirschman index is the probability that two random individuals in a population belong to the same group. It may be converted into a diversity index (where higher values imply a more even distribution) by subtracting its value from 1. The resulting quantity is also known as the Gini–Simpson index and Hurlburt’s probability of interspecific encounter [16]. Richness gives equal weight to all groups present, while Simpson and Shannon diversity have values that are more affected by the evenness of the biggest groups. Because of the log term in the calculation of Shannon entropy, small populations have a bigger effect than in Simpson diversity.

Whittaker [57] [58] separated the diversity across a set of regions ( $\gamma$ -diversity) into diversity within regions ( $\alpha$ -diversity) and between regions ( $\beta$ -diversity), which is known as turnover diversity. The formula is  $D_\gamma = \bar{D}_\alpha + D_\beta$ , where  $\bar{D}_\alpha$  is a weighted mean over the surveyed regions.

Table 1 shows each diversity index for the United States and their separation into within-

region and turnover diversity. These values reflect diversity at the denominational level. Different taxonomic groupings will produce smaller values. The scale of geographic unit affects the values of  $\alpha$ - and  $\beta$ - diversity. If the country is partitioned into larger regions, there will likely be more diversity within regions and less turnover diversity. Here, our unit is the county, the smallest geographical region in the RCM data.

Using richness, turnover diversity is the greater part, but this pattern is reversed for Shannon and Simpson diversity. This reveals that there are many small religions with localized extent. That is, there is a lot of diversity in the set of churches present in different parts of the country, but the largest denominations are widespread. Applying different diversity measures at the level of religious denomination and separating local diversity from turnover diversity enables researchers to more precisely describe the religious diversity within a community and to meaningfully compare differences in diversity among communities.

### 2.2.2 The Group Abundance Distribution

Diversity indices are insufficient for characterizing a population. Diversity manifests in the distribution of groups within the population, and for any diversity index, one can describe a whole set of distributions including a wide qualitative range whose members have the same calculated diversity. Ecology provides a rich set of tools for measuring biological diversity by characterizing the distributions of biological species which will be employed to describe American religious populations.

Preston presents a method for studying species abundance by examining logarithmically binned histograms. Abundance classes, or “octaves” in the base 2 case, are given by the sequence of intervals  $\{[k^n, k^{n+1})\}_{n=0}^{\infty}$  where  $k$  is conventionally 2, 3, or 10. When  $k = 2$ , the upper limit of the abundance included in each octave is twice as big as the previous one. [23]

If species abundance follows a log-normal distribution, the histogram produced by such a plot will have a Gaussian shape. That species abundances are lognormally distributed is among the strongest results in ecology, with the pattern observable across a diverse range of organisms and in geographical regions of every size. [51]

Fitting a lognormal distribution to religious nation-level group membership data shows a good match (Figure 1). A Kolmogorov-Smirnov goodness of fit test (as recommended by Tokeshi) was performed, resulting in a KS test statistic of 0.55 giving a  $p$ -value of 0.67, meaning the lognormal distribution cannot be rejected as a statistical model of the empirical data [54]. The lognormal model provides a robust fit across geographical regions (Figure 2), states, and when counties are divided between rural and metropolitan (according to RUCC), and also when adherents are separated by religious family, rather than at the more fine-grained level of denomination (Figure 3). KS tests were performed for all of the empirical distributions corresponding to these conditions and in no case was the lognormal hypothesis rejected.

### 2.2.3 Canonical Lognormal Distribution

Preston’s 1948 canonical hypothesis (CH) [37] [38] characterizes a common pattern in species abundances. Describing religion, abundances follow a canonical lognormal distribution if a randomly picked individual is more likely to come from one of the largest groups in a region than from a collection of intermediate sized groups.

In a Preston plot, label the bin where the most abundant species is expected to lie  $R_{\max}$ . An individuals curve can be drawn by associating with each bin the number of individuals (instead of species) present in the class. The mode of this individuals curve is the bin which contains more individuals than any other. Call it  $R_N$ . A canonical lognormal distribution is one where these values match, that is  $\gamma = \frac{R_{\max}}{R_N} = 1$  [23].

The CH is a constraint on the parameters of lognormal distributions that describe species abundances. Specifically, Preston’s CH constrains the relationship between  $s$ , the number of species, and the variance  $\sigma^2$  such that species richness (the number of species represented) and evenness of abundances are inversely related. The CH has been empirically borne out, with many ecological assemblages being well described by canonical lognormal distributions [51]. Preston asserts that the CH describes the natural abundance distribution, and when assemblages do not fit the hypothesis, it may be because of poor sampling, or a failure to select a homogeneous community (Preston 1980).

The religious GADs for US Census regions are well approximated by canonical lognormal distributions. Dennis and Patil’s approximation,  $2 \log s - \log \log s - \log(4\pi) \approx \sigma^2$ , where  $s = 176$  is the number of groups included in the analysis, gives a variance  $\sigma^2 = 6.17$ , which is close to that  $\hat{\sigma}^2 = 6.07$  of the fit lognormal CDF [7]. The US can be geographically partitioned and in almost every case the same features remain: a great number of intermediate-sized denominations constitute the majority of groups, but most individuals belong to one of a few churches that are orders of magnitude larger than the rest.

### 2.2.4 Power-law behavior

The largest religious denominations have thousands of times as many members as the mean-sized group. Membership of religious groups, like populations of cities, varies across scales of different orders of magnitude, and exhibits a clear right skew. American city populations are supposed to follow a power-law, that is

$$p(X) \sim x^{-\alpha}$$

Many natural and social phenomena exhibit power-law distributions, such as the populations of American cities, the magnitude of earthquakes in California, and the frequency of words occurring in a corpus of text, and controversy is common in debates on whether purported power-laws are actually lognormal and vice versa [28].

For religious GADs, a power law might be an apt description of religious groups above a certain size. The problem is, there are just too few really small denominations for the power-law to fit over the entire range. This is a typical issue, and many phenomena are said to have a “power-law tail” if they exhibit power-law behavior for measured quantities larger than some  $x_{\min}$  [28].

The lognormal distribution is an adequate description of religious abundances across the entire range of group sizes, and does not require cutting out small denominations from the analysis. It takes data that spans many orders of magnitude above  $x_{\min}$ , and lots of it, to distinguish a lognormal distribution from a power-law. Unless there is a strong theoretical reason to expect a power-law, it is not an appropriate model here.

Yule (1922) presents a biological example of power-law distributions. He considers the number of species belonging to various genera within a taxonomic family. The empirical observation is made that the size of a genus (given by the number of species it includes) follows a power-law. Yule proposed a model that would now be called a preferential attachment process. Supposing any species is as likely to speciate as any other, and that new species remain in the same genus as their parent species, the number of species in a genus increases with a probability proportional to the number of species that are already members of the genus [61].

The Yule model includes the possibility that a new species will be sufficiently different from its parent to start a new genus. In the time limit, the process produces a Yule-Simon distribution, a discrete distribution exhibiting a fat tail.

A similar analysis can be performed in the religious taxonomy. Christian denominations belong to a religious family—there are many Baptist, Methodist, etc. denominations. The ARDA presents this categorization following the process of schisms and mergers that gives rise to the contemporary religious landscape. The religious family generally may include any number of related denominations, and provides a more specific focus than the very broad “religious tradition” categorization.

Taking religious family as analogous to genus, and denomination to biological species, the number of denominations per family is fairly well described by a power-law distribution (Figure 6). Judaism, Catholicism, and Latter-Day Saints are religious families which are among the majority that include very few sects. A preferential attachment model tells the story that these religious families have experienced relatively few sectarian splits, most of the ones that did occur being different enough to produce all-new religious families, and so now they continue to have a low probability of new sects emerging. The European Free Church Family, on the other hand, comprises a set of Protestant churches splitting from European state churches believing in voluntary membership. It now includes 35 denominations. Many contemporary denominations trace their history to churches in this family. Since the Yule model gives a probability of any sect splitting being the same as any other, it stands to reason that this historically rich might now be among the most diverse.

Fitting a Pareto distribution to the empirical distribution of denominations per religious family gives a distribution that is not significantly different. A power-law distribution scaled so that its support is  $[0, 35]$  gives an even better fit (Figure 6).

## 2.3 Spatial Statistics

Religion and geography are closely linked. Most simply, religious activity may be constrained by proximity to an appropriate place of worship. Other geographical features have religious significance. Religious populations may congregate around sacred sites [34]. Beyond the specifically religious features of the geography are the historical demographics. If a group is well-established in one place, its population might be expected to spread locally rather than randomly across the country.

The dynamics of distance-dependent religious spread can be expected to work in two ways. A person belonging to one religious group is more likely to remain in-place than to move randomly. Potential converts are more likely to join a group with a substantial presence in their area than an arbitrary other group.

These intuitions about the spatial properties of religious composition across the country must be verified. Tobler’s first law of geography, “everything is related to everything else, but near things are more related than distant things,” defines a criterion for something to be a geographical phenomenon. Our intuitions suggest religion to be one of these things. There are fewer Mormons as you go further from Utah. Southern Baptists are more common in the South. Choropleth maps of the proportion of a county’s population belonging to some religious group give a visual confirmation of this suspicion.

### 2.3.1 Spatial Autocorrelation Measures

Moran’s  $I$  is a statistical measure of spatial autocorrelation given by the formula

$$I = \frac{N}{W} \frac{\sum_i \sum_j w_{ij} (x_i - \bar{x})(x_j - \bar{x})}{\sum_i (x_i - \bar{x})^2} \in [-1, 1]$$

where  $x_i$  is the proportion of county  $i$ 's population belonging to the religion,  $\bar{x}$  is the mean proportion,  $w_{ij}$  is the value in the matrix of spatial weights relating counties  $i$  and  $j$ ,  $N$  is the number of counties, and  $W$  is the sum of all  $w_{ij}$ .

The values of  $w$  reflect the hypothesized sensitivity to distance. Typical choices are using an adjacency matrix with  $w_{ij} = 1$  if county  $i$  is adjacent to county  $j$ , otherwise 0, or to populate the matrix using some function that decays with distance. Investigating which distance decay function is most appropriate is an interesting problem, and might be informed by semivariogram analysis. The county adjacency matrix is sufficient for investigating the hypothesis that religious abundances are spatially correlated, and allows computational optimizations that enable testing the property for all groups.

Under the null hypothesis of no spatial autocorrelation Moran's  $I$  has an expected value of 0. Negative values suggest negative autocorrelation while values significantly above 0 indicate positive spatial autocorrelation.

Calculating  $I$  for religious groups gives the expected result. The proportion of a population belonging to a religious group obeys Tobler's first law. All religious groups have a positive  $I > 0.2$ . The Assemblies of God have a substantially smaller degree of spatial autocorrelation than any other denomination with a value of 0.22 while for all other groups  $I > 0.3$ . For many small churches, values for  $I$  are larger than 0.9 and there are more than a dozen with  $I > 0.99$ , indicating an extremely high degree of spatial clustering for these denominations/ See table 2 for values of Moran's  $I$  for the largest denominations.



Group Name	Moran's $I$
Catholic Church	0.6113
Southern Baptist Convention	0.8000
The United Methodist Church	0.5388
The Church of Jesus Christ of Latter-day Saints	0.8700
Evangelical Lutheran Church in America	0.7577
Assemblies of God	0.2153
Muslim Estimate	0.5799
Presbyterian Church (USA)	0.3333
Lutheran Church, The Missouri Synod	0.5366
Episcopal Church Groups Combined	0.3584

Table 2.2: Values of Moran's  $I$  for the proportion of counties' populations belonging to denominations with more than 20 million members

## Semivariogram

In order to investigate how this spatial dependence manifests, how religious power decays with distance, and whether there are differences between religions in the degree or type of spatial autocorrelation, semivariograms are produced.

The semivariogram  $\gamma(h)$  of a spatial stochastic process is half the expected squared distance between points separated by a distance  $h$ .

$$\gamma(h) = \frac{1}{2}E[(z(x) - z(y))^2]$$

where  $d(x, y) = h$  and  $z$  is the quantity in question.

For real spatial phenomena this cannot be obtained exactly. We cannot measure  $z$  at all points, and we do not know the underlying stochastic process from which to derive the expectation. Instead observations are binned by distance and the empirical semivariogram is plotted.

Call  $\delta > 0$  be the spatial "lag" we define the bin  $N_{(h, h+\delta]}$  to be the set of pairs  $(x, y)$  such that  $d(x, y) \in (h, h + \delta]$ . The empirical semivariogram is

$$\hat{\gamma}_\delta(h) = \frac{1}{2|N_{(h,h+\delta]}|} \sum_{(x,y) \in N_{(h,h+\delta]}} (z(x) - z(y))^2$$

Plotting the empirical semivariogram reveals both the degree (intensity) of spatial interdependence, and how correlation decays as a function of distance.

Three statistics are often used to describe the semivariogram. The nugget  $n$  is half the variance at points close to  $h = 0$ . It captures the basic variation present among nearest neighbors. The sill  $s$  is the maximum of the semivariance as  $h \rightarrow \infty$ , denoting the level of difference expected between regions with no spatial similarity. The range,  $r$  is the distance where the variogram gets very close to the sill (beyond this point spatial correlation is supposed to be negligible).

For large, widely spread religions, the sill of the proportion semivariogram takes a value of about  $s \approx 0.025$ , and the nugget is apparently negligible. For relatively much smaller religions, the proportion of adherents never differs much from zero, so in absolute terms the sill is much smaller.

The variograms for Catholics, LDS, and Southern Baptists (figures at the end of the paper) suggest there is something qualitatively different about the spatial arrangement of these groups. The concave curves of the Catholic Church and Southern Baptist Convention resemble spherical or exponential variogram models, while the initially convex LDS figure better matches a Gaussian or cubic model. The downward trend at about 1500 km for the Southern Baptist Convention results from the breakdown of isotropy at long distances. Many Midwestern counties have zero Southern Baptists, having churches affiliated with a different Baptist group. In this distance range there are many county pairs between Southern and Midwestern counties.

The range of the graphed semivariograms cuts off at about 2300 km. This is about 1/2 the distance between the furthest pair of counties in the contiguous US. Beyond this, the number of paired counties in any particular “bin” begins to shrink and invalid conclusions may be drawn from the variogram. Also, the assumption of isotropy (direction invariance) breaks down if distance isn’t restricted, e.g., for distances in a certain range most pairs will be East Coast/West Coast comparisons.

## 2.4 Investigating Theoretical Models

The fact that biological species numbers grow multiplicatively makes the lognormal model a natural choice [5]. Seeing a similar pattern in American religious group membership demands a theoretical justification.

### CLT and spatial analogues

Taking the product of independent random variables that take on only positive values gives a lognormal distribution. When the logarithm of values is taken, multiplication becomes addition so the central limit theorem can be applied, giving a normal distribution for the logarithm of values taken by the product random variable.

There are two basic problems facing such this simplest statistical explanation. In the first place, what are the variables being multiplied, and why are they multiplied? In biological species, it is natural to model a species’ abundance as a product of, e.g., the fertile population of the previous generation, resource abundance, and the mortality rate. If many species grow in this fashion over many generations, the collection will exhibit lognormal abundance. Without specifying a model, researchers can point to the “natural” assumption that a process is mostly multiplicative to explain the lognormal distribution of outcomes.

The second problem is more difficult. One aspect of producing GADs is essentially additive: they comprise a spatial aggregation of abundances of non-overlapping subgroups. The GAD for the United States is, by definition, the sum of group abundances within each state, and each state has a GAD given by summing abundances for each county. We cannot explain the lognormal distribution of the national GAD by appealing only to an underlying multiplicative process. The fact individual states and counties also exhibit lognormal distributions is at least as much of a riddle as it is evidence for the robustness of the result.

Šizling et al. present a statistical model that is a spatial extension of the CLT. Whereas the CLT considers the sum of independent random variables, their model derives from repeatedly splicing adjacent subsets whose distributions depend on the spatial correlation of abundance patterns as well as species turnover (the rate at which species emerge and go extinct).

## **Ecological models**

Biologists have presented theoretical models to explain patterns of species abundance. Biological models assume species divide an ecological niche space, viewed, roughly, as a multi-dimensional volume of environmental resources, into niches which each species occupies [23]. The relative abundances of various species are imagined to follow from the proportions of some finite set of resources they have access to.

In the case of religious diversity, one measure of the volume of the ambient niche space is the population, with different dimensions corresponding to various religious practices, tenets, proscriptions, within which a church positions itself and attracts those individuals whose preferences correspond to its doctrine.

This sort of modeling is distinct from models which present agents' choice of religious group as a coordination game. In these, churches are not distinguished and (homogeneous, except perhaps for network structure) individuals conform according to pressure from neighbors.

Sugihara presents a niche apportionment model producing a canonical log-normal distribution of species abundance. The process involves a niche space being repeatedly split until the partition has as many elements as there are species. At each round, a random niche is split into pieces 0.75 and 0.25 of its original size, corresponding to the average ratio of the larger resultant piece to the smaller [51]. Other models have the probability of a niche being selected being a function of its size.

In the case of religious diversity, one might imagine a population with members distributed across a preference space (e.g., with preferences for strictness, worship frequency, congregation size) or, indeed, physical space. At each epoch, an existing church is selected to have its niche “invaded”, either by a competing religious group or splitting-off by a sect of the original group. The chosen niche is divided, and the entire process repeated.

Niches being randomly chosen presents a problem if invasion is the major mechanism by which they are divided. A larger group presents a potentially more profitable target, and it is implausible that some greater coherence with bigger group size would exactly counterbalance that. On the other hand, if churches independently undergo church-sect splitting at some fixed rate, then the assumption is sound. This is a heavily stylized picture of the mechanisms truly giving rise to the distribution of religious group sizes, but the sequential splitting of a population of potential adherents by competitors gives a dynamic model amenable to studying regions with various numbers of religious groups, and at least maintains the realistic assumption that groups do not appear all at once.

Furthermore, sequential breakage models produce a hierarchical structure of groups where a pair resulting from a recent division is more closely related, in some sense, than an arbitrary pair of religious groups. For example, two recently formed Pentecostal churches are taxonomically more similar than either one of them to the Catholic church, and this structure is naturally captured by sequential breakage [51].

It should be noted that invasion or colonization events diverge from the hierarchical structure interpretation while still fitting the breakage model. An invading church may target the same subset of the underlying population as an existing group without being taxonomically related.

Tokeshi presents a class of models all following this basic paradigm but differing in how the niche to be divided is selected at each step. From dominance decay, to dominance preemption, the models produce more or less even abundance distributions [53]

Sugihara's notes that when a mass is randomly split, in expectation, the larger of the resulting pieces will have .75 of the original size. His choice of taking this value at every split is empirically motivated.

## 2.5 Discussion

Classic statistical results from the macroecology are reproduced when human religious groups are considered instead of species. This curious connection between biology and the social sciences motivates further research into the source of the shared pattern. Theoretical ecology offers a variety of mechanistic models that give rise to the observed phenomena. Opposing these are statistical and mathematical arguments suggesting that observed patterns are consistent with entire classes of generative processes, with only a few assumptions about symmetry [10] or how values are combined [46]. Whether mechanistic ecological models are adopted by social scientists, or commonality is revealed to be part of a more fundamental mathematical property, the disciplines are linked, and explicating the connection between the fields is a promising and exciting research program.

Future research will investigate whether similar mechanisms underlie the common statistical properties. There are cases where ecological mechanisms might sensibly describe the religious distribution. The mathematics of niche subdivision models can be adapted, swapping out

terms “species” and “speciation” for “denomination” and “sect formation”. Of course, the wholesale adoption of theoretical models from other sciences is inadvisable without careful consideration. Many models attempting to explain species abundance distributions have been formulated to be mathematically general and avoid relying on particular mechanisms unique to biology. Species abundance distributions share common features across such a diversity of biological populations that the theory has been developed to be, in large part, agnostic to biologically specific parameters.

Adopting techniques already used in ecology is one way forward. On the other hand, the fact that ecological statistical patterns can be found outside of biological contexts motivates the development of theory that connects and generalizes both ecological and social-dynamic models. This is in some sense the reverse of adopting models so far specifically ecological in concept. Instead, species abundance theory can be informed by placing it in a general framework of population models giving rise to desirable statistical features.

The application of lognormal distributions across many scientific problems has already driven the development of some general descriptions of mathematical phenomena producing it [7]. Power-law distributions, seen in the number of species per genus and also denominations per religious family can be explained as well by the familiar preferential attachment models in either case.

Similarity in mechanism is one avenue on which macroecology and the study of religion can inform each other. Another is investigating commonalities in how measurement and categorization have been done in each field.

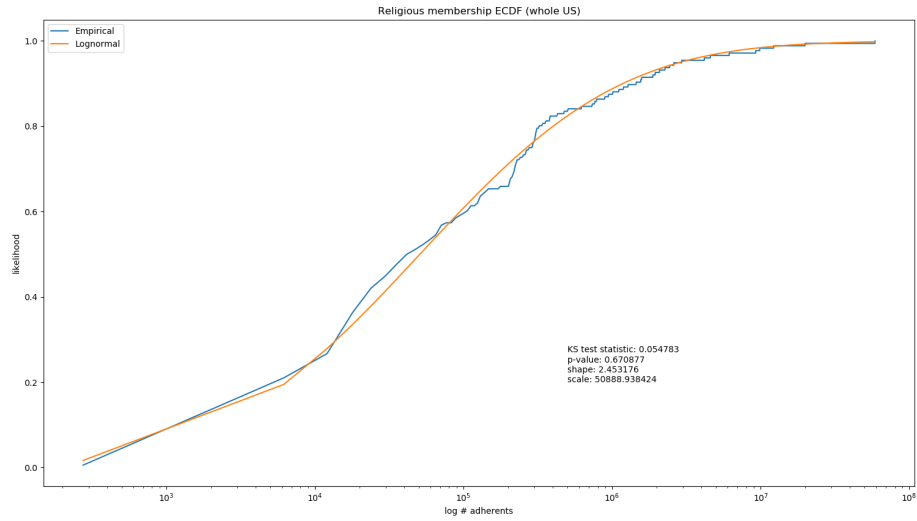


Figure 2.1: Empirical cumulative distribution of religious membership and the best-fit log-normal CDF

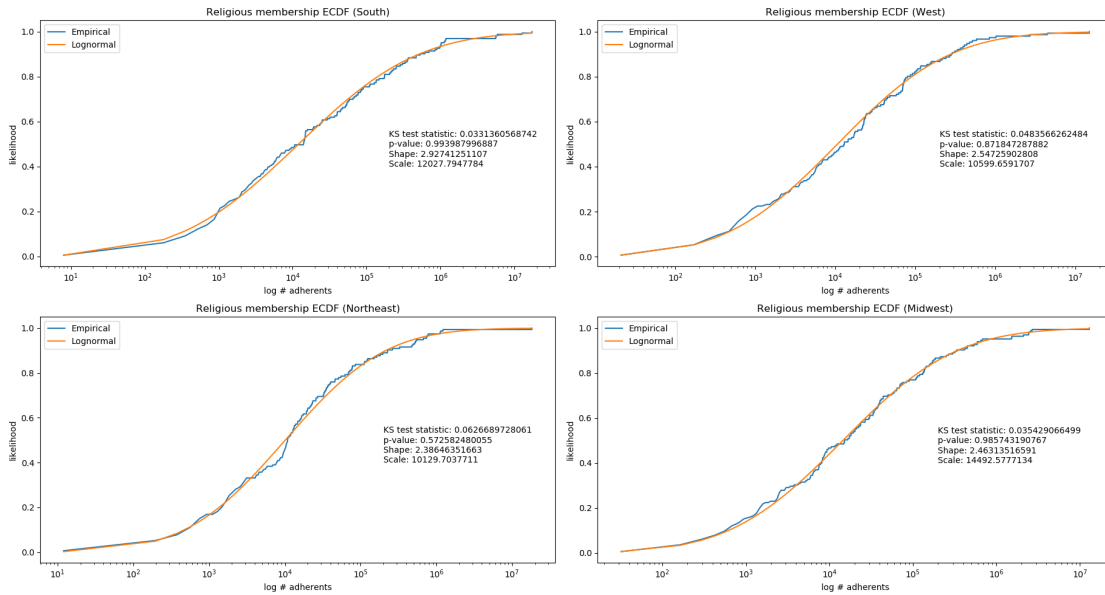


Figure 2.2: ECDFs of religious membership for US geographical regions



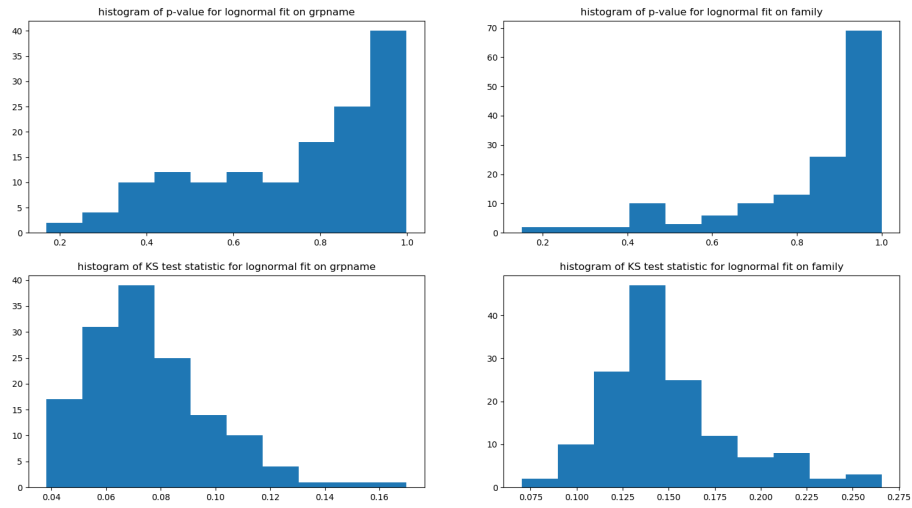


Figure 2.3: KS test statistic and p-values for different metro categories per state. This is a robustness check on the lognormal hypothesis, which is not rejected in any case when US counties are divided into groups by RUCC in each state.

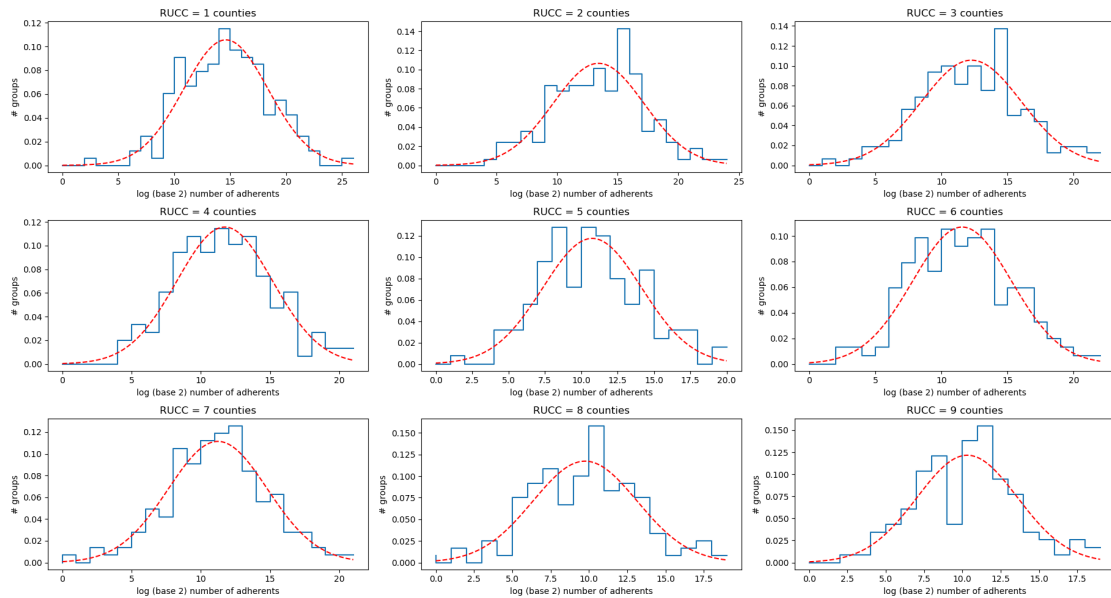


Figure 2.4: Histogram of proportion of religious groups falling into logarithmic (base 2) membership bins in US counties separated by RUCC.

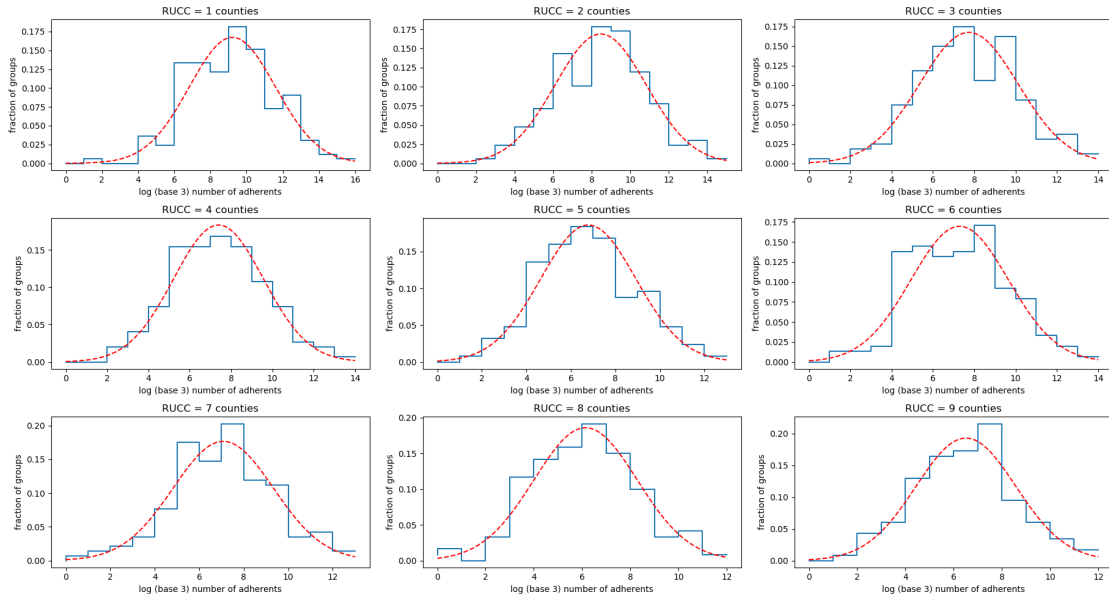


Figure 2.5: Histogram of proportion of religious groups falling into logarithmic (base 3) membership bins in US counties separated by RUCC.

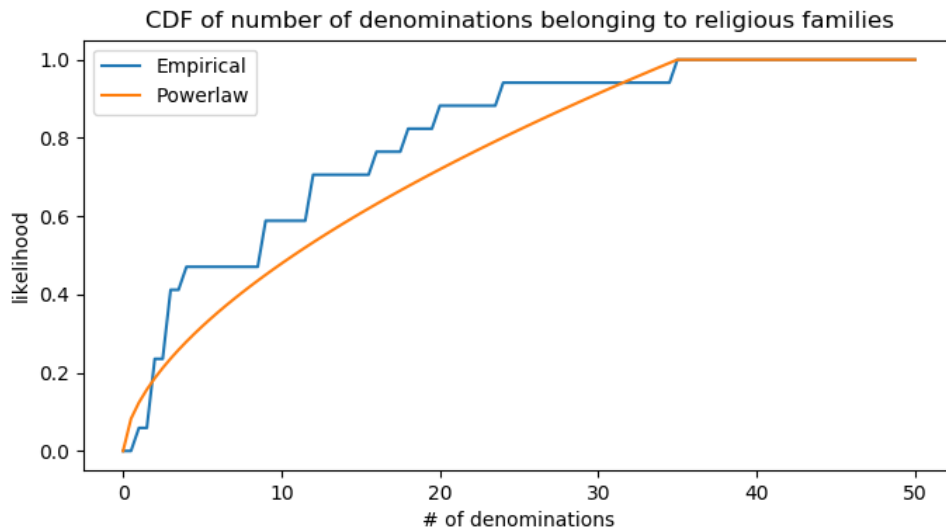


Figure 2.6: The CDF of a power-law distribution with support  $[0, 35]$  and the empirical CDF of denominations per religious family as in the case of a Yule process. The distribution cannot be rejected as having produced the data with KS test statistic 0.19 and  $p$ -value 0.51.

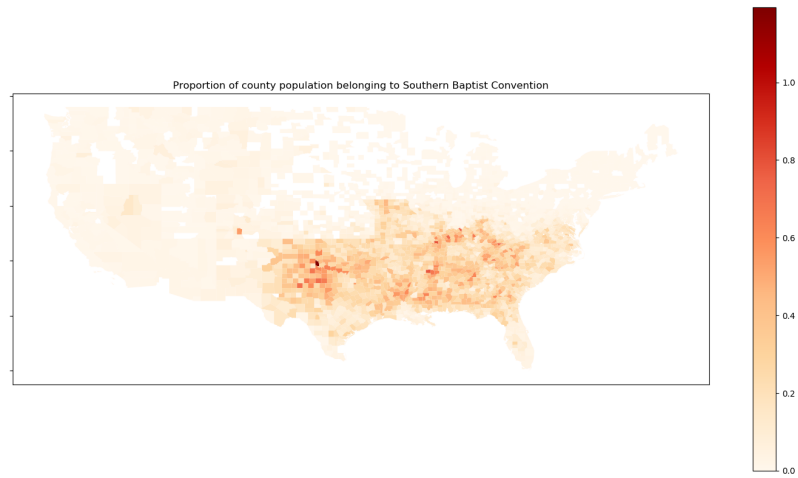


Figure 2.7: Proportion of population belonging to Southern Baptist Convention

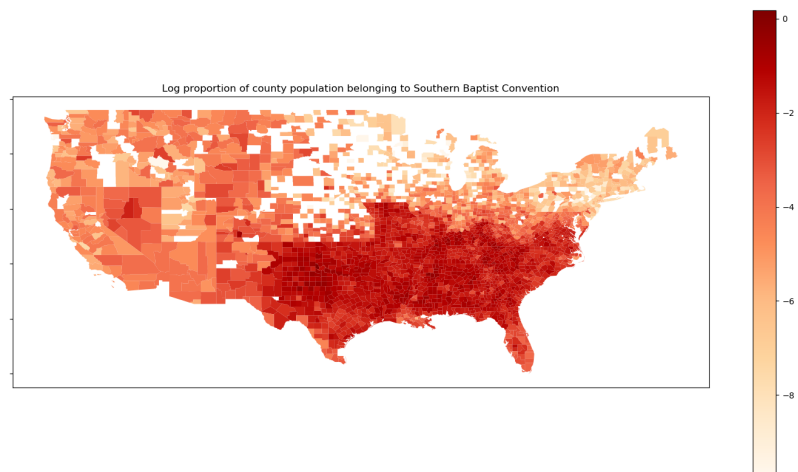


Figure 2.8: Log-proportion of population belonging to Southern Baptist Convention (to highlight differences)

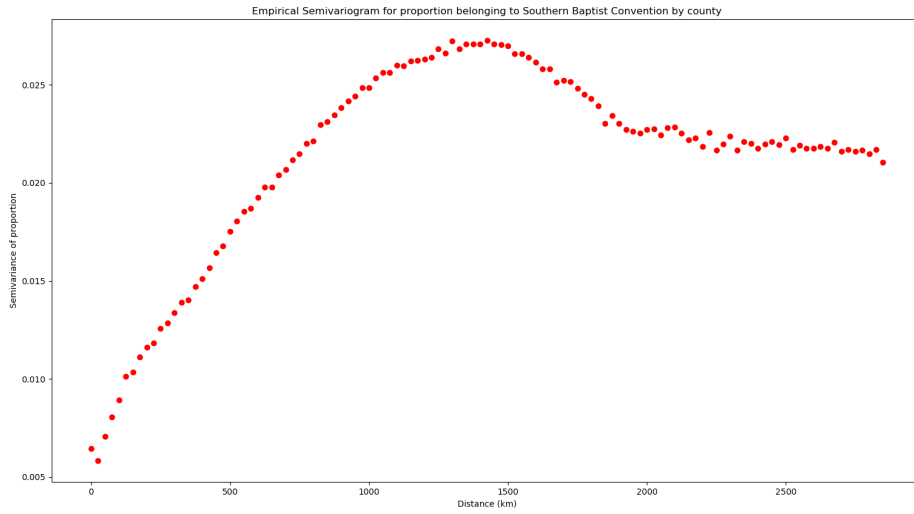


Figure 2.9: Empirical semivariogram of proportion of county population belonging to the Southern Baptist Convention

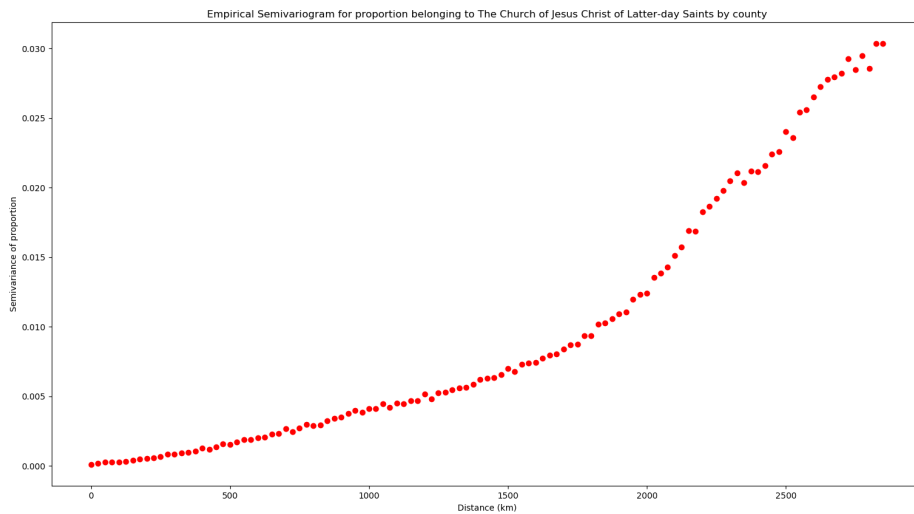


Figure 2.10: Empirical semivariogram of proportion of county population belonging to the Church of Jesus Christ of Latter-day Saints

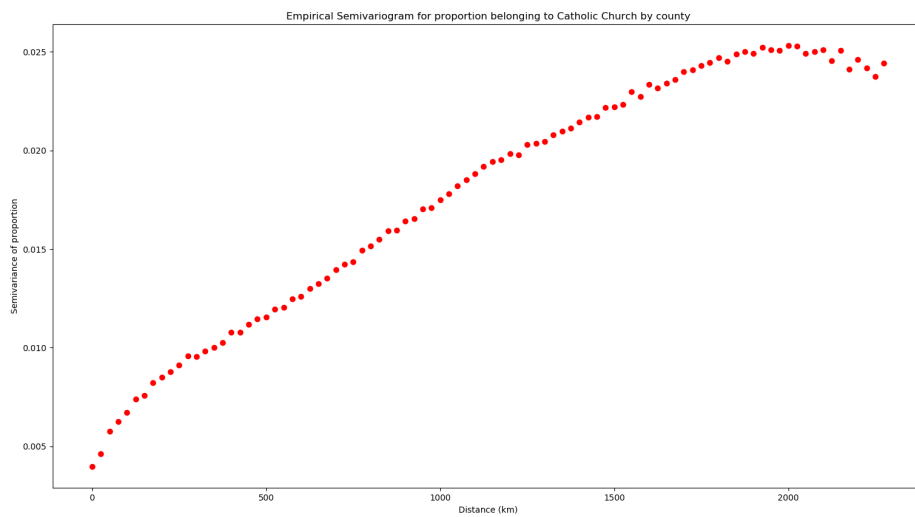


Figure 2.11: Empirical semivariogram of proportion of county population belonging to the Catholic church

# Chapter 3

## Chaos in a two-population rock-paper-scissors game

### 3.1 Introduction

The simple game of rock-paper-scissors (RPS) provides a bounty of theoretical properties and practical applications. Derived from the schoolyard game, RPS players invoke one of three strategies with the winner determined by the relation: rock beats scissors, scissors beats paper, and paper beats rock. It is the simplest specification in game theory featuring cyclic dominance. In dynamical models where populations evolve or learn to gain an advantage, it is an easy to understand model giving rise to limit cycles.

In this chapter, payoff matrices will be given as regular matrices  $M$  where the element  $M_{ij}$  should be read as the payoff from playing the strategy represented by the  $i$ -th row against the strategy in the  $j$ -th column. The single population rock paper scissors dynamics in its most basic form has the payoff matrix

$$A = \begin{pmatrix} 0 & -1 & 1 \\ 1 & 0 & -1 \\ -1 & 1 & 0 \end{pmatrix} \tag{3.1}$$

The replicator dynamics for this system are given by

$$\frac{d(x_i)}{dt} = x_i((A\mathbf{x})_i - \mathbf{x}A\mathbf{x}), i = 1, 2, 3$$

where  $\mathbf{x} = (x_1, x_2, x_3)$  is the 3-vector of proportions playing each strategy, so  $\sum_{i=1}^3 x_i = 1$ .  $(A\mathbf{x})_i$  is the payoff from playing strategy  $i$ , while  $\mathbf{x}A\mathbf{x}$  is the average payoff. This is a standard replicator equation and is typically interpreted with a biological metaphor. The difference in payoff between a given type and the population average determines the fitness of that type, that is, a member's rate of reproduction relative to the population average. This value is justified by imagining a scenario where random individuals are selected to play against one another and taking the limit of the population size to infinity, giving a continuous representation. The proportional rate of growth of that type, then, is that reproduction rate multiplied by the current proportion of the population belonging to the type.

When the proportion belonging to each type is nonzero, these dynamics have solutions that are limit cycles around the center. To illustrate, suppose a population has a high proportion of rock-players. These players get nothing when they are paired together, but the paper-players benefit greatly from pairings with the majority. Thus, the average paper-player does very well, and the proportion of the population playing paper grows until, eventually, the success of this strategy wanes and scissors becomes the best. Note that the periodic orbit is an artifact particular to the zero-sum (skew-symmetric) payoff matrix and the choice of replicator dynamics. Changing either one of these things may result in a system where the

mixed Nash equilibrium with  $\frac{1}{3}$  of the population playing each strategy is an attractor, or where solutions spiral away from the center until one of the types goes extinct.

Situations featuring cyclic dominance are simply represented by RPS and so it has featured in models in biology and economics. A famous biological example examines the persistent coexistence of three distinct types of males in side-blotched lizards. These types are distinguished by the colors of the markings on their throat and also by their territorial behaviors in finding and guarding mates. Orange-throated lizards are aggressive and control large areas, blue-throated males focus their energy on smaller regions but can be driven off by an orange male, while males with yellow throats have female morphology and can sneak around in an orange male's territory, but can be caught by the males of the blue variety. Observing periodic fluctuations in the populations belonging to each type, Sinervo and Lively found RPS dynamics and frequency-dependent fitness to give a plausible explanation for the persistent heterogeneity [45]. Other biological phenomena share this same pattern. The high degree of biodiversity in *E. coli*, manifests in one such pattern. There is a trio of types of the bacteria. The first, a "killer" type, produces an antimicrobial toxin, a second type is sensitive to the toxin, and a third, resistant type expends some energy (less than is required to produce the toxin) to protect itself. Each population of *E. coli* has a relative fitness advantage against one of the others and so RPS proves to be an effective model[6]. Bacteria are a particularly rich domain of organisms and exhibit a wide variety of competitive arrangements [15], but the puzzle of persistent coexistence of biological diversity when participating species face different evolutionary pressures is perennial in the field [55], and the stable cycle derived in the RPS model offers one mechanism for its maintenance.

The basic evolutionary dynamics may be generalized in many ways. Some models introduce asymmetry in the payoffs for wins and losses. Others include a non-zero payoff for ties. Depending on the particulars, such changes drive the dynamics towards a stable fixed point at the center or outwards towards extinction for one of the types.



A class of derived models consider two player or two population systems, given by introducing a second matrix

$$B = \begin{pmatrix} 0 & -b & b \\ b & 0 & -b \\ -b & b & 0 \end{pmatrix} \tag{3.2}$$

,

and a second population vector  $y = (y_i)$ ,  $i = 1, 2, 3$ . The replicator dynamics in this case are given by

$$\frac{dx}{dt} = x((Ay) - xAy) \tag{3.3}$$

$$\frac{dy}{dt} = y((Bx) - yBx) \tag{3.4}$$

The value of  $b$  determines the relative speed of population  $y$ 's updating in response to  $x$ 's strategy. It determines something analogous to the “natural frequency” of the population's cyclic orbit. most models consider the special case where  $b = 1$  and both populations update at the same rate. Such symmetry between the populations is a hefty assumption, but it is natural enough: when looking at a single population, changing  $b$  has no affect on the shape of solutions, and in most situations modeled as games, only the ordering of payoffs matters. Only with particular specifications of the dynamics do interesting effects of varying relative payoffs emerge.

Sato, Akiyama, and Farmer observe chaos in a system where  $b = 1$  but

$$A = \begin{pmatrix} \epsilon_x & -1 & 1 \\ 1 & \epsilon_x & -1 \\ -1 & 1 & \epsilon_x \end{pmatrix}$$

$$B = \begin{pmatrix} \epsilon_y & -1 & 1 \\ 1 & \epsilon_y & -1 \\ -1 & 1 & \epsilon_y \end{pmatrix}$$

They found chaos for some  $0 < \epsilon_x < 1$  and  $\epsilon_x = -\epsilon_y$ . The asymmetric  $\epsilon$  perturbation of payoffs on the diagonal incentivizes one population to play a common strategy with the other, while the second must avoid this scenario. This game is simply two-player RPS combined with a small “matching pennies” component[42]. It is one of the simplest chaotic models in evolutionary game theory and reveals how a minor deviation from a classic toy model may lead to substantially different behavior.

Keeping zeros on the diagonal, Griffin, Semonsen, & Belmonte present a chaotic system with three populations on the 3-cycle ( $K_3$ ) where each population evolves according to the replicator dynamics in games against adjacent populations (nodes of the graph that share an edge). This paper introduces the analogy between the rich networks of oscillators literature in physics and work on evolutionary games on graphs [11].

This chapter investigates an alternative route to chaos in a two-population system. The payoff matrices follow the traditional form with zero payoff in case of ties and the penalty for losing being equal to the negative of the winner’s payoff. The novelty is that populations engage in self-play at the same time they compete with one another, and update on their own composition as well as the opposing population’s. Before we explicitly define the model, it may be useful to keep in mind that this is simply a the coupling of familiar systems—the

single- and two-population RPS games—by adding the payoff from each separate interaction.

### 3.1.1 Motivation

Cyclic dominance is a common motif in game theory. Replicator dynamics models of cyclic dominance exhibit limit cycles as each strategy becomes popular in turn. In a single-population RPS game, the particular choice of off-diagonal payoffs typically doesn't matter, only appearing as a constant multiple for  $\frac{dx}{dt}$  denoting the period of solutions around the same limit cycles.

When there are several populations, solution cycles with different periods begin to resemble physical oscillators with different natural frequencies. Systems of coupled oscillators are a fruitful topic of study. As the strength of coupling is increased, systems of Kuramoto oscillators, for instance, exhibit a phase transition to spontaneous synchronization [50], and have been used to model the synchronization of neurons in the case of resting tremors in individuals with Parkinson's disease [24].

This chapter is an attempt to draw from this well-developed topic for analogous problems in population models and to present a minimal example exhibiting interesting behavior when “out-of-sync” populations are linked.

There are some key differences between dominance cycle population models and physical oscillators. The state of a Kuramoto oscillator is fully described by its phase, and while a similar idea may be defined in RPS (taking the interior equilibrium  $X = (\frac{1}{3}, \frac{1}{3}, \frac{1}{3})$  to be the origin we could say the phase is the angle from vertical) there is some difficulty adequately capturing the amplitude: how “far” is this solution from the new origin.

It may be useful to keep a real-world scene in mind when considering the present model. One plausible scenario modeled by such dynamics is competition between two broadcasting

firms where audiences have cyclic preferences, and producers at each company compete for viewership. The fickle audience prefers sports to news, news to drama, and drama to sports.

RPS has been used by economists to model such inter-firm competition, and the model here extends the scope to companies where employees within a firm compete with one another to produce the most appealing product. One might imagine various production teams vying for favor in the eyes of management while the networks themselves compete for viewers. It is natural enough to suppose that differences in access to information and corporate policies would lead to differences in the speed with which production teams update strategies based on internal and external states.

An alternative ecological application is a simple metapopulation involving two sub-populations engaged in dominance cycle competition where updating occurs at different rates from between- and within-population competition. Consider a region inhabited by two groups of side-blotched lizards separated by some sort of imperfect natural barrier, or two differently sized vessels of *E. coli* bacteria intermixed at some relatively slow rate.

## 3.2 The Model

The states of the populations are given by two vectors  $X = (x_r, x_p, x_s)$  and  $Y = (y_r, y_p, y_s)$  whose elements denote the proportion playing each strategy.  $\sum x_i = \sum y_i = 1$

There are four payoff matrices  $A_w, A_e, B_w, B_e$  whose entries correspond to payoffs from within-population and inter-population play for  $X$  and  $Y$ :

$$A_w = \begin{pmatrix} 0 & -1 & 1 \\ 1 & 0 & -1 \\ -1 & 1 & 0 \end{pmatrix} \quad (3.5)$$

$$B_w = \begin{pmatrix} 0 & -a & a \\ a & 0 & -a \\ -a & a & 0 \end{pmatrix} \quad (3.6)$$

$$A_e = \begin{pmatrix} 0 & -b & b \\ b & 0 & -b \\ -b & b & 0 \end{pmatrix} \quad (3.7)$$

$$B_e = \begin{pmatrix} 0 & -c & c \\ c & 0 & -c \\ -c & c & 0 \end{pmatrix} \quad (3.8)$$

The dynamics are

$$\dot{x}_i(\text{within}) = x_i((A_w X)_i - X A_w X) \quad (3.9)$$

$$\dot{x}_i(\text{external}) = x_i((A_e Y)_i - X A_e Y) \quad (3.10)$$

$$\dot{x}_i = \dot{x}_i(\text{within}) + \dot{x}_i(\text{external}) \quad (3.11)$$

and for the second population,

$$\dot{y}_j(\text{within}) = y_j((B_w Y)_j - Y B_w Y) \quad (3.12)$$

$$\dot{y}_j(\text{external}) = y_j((B_e X)_j - Y B_e X) \quad (3.13)$$

$$\dot{y}_j = \dot{y}_j(\text{within}) + \dot{y}_j(\text{external}) \quad (3.14)$$

While the payoffs and interactions are complicated, this is still a two-population system with only three strategies per population as players must play the same strategy whether playing within or across populations.

Since  $\sum_i x_i = \sum_j y_j = 1$  the phase space is the product of two standard 2-simplices  $\Delta^2 \times \Delta^2$ .

### 3.2.1 Identifying chaos

A Poincare section or Poincare map tracks the values of variables as a trajectory crosses a low-dimensional subspace of the phase space transverse to the flow. Here, we consider the plane  $x_1 - x_0 + y_1 - y_0 = 0$ . In even complicated periodic solutions, the Poincare section traces a closed loop, while in a chaotic solution, trajectories cross the subspace within a region of the same dimension rather than a lower-dimensional loop (Fig 1). The 2-dimensional subspace visualized by the Poincare map allows for easier visual distinction of “clouds” from closed loops and offers a useful tool for identifying or confirming a chaotic solution. Visual inspection of a Poincare section with payoffs  $a = \sqrt{2}$ ,  $b = 15.4$ ,  $c = 1$  shows a cloud of points more or less filling a region of phase space, which is characteristic of a chaotic system. (Fig 2)

The hallmark of chaos is sensitivity to initial conditions. Simulating two trajectories with ini-

tial conditions  $X_1(0) = [0.5, 0.2, 0.3]$ ,  $Y_1(0) = [0.2, 0.5, 0.3]$  and  $X_2(0) = X_1(0) + [10^{-6}, -10^{-6}, 0]$ ,  $Y_2(0) = Y_1(0)$  and observing the evolution of the distance between the solutions gives a first glimpse at how nearby initial conditions evolve.

Figure 3.3 shows the trajectories remain near for about 75 time steps, and then rapidly diverge to a maximum. Since the state space is bounded, distances cannot grow past this. Visual inspection does suggest a period of exponential separation which strongly supports the conclusion that this is a chaotic dynamical system.

Lyapunov exponents were estimated using the JiTCODE differential equations library [3]. The maximal Lyapunov exponent (MLE) characterizes the rate of separation for nearby trajectories. The MLE for this system was estimated by simulating a solution beginning at  $[X_1(0), Y_1(0)]$  and discarding 1000 time steps to allow the system to approach an attractor if any exists. The MLE was found to be  $\lambda = 0.17280.0183$ . The phase space is compact so a positive value for  $\lambda$  indicates the system is chaotic.

### 3.2.2 Chaotic subspace

Identifying chaotic dynamics motivates a more thorough investigation of the parameter space. This dynamical system in some qualitative sense resembles systems of coupled oscillators which in some cases only result in chaotic solutions when the oscillators natural frequencies are not rational multiples. Accounting for this possibility requires a two-stage exploration of the parameter space. In all cases, the payoff for internal play in population  $X$  was fixed at 1, and the other three payoffs varied. The first stage simulated solutions on a lattice of  $15 \times 15 \times 15$  points in  $1 \leq a, b, c, \leq 22$ . In order to determine the role of irrational payoffs, a second round of simulations was performed on points  $(b, c)$ , where 15 selections of each  $b$  and  $c$  were chosen uniformly at random from the interval  $[1, 22]$ . The values for  $a$  are the same evenly-spaced points as in stage 1. Figure 3.4 presents the results of these simulations.

When one of  $b$  or  $c$  is relatively large and each of the other payoffs is small. The symmetric appearance of chaotic solutions along the  $b$ - and  $c$ - dimensions is to be expected as each parameter plays a similar role, governing the payoffs from external interactions for each population.

### 3.3 Conclusion

This paper supplements ongoing scholarship that investigates chaotic phenomena in evolutionary dynamics driven by rock-paper-scissors games. When a member of a population must play against its own cohort and simultaneously against a separate population, the system evolves chaotically even though individual interactions are all simple rock-paper-scissors games.

This sort of interaction is an alternative route to chaos with two populations. For three-strategy games, two populations are required, so this is a minimal example. The model suggests that chaotic outcomes in economic or biological scenarios do not require an asymmetry from non-equal payoffs in case of ties, but may result from intra-population interactions occurring simultaneously with between-population play. In this case, asymmetry in the rates of updating enables the chaotic solution.



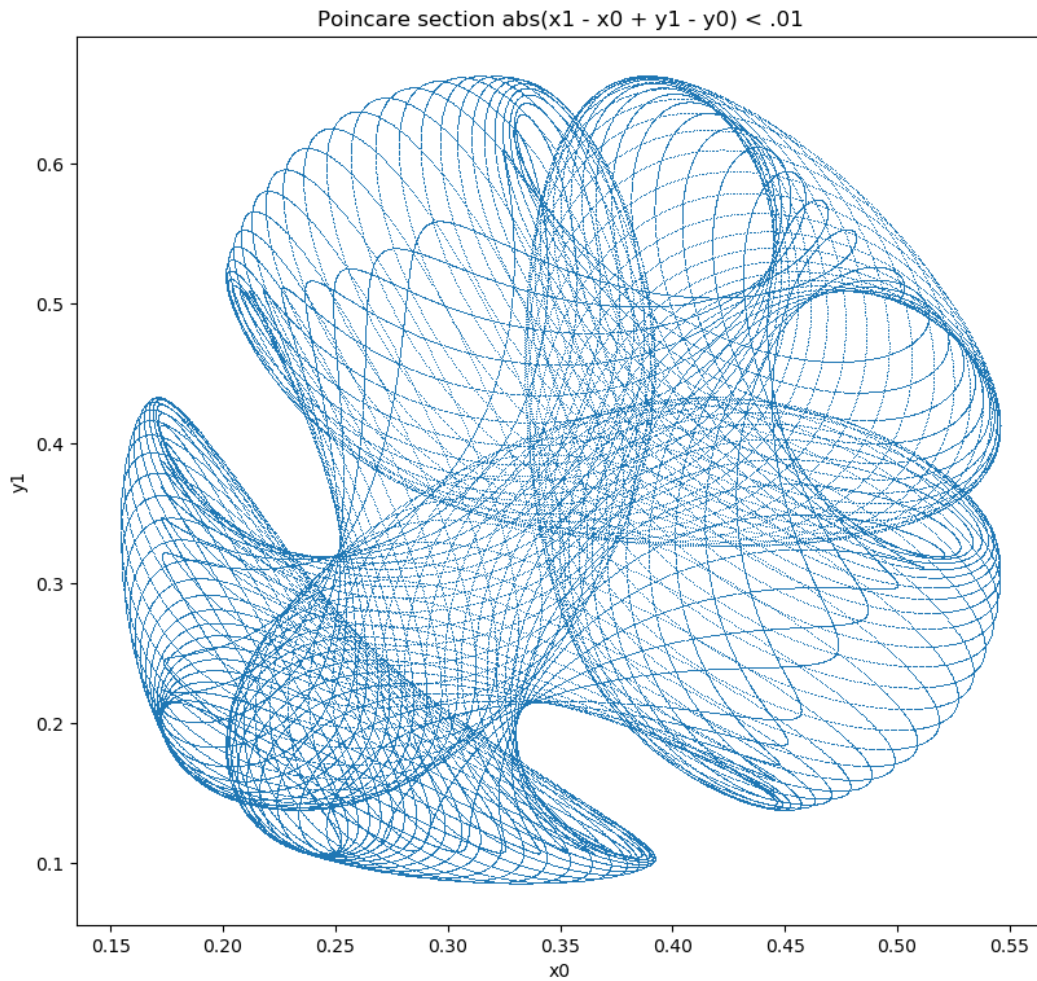


Figure 3.1: Poincaré section of the dynamics of a non-chaotic solution.  $x_0$  and  $y_1$  are the proportion of rock and paper players in the first and second population, respectively. The orbit traces an intricate space, but it is still one dimensional.

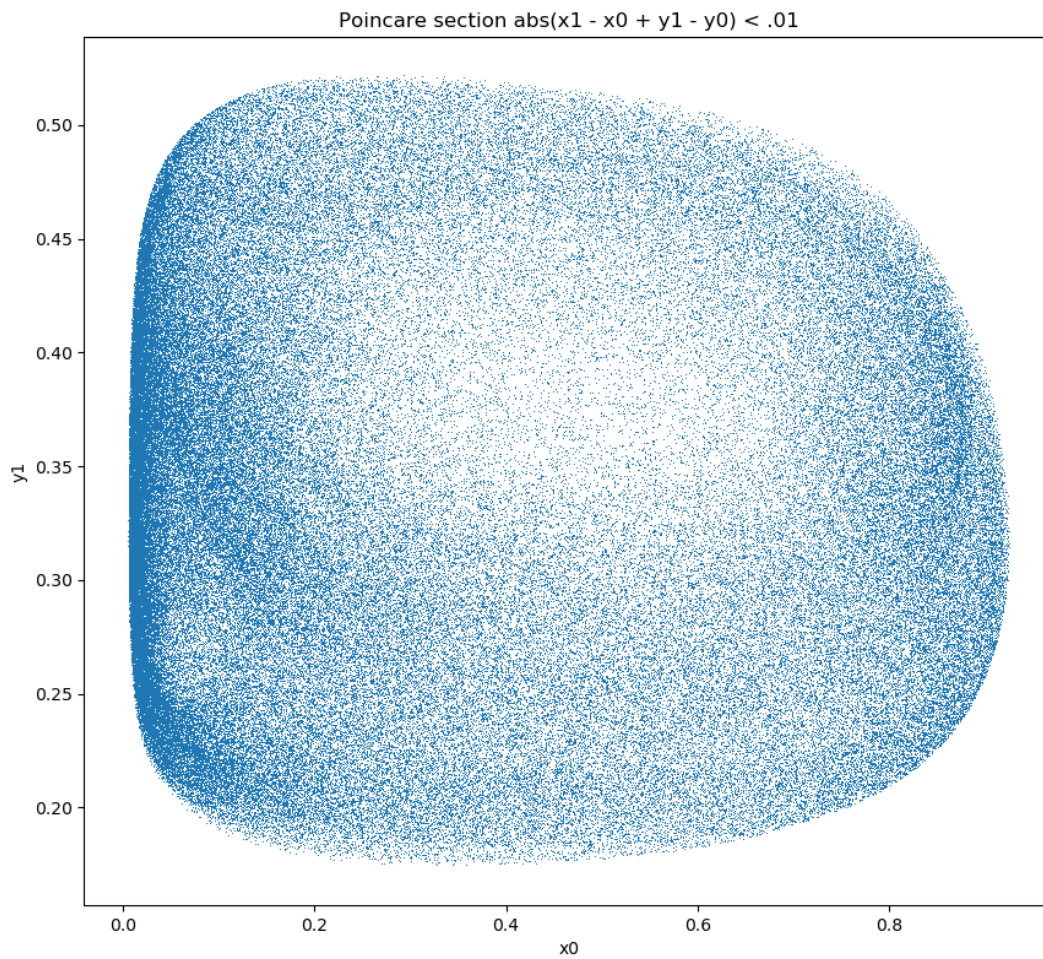


Figure 3.2: Poincaré section of the models dynamics with payoffs  $a = \sqrt{2}$ ,  $b = 15.4$ ,  $c = 1$ .  $x_0$  and  $y_1$  are the proportion of rock and paper players in the first and second population, respectively. The orbit crosses the section throughout a subset of the same dimension rather than tracing a closed loop.

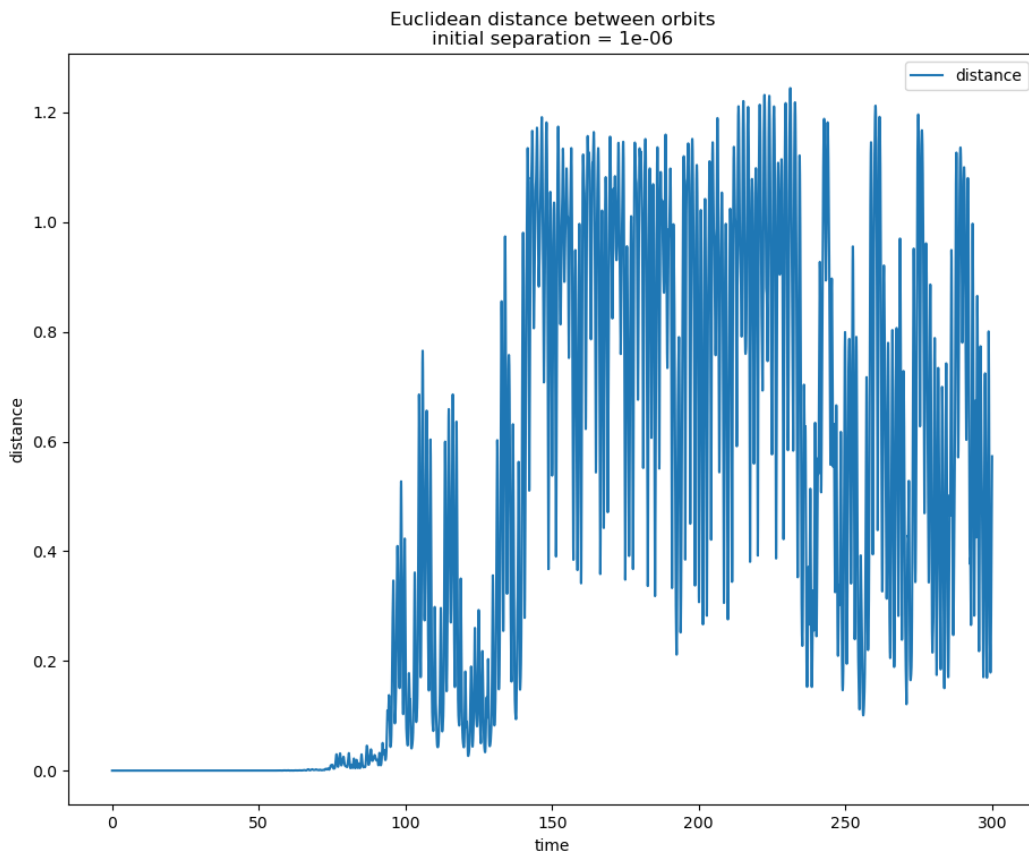


Figure 3.3: Distance between two trajectories with nearby initial conditions. The trajectories remain close for early time steps and then rapidly diverge.

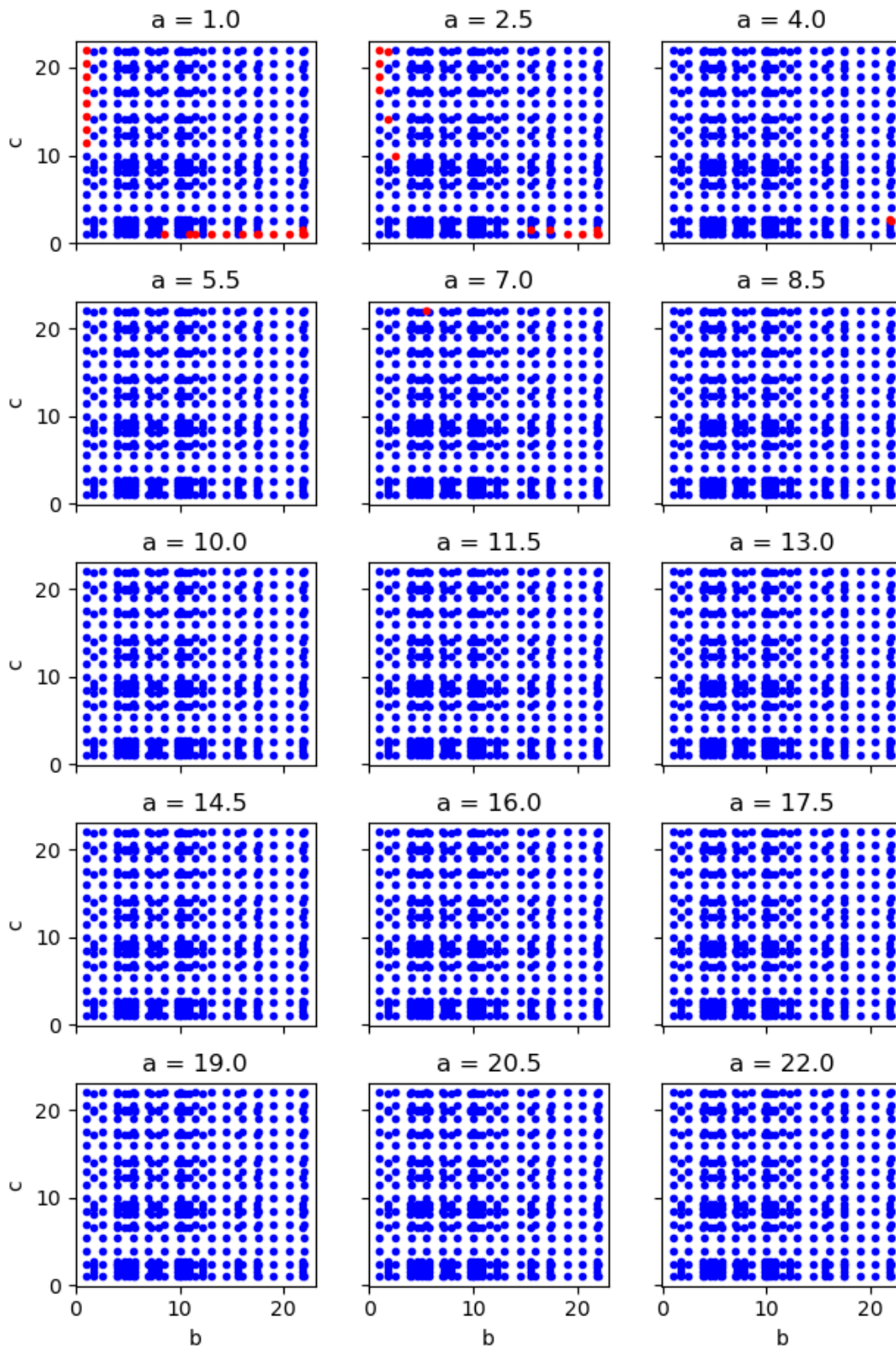


Figure 3.4: Red points represent parameter sets with  $MLE \geq 0.02$  which are likely to exhibit chaotic solutions. The blue points are the other parameters that were tested.

# Chapter 4

## Weak Points

This chapter investigates the evolutionary dynamics of invasions of non-cooperators into a population of cooperators playing a two-player Stag Hunt game on graphs. The dynamics are shown to be linked to endogenous graph properties as well as the selection of values in the payoff matrix. The first section situates the findings within contemporary research in evolutionary game theory (EGT), evolutionary graph theory, and work describing graph-cellular automata (CA). The second section presents new findings and describes location-dependent invadable graphs. The third section describes directions for future research and possible connections to other domains of study in evolutionary dynamics.

## 4.1 Background

### 4.1.1 Evolutionary Game Theory

Coordination games like the Stag Hunt feature multiple Nash equilibria and so feature the problem of selecting between them. Unlike the Prisoner's Dilemma, where agents are driven towards defecting by the simple calculus of choosing more over less, coordination games pose a problem where the best choice is to match one's partner.

		Player Y	
		<i>S</i>	<i>H</i>
Player X	<i>S</i>	(4, 4)	(0, 3)
	<i>H</i>	(3, 0)	(3, 3)

Table 4.1: Stag Hunt payoff matrix

In what is called the cooperative case,  $(S, S)$ , both players hunt the stag, each is receiving the highest payoff and there is nothing to be gained by switching strategy. If both players hunt the hare, neither can unilaterally profit by switching to  $S$ . The stag hunt fails unless the parties are coordinated. Hare-hunting is the safe alternative.

		<i>S</i>	<i>H</i>
		<i>a</i>	0
<i>S</i>	<i>b</i>	<i>b</i>	

Table 4.2: General form payoff matrix. We require  $a > b$

The Stag Hunt has been used to model coordinative behaviors in biological and social systems [2, 1, 8, 47, 48]. Cooperative and noncooperative strategies may correspond to genotypes, to reasoned selections between alternatives, or be the outcome of a social imitation process [44].

### 4.1.2 Network Effects

Brian Skyrms calls correlation “the key to the evolution of cooperation” [47]. Evolutionary coordination game models show that interactions between neighbors, instead of global, well-mixed interactions, can significantly alter the dynamics within a population of agents [8, 26]. Much work has been done to formulate a theory for games played by agents arranged on the vertices of infinite graphs with some sort of regular structure. Games played with local interaction on infinite lattices, regular small-world networks, and tree-like structures form a rich domain of study, sometimes called evolutionary graph theory, which has seen its models applied in economics, theoretical evolutionary biology, and physics [26, 29, 31, 32, 52].

In biological models it can be advantageous to update strategies according to rules which do not presuppose agents being rational in any capacity. Prominent examples of update rules include Birth-Death updating, in which fitness (or equivalently, utility) determines the likelihood an agent is chosen to reproduce, replacing one neighbor, Death-Birth updating, where a random agent is replaced by a neighbor according to their fitness distribution, and Imitation updating, where an agent is randomly selected to copy a neighbor’s strategy or keep its own strategy with a chance determined by its fitness [32].

Models in which agents exhibit boundedly rational behavior lose biological generality but gain some social plausibility. Instead of update rules that resemble reproduction, social scientists have considered models where agents are given behavioral rules incorporating interactions with, or observations of neighbors beyond random pairing [8, 26, 44, 47, 48, 56]. In this paper, the update rule is given by a best response dynamics in which each agent is given the chance to update its strategy at every period. The process of updating has an agent choose a strategy for period  $t$  by picking the strategy which would maximize the sum of payoffs in games against neighbors according to their states at  $t - 1$ .

Two of the articles cited above are especially relevant to the research presented here. In [8],

Ellison considers populations playing a two-strategy coordination game with a risk-dominant equilibrium. This paper considers in particular those configurations which start in some mixed state and eventually reach a homogenous population state where every agent plays the risk-dominant strategy (i.e., hunts hare). Ellison's focus is on the role local interaction plays on time to reach equilibrium. His main observation is that local interaction enables a faster fixation to the risk-dominant equilibrium since an agent only needs some fraction of neighbors, rather than some fraction of the whole population, to be hunting hare in order for switching to be the best response. In the most extreme case, where the population is arranged on a line or circle graph and each agent only has two neighbors, a single invader playing the risk-dominant strategy will cause the population to reach equilibrium in a number of time steps proportional to the population size. This is in contrast with models of well-mixed populations of agents where only a sequence of improbable events leads to the risk-dominant fixation, and the expected time for such an occurrence can be immense (in one model it took  $10^{100}$  time steps!).

The second is [26] which also discusses a model with agents playing a coordination game and revising their play based on simultaneous best response updates. Morris considers the theoretical properties of infinite graphs that allow "contagion" to occur. Contagion here refers to the possibility of a strategy introduced at some finite subset of agents spreading through the whole population. Morris' paper clarifies the dynamics of local interaction coordination games and gives precise and useful mathematical conditions that guarantee this particular sort of invadability. The present chapter is in this line of research, considering the structural properties of graphs that allow for invasions, but there are significant differences. In the first place, rather than considering a special kind of invasion on infinite graphs, this chapter is concerned with finite graphs, and the finite analogue to evolutionary stability, that is resistance to a single invader. Second, this chapter does not concern the question of which graphs can possibly be invaded, but explores those invadable networks have particular weak points.



An interesting side effect of the deterministic best response dynamics with discrete time periods (generations) is that, because each agent's state at time  $t$  is determined by the states of a fixed subset of agents at  $t - 1$ , the process can be described as a cellular automata process [60]. Indeed, the traditional study of CA processes on lattices has been generalized in the theory of graph-cellular automata (graph-CA) which offers a framework which might be applied to evolutionary models more broadly [33].

## 4.2 Model & Discussion

Let  $V$  be a finite set. Call  $V$  the set of vertices or the population and an element  $i$  of  $V$  a vertex or an agent.  $E \subseteq \{(x, y) | x, y \in V\}$  is the set of edges. We require  $(x, y) \in E \iff (y, x) \in E$ . For any agent  $i$ ,  $N(i) = \{j \in V | (i, j) \in E\}$  is the neighborhood of  $i$  and its elements are called  $i$ 's neighbors. The number of  $i$ 's neighbors will be denoted  $|N(i)|$ . Possible payoffs for a single, two-player interaction are  $\{0, a, b\}$  with  $a > b > 0$ .

The strategy set  $M = \{S, H\}$  is the domain for the family of utility functions  $u_{(i,t)}(x) : M \rightarrow \mathbb{R}$  where  $t = \{0, 1, 2, \dots\}$  denotes the time step. We use  $m_i(t)$  to refer to  $i$ 's strategy at time  $t$ .  $u_{(i,t)}(H) = b|N(i)|$ : each  $i$  gets a constant payoff from playing  $H$  at any time.  $u_{(i,t)}(S) = a(\#\{j | j \in N(i), m_j(t-1) = S\})$ , on the other hand, depends on the number of neighbors playing  $S$  on the previous round.

This gives rise to a deterministic dynamics where agents pick strategies by maximizing each  $u_{(i,t)}$  given the state of the system at  $t - 1$ . In case of ties,  $u_{(i,t)}(S) = u_{(i,t)}(H)$  the agent chooses  $m_i(t) = H$ . The agent opts for the guaranteed payoff from hunting hare, all else being equal.

### 4.3 Results

**Definition 4.1.** *A network  $G_A$  of agents uniformly playing strategy  $A$  is called **evolutionary stable** if it cannot be invaded by a single mutant.*

This definition is in line with Ohtsuki et al. who characterize evolutionary stable strategies (ESS) based on “rare mutants” having “a selective advantage over residents” [32]. In the case of discrete, finite networks the rare mutant is realized as a single agent changing from strategy state  $A$  to state  $B$ .

Recall the hare hunter’s payoff for any single interaction is  $b$  in all cases and the stag hunter’s is  $a$  when matched with another stag hunter. In general, if an agent governed by the best response dynamics is adjacent to  $k$  neighbors, one hare-hunting invader and  $k - 1$  stag hunters, it will continue hunting stag on the following round if and only if  $(k - 1)a > kb$ .

The **critical ratio** for agent  $i$  is given by

$$\frac{a}{b} > \frac{|N(i)|}{|N(i)| - 1} \tag{4.1}$$

It gives the specific ratio of values in the payoff matrix required for  $i$  to resist a single defecting neighbor. The existence of such a relationship shows the contingency of the evolutionary dynamics on the local graph structure as well as the particular selection of parameters. It is useful to note that in the limit as  $k \rightarrow \infty$ ,  $\frac{k}{k-1} \rightarrow 1$ . The finite model approaches the case for a continuous, well-mixed population and this calculation of the critical ratio agrees with the requirement in the replicator dynamics, where  $a > b$  is the threshold for  $S$  being an evolutionary stable strategy.

The critical ratio resembles Ellison’s description of  $\frac{1}{2}$ -dominant strategies, which describe those states that are a best response for players who have one or more neighbors in the state

[8]. In the context of games played by agents arranged on a line, a pair of neighboring vertices in a  $\frac{1}{2}$ -dominant state will result in convergence to an equilibrium where every agent plays the strategy. Morris generalizes this idea, defining the “critical number”  $q$ , the proportion of neighbors playing strategy  $A$  beyond which switching to  $A$  is the best response [26].

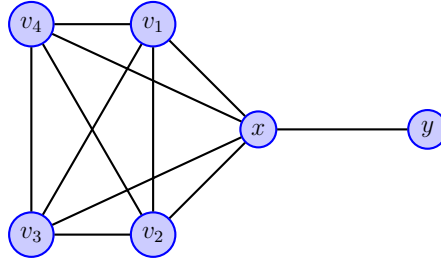


Figure 4.1: An example of a location-dependent invadable graph of type  $G$ . If  $m_{v_i}(0) = H$  then all vertices will play  $H$  after several steps. However if  $m_y(0) = H$  but  $m_{v_i}(0) = m_x(0) = S$  for all  $i$ ,  $H$  will not spread to the other vertices.

**Definition 4.2.** A graph  $G_A$  with all vertices in state  $A$  (i.e., playing strategy  $A$ ) is called  **$B$ -invadable** if  $\exists U_\alpha \subseteq V(G_A)$  on which  $u \in U_\alpha$  switching to state  $B$  implies every vertex will be in state  $B$  and stable after a finite number of steps.  $U = \bigcup U_\alpha$  is the invadable set.

**Definition 4.3.**  $G_A$  is **location-dependent invadable** if  $\exists v \in V(G_A)$ ,  $v \notin U$  where  $U$  is the nonempty invadable set, and  $G_A$  is invadable. In other words, there are vertices where invasion cannot begin despite  $G_A$  being invadable.

Graphs of this second type are of particular interest because they feature strategies which defy categorization in terms of evolutionary stability. Systems that are location-dependent invadable may switch to a stable equilibrium by introducing a single invader but this process requires the invasion to begin at a particular vulnerable proper subset of the vertices. This definition introduces a sort of sensitivity to context and network structure that is related to, but goes beyond the strategic information encoded in the payoff matrix.

I will now show that the class of location-dependent invadable graphs is not vacuous by introducing several families of graphs.

Let  $n \in \mathbb{N}$ ,  $n \geq 4$  and  $K_n$  be the complete graph on  $n$  vertices. Label the vertices  $V(K_n) = \{x, v_1, v_2, \dots, v_{n-1}\}$ . Take the graph  $G$  given by  $V(G) = V(K_n) \cup \{y\}$  with edge set  $E(G) = E(K_n) \cup \{xy\}$ . Consider a Stag Hunt with payoffs  $u_S = a$  and  $u_H = b$  with  $a > b > 0$ . If  $G_S$  is  $G$  populated by vertices playing strategy  $S$

**Theorem 4.1.**  $G_S$  is location-dependent invadable

*Proof.* Suppose  $\frac{n}{n-1} < \frac{a}{b} < \frac{n-1}{n-2}$ . If the invasion begins at vertex  $v_i$ ,  $1 \leq i \leq n-1$  then for any  $v_j$ ,  $j \neq i$ ,  $u_S(v_j) = a(n-2) < b(n-1) = u_H(v_j)$ , so  $v_j$ 's best response is to switch to state  $H$  in the next generation.

At this stage, though,  $v_i$  has switched to  $S$  but every other  $v_j$  is in state  $H$ . It is easy to see the best response for  $v_i$  is now to return to  $H$ , and for vertex  $x$ ,  $u_S(x) = 2a < b(n-1) = u_H(x)$ , so the invasion spreads to  $x$  as well.

By now,  $y$  is the only vertex remaining in state  $S$  so, for  $y$ ,  $u_S(y) = 0 < b = u_H(y)$  and the invasion will be complete.

However, if  $y$  is the initial invasion site in  $G_S$ , considering the payoff functions for  $x$  gives  $u_S(x) = a(n-1) > bn = u_H(x)$ , so the  $H$  state cannot spread across the graph.  $\square$

The same principle can be generalized to pairs of complete graphs  $K_m$ ,  $K_n$  where  $m \neq n$ , connected by a single edge. Let  $V(K_m) = \{x, v_1, \dots, v_{m-1}\}$  and  $V(K_n) = \{y, u_1, \dots, u_{n-1}\}$ . Construct the graph

$$L = (V(K_m) \cup V(K_n), E(K_m) \cup E(K_n) \cup xy)$$

It can be shown that  $L_S$  is location dependent invadable

*Proof.* Suppose  $m > n$  and  $\frac{m}{m-1} < \frac{a}{b} < \frac{m-1}{m-2} \leq \frac{n}{n-1}$ . If the invasion begins at a vertex  $v_i$  on

the subgraph  $K_m$ , all of the vertices in  $K_m$  will switch to state  $H$  as in the previous proof. The next step is the invasion jumping from  $K_m$  to  $K_n$  across the edge  $xy$ .

Consider the best response for  $y$ .  $u_S(y) = a(n - 1) < bn = u_H(y)$  by the hypothesis.  $y$  converts to state  $H$  and on the next generation,  $u_S(u_i) = a(n - 2) < b(n - 1) = u_H(u_i)$ , so all of the vertices in  $L$  will ultimately be in state  $H$ , and  $L_S$  is  $H$ -invadable.

However, if the first appearance of state  $H$  is on a vertex  $u_i$  on the subgraph  $K_n$ , the invasion will cover the vertices of  $K_n$  before stopping. That it spreads at first follows from the hypothesis,  $|K_m| > |K_n|$  and  $K_m$  being invadable. At this point, consider the best response for position  $x$ .  $u_S(x) = a(m - 1) > bm = u_H(x)$ .  $S$  remains the best response, and the invasion falters. □

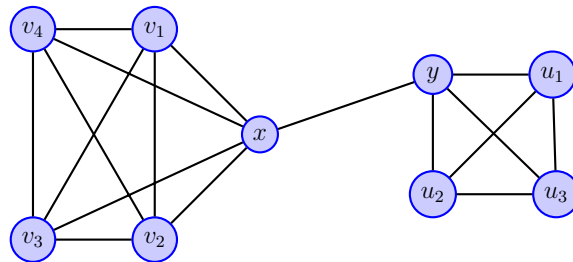


Figure 4.2: An example of a location-dependent invadable graph of type  $L$

One may choose whatever integers  $m \neq n$  for the complete components of an  $L$ -graph so it is clear these networks constitute an infinite family of location-dependent invadable graphs (with carefully chosen payoffs). This construction does not cover all of the cases, however. Taking the pattern of linked complete graphs as a starting point, one can construct many different structures sharing the same feature. In particular consider  $K_5$  linked by a single edge to  $K_4$  which is linked by an edge, with a different endpoint, to another  $K_4$ , and continue adding more copies of  $K_4$  in this way. It is easy to show that any mutation from a cooperative equilibrium beginning on the long tail of  $K_4$ s will be halted by the bottleneck once it reaches  $K_5$ , but if the first hare-hunter appears inside  $K_5$ , the whole network will eventually switch

over.

The fixation probability of the invading variety, that is the probability that the heterogeneous state induced by a single mutation will eventually reach a situation where only mutant types remain, is simply  $\frac{\#U}{\#V}$  where  $U$  is the invadable set. Graphs may be constructed where this probability is arbitrarily large or small.

Another interesting pattern is the construction resembling a star graph, with a central hub joined to many spokes. If the hub is a complete graph  $K_m$  with large degree with  $l \ll m$  of its vertices joined to chains of smaller complete graphs  $K_n$  as above, the “hub” subgraph acts as a bastion against invasions beginning anywhere on one of the spokes. In this case the entire spoke may play the invading strategy, but the hub and the other spokes will maintain cooperative play. The details of such constructions will not be given here as each of the parts is the same as a step in the previous cases.

It is worth taking a detour to consider the complete bipartite graphs  $K_{m,n}$  with  $m, n \geq 1$ . Because the vertices may be partitioned into disjoint sets  $U = \{u_1, \dots, u_m\}$  and  $V = \{v_1, \dots, v_n\}$  so every edge in  $E(K_{m,n})$  may be written  $u_i v_j$  where  $1 \leq i \leq m$  and  $1 \leq j \leq n$ , any initial invasion site  $x$  must be an element of  $U$  or  $V$ , and all of its neighbors will be in  $V$  or  $U$ , respectively.

Suppose  $x \in U$ . Even if for any neighbor  $y$  of  $x$ ,  $u_S(y) < u_H(y)$ , because all of  $x$ 's neighbors are initially in state  $S$ ,  $x$ 's best response will be to switch to state  $S$ , as is typical for the second generation of any invasion. However, now for every  $y \in V$ , all of its neighbors are in state  $S$ , so switching to  $H$  is the best response. Payoff parameters  $a$  and  $b$  may be selected so on alternate generations all of  $U$  is in  $S$  while  $V$  is in  $H$  and vice versa. Permanent oscillations can occur on bipartate graphs, but invasion cannot.

This gives a graph-theoretic explanation from one result presented by Ellison. He presents similar dynamics and shows that one-dimensional circular graphs where  $|V|$  is even the homo-

geneous steady states are joined by the period-two cycle  $(S, H, S, H, \dots) \rightarrow (H, S, H, S, \dots) \rightarrow \dots$ . Any circular graph with an even number of vertices is bipartite, and so each part comprises agents who respond only to agents belonging to its complement. Ellison also shows that risk-dominant strategies only invade line graphs when played by a pair of neighbors: line graphs are bipartite and with one invader there will always be one part uniformly playing the other strategy [8, 26].

Ellison's observation has been extended from circle and line graphs to the class of all bipartite graphs. He observes that the former case can hardly be said to well describe any economic systems, and with bipartite graphs being such a strong restriction, perhaps we ought to share his concern. However, there are social scenarios where bipartite graphs joined with simultaneous updating offer a plausible starting point [39]. Any periodic, be it seasonal or daily, market where customers match with sellers can be modeled with a bipartite graph. One can imagine a set of such transactions involving some sort of norm where an optimal outcome requires the cooperation of buyers and sellers, but if either player fails to adhere to the norm, the other would be better off avoiding it, too.

The classic example of bipartite social networks is heterosexual interactions. A contrived example to illustrate the plausibility of the model has groups of men and women who only date members of the other group and must decide whether to spend time and money on tango lessons, which are only worthwhile if your partner does the same, or to settle for line dancing, which is less fun, but doesn't require as much effort to learn. If the payoffs are appropriately chosen for a network of men and women who have a consistent schedule of dance dates, we are relieved to report that a single missed lesson will not result in the extinction of tango.

This chapter describes location-dependent invadable graphs, introducing a novel result in the underexplored domain of evolutionary processes on finite graphs. This work suggests several possibilities for extension. A more general structural description of networks in this

category would be more useful than the given examples of classes of graphs which satisfy the definition. Invasions beginning with a single individual match a framework derived from the idea of an ESS, but because a common family of graphs (the bipartite graphs) can only be taken over when a pair of neighboring agents switch strategies, it makes sense for the theory to explore invasions beginning with two (or  $n$ ) individuals.

If this new notion of invadability can be constructed it will open the door to the study of invasions of cooperators into graphs populated by noncooperators. Indeed, descriptions of networks which structurally favor stag hunting might be of greater theoretical interest since the emergence of cooperation is intuitively seen as a “good” outcome [8, 47].

Fully deterministic dynamics provides considerable power for deriving analytic results, but many mostly deterministic evolutionary models feature small stochastic components which corresponds to genetic mutation or the “trembling hand” when selecting among strategies [8, 48]. The constructions in this chapter depend on deterministic dynamics and fully synchronous updating. Thus, they only describe the “short-run” dynamics of systems directly after a mutation or invasion is introduced. Whether location-dependent invadable graphs remain a useful construct in models with stochastic, asynchronous updating is a logical next question to ask.

The social scenarios described by stag hunt games are interesting in part because of the tension between socially optimal and stable, but suboptimal equilibria. Because these games are inherently dyadic, standard techniques from evolutionary game theory and graph theory may be used. However, similar situations may be better described by public goods games [41], or other types of group-coordination tasks which cannot be decomposed as sums of pairwise interactions. This is a trade-off that must be made when modeling strategic interactions using networks: giving up some flexibility in the features that can be modelled in how payoffs are allocated to enable studying a structured population.



# Chapter 5

## Concluding Remarks

A social scientist's adage says that it's hard to predict a single person's actions, but it's easy to predict those of a million. Population dynamical models are at their richest and most interesting when they invert that truism. Agents may be simply described automata full specified with a few rules governing their behavior, but when joined into an interacting population engage in unpredictable and interesting behaviors. Seminal work in population dynamics established this as fact and enchanted a generation of researchers, the author of this work included, who found that rather than standing as monolithic contributions to science, answering a single question once and for all, the domain of evolutionary models offers a wellspring for deriving new models that are just as vivid and surprising as the originals. It is so in human populations as well. A researcher must not be intimidated by the millions of researchers scrutinizing thousands of data sets. Always bear in mind the depth and complexity of human behavior, and the breadth of investigative tools to be employed and see that neither insight nor genius is required to make new discoveries, rather it is just that same richness that draws so many to study human populations. The projects included in this dissertation follow this theme and serve as proof of the strength of the interdisciplinary approach, that is, asking naive and basic questions, and then trying to answer them using

any tools at hand. Curiosity outside of one's field of expertise is a boon to any scientist. There are analogous problems across scientific disciplines ripe for recognition, just as there are so many mathematical techniques not yet in use by social scientists that sit ready to be employed to clarify or develop our models. It is not easy to search out these connections themselves. What is easy is studying broadly and maintaining an open mind, ready to try a solution from one place on a problem from another.

## Future Work

This interdisciplinary style naturally offers a multiplicity of new scientific hypotheses and new mathematical possibilities. “Multiplicity” should be read literally. With  $X$  existing models or unanswered questions from one domain and  $Y$  techniques from another one has  $X \times Y$  pairs and so the puzzle is to select a good problem rather than to construct a novel one. However, each of the chapters presented here suggests some research questions that seem especially promising. Uncovering the resemblance between religious membership and species abundance numbers presents the puzzle of answering why one would be like the other. There has not been a mathematical, mechanistic attempt to model the sizes of religious denominations, and the qualitative similarities between speciation and religious groups' splitting joins the common statistical pattern to suggest adopting ecological models in the study of religion. Even if the ecological-religious similarities prove to be vacuous, or if they are found to be statistical artifacts (either as a consequence of the central limit theorem or peculiarities of measurement), theoretical ecology offers an abundance of models which may be introduced as hypothesis to be tested against the data. The tradition of fitting statistical models to abundances goes back to at least Fisher [9], but social scientists may do better than testing statistical models without any definite theoretical meaning by considering those simple ecological models which might plausibly serve as simple and sensible

hypotheses. For example, we might consider a population of potential adherents to be analogous to an ecological niche, that is, as a collection of available resources. One supposes that relative species abundances match the proportion of resources captured by each type, and so the population of people might be divided up by competing churches whose doctrines best match those of some subset of the population. MacArthur proposed the first set of such hypotheses with his “broken stick” model where the ecological niche is modeled as a line segment which is repeatedly and randomly divided between species [22]. Testing this against religious membership data is an empirical question, and the advantage is researchers can begin the scientific process of testing logically coherent hypotheses rather than being limited to matching statistical models.

Evolutionary game theory is uniquely poised to grow in popularity along with fashionable fields like complexity science, computational or simulation-based social science, and socio-physics. In each of these disciplines, the individual unit (often representing a person) is immersed in a rich, structured population, where emergent behavior is the norm and the individual looks more like a material particle than a person. EGT offers the best body of work describing the dynamics of strategic agents and so it already provides the foundation for many complex systems models. There remains a lot of work to be done, not just in bridging the gap between EGT and these other fields, but by producing research that itself contributes to the understanding of the key problems of complex and sociophysical systems. Understanding the fundamental mathematical properties of evolving populations is critical to achieving this goal. Chapter 3 was an attempt to make a small contribution to our understanding of chaos in evolutionary dynamics by providing one simple case where chaotic solutions may occur. Most of the related work takes a similar form: a special case or a particular proof of concept exhibiting chaos. The nonlinear dynamical systems that exhibit chaos are notoriously intractable to analytic techniques, but it is desirable to have a more general understanding of the sorts of payoff matrices that produce chaotic solutions under the replicator dynamics rather than having to perform the standard suite of mathematical

tests on every particular model. Making such a distinction is impossible for systems of ODEs in general, but perhaps limiting the scope to those consistent with the replicator equations will enable some more general claims to be verified.

The obvious empirical work, investigating the possibility of chaotic dynamics *in vitro* using biological instances of RPS dynamics (e.g., colicin-producing *E. coli*) should not be attempted until the theoretical model of chapter 3 is found to generalize. The chapter presents a model where the growth rates of each strategy (within each population) are identical. This symmetry gives a mathematically neat and easy to understand form. It also yields symmetric orbits: solutions that match our intuitions about physical oscillators with various natural frequencies. However, no such symmetry can be imagined to exist in biology. Among *E. coli*, colicin-producing and colicin-resistant strains in isolation have fundamental reproductive and metabolic disadvantages compared to the susceptible strain. Colicin is metabolically expensive to produce and is only released on cell death. Resistance to colicin is achieved by deleting the gene for producing a particular protein which may result in nutrient deficiency [20]. Competitive dynamics aside, there is an absolute disadvantage to either of these strategies and symmetric payoffs are clearly unrealistic. The next project will examine the general case where payoffs have an ordinal dominance cycle property, but have different absolute sizes.

One cannot read about complex systems or networks without seeing the other mentioned. There is a maxim among networks researchers that the space of networks is so huge and there is so much structural variety that one's readers will take for granted that analytic work is impossible, and won't push back against results that rely on simulations. There is truth to this. Writing a model that uses networks tends to introduce a level of complexity that makes full mathematical specification, at best, too time-consuming or specific to be useful, and at worst, impossible. The vastness of networks has the converse effect, too. There are entire families of graphs, often generated by simple algorithms, which all maintain some desired

mathematical features. This fact is of little use to those studying natural or social networks that have enough randomness to make the possibility of encountering a member of one of these sets minute, but it is particularly valuable to engineers linking systems of devices, or organizational researchers who have control over the structure of social interactions. Future work will expand the set of known location-dependent invadable graphs, and to take a deeper look at the role and structure of network bottlenecks in both real networks as well as coordination games and imitation dynamics beyond the synchronous stag hunt. This sort of research is key to understanding of the spread of political and social ideas and has become even more important as (sometimes radical) ideas are shared online.

One theme of this dissertation is that interdisciplinary work that combines techniques from two fields offers a cornucopia of unexplored research topics. Evolutionary games on graphs is an exemplar. The problems are easy to describe, often have practical applications, and most of them are not adequately understood. Ongoing work investigates a puzzling property of a model that is almost a perfect inversion of that presented in chapter 4. When an anti-coordination game is played by humans on a network, adding an extra link across the graph speeds up the propagation of information and naturally leads to the population finding an equilibrium more quickly. However, simulations where agents randomize their strategy when they lose the anti-coordination game (when there is a match with a neighbor) and maintain it when it is optimal to do so have precisely the opposite property: the extra link slows the time to equilibrium [19]! The working paper explores the structural reasons for this mathematically, and provides a suite of simulation results to provide a more general and precise description of this property.

## Conclusion

Each chapter presents research made possible by an interdisciplinary unification of a mathematical technique and an existing problem or model in the social sciences. The success of these projects shows the utility of this approach. Beyond that, the very existence of these projects ought to suggest beyond being scientifically useful for solving problems, having a broad understanding of both mathematical ideas and scientific models enables the creation of new models and hypotheses that are both intrinsically interesting, but also novel and tractable. Of these two halves, producing new answers and also new questions, it is the latter that makes me most happy. The research presented here gives a sample of of the power drawing from mathematics offers to social scientists solving problems in population dynamics, and only a tiny taste of the richness of a field that is being uncovered by researchers willing to create new ones.

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