SOCIAL AND ECONOMIC NETWORKS

Matthew O. Jackson

Social and Economic Networks [1]

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Preface

This book provides an overview and synthesis of models and techniques for analyzing social and economic networks. This is meant to serve both as a resource for researchers and a text on the subject for graduate students. The focus is primarily on the modeling of and theory behind the structure, formation, and implications of social networks. Statistical and experimental analyses of networks are also discussed throughout, especially when they help set the stage for issues to be investigated. The main emphasis is on providing a foundation for analyzing and understanding social and economic networks.

The organization of the book can be split into four main parts. The first part introduces network analysis and provides some background on what is known about various networks, how they are measured and useful ways of representing them. The second part presents some of the models that have been used to understand how networks are formed. This draws from two very different perspectives: random graph models, where there is some stochastic process which governs the development of the links in a network, as well as strategic models of network formation, where the development of links is based on costs and benefits and game theoretic techniques are used. These approaches to modeling provide different insights into networks, how they are formed, and why the exhibit certain characteristics. The third main part of the book looks at the implications of network structure. Much of the interest in networks has to do with the fact that their structure is an important determinant of how societies and economies function. This part examines how network models are used to predict the spread of disease, the dissemination of information, the choice of behavior by people, and how markets function. The final part of the book covers empirical analyses of networks and methods of identifying social interaction.

A specific outline of the grouping by chapters is as follows:

- Part I: Some Background and the Fundamentals of Network Analysis
  - Introduction (Chapter 1)

  - Representing and measuring networks (Chapter 2)
  - Empirical Background on Social and Economic Networks (Chapter 3)

- Part II: Models of Network Formation
  - Modeling network formation through random graph models, (Chapters 4 and 5),
  - Modeling network formation through strategic models, (Chapter 6),

- Part III: Implications of Network Structure
  - How information, diseases, and behaviors propagate through networks, (Chapters 7, 8, and 9),
  - How network structure impacts behavior (Chapter 9),
  - Analysis of some networked markets (Chapter 10),

- Part IV: Methods, Tools, and Emprical Analyses
  - Game theoretic foundations of network formation, (Chapter 11)
  - The allocation of productive value and utility through a network (Chapter 12).
  - Observing and Measuring Social Interaction through Data and Experiments and Community Structures (Chapter 13).

Although this represents a categorization of the chapters by subject, the relationship between the chapters is not entirely linear. I have intermingled some subjects to tie different approaches together, and the chapters will refer to each other. Also, there is a progression in the book with some of the more technically demanding chapters coming later, as well as those that draw on concepts from earlier chapters.

The modeling of networks requires some mathematical background, but I have made the book as self-contained as possible. I do not presume any knowledge beyond some familiarity with linear algebra (vectors and matrices), calculus, and some familiarity with probability and statistics. The discussions employing graph theory and game theory are self-contained and there are appendices with introductions to some of the topics, including various useful results from graph theory, math, game theory and

probability theory. There are some sections and exercises that are more mathematical in nature, and those are marked with an *.

There are several reasons for writing this book. First, and foremost, networks of relationships play central roles in a wide variety of social, economic, and political interactions. For example, many, if not most, markets function not as centralized and anonymous institutions, but rather involve a variety of bilateral exchanges or contracts. As a case in point, most jobs are filled by people who were informed about the job through a social contact. This fact has consequences for patterns of employment, inequality in wages across groups, and social mobility. As such, understanding social network structure and how it influences human interaction is not only important to science (and the social sciences in particular), it is essential. Second, the topic is timely for two reasons. One is that recent technological advances have made information networks much more prominent (e.g., the world wide web), and people are more conscious of the role of networks in their lives. Another is that the formal modeling of networks has now reached a maturity across fields that permits a book-length treatment devoted to it. Finally, the inter- and multi-disciplinary nature of research on networks means that knowledge is quite diffuse, and there is much to be gained by collecting aspects of it from different fields in a unified treatment. Substantial research on networks has been conducted in sociology, economics, physics, mathematics, and computer science, and these disciplines take different approaches and ask varied questions.[1] This makes it important to bridge the literatures and produce a text that collects and synthesizes different modeling approaches and techniques and makes them all available to researchers from any discipline who are interested in the study of networks.

At the end of each chapter in this book you will find "exercises." The exercises here are meant to serve several purposes. They serve the usual purpose of problems in a textbook: that is, to help ensure that students have a chance to work with concepts and more fully familiarize themselves with the ideas presented in a given chapter; and thus can be made part of a course material. And, of course, the interested researcher can work the exercises as well. But beyond this, the exercises also introduce *new* material. I have used the exercises to introduce new concepts and material that is not

[1] Social network analysis is a central and well-developed area of study in sociology, with societies, journals, conferences and decades of research devoted to it. With occasional overlap, a literature on graph theory has matured in mathematics over the same period. While the literature on networks has been thriving in sociology for over five decades, it has emerged in economics primarily over the last ten to fifteen years. Its explosion in computer science and statistical physics has been rapid and mostly during the past decade.

covered in the text. These are meant to be closely related to material in the text, but complementary to it. These are often ideas that I feel are important enough to include here, but for one reason or another did not fit easily with the main thread of a chapter without making it longer than I desired or taking us on a tangent. This means that researchers consulting this book as a reference should not ignore the exercises, and may in many instances actually find what they are looking for in exercises.[2]

As with any such undertaking, there are many acknowledgements due, and they do not adequately represent the scope and depth of the help received. This project would not have been possible without financial support from the Center for Advanced Studies in the Behavioral Sciences, the Guggenheim Foundation, and the Lee Center for Advanced Networking, as well as the NSF under grants SES–0316493 and SES–0647867. I began this project while I was at the California Institute of Technology and concluded it while at Stanford University, and their support is gratefully acknowledged. In terms of the content of this monograph, I have been deeply influenced by a number of collaborators. First and foremost, my initial interest in this subject arose through conversations and subsequent research with Asher Wolinsky. I have continued to learn about networks and enjoy the interaction with a group of co-authors (in chronological order): Alison Watts, Bhaskar Dutta, Anne van den Nouweland, Toni Calvó-Armengol, Francis Bloch, Gary Charness, Alan Kirman, Jernej Copic, Brian Rogers, Dunia Lopez-Pintado, Leeat Yariv, Andrea Galeotti, Sanjeev Goyal, Fernando Vega-Redondo, Ben Golub, Sergio Currarini, and Paolo Pin. Their collaboration and friendship is greatly appreciated. Although not co-authors on network-related projects, Salvador Barbera, Darrell Duffie and Hugo Sonnenschein have been great mentors (and friends) and profoundly shaped my approach and writing. I thank Lada Adamic, Marika Cabral, Toni Calvó-Armengol, Jon Eguia, Marcel Fafchamps, Ben Golub, Carlos Lever, Laurent Mathevet, and Tim Sullivan for extensive comments on earlier drafts. For all of the emotional support and enthusiasm needed to keep such a project afloat, I owe profound thanks to my wife, Sara, my daughters, Emily and Lisa, and to my parents. Special thanks are due to Sara, whose encouragement through the persistent asking of the question "Did you get to work on your book today?" always kept me pointed in the right direction, and whose juggling of many tasks allowed me to answer "yes" more often than "no."

[2] This is obviously not the first text to do this, as one sees important results appearing as exercises in many mathematical texts. The usefulness of this technique was made obvious to me through the superb text on axiomatic social choice by Hervé Moulin [469].

Matthew O. Jackson
Stanford University, February 2008

Chapter 1

Introduction

This chapter provides an introduction to the analysis of networks through the presentation of several examples of research. This provides not only some idea of why the subject is interesting, but also of the range of networks studied, approaches taken and methods used.

1.1 Why Model Networks?

Social networks permeate our social and economic lives. They play a central role in the transmission of information about job opportunities, and are critical to the trade of many goods and services. They are the basis of the provision of mutual insurance in developing countries. Social networks are also important in determining how diseases spread, which products we buy, which languages we speak, how we vote, as well as whether or not we decide to become criminals, how much education we obtain, and our likelihood of succeeding professionally. The countless ways in which network structures affect our well-being make it critical to understand: (i) how social network structures impact behavior, and (ii) which network structures are likely to emerge in a society. The purpose of this monograph is to provide a framework for an analysis of social networks, with an eye on these two questions.

As the modeling of networks comes from varied fields and employs a variety of different techniques, before jumping into formal definitions and models, it is useful to start with a few examples that help give some impression of what social networks are and how they have been modeled. The following examples illustrate widely different perspectives, issues, and approaches; previewing some of the breadth of the range of

topics to follow.

1.2 A Set of Examples:

The first example is a detailed look at the role of social networks in the rise of the Medici.

1.2.1 Florentine Marriages

The Medici have been called the "godfathers of the Renaissance." Their accumulation of power in the early fifteenth century in Florence, was orchestrated by Cosimo de' Medici despite the fact that his family started with less wealth and political clout than other families in the oligarchy that ruled Florence at the time. Cosimo consolidated political and economic power by leveraging the central position of the Medici in networks of family inter-marriages, economic relationships, and political patronage. His understanding of and fortuitous position in these social networks enabled him to build and control an early forerunner to a political party, while other important families of the time floundered in response.[1]

Padgett and Ansell [491] provide powerful evidence for this by documenting the network of marriages between some key families in Florence in the 1430's. The following figure provides the links between the key families in Florence at that time, where a link represents a marriage between members of the two linked families.[2]

As mentioned above, during this time period the Medici (with Cosimo de' Medici playing the key role) rose in power and largely consolidated control of the business and politics of Florence. Previously Florence had been ruled by an oligarchy of elite families. If one examines wealth and political clout, however, the Medici did not stand out at this point and so one has to look at the structure of social relationships to understand why it was the Medici who rose in power. For instance, the Strozzi had

[1] See Kent [367] and Padgett and Ansell [491] for detailed analyses, as well as more discussion of this example.

[2] The data here were originally collected by Kent [367], but were first coded by Padgett and Ansell [491], who discuss the network relationships in more detail. The analysis provided here is just a teaser that offers a glimpse of the importance of the network structure. The interested reader should consult Padgett and Ansell [491] for a much richer analysis.

Figure 1.2.1 15th Century Florentine Marriges Data from Padgett and Ansell [491] (drawn using UCINET)

both greater wealth and more seats in the local legislature, and yet the Medici rose to eclipse them. The key to understanding this, as Padgett and Ansell [491] detail, can be seen in the network structure.

If we do a rough calculation of importance in the network, simply by counting how many families a given family is linked to through marriages, then the Medici do come out on top. However, they only edge out the next highest families, the Strozzi and the Guadagni, by a ratio of 3 to 2. While this is suggestive, it is not so dramatic as to be telling. We need to look a bit closer at the network structure to get a better handle on a key to the success of the Medici. In particular, the following measure of betweenness is illuminating.

Let $P(ij)$ denote the number of shortest paths connecting family i to family j. [3] Let $P_k(ij)$ denote the number of these paths that family k lies on. For instance, the shortest path between the Barbadori and Guadagni has three links in it. There are two such paths: Barbadori - Medici - Albizzi - Guadagni, and Barbadori - Medici -

[3] Formal definitions of path and some other terms used in this chapter appear in Chapter 2. The ideas should generally be clear, but the unsure reader can skip forward if they wish. Paths represent the obvious thing: a series of links connecting one node to another.

Tournabouni - Guadagni. If we set i = Barbadori and j = Guadagni, then $P(ij) = 2$. As the Medici lie on both paths, $P_k(ij) = 2$ when we set k = Medici, and i = Barbadori and j = Guadagni. In contrast this number is 0 if we set k = Strozzi, and is 1 if we set k = Albizzi. Thus, in a sense, the Medici are the key family in connecting the Barbadori to the Guadagni.

In order to get a fuller feel for how central a family is, we can look at an average of this betweenness calculation. We can ask for each pair of other families, what fraction of the total number of shortest paths between the two the given family lies on. This would be 1 if we are looking at the fraction of the shortest paths the Medici lie on between the Barbadori and Guadagni, and 1/2 if we examine the corresponding fraction that the Albizzi lie on. Averaging across all pairs of other families gives us a sort of betweenness or power measure (due to Freeman [237]) for a given family. In particular, we can calculate

$$\sum_{ij:i\neq j,k\notin\{i,j\}} \frac{P_k(ij)/P(ij)}{(n-1)(n-2)/2} \tag{1.1}$$

for each family k, where we set $\frac{P_k(ij)}{P(ij)} = 0$ if there are no paths connecting i and j, and the denominator captures that a given family could lie on paths between up to $(n-1)(n-2)/2$ pairs of other families. This measure of betweenness for the Medici is .522. That means that if we look at all the shortest paths between various families (other than the Medici) in this network, the Medici lie on over half of them! In contrast, a similar calculation for the Strozzi comes out at .103, or just over ten percent. The second highest family in terms of betweenness after the Medici is the Guadagni with a betweenness of .255. To the extent that marriage relationships were keys to communicating information, brokering business deals, and reaching political decisions, the Medici were much better positioned than other families, at least according to this notion of betweenness.[4] While aided by circumstance (for instance, fiscal problems resulting from wars), it was the Medici and not some other family that ended up consolidating power. As Padgett and Ansell [491] put it, "Medician political control was produced by network disjunctures within the elite, which the Medici alone spanned."

[4] The calculations here are conducted on a subset of key families (a data set from Wasserman and Faust [615]), rather than the entire data set which consists of hundreds of families. As such, the numbers differ slightly from those reported in footnote 31 of Padgett and Ansell [491]. Padgett and Ansell also find similar differences in centrality between the Medici and other families in terms of a network of business ties.

This analysis shows that network structure can provide important insights beyond those found in other political and economic characteristics. The example also illustrates that the network structure is important beyond a simple count of how many social ties each member has, and suggests that different measures of betweenness or centrality will capture different aspects of network structure.

This example also suggests a series of other questions that we will be addressing throughout this book. For instance, was it simply by chance that the Medici came to have such a special position in the network or was it by choice and careful planning? As Padgett and Ansell [491] say (footnote 13), "The modern reader may need reminding that all of the elite marriages recorded here were arranged by patriarchs (or their equivalents) in the two families. Intra-elite marriages were conceived of partially in political alliance terms." With this perspective in mind we then might ask why other families did not form more ties, or try to circumvent the central position of the Medici. We could also ask whether the resulting network was optimal from a variety of perspectives: was it optimal from the Medici's perspective, was it optimal from the oligarchs' perspective, and was it optimal for the functioning of local politics and the economy of 15th century Florence? These types of questions are ones that we can begin to answer through explicit models of the costs and benefits of networks, as well as models of how networks form.

1.2.2 Friendships Among High School Students

The next example comes from the The National Longitudinal Adolescent Health Data Set, known as "Add Health."[5] These data provide detailed social network information for over ninety thousand high school students from U.S. high schools interviewed during the mid 1990s; together with various data on the students' socio-economic background, behaviors and opinions. The data provide a number of insights and illustrate some features of networks that are discussed in more detail in the coming chapters.

Figure 1.2.2 shows a network of romantic relationships as found through surveys of

[5] Add Health is a program project designed by J. Richard Udry, Peter S. Bearman, and Kathleen Mullan Harris, and funded by a grant P01-HD31921 from the National Institute of Child Health and Human Development, with cooperative funding from 17 other agencies. Special acknowledgment is due Ronald R. Rindfuss and Barbara Entwisle for assistance in the original design. Persons interested in obtaining data files from Add Health should contact Add Health, Carolina Population Center, 123 W. Franklin Street, Chapel Hill, NC 27516-2524 (addhealth@unc.edu). The network data that I present in this example were extracted by James Moody from the Add Health data set.

Figure 1.2.2. A Figure from Bearman, Moody and Stovel [47] based the Add Health Data Aet. A Link Denotes a Romantic Relationship, and the Numbers by Some Components Indicate How Many Such Componets Appear.

students in one of the high schools in the study. The students were asked to list the romantic liasons that they had during the six months previous to the survey.

There are several things to remark about Figure 1.2.2. The network is nearly a *bipartite* network, meaning that the nodes can be divide into two groups, male and female, so that links only lie between groups (with a few exceptions). Despite its nearly bipartite nature, the distribution of the degrees of the nodes (number of links each node has) turns out to closely match a network where links are formed uniformly at random (for details on this see Section 3.2.3), and we see a number of features of large random networks. For example, we see a "giant component," where over one hundred of the students are connected via sequences of links in the network. The next largest component (maximal set of students who are each linked to one another via sequences of links) only has ten students in it. This component structure has important implications for the diffusion of disease, information, and behaviors, as discussed in detail in Chapters 7, 8, and 9. Next, note that the network is quite "tree-like" in that there are very few loops or cycles in the network. There is a very large cycle visible in the giant component, and then a couple of smaller cycles present, but very few overall.

The absence of many cycles means that as one walks along the links of the network until hitting a dead-end, most of the nodes that are met are new ones that have not been encountered before. This is important in navigation of networks. This feature is found in many random networks in cases where there are enough links so that a giant component is present, but there are also few enough links so that the network is not fully connected. This contrasts with what we see in the denser friendship network pictured in Figure 1.2.2, where there are many cycles, and a shorter distance between nodes.

The network pictured in Figure 1.2.2 is also from the Add Health data set and connects a population of high school students.[6] Here the nodes are coded by their race rather than sex, and the relationships are friendships rather than romantic relationships. This is a much denser network than the romance network, and also exhibits some other features of interest.

A strong feature present in Figure 1.2.2 is what is known as "homophily," a term due to Lazarsfeld and Merton [404]. That is, there is a bias in friendships towards similar individuals; in this case the homophily concerns the race of the individuals. This bias is above what one would expect due to the makeup of the population. In this school, 52 percent of the students are white and yet 86 percent of whites' friendships are with other whites. Similarly, 38 percent of the students are black and yet 85 percent of blacks' friendships are with other blacks. Hispanics are more integrated in this school, comprising 5 percent of the population, but having only 2 percent of their friendships with Hispanics.[7] If friendships were formed without race being a factor, then whites would have roughly 52 percent of their friendships with other whites rather than 85 percent.[8] This bias is referred to as "inbreeding homophily" and has strong consequences. As we can see in the figure, it means that the students end up somewhat segregated by race, and this will impact the spread of information, learning, and the

[6] A link indicates that at least one of the two students named the other as a friend in the survey. Not all friendships were reported by both students. For more detailed discussion of these particular data see Curarrini, Jackson and Pin [171].

[7] The Hispanics in this school are exceptional compared to what is generally observed in the larger data set of 84 high schools. Most racial groups (including Hispanics in many of the other schools) tend to have a greater percentage of own-race friendships than the percentage their race in the population, regardless of their fraction of the population. See Currarini, Jackson and Pin [171] for details.

[8] There are a variety of possible reasons for the patterns observed, as it could be that race is correlated with other factors that affect friendship opportunities. For more discussion of this with respect to these data see Moody [458] and Currarini, Jackson and Pin [171]. The main point here is that the resulting network has clear patterns and those will have consequences.

Figure 1.2.2 "Add Health" Friendships among High School Students Coded by Race: Blue=Black, Yellow=White, Red=Hispanic, Green=Asian, White=Other

speed with which things propagate through the network; themes that are explored in detail in what follows.

1.2.3 Random Graphs and Networks

The examples of Florentine marriages and high school friendships suggest the need for models of how and why networks form as they do. The last two examples in this chapter illustrate two complementary approaches to modeling network formation.

The next example of network analysis comes from the graph-theoretic branch of mathematics, and has recently been extended in various directions by the computer science, statistical physics, and economics literatures (as will be examined in some of the following chapters). This is perhaps the most basic model of network formation that one could imagine: it simply supposes that a completely random process is responsible for the formation of the links in a network. The properties of such random networks provide some insight into the properties that some social and economic networks have. Some of the properties that have been extensively studied are how links are distributed across different nodes, how connected the network is in terms of being able to find paths from one node to another, what the average and maximal path lengths are, how many isolated nodes there are, and so forth. Such random networks will serve as a very useful benchmark against which we can contrast observed networks; as such comparisons help identify which elements of social structure are not the result of mere randomness, but must be traced to other factors.

Erdös and Rényi [211], [212], [213] provided seminal studies of purely random networks.[9] To describe one of the key models, fix a set of n nodes. Each link is formed with a given probability p, and the formation is independent across links.[10] Let us examine this model in some detail, as it has an intuitive structure and has been a springboard for many recent models.

Consider a set of nodes $N = \{1, \ldots, n\}$, and let a link between any two nodes, i

[9] See also Solomonoff and Rapoport [576] and Rapoport [524], [525], [526], for related predecessors.

[10] Two closely related models that they explored are as follows. In one of the alternative models, a precise number M of links is formed out of the $n(n-1)/2$ possible links. Each different graph with M links has an equal probability of being selected. In the second alternative model, the set of all possible networks on the n nodes is considered and one is randomly picked uniformly at random. This can also be done according to some other probability distribution. While these models are clearly different, they turn out to have many properties in common. Note that the last model nests the other two (and any other random graph model on a fixed set of nodes) if one chooses the right probability distributions over all networks.

and j, be formed with probability p, where $0 < p < 1$. The formation of links is independent. This is a binomial model of link formation, which gives rise to a manageable set of calculations regarding the resulting network structure.[11] For instance, if $n = 3$, then a complete network forms with probability p^3, any given network with two links (there are three such networks) forms with probability $p^2(1-p)$, any given network with one link forms with probability $p(1-p)^2$, and the empty network that has no links forms with probability $(1-p)^3$. More generally, any given network that has m links on n nodes has a probability of

$$p^m(1-p)^{\frac{n(n-1)}{2}-m} \tag{1.2}$$

of forming under this process.[12]

We can calculate some statistics that describe the network. For instance, we can find the degree distribution fairly easily. The degree of a node is the number of links that the node has. The degree distribution of a random network describes the probability that any given node will have a degree (number of links) of d.[13] The probability that any given node i has exactly d links is

$$\binom{n-1}{d} p^d(1-p)^{n-1-d}. \tag{1.3}$$

Note that even though links are formed independently, there will be some correlation in the degrees of various nodes, which will affect the distribution of nodes that have a given degree. For instance, if $n = 2$, then it must be that both nodes have the same degree: the network either consists of two nodes of degree 0, or two nodes of degree 1. As n becomes large, however, the correlation of degree between any two nodes vanishes, as the possible link between them is only one out of the $n-1$ that each might have. Thus, as n becomes large, the fraction of nodes that have d links will

[11] See Section 4.5.4 for more background on the binomial distribution.

[12] Note here that there is a distinction between the probability of some specific network forming and some network architecture forming. With four nodes the chance that a network forms with a link between nodes 1 and 2 and a link between nodes 2 and 3 is $p^2(1-p)^4$. However, the chance that a network forms which contains two links involving three nodes is $12\,p^2(1-p)^4$, as there are 12 different networks we could draw that have this same shape. The difference between these counts is whether we pay attention to the labels of the nodes in various positions.

[13] The degree distribution of a network is often given for an observed network, and thus is a frequency distribution. Here, when dealing with a random network, one can talk about the degree distribution before the network has actually formed, and so we refer to probabilities of nodes having given degrees, rather than observed frequencies of nodes with given degrees.

approach the expression in (1.3). For large n and small p, this binomial expression is approximated by a Poisson distribution, so that the fraction of nodes that have d links is approximately[14]

$$\frac{e^{-(n-1)p}((n-1)p)^d}{d!}. \tag{1.4}$$

Given the approximation of the degree distribution by a Poisson distribution, the class of random graphs where each link is formed independently with an identical probability is often referred to as the class of *Poisson random networks*, and I will use this terminology in what follows.

To provide a better feeling for the structure of such networks, I generated a couple of Poisson random networks for different p's. I chose $n = 50$ nodes as this produces a network that is easy to visualize. Let us start with an expected degree of 1 for each node. This is equivalent to setting p at roughly .02. Figure 1.2.3 pictures a network generated with these parameters.[15] This network exhibits a number of features that are common to this range of p and n. First, we should expect some isolated nodes. Based on the approximation of a Poisson distribution (1.4) with $n = 50$ and $p = .02$, we should expect about 37.5 percent of the nodes to be isolated (i.e., have $d = 0$), which is roughly 18 or 19 nodes. There are 19 isolated nodes in the network, by chance. Figure 1.2.3 compares the realized frequency distribution of degrees with the Poisson approximation.

The distributions match fairly closely. The network also has some other features that are common to random networks with p's and n's in this relative range. In graph theoretical terms, the network is a "forest," or a collection of trees. That is, there are no cycles in the network (where a cycle is a sequence of links that lead from one node back to itself, as described in more detail in Section 2.1.3). The chance of there being a cycle is relatively low with such a small link probability. In addition, there are six components (maximal subnetworks such that every pair of nodes in the subnetwork is connected by a path or sequence of links) that involve more than one node. And one

[14] To see this, note that for large n and small p, $(1-p)^{n-1-d}$ is roughly $(1-p)^{n-1}$. Then, we write $(1-p)^{n-1} = (1 - \frac{(n-1)p}{n-1})^{n-1}$ which, if $(n-1)p$ is either constant or shrinking (if we allow p to vary with n), is approximately $e^{-(n-1)p}$. Then for fixed d, large n, and small p, $\begin{pmatrix} n-1 \\ d \end{pmatrix}$ is roughly $\frac{(n-1)^d}{d!}$.

[15] The networks in Figures 1.2.3 and 1.2.3 were generated and drawn using the random network generator in UCINET [89]. The nodes are arranged to make the links as easy as possible to distinguish.

Figure 1.2.3. A Randomly Generated Network with Probability .02 on each Link

Figure 1.2.3 Frequency Distribution of a Randomly Generated Network and the Poisson Approximation for a Probability of .02 on each Link

of the components is much larger than the others: involving 16 nodes, while the next largest component only has 5 nodes in it. As we shall discuss shortly, this is to be expected.

Next, let us start with the same number of nodes, but increase the probability of a link forming to $p = \log(50)/50 = .078$, which is roughly the threshold where isolated nodes should start to disappear. (This threshold is discussed in more detail in Chapter 4.) Indeed, based on the approximation of a Poisson distribution (1.4) with $n = 50$ and $p = .08$, we should expect about 2 percent of the nodes to be isolated (with degree 0), or roughly 1 node out of 50. This is exactly what we see in the realized network in Figure 1.2.3 (again, by chance). With the exception of the single isolated node, the rest of the network is connected into one component.

As shown in Figure 1.2.3, the realized frequency distribution of degrees is again similar to the Poisson approximation, although, as one should expect at this level of randomness, not a perfect match.

The degree distribution tells us a great deal about a network's structure. Let us

Figure 1.2.3 A Randomly Generated Network with Probability .08 of each Link

Figure 1.2.3 Frequency Distribution of a Randomly Generated Network and the Poisson Approximation for a Probability of .08 on each Link

examine this in more detail, as it provides a first illustration of the concept of a *phase transition*, where the structure of a random network changes as we change the formation process.

Consider what fraction of nodes are completely isolated; i.e., what fraction of nodes have degree $d = 0$? From (1.4) it follows that this is approximated by $e^{-(n-1)p}$ for large networks, provided the average degree $(n-1)p$ is not too large. To get a more precise expression, let us examine the threshold where this fraction is just such that we expect to have one isolated node on average. That is where $e^{-(n-1)p} = \frac{1}{n}$. Solving this yields $p(n-1) = log(n)$, or right at the point where average degree $(n-1)p$ is $log(n)$. Indeed, this is a threshold for a "phase transition," as we shall see in Section 4.2.2. If the average degree is substantially above $log(n)$, then probability of having any isolated nodes goes to 0, while if the average degree is substantially below $log(n)$, then the probability of having at least some isolated nodes goes to 1. In fact, as we shall see in Theorem 4.2.1, this is the threshold such that if the average degree is significantly above this level then the network is path-connected with a probability converging to 1 as n grows (so that any node can be reached from any other via a path in the network), while below this level the network will consist of multiple components with a probability going to 1.

Other properties of random networks are examined in much more detail in Chapter 4. While it is clear that completely random networks are not always a good approximation for real social and economic networks, the analysis above (and in Chapter 4) shows us that much can be deduced in such models; and that there are some basic patterns and structures that we will see emerging more generally. As we build more realistic models, similar analyses can be conducted.

1.2.4 The Symmetric Connections Model

Although random network formation models give us some insight into the sorts of characteristics that networks might have, and exhibit some of the features that we see in the Add Health social network data, it does not provide as much insight into the Florentine marriage network. There, marriages were carefully arranged. The last example comes from the game-theoretic, economics literature and provides a basis for the analysis of networks that are formed when links are chosen by the agents in the network. Through this example, we can begin to look at the questions about which networks might be best for a society and which networks might arise if the players have discretion in choosing their links.

Figure 1.2.4 ***The utilities to the players in a three-link four-player network in the symmetric connections model.***

It is a simple model of social connections that was developed by Jackson and Wolinsky [343]. In this model, links represent social relationships, for instance friendships, between players. These relationships offer benefits in terms of favors, information, etc., and also involve some costs. Moreover, players also benefit from indirect relationships. A "friend of a friend" also results in some indirect benefits, although of a lesser value than the direct benefits that come from a "friend." The same is true of "friends of a friend of a friend," and so forth. The benefit deteriorates with the "distance" of the relationship. This is represented by a factor δ that lies between 0 and 1, which indicates the benefit from a direct relationship and is raised to higher powers for more distant relationships. For instance, in the network where player 1 is linked to 2, 2 is linked to 3, and 3 is linked to 4: player 1 gets a benefit of δ from the direct connection with player 2, an indirect benefit of δ^2 from the indirect connection with player 3, and an indirect benefit of δ^3 from the indirect connection with player 4. The payoffs to this four players in a three-link network is pictured in Figure 1.2.4.

For $\delta < 1$ this leads to a lower benefit from an indirect connection than a direct one. Players only pay costs, however, for maintaining their direct relationships.[16]

Given a network g,[17] the net utility or payoff $u_i(g)$ that player i receives from a network g is teh sum of benefits that the player gets for his or her direct and indirect connections to other players less the cost of maintaining his or her links. In particular, it is

$$u_i(g) = \sum_{j \neq i:\ i \text{ and } j \text{ are path-connected in } g} \delta^{\ell_{ij}(g)} - d_i(g)c,$$

where $\ell_{ij}(g)$ is the number of links in the shortest path between i and j, $d_i(g)$ is the

[16] In the most general version of the connections model the benefits and costs may be relation specific, and so are indexed by ij. One interesting variation is where the cost structure is specific to some geography, so that linking with a given player depends on their physical proximity. That variation has been studied by Johnson and Gilles [349] and is discussed in Exercise 6.13.

[17] For complete definitions, see Chapter 2. For now, all that is important is that this tells us which pairs of players are linked.

number of links that i has (i's degree), and $c > 0$ is the cost for a player of maintaining a link.

The highly stylized nature of the connections model allows us to begin to answer questions regarding which networks are "best" (most "efficient") from society's point of view, as well as which networks are likely to form when self-interested players choose their own links.

Let us define a network to be *efficient* if it maximizes the total utility to all players in the society. That is, g is efficient if it maximizes $\sum_i u_i(g)$.[18]

It is clear that if costs are very low, it will be efficient to include all links in the network. In particular, if $c < \delta - \delta^2$, then adding a link between any two agents i and j will always increase total welfare. This follows because they are each getting at most δ^2 of value from having any sort of indirect connection between them, and since $\delta^2 < \delta - c$, the extra value of a direct connection between them increases their utilities (and might also increase, and cannot decrease, the utilities of other agents).

When the cost rises above this level, so that $c > \delta - \delta^2$ but c is not too high (see Exercise 1.3), it turns out that the unique efficient network structure is to have all players arranged in a "star" network. That is, there should be some central player who is connected to each other player, so that one player has $n-1$ links and each of the other players has 1 link. The idea behind why a star among all players is the unique efficient structure in this middle cost range, is as follows. A star involves the minimum number of links needed to ensure that all pairs of players are path connected, and it has each player within two links of every other player. The intuition behind this dominating other structures is then easy to see. Suppose for instance we have a network with links between 1 and 2, 2 and 3, and 3 and 4. If we change the link between 3 and 4 to be one between 2 and 4, we end up with a star network. The star network has the same number of links as our starting network, and thus the same cost and payoffs from direct connections. However, now all agents are within two links of each other whereas before some of the indirect connections involved paths of length three. This is pictured in Figure 1.2.4.

As we shall see, this is the key to the set of efficient networks having a remarkably simple characterization: either costs are so low that it makes sense to add links, and then it makes sense to add all links, or costs are so high that no links make sense, or

[18] This is just one of many possible measures of efficiency and societal welfare, which is a well-studied subject in philosophy and economics. How we measure efficiency has important consequences in network analysis and is discussed in more detail in Chapter 6.

Figure 1.2.4 ***The Gain in Total Utility from Changing a "Line" into a "Star".***

costs are in a middle range and the unique efficient architecture is a star network. This characterization of efficient networks being either stars, empty or complete, actually holds for a fairly general class of models where utilities depend on path length and decay with distance, as is shown in detail in Section 6.3.

We can now compare the efficient networks with those that arise if agents form links in a self-interested manner. To capture how agents will act, let us consider a simple equilibrium concept introduced in Jackson and Wolinsky [343]. This concept is called "pairwise stability" and involves checking two things about a network: first, no agent would raise his or her payoff by deleting some link that he or she are directly involved in; and second, no two agents would both benefit by adding a link between themselves. This stability notion captures the idea that links are bilateral relationships and require the consent of both individuals. If some individual would benefit by terminating some relationship that he or she is involved in, then that link would be deleted; while if two individuals would each benefit by forming a new relationship, then that link would be added.

In the case where costs are very low $c < \delta - \delta^2$, as we have already argued, the direct benefit to the agents from adding or maintaining a link is positive, even if they are already indirectly connected. Thus, in that case the unique pairwise stable network will be the efficient one which is the complete network. The more interesting case comes when $c > \delta - \delta^2$, but c is not too high, so that the star is the efficient network.

If $\delta > c > \delta - \delta^2$, then a star network (that involves all agents) will be both pairwise stable and efficient. To see this we need only check that no player wants to delete a link, and no two agents both want to add a link. The marginal benefit to the center

player from any given link already in the network is $\delta - c > 0$, and the marginal benefit to a peripheral player is $\delta + (n-2)\delta^2 - c > 0$. Thus, neither player wants to delete a link. Adding a link between two peripheral players only shortens the distance between them from two links to one, and does not shorten any other paths - and since $c > \delta - \delta^2$ adding such a link would not benefit either of the players. While the star is pairwise stable, in this cost range so are some other networks. For example if $c < \delta - \delta^3$, then four players connected in a "circle" would also be pairwise stable. In fact, as we shall see in Section 6.3, many other (inefficient) networks can be pairwise stable.

If $c > \delta$, then the efficient (star) network will not be pairwise stable, as the center player gets only a marginal benefit of $\delta - c < 0$ from any of the links. This tells us that in this cost range there cannot exist any pairwise stable networks where there is some player who just has one link, as the other player involved in that link would benefit by severing it. For various values of $c > \delta$ there will exist nonempty pairwise stable networks, but they will not be star networks: as just argued, they must be such that each player has at least two links.

This model makes it clear that there will be situations where individual incentives are not aligned with overall societal benefits. While this connections model is highly stylized, it still captures some basic insights about the payoffs from networked relationships and it shows that we can model the incentives that underlie network formation and see when resulting networks are efficient.

This model also raises some interesting questions that we will examine further in the chapters that follow. How does the network that forms depend on the payoffs to the players for different networks? What are alternative ways of predicting which networks will form? What if players can bargain when they form links, so that the payoffs are endogenous to the network formation process (as is true in many market and partnership applications)? Uow does the relationship between the efficient networks and those which form based on individual incentives depend on the underlying application and payoff structure?

1.3 Exercises

EXERCISE **1.1** *A Weighted Betweenness Measure*

Consider the following variation on the betweenness measure in (1.1). Any given shortest path between two families is weighted by inverse of the number of intermediate

Figure 1.3 Differences in Betweenness measures.

nodes on that path. For instance, the shortest path between the Ridolfi and Albizzi involves two links and the Medici are the only family that lies between them on that path. In contrast, between the Ridolfi and the Ginori the shortest path is three links and there are two families, the Medici and Albizzi, that lie between the Ridolfi and Ginori on that path.

More specifically, let ℓ_{ij} be the length of the shortest path between nodes i and j and let $W_k(ij) = P_k(ij)/(\ell_{ij} - 1)$, (setting $\ell_{ij} = \infty$ and $W_k(ij) = 0$ if i and j are not connected). Then the weighted betweenness measure for a given node k be defined by

$$WB_k = \sum_{ij:i\neq j, k\notin\{i,j\}} \frac{W_k(ij)/P(ij)}{(n-1)(n-2)/2}. \tag{1.5}$$

where we take the convention that $\frac{W_k(ij)}{P(ij)} = 0/0 = 0$ if there are no paths connecting i and j.

Show that

- $WB_k > 0$ if and only if k has more than one link in a network and some of k's neighbors are not linked to each other,
- $WB_k = 1$ for the center node in a star network that includes all nodes (with $n \geq 3$), and
- $WB_k < 1$ unless k is the center node in a star network that contains all nodes.

Calculate this measure for the the network pictured in Figure 1.3 for nodes 5 and 6.

Contrast this measure with the betweenness measure in (1.1).

Exercise **1.2** *Random networks*

Fix the probability of any given link forming in a Poisson random network to be p where $1 > p > 0$. Fix some arbitrary network g on k nodes. Now, consider a sequence of random networks indexed by the number of nodes n, as $n \to \infty$. Show that the probability that a copy of the k node network g is a subnetwork of the random network on the n nodes goes to 1 as n goes to infinity.

[Hint: partition the n nodes into as many separate groups of k nodes as possible (with some leftover nodes) and consider the subnetworks that end up forming on each of these groups. Using the expression in (1.2) and the independence of link formation, show that the probability that the none of these match the desired network goes to 0 as n grows.]

EXERCISE **1.3** *The Upper Bound for a Star to be Efficient*

Find the maximum level of cost in terms of δ and n, for which a star is an efficient network in the symmetric connections model.

EXERCISE **1.4** *The Connections Model with Low Decay**

Consider the symmetric connections model in a setting where $1 > \delta > c > 0$.

Show that if δ is close enough to 1, so that there is "low decay" and δ^{n-1} is nearly δ, then in every pairwise stable network every pair of players have some path between them and that there are at most $n-1$ total links in the network.

In a case where δ is close enough to 1 so that any network that has $n-1$ links and connects all agents is pairwise stable, what fraction of the pairwise stable networks are also efficient networks?

How does that fraction behave as n grows (adjusting δ to be high enough as n grows)?

EXERCISE **1.5** *Homophily and Balance Across Groups*

Consider a society of two groups, where the set N_1 comprises the members of group 1 and the set N_2 comprises the members of group 2, with cardinalities n_1 and n_2, respectively. Suppose that $n_1 > n_2$. For an individual i, let d_i be i's degree (total number of friends) and let s_i denote the number of friends that i has that are within own group. Let h_k denote a simple homophily index for group k, defined by $h_k = \frac{\sum_{i \in N_k} s_i}{\sum_{i \in N_k} d_i}$. Show that if h_1 and h_2 are both above 0 and below 1, and the average degree in group 1 is at least as high as the average degree in group 2, then $h_1 > h_2$. What are h_1 and h_2 in the case where friendships are formed in percentages that correspond to the relevant populations.

Chapter 2

Representing and Measuring Networks

With some feeling for network analysis under our belts, this chapter presents some of the fundamentals of how networks are represented, measured and characterized. This provides basic concepts and definitions that are the basis for the language of network research. Sprinkled throughout are some observations from case studies that illustrate some of the concepts. More discussion about observed social and economic networks appears in Chapter 3.

2.1 Representing Networks

As networks of relationships come in many shapes and sizes, there is no single way of representing networks that will encompass all applications. Nevertheless, there are some representations that serve as a useful basis for capturing many applications. Here I focus on a few standard ways of denoting networks that are broad and flexible enough to capture a multitude of applications, and yet simple enough to be compact, intuitive, and tractable. As we proceed, I will try to make clear what is being admitted and what is being ruled out.

2.1.1 Nodes and Players

The set $N = \{1, \ldots, n\}$ is the set of *nodes* that are involved in a network of relationships.

Nodes will also be referred to as "vertices," "individuals," "agents," or "players," depending on the setting. It is important to emphasize that nodes might be individual people, firms, countries, or other organizations; or a node might even be something like a web page belonging to some person or organization.

2.1.2 Graphs and Networks

The canonical network form is an undirected graph, where two nodes are either connected or not. This applies to situations where two nodes are either in a relationship with each other or not, but it cannot be that one is related to the second without the second being related to the first. This is generally true of many social and/or economic relationships, such as partnerships, friendships, alliances, acquaintances, etc. This sort of network will be central to most of the chapters that follow. However, there are other situations that we will examine that are better modeled as directed networks, where one node may be connected to a second without the second being connected to the first. For instance, a network that keeps track of which authors cite which other authors, or which web pages have links to which others would naturally take the form of a directed graph.

The distinction between directed and undirected networks is not a mere technicality. It is fundamental to the analysis, as the applications and modeling are quite different. In particular, when links are necessarily reciprocal, then it will generally be the case that joint consent is needed to establish and/or maintain the relationship. For instance, in order to form a trading partnership, both partners need to agree. To maintain a friendship the same is generally true, as is maintaining a business relationship, alliance, etc. In the case of directed networks, one individual may direct a link at another without the other's consent, which is generally true in citation networks or in links between web pages. These distinctions result in some basic differences in the modeling of network formation as well as different conclusions about which networks will arise and which are optimal, etc.

In what follows the default is that the network is undirected and I will be explicit when directed networks are considered. Let us begin with the formal definitions of graphs that represent networks.

A *graph* (N, g) consists of a set of nodes $N = \{1, \ldots, n\}$ and a real-valued $n \times n$ matrix, g, where g_{ij} represents the (possibly weighted and/or directed) relation between i and j. This matrix is often referred to as the *adjacency matrix*, as it lists which nodes

Figure 2.1.2. ***A network with two links.***

are linked to each other, or in other words which nodes are adjacent to one another.[1] In the case where the entries of g take on more than two values, and can keep track of the intensity of level of relationships, the graph is referred to as a *weighted* graph. Otherwise, it is standard to use the values of either 0 or 1, and the graph is *unweighted*.

In much of what follows, N will be fixed or given. As such, I will often refer to g as being a network or graph.

A network is *directed* if it is possible that $g_{ij} \neq g_{ji}$, and a network is *undirected* if it is required that $g_{ij} = g_{ji}$ for all nodes i and j. Parts of the literature refer to directed graphs as *digraphs*.

For instance, if $N = \{1, 2, 3\}$, then

$$g = \begin{pmatrix} 0 & 1 & 0 \\ 1 & 0 & 1 \\ 0 & 1 & 0 \end{pmatrix} \tag{2.1}$$

is the (undirected and unweighted) network where there is a *link* between nodes 1 and 2, a link between nodes 2 and 3, but no link between nodes 1 and 3.

Nodes are also often referred to as *vertices* and links are often referred to as *edges* or *ties*; and as *arcs* in the case of directed graphs.

Self-links or *loops* will often not have any real meaning or consequence, and so whether we set $g_{ii} = 1$ or $g_{ii} = 0$ as a default will most often (but not always!) be irrelevant. Unless otherwise indicated in what follows, assume that $g_{ii} = 0$ for all i.[2]

[1] There are more general graph structures that can represent the possibility of multiple relationships between different nodes; for instance, having different links for being friends, relatives, co-workers, etc. These are sometimes referred to as a multiplex networks. One can also allow for relationships that involve more than two nodes at a time. For example, see Page and Wooders [493] for some more general representations.

[2] Sometimes, graphs without any self-links (and without multiple links) are referred to as *simple graphs*. Here unless, unless otherwise stated, the term graph refers to a simple graph. If self-links and multiple links between nodes are permitted, the resulting structure is termed a *multigraph*.

There are equivalent ways of representing a graph. Instead of viewing g as an $n \times n$ matrix, it is sometimes easier to describe a graph by listing of all the links or edges that are in the graph. That is, we can then view a graph as a pair (N, g), where g is the a collection of links which are just listed as a subsets of N of size 2. So, for instance, the network g in (2.1) can equivalently be written as $g = \{\{1, 2\}, \{2, 3\}\}$, or simplifying notation a bit $g = \{12, 23\}$. So, we write ij to represent the link connecting nodes i and j. Then we can write $ij \in g$ to indicate that i and j are linked under the network g; that is, writing $ij \in g$ is equivalent to writing $g_{ij} = 1$.

I alternate between the different representations as is convenient. It will also be useful to write $g' \subset g$, to indicate that

$$\{ij \ : \ ij \in g'\} \subset \{ij \ : \ ij \in g\}.$$

Let the shorthand notation of $g + ij$ represent the network obtained by adding the link ij to an existing network g, and and let $g - ij$ represent the network obtained by deleting the link ij from the network g.

We can represent directed networks in an analogous manner, viewing ij as a directed link and distinguishing between ij and ji.

Let $G(N)$ be the set of all undirected and unweighted networks on N.

In some cases we will be interested in the exact labels of which nodes are in which positions in a network, and in other situations we will just care about the structure of the network. The idea that two networks or graphs are have the same structure is captured through the concept of an isomorphism. The networks (N, g) and (N', g') are *isomorphic* if there exists a one-to-one and onto function (a bijection) $f : N \to N'$, such that $ij \in g$ if and only if $f(i)f(j) \in g'$. Thus, f just relabels the nodes and the networks are the same up to that relabeling.

Given a subset of nodes $S \subset N$ and a network g, let $g|_S$ denote the network g restricted to the set of nodes S, so that

$$[g|_S]_{ij} \quad = \quad \begin{cases} 1 & \text{if } i \in S, j \in S, g_{ij} = 1, \text{ and} \\ 0 & \text{otherwise.} \end{cases}$$

Thus $g|_S$ is the network obtained by deleting all links except those that are between nodes in S. An example is pictured in Figure 2.1.2.

Figure 2.1.2 A Network and the Network Restricted to $S = \{1, 2, 5\}$

For any network g, let $N(g)$ be the set of nodes that have at least one link in the network g. That is, $N(g) = \{i \mid \exists j \text{ s.t. } ij \in g, \text{ or } ji \in g\}$.[3]

2.1.3 Paths and Cycles

Much of the interest in networked relationships comes from the fact that individual nodes benefit (or suffer) from indirect relationships. Friends might provide access to favors from their friends and information might spread through the links of a network. In order to capture the indirect interactions in a network, it is important to model paths through a network. In the case of an undirected network, a path is an obvious object. As there are multiple definitions in the case of a directed network, I return to those after providing definitions for an undirected network.

A *path* in a network $g \in G(N)$ between nodes i and j is a sequence of links $i_1 i_2, \ldots, i_{K-1} i_K$ such that $i_k i_{k+1} \in g$ for each $k \in \{1, \ldots, K-1\}$, with $i_1 = i$ and $i_K = j$, and such that each node in the sequence $i_1, \ldots, i_K$ is distinct.[4] A *walk* in a

[3]Here it matters whether $g_{ii} = 1$, in which case $i \in N(g)$, or whether $g_{ii} = 0$, in which case $i \notin N(g)$.

[4]A path may also be defined to be a subnetwork, so that it consists of the set of involved nodes

network $g \in G(N)$ between nodes i and j is a sequence of links $i_1 i_2, \ldots, i_{K-1} i_K$ such that $i_k i_{k+1} \in g$ for each $k \in \{1, \ldots, K-1\}$, with $i_1 = i$ and $i_K = j$.

The distinction between a path and a walk is whether all the involved nodes are distinct. A walk may come back to a given node more than once, whereas a path is a walk that never hits the same node twice.[5]

A *cycle* is a walk $i_1 i_2, \ldots, i_{K-1} i_K$ that starts and ends at the same node (so $i_1 = i_K$), and such that all other nodes are distinct ($i_k \neq i_{k'}$ when $k < k'$ unless $k = 1$ and $k' = K$). Thus, a cycle is a walk such that the only node that appears more than once is the starting/ending node.

A cycle can be constructed from any path by adding a link from the end to the starting node; and conversely, deleting the first or last link of a cycle results in a path.

A *geodesic* between nodes i and j is a shortest path between these nodes; that is, a path with no more links than any other path between these nodes.

To briefly summarize:

- A walk is a sequence of links connecting a sequence of nodes.
- A cycle is a walk that starts and ends at the same node, with all nodes appearing once except the starting node which also appears as the ending node.
- A path is a walk where a node appears at most once in the sequence.
- A geodesic between two nodes is a shortest path between them.

Note that if we follow the convention of setting $g_{ii} = 0$, then $g^2 = g \times g$ tells us how many walks there are of length 2 between any two nodes.

For instance if we start with a network

$$g = \begin{pmatrix} 0 & 1 & 1 & 0 \\ 1 & 0 & 0 & 1 \\ 1 & 0 & 0 & 1 \\ 0 & 1 & 1 & 0 \end{pmatrix},$$

and the set of links.

[5] The definition of path here is the standard one from the graph theory literature. In some of the network literature, the term path is used more loosely and is actually that of a "walk," so that nodes can be visited more than once. This can cause some confusion, which the reader should be aware of when reading the broader literature.

then g^2 is

$$g^2 = \begin{pmatrix} 2 & 0 & 0 & 2 \\ 0 & 2 & 2 & 0 \\ 0 & 2 & 2 & 0 \\ 2 & 0 & 0 & 2 \end{pmatrix}.$$

So, for instance there are two walks between 1 and 4 of length 2 (passing between 2 and 3, respectively). There are two walks from 1 back to 1 (passing through 2 and 3, respectively). Then g^3 is

$$g^3 = \begin{pmatrix} 0 & 4 & 4 & 0 \\ 4 & 0 & 0 & 4 \\ 4 & 0 & 0 & 4 \\ 0 & 4 & 4 & 0 \end{pmatrix}$$

There are four walks of length 3 between 1 and 2 (namely, (12,24,42), (13,34,42), (12,21,12), and (13,31,12)). Note that we are seeing walks that have some cycles in them (and hence the use of the term "walk" rather than "path"). The k-th power of the network, g^k, keeps track of all possible walks of length k between any two nodes, including walks with many cycles within them.

2.1.4 Directed Paths, Walks, and Cycles

In the case of directed networks, there are different possible definitions of paths and cycles. The definitions depend on whether we want to keep track of the direction of the links or not, and in various applications will depend on whether things like communication are restricted only to follow the direction of the links or can move in both directions along a directed link, as for example in a network of links between web pages.

In the case where direction is important, the definitions are just as stated above for undirected networks, but where the ordering of the nodes in each link now takes on an important role. For instance, we might be interested in knowing whether one can find one web page from another by following (directed) links starting from one page and leading to the other. In that case, I will refer to directed paths, directed walks, and directed cycles.

A *directed walk* in a network $g \in G(N)$ is a sequence of links $i_1 i_2, \ldots, i_{K-1} i_K$ such that $i_k i_{k+1} \in g$ (that is, $g_{i_k i_{k+1}} = 1$) for each $k \in \{1, \ldots, K-1\}$.

Figure 2.1.4 A Directed Path from 2 to 4 (via 1 and 3); a Directed Cycle from 1 to 3 to 2 to 1; and a Directed Walk from 3 to 2 to 1 to 3 to 4.

A *directed path* in a directed network $g \in G(N)$ from node i to node j is a sequence of links $i_1 i_2, \ldots, i_{K-1} i_K$ such that $i_k i_{k+1} \in g$ (that is, $g_{i_k i_{k+1}} = 1$) for each $k \in \{1, \ldots, K-1\}$, with $i_1 = i$ and $i_K = j$, and such that each node in the sequence $i_1, \ldots, i_K$ is distinct.

A *directed cycle* in a network $g \in G(N)$ is a sequence of links $i_1 i_2, \ldots, i_{K-1} i_K$ such that $i_k i_{k+1} \in g$ (that is, $g_{i_k i_{k+1}} = 1$) for each $k \in \{1, \ldots, K-1\}$, with $i_1 = i_K$.

These definitions are illustrated in Figure 2.1.4.

In cases where the direction of the link just indicates who initiated the link, but where links can conduct in both directions, we can keep track of undirected paths. There we think of i and j being linked if either $g_{ij} = 1$ or $g_{ji} = 1$. In that case, we can simply define the undirected network that comes from considering i and j to be linked if there is a directed link in either direction. In general, I will refer to such paths, walks, and cycles as "undirected".

To be more specific, given a directed network g let $\widehat{g}$ denote the undirected network obtained by allowing an (undirected) link to be present whenever there is a directed link present in g. That is, let $\widehat{g}_{ij} = \max(g_{ij}, g_{ji})$. Then we say that there is an *undirected path* between nodes i and j in g if there is a path between them in $\widehat{g}$. Similarly, we

define an undirected cycle or walk.

In Figure 2.1.4 there is no directed path from node 4 to any other node, but there is an undirected path from node 4 to each of the other nodes.

2.1.5 Components and Connected subgraphs

An important thing to keep track of in many applications of networks is which nodes can reach which other nodes through paths in the network. This plays a critical role in things like contagion, learning, and the diffusion of various behaviors through a social network. Looking at the path relationships in a network naturally partitions a network into different connected subgraphs that are commonly referred to as components. Again, definitions are first provided for undirected networks, and later for directed networks.

A network (N, g) is *connected* (or path-connected) if every two nodes in the network are connected by some path in the network. That is, (N, g) is connected if for each $i \in N$ and $j \in N$ there exists a path in (N, g) between i and j.

A *component* of a network (N, g), is a nonempty subnetwork (N', g') such that $\emptyset \neq N' \subset N$, $g' \subset g$, and

- (N', g') is connected, and
- if $i \in N'$ and $ij \in g$, then $j \in N'$ and $ij \in g'$.

Thus, the components of a network are the distinct maximal connected subgraphs of a network. In the network below there are four components: the node 2 together with an empty set of links, the nodes $\{1, 3, 4, 5\}$ together with links $\{15, 35, 34, 45\}$, the nodes 6 and 10 together with the link $6, 10$, and the nodes $\{7, 8, 9\}$ together with the links $\{78, 79, 89\}$.

Note that under this definition of component, a completely isolated node that has no links is considered a component.[6]

The set of components of a network (N, g) is denoted $C(N, g)$. In cases where N is fixed or obvious, I use a notation where components are simply denoted $C(g)$. The component containing a specific node i is denoted $C_i(g)$.

Components of a network partition the nodes into groups within which nodes are path-connected. Let $\Pi(N, g)$ denote the partition of N induced by the network (N, g).

[6] This is a matter of convention, and one can also find definitions of components that only allow for subnetworks with links.

Figure 2.1.5. *A network with four components.*

That is, $S \in \Pi(N, g)$, if and only if $(S, h) \in C(N, g)$ for some $h \subset g$. For example, the network in Figure 2.1.5 induces the partition $\Pi(N, g) = \{\{1, 3, 4, 5\}, \{2\}, \{6, 10\}, \{7, 8, 9\}\}$ over the set of nodes.

So, a network is connected if and only if it consists of a single component (and so $\Pi(N, g) = \{N\}$).

A link ij is a *bridge* in the network g if $g - ij$ has more components than g.[7]

In the case of a directed network, there are again several different approaches. One ways is to again work by ignoring the directed nature of links, and to consider the undirected network that has a link present if one is present in either direction. This defines one notion of connection and components. In some applications, where direction is important, for instance in the transmission of information, we will want to keep track of the directed nature of the network. In such cases, I will refer to *strongly connected* graphs or subgraphs, so that each node can reach each other via a directed path. Further definitions are specified as needed in what follows.

[7] There are variations on this definition, with some requiring that the components that are connected by the bridge both involve more than one node.

Figure 2.1.6 Four Trees in a Forest

2.1.6 Trees, Stars, Circles, and Complete Networks

There are a few particular network structures that are commonly referred to.

A *tree* is a connected network that has no cycles.

A *forest* is a network such that each component is a tree. Thus any network that has no cycles is a forest, as in the example pictured in Figure 2.1.6.

A particularly prominent forest network is a star. A *star* is a network such that there exists some node i such that every link in the network involves node i. In this case i is referred to as the *center* of the star.

There are a few facts about trees that are easy to derive (see Exercise 2.2) and worth mentioning.

- A connected network is a tree if and only if it has $n - 1$ links.
- A tree has at least two leaves, where leaves are nodes that have exactly one link.
- In a tree, there is a unique path between any two nodes.

The *complete network* is one where all possible links are present, so one where where $g_{ij} = 1$ for all $i \neq j$.

Figure 2.1.6 A Complete Network on Six Nodes and a Star Network on Six Nodes

A *circle* (also known as a cycle-graph) is a network that has a single cycle and such that each node in the network has exactly two neighbors.

In the case of directed networks, there can be many different stars involving the same set of nodes and having the same center, depending on which directed links are present between any two linked nodes. On occasion, it will be useful to distinguish between these.

2.1.7 Neighborhood

The *neighborhood of a node* i is the set of nodes that i is linked to.[8]

$$N_i(g) = \{j : g_{ij} = 1\}.$$

[8]Note that whether i is in i's neighborhood depends on whether or not we have allowed $g_{ii} = 1$. As I am following a default convention of $g_{ii} = 0$, i will generally not be considered to be in i's neighborhood. This ensures that i's degree is the number of other nodes that i is linked to, which is then the cardinality i's neighborhood.

Given some set of nodes S, the *neighborhood of* S is the union of the neighborhoods of its members. That is

$$N_S(g) = \bigcup_{i \in S} N_i(g) = \{j : \exists i \in S, g_{ij} = 1\}.$$

We can also talk about extended neighborhoods of a node, for instance of all the nodes that can be reached by paths of no more than length 2, etc. The *two-neighborhood of a node* i is

$$N_i^2(g) = N_i(g) \cup \left(\bigcup_{j \in N_i(g)} N_j(g) \right)$$

Inductively, all the nodes that can be reached from i by paths of length no more than k is the *k-neighborhood* of i, which can be defined by

$$N_i^k(g) = N_i(g) \cup \left(\bigcup_{j \in N_i(g)} N_j^{k-1}(g) \right).$$

Similar definitions of k-neighborhoods hold for any set of nodes S, so that $N_S^k(g) = \cup_{i \in S} N_i^k(g)$ is the set of nodes that can be reached from some node in S by a path of length no more than k.

Generally when referring to the *extended neighborhood* of a node i, that is all of the nodes it is path connected to or $N_i^n(g)$.

The above definitions also work for directed networks, where then the interpretation is that the nodes in $N_i^k(g)$ are the nodes that can be reached from i via a directed path.

2.1.8 Degree and Network Density

The *degree* of a node is the number of links that involve that node, which is the cardinality of i's neighborhood. Thus, a node i's degree in a network g, denoted $d_i(g)$, is

$$d_i(g) = \#\{j : g_{ji} = 1\} = \#N_i(g).$$

In the case of a directed network, the above calculation would be the *in-degree*. The *out-degree* of node i is the corresponding calculation $\#\{j : g_{ij} = 1\}$. These coincide in the case of an undirected network.

The *density* of a network keeps track of the relative fraction of links that are present, and is simply the average degree divided by $n - 1$.

Figure 2.1.8 A Directed Network on Five Nodes, Node 1 has In-Degree 2 and Out-Degree 4

2.2 Some Summary Statistics and Characteristics of Networks

While a small network can be usefully described directly by its graph g, and can be illustrated easily in a figure, larger networks can be more difficult to envision and describe. Moreover, it is important to be able to compare networks and to classify them according to properties that they exhibit, and thus to have a stable of summary statistics that provide us with meaningful insight into the structure of a network.

2.2.1 Degree Distributions

A fundamental characteristic of a network is its degree distribution. The degree distribution of a network is a description of the relative frequencies of nodes that have different degrees. That is, $P(d)$ is the fraction of nodes that have degree d under a degree distribution P.[9]

[9] P can be a frequency distribution if we are describing data, or it can be a probability distribution if we are working with random networks.

For instance, a *regular* network is one where all nodes have the same degree. A network is *regular of degree* k if $P(k) = 1$ and $P(d) = 0$ for all $d \neq k$. Such a network is quite different from the random network we described in Section 1.2.3, where there is a great deal of heterogeneity in the degrees of nodes and the distribution is a Poisson distribution.

Beyond the degenerate degree distribution associated with a regular network, and the Poisson degree distribution associated with Poisson random networks that we saw in Section **??**, another prominent degree distribution is what is referred to as a "scale-free" degree distribution. These distributions date to Pareto [501], and appear in a wide variety of settings ranging from incomes , to word usage, to city populations, to degrees in networks (as is discussed in more detail in Chapter 3).[10]

A *scale-free distribution* (or power distribution) $P(d)$ satisfies[11]

$$P(d) = cd^{-\gamma}, \tag{2.2}$$

where $c > 0$ is a scalar (which depends on the support of the distribution).[12] This means that if we increase the degree by a factor k, then we end up with a frequency that goes down by a factor of $k^{-\gamma}$. As this is true regardless of the starting degree d, it means that relative probabilities of degrees of a fixed relative ratio are the same regardless the scale of those degrees. That is, $P(2)/P(1)$ is the same as $P(20)/P(10)$. Hence, the term scale-free.

Scale-free distributions are often said to exhibit a *power law*, with reference to the power function $d^{-\gamma}$.

Generally, given a degree distribution P, let $\langle d \rangle_P$ denote the expected value of d, and $\langle d^2 \rangle_P$ denote the expectation of the square of the degree, etc. I will often omit the $_P$ notation when P is fixed.

Such distributions have "fat tails." That is, there tend to be many more nodes with very small and very large degrees than one would see if the links were formed completely independently so that degree followed a Poisson distribution. We can see this comparison in the following plots of these degree distributions when the average degree is ten (comparing the Poisson degree distribution from (1.4) with the secale free distribution from (2.2)) :

[10] For an informative overview, see Mitzenmacher [446].

[11] One has to be careful about defining the value at $d = 0$, as it might not be well defined; so let us keep track of nodes with degree at least 1.

[12] When the support is $\{1, 2, \ldots\}$, then the scalar is the inverse of what is known as the Riemann Zeta Function, $z(\gamma) = \sum_{d=1}^{\infty} \frac{1}{d^\gamma}$.

Figure 2.2.1. Comparing a Scale-Free Distribution to a Poisson Distribution

We can easily see the fatter tail of the scale-free distribution in the lower tail (for lower degrees), while for higher degrees it is harder to see the differences. If we convert the plot to a log-log plot (that is, we plot the log(frequency) versus the log(degree) instead of the raw numbers), then the differences in the upper tail (for higher degrees) become more evident:

Figure **??** also points out another interesting aspect of scale-free distributions: they are linear when plotted on a log-log plot. That is, we can rewrite (2.2) by taking logs of both sides to obtain:

$$log(f(d)) = log(c) - \gamma log(d).$$

This is useful in trying to estimate γ from data, as then linear regression can be used.

2.2.2 Diameter and Average Path Length

The *distance* between two nodes is the length of (number of links in) the shortest path or *geodesic* between them. If there is no path between the nodes, then the distance between them is infinite.

Figure ?? Comparing a Scale-Free Distribution to a Poisson Distribution: LOG-LOG Plot

This leads us to another important characteristic of a network: namely its diameter. The *diameter* of a network is the largest distance between any two nodes in the network.[13]

To see how diameter can vary across networks with the same number of nodes and links, consider two different networks where each node has on average two links as in Figure 2.2.2 - the first network is a circle and the second is a tree.

Despite the fact that both networks have an average degree of 2, they are very clearly different in structure. The degree distribution picks up some aspect of the difference in that the circle is regular so that every node has exactly two links, while in the binary tree (almost) half of the nodes have degree 3 and (almost) half of the nodes have degree 1 (the exception is the root node that has degree exactly 2). However, we need other measures to pick up clear differences in these networks. For instance, the

[13]Related measures, working with cycles rather than paths, are the girth and circumference of a network. The *girth* is the length of the smallest cycle in a network (set to infinity if there are no cycles), and the *circumference* is the length of the largest cycle (set to zero if there are no cycles).

Figure 2.2.2. Circle and Tree

diameter of a circle of n nodes is either $n/2$ or $(n-1)/2$, while the diameter of a binary tree of n nodes is roughly $2log_2(n+1)$.[14]

While the diameter is one measure of path length, it only provides an upper bound on path length. *Average path length* (also referred to as "characteristic path length") between nodes is another measure that captures related properties. The average is taken over geodesics, or shortest paths. Clearly, the average path length will be bounded above by the diameter; and in some cases can be much shorter than the diameter. Thus, it is often useful to see whether the diameter is being determined by a few outliers (literally), or whether it is of the same order as the average geodesic.

Many networks are not fully connected, and may consist of a number of separate components. In such cases, one often reports the diameter and average path length within the largest component, being careful to specify whether or not that component is a "giant" component (containing a non-trivial fraction of nodes).[15]

[14] This holds precisely if there is an integer K so that $n = 2^K - 1$ in the case of a binary tree.

[15] There is a way to circumvent these problems. As Newman [480] suggests, the measure $\frac{n(n+1)}{2\sum_{ij}\frac{1}{\ell(i,j,g)}}$, where $\ell(i,j,g)$ is the length of the shortest path between i and j in g and is set to infinity if the nodes are not connected. This can be calculated regardless of component structure. So rather than averaging path lengths, one looks at the reciprocal of the average of the reciprocal path lengths. Taking the

Recalling that raising the adjacency matrix g to a power k provides as its ij-th entry the number of walks of length k between nodes i and j, we can easily calculate shortest path lengths. That is, the shortest path length between nodes i and j can be found by finding the smallest ℓ such that the ij-th entry g^ℓ is positive, and then that entry is the number of shortest paths between those nodes. This same calculation provides shortest directed paths in the case of directed networks. Calculating shortest path lengths for all pairs of nodes, through successive powers of the adjacency matrix g, then provides a basic method of calculating diameter. There are more computationally efficient algorithms for calculating or estimating diameter,[16] and most network software programs include such calculations as built-in features.

2.2.3 Cliquishness, Cohesiveness, and Clustering

One fascinating and important aspect of social networks is how tightly clustered they are. For example, the extent to which my friends are friends with each other captures one facet of this. There are a variety of concepts that measure how cohesive or closely knit a network is.

An early concept related to this is the idea of a clique. A *clique* is a maximal completely connected subnetwork of a given network.[17] That is, if some set of nodes $S \subset N$ are such that $g|_S$ is the complete network on the nodes S, and for any $i \in N \setminus S$ $g|_{S \cup \{i\}}$ is not complete, then the nodes S are said to form a clique.[18] Cliques are generally required to contain at least 3 nodes, otherwise each link could potentially define a clique of two nodes. Note that a given node can be part of several cliques at once. For example, in Figure 2.2.3 both nodes 2 and 3 are in two different cliques.

One measure of cliqueshness is to count the number and size of the cliques of a network. One difficulty with this is that removing one link from a large clique can change the clique structure completely. For instance, removing one link from a complete

reciprocal twice leads to something similar to averaging path lengths directly, but working with the reciprocals eliminates the influence of infinite path lengths.

[16] For instance, there are more efficient ways of calculating powers of g when it is diagonalizable (see Section 2.4.1), and computational efficiency can be important when n is large.

[17] Note the distinction between a clique and a component. A clique must be completely connected and not be a strict subset of any subnetwork that is completely connected, while a component must be path-connected and not be a strict subset of any subnetwork that is path-connected. Neither implies the other.

[18] An early definition of this is from Luce and Perry [**?**].

Figure 2.2.3 A Network on Four Nodes and its Two Cliques

network among four nodes changes the clique structure from having one clique involving four nodes to two cliques of three nodes. More generally, the clique structure is very sensitive to slight changes in a network.

The most common way of measuring some aspect of cliqueshness is based on "transitive triples" or "clustering."[19] Examining undirected networks, the most basic clustering measure is simply to perform the following exercise. Look across all situations where two links both emanate from the same node, so for instance ij and ik both involve node i, and ask what proportion of the time it is that jk is then also in the network. So, if i has relationships with both j and k, how likely on average is it that j and k are related in the network? This clustering measure is represented by

$$Cl(g) = \frac{\sum_i \#\{jk \in g | k \neq j, j \in N_i(g), k \in N_i(g)\}}{\sum_i \#\{jk | k \neq j, j \in N_i(g), k \in N_i(g)\}} = \frac{\sum_{i;j\neq i;k\neq j;k\neq i} g_{ij}g_{ik}g_{jk}}{\sum_{i;j\neq i;k\neq j;k\neq i} g_{ij}g_{ik}}.$$

I will often refer to this as *overall* clustering, in order to distinguish it from the other

[19] Clustering in the way it is used here is a term that has come out of the recent random network literature (e.g., see Newman [480]). "Clustering" has an interesting history as a term, growing out of the earlier sociology literature, based on partitioning signed graphs into subsets where nodes within elements of the partition have only positive relationships between them, and only negative relationships exist across elements of the partition (e.g, see Chapter 6 in Wasserman and Faust [615]).

measures of clustering that follow.

A different measure that has also been used in the literature is similar to the clustering coefficient $Cl(g)$ above, except that instead of considering the fraction of fully connected triples out of the potential triples where at least two links are present, the measure does this on a node-by-node basis, and then averages across nodes. This is based on the following definition of *individual clustering for a node* i:

$$Cl_i(g) = \frac{\#\{jk \in g | k \neq j, j \in N_i(g), k \in N_i(g)\}}{\#\{jk | k \neq j, j \in N_i(g), k \in N_i(g)\}} = \frac{\sum_{j \neq i; k \neq j; k \neq i} g_{ij} g_{ik} g_{jk}}{\sum_{j \neq i; k \neq j; k \neq i} g_{ij} g_{ik}}.$$

Thus, $Cl_i(g)$ looks across all pairs of nodes that are linked to i, and then considers how many of them are linked to each other.[20] Another way to write the individual clustering coefficient is then

$$Cl_i(g) = \frac{\#\{jk \in g | k \neq j, j \in N_i(g), k \in N_i(g)\}}{d_i(g)(d_i(g) - 1)/2}$$

The *average clustering* coefficient is then

$$Cl^{Avg}(g) = \sum_i Cl_i(g)/n.$$

Note that this is a different calculation than the overall clustering coefficient $Cl(g)$, where the average is taken over all triples. Under average clustering, one computes a clustering for each node and then averages across nodes. This gives more weight to low-degree nodes than the clustering coefficient.

As an illustration of these two measures, let us compute them relative to the Florentine Marriage Network pictured in Figure **??**.

To compute the overall clustering coefficient, we first count how many configurations of the form ij, jk there are in the network. For instance, there is one with Barbadori-Medici and Barbadori-Castellan. There are three with the Ridolfi at the center. There are fifteen with the Medici at the center and so forth. Totaling across all such configurations, we find that there are 47 such configurations in the network. Out of those 47 such configurations, 9 of them are completed. Thus, $Cl(g) = 9/47$. In terms of the average clustering, we compute the clustering for each family separately. For instance, the Barbadori have one possible pair and they are not connected, so the Barbadori have $Cl_{Barbadori}(g) = 0/1 = 0$. The Pazzi, Acciaiuol, Ginori, Lambertes, and Pucci are all 0 by convention (they each have one or no links). The Bischeri, Castellan,

[20] A convention is to set $Cl_i(g) = 0$ if i has no more than one link.

Figure 2.2.3. Differences in Clustering Measures

Ridolfi, and Tornabuon each have clustering 1/3. The Strozzi are also 1/3 (2 out of 6). The Peruzzi are 2/3, the Medici 1/15, and the Guadagni and Albizzi have at least two neighbors each, but still have clusterings of 0.[21] When we average across all of these, we get $Cl^{Avg}(g) = .15$ or 3/20. This is a bit less than the overall clustering $Cl(g)$, as we are including a number of 0's in the average clustering.

The above calculations show that it is possible to have these two common measures of clustering differ. While in that example the average clustering is lower than the overall clustering, it can also go the other way. Moreover, it is not hard to generate networks where the two measures can produce very different numbers for the same network. For instance, consider the following variation of a star network. Begin with a large number of triads (complete networks among three nodes), and then add a center node, to which we connect every other node. This is pictured in Figure 2.2.3.

As the number of nodes involved gets large, average clustering goes to 1, while overall clustering goes to 0! To see this note that all of the nodes other than the center

[21] This relates back to the important role of the Medici, as many of their neighbors were not directly connected, but only indirectly through the Medici.

node have individual clustering measures of 1. Thus, when averaging across them we end up with an average clustering coefficient converging to 1. However, with regards to the overall clustering coefficient, each time that a new triad is added the number of possible pairs of links goes up by 2 times how many links the center node already had (plus 3), while the number of those pairs that are completed only goes up by 3. Thus, overall clustering goes to 0.

Clearly, the two different measures of clustering are capturing different things and so there is no "right" or "wrong" measures. This does point out that such simple coefficients cannot give a full picture of the inter-relatedness of a network, but only an impression of some aspect of it.

In the case of directed networks one has further choices with regard to measuring clustering. One option is simply to ignore the direction of a link and consider two nodes to be linked if there is a directed link in either direction between them. Based on this derived undirected network, one can then apply the above measures of overall and average clustering. A different approach is to keep track of the percentage of "transitive triples." This looks at situations where node i has a directed link to j, and j has a directed link to k, and then asks whether i has a directed link to k; which follows the usual notion of "transitivity" of relationships.[22] The percentage of times in a network that the answer is "yes" is the *fraction of transitive triples*. This fraction is represented as follows.

$$Cl^{TT}(g) = \frac{\sum_{i;j\neq i;k\neq j} g_{ij}g_{jk}g_{ik}}{\sum_{i;j\neq i;k\neq j} g_{ij}g_{jk}}.$$

While the above fraction of transitive triples is a standard measure, much of the empirical literature has instead simply ignored the directed nature of relationships.[23]

2.2.4 Centrality

Most of the measures I have discussed to this point are predominately "macro" in nature, that is, they describe broad characteristics of a network. In many cases, we might also be interested in "micro" measures, that allow us to compare nodes and to say something about how a given node relates to the overall network. For instance, as

[22] Alternatively, one could examine the percentage of times that k has a directed link to i so that a directed cycle emerges. This can be a very different calculation depending on the context.

[23] There are also hybrid measures (mixing ideas of directed and undirected links) where one counts the percentage of possible directed links among a node's direct neighbors that are present on average, as in, for example, Adamic's [1] study of the www.

we saw in the Florentine Marriage example in Section 1.2.1, the idea of how central a node is can be very important. In particular, notions that somehow capture a node's position in a network are useful. As such, many different measures of centrality have been developed, and they each tend to capture different aspects of the position that a node has, which can be useful when working with information flows, bargaining power, infection transmission, influence and other sorts of important behaviors on a network.

Measures of centrality can be categorized into four main groups depending on the types of statistics on which they are based. The four main measurements that go into centrality measures are:[24]

1. degree - how connected a node is,
2. closeness - how easily a node can reach other nodes,
3. betweenness - how important a node is in terms of connecting other nodes,
4. neighbors' characteristics - how important, central, or influential a node's neighbors are.

Given how different these notions are, even without looking at formal definitions it is easy to foresee that they will capture complementary aspects of a node's position, and any particular measure will be better suited for some applications and less well suited for others. Let me discuss some of the more standard definitions of each type.

Degree Centrality

Perhaps the simplest measure of the position of a given node in a network is simply to keep track of its degree. A node with degree $n-1$ would be directly connected to all other nodes, and hence quite central to the network. A node connected to only 2 other nodes (for large n) would be, at least in one sense, less central. The *degree centrality* of a node is simply $d_i(g)/(n-1)$, so that it ranges from 0 to 1 and tells us how well a node is connected, in terms of direct connections.

Of course, degree centrality is clearly missing many of the interesting aspects of a network. In particular, it completely misses any aspect of how well located a node is in a network. It might be that a node has relatively few links, but lies in a critical location in the network. For many applications, where the influence or marginal contribution

[24] See Borgatti **??** for more discussion about categorizing measures of centrality.

Figure 2.2.4. A Central Node with Low Degree Centrality

of a node to a network is important, we would prefer to have a centrality measure that would pick this up. For example, consider the network in Figure 2.2.4.

In the network in Figure 2.2.4 the degree of nodes 3 and 5 are three, and the degree of node 4 is only two. Arguably, node 4 is at least as central as nodes 3 and 5, and far more central than the other nodes that each have two links (nodes 1, 2, 6, and 7). There are several senses in which we see a powerful or central role of node 4. If one deletes node 4, the component structure of the network changes. This might be very important if we are thinking about something like information transmission, where node 4 is critical in path-connecting nodes 1 and 7. This will be picked up by a measure such as betweenness. We also see that node 4 is relatively close to all of the other nodes, in that it is at most two links away from any other node, whereas each other node has at least one node at a distance of three or more. This would be important in applications where something is being conveyed or transmitted through the network (say an opinion or favor) and there is a decay of the strength with distance. In that case, being closer can either help a node make use of other nodes (e.g., having access to favors) or to have influence (e.g., conveying opinions). This brings us to the

next category of centrality measures.

Closeness Centrality

This second class of measures keeps track of how close a given node is to each other node. One obvious "closeness"-based measure is just the inverse of the average distance between i and any other node: $(n-1)/\sum_{j\neq i}\ell(i,j)$, where $\ell(i,j)$ is the number of links in the shortest path between i and j. There are various conventions for handling networks that are not connected, as well as other possible measures of distance, which leads to a whole family of closeness measures.

A richer way of measuring centrality based on closeness is to consider a decay parameter δ, where $1 > \delta > 0$ and then consider the proximity between a given node and each other node weighted by the decay. In particular, let the *decay centrality* of a node be defined as

$$\sum_{j\neq i}\delta^{\ell(i,j)},$$

where $\ell(i,j)$ is set to infinity if i and j are not path-connected. This is a centrality measure that is related to the symmetric connections model of Jackson and Wolinsky [343], as it is just the benefit that a node gets in that model of a network.

As δ gets close to one, it is easy to see that decay centrality measures how large a component a node lies in. As δ gets close to 0, then decay centrality gives infinitely more weight to closer nodes than farther nodes, so it becomes proportional to degree centrality. For intermediate values of δ, a node is rewarded for how close it is to other nodes, but in a way that very distant nodes are weighted less than closer nodes.

Betweenness Centrality

A measure of centrality that is based on how well situated a node is in terms of the paths that it lies on, was first proposed by Freeman [237], and we first discussed it in Section **??** in the context of the Florentine marriages (see (**??**).

Letting $P_i(kj)$ denote the number of geodesics (shortest paths) between k and j that i lies on, and $P(kj)$ the total number of geodesics between k and j, we get an idea of how important i is in terms of connecting k and j by looking at the ratio $P_i(kj)/P(kj)$. If this is close to 1, then i lies on most of the shortest paths connecting k to j, while if this is close to 0, then i is less critical to k and j. Averaging across all

pairs of nodes, the *betweenness centrality* of a node i is

$$Ce_i^B(g) = \sum_{k \neq j : i \notin \{k,j\}} \frac{P_i(kj)/P(kj)}{(n-1)(n-2)/2}$$

When we examine the network in Figure 2.2.4 with respect to betweenness centrality, we find that $Ce_4^B(g) = 9/15$, $Ce_3^B(g) = 8/15$, and $Ce_1^B(g) = 0$. This makes it clear that nodes 3, 4 and 5 are much more central than the other nodes, and that 4 is the most "central" node in terms of connecting the other pairs of nodes.

Prestige, Power, and Eigenvector Related Centrality Measures

Beyond these fairly direct measures of centrality, there are more intricate ones. One of the more elegant, both mathematically and in terms of the ideas that it captures, is a notion developed by Bonacich [84]. Bonacich's measure is based on ideas that trace back to Seeley [**?**], Katz [361], and earlier work of Bonacich [83], and it is useful to start by discussing those ideas. These measures are based on the premise that a node's importance is determined by how important its neighbors are. That is, we might like to not only account for the fact that a node is connected or close to many other nodes, but that it is close to many other "important" nodes. This notion is central to citation rankings and things like Google page rankings. The difficulty is that such a measure becomes self-referential. The centrality of a node depends on how central its neighbors are, which depends on the centrality of their neighbors, and so forth. There are various approaches to dealing with this issue this is a nice application of some basic ideas from matrix algebra and fixed point theory.

Define the *Katz prestige* of a node i, denoted $P_i^K(g)$, to be a sum of the prestige of i's neighbors divided by their respective degrees. Here I am using the term "prestige" to keep with the original, but one can also think of this as a way to measure "centrality." So, i gains prestige from having a neighbor j who has high prestige. However, this is corrected by how many neighbors j has, so that as j has more relationships then i gets less prestige from being connected to j, all else held equal. This correction for the number of relationships that j has might be thought of as correcting for the relative access or time that i gets to spend with j. That is, the Katz prestige of a node i is

$$P_i^K(g) = \sum_{j \neq i} g_{ij} \frac{P_j^k(g)}{d_j(g)}. \tag{2.3}$$

This is a self-referential definition, so it is not immediately obvious that it is uniquely

(or always) defined. It does provide us with a series of equations and unknowns, so in principle is solvable. We can see this as follows.

Let $\widehat{g}_{ij} = g_{ij}/d_j(g)$, be the normalized adjacency matrix g so that the sum across any (non-zero) *column* is normalized to 1.[25] The relationship in (2.3) can then be rewritten as

$$P^K(g) = \widehat{g}P^K(g), \tag{2.4}$$

or

$$(I\!I - \widehat{g})P^K(g) = 0, \tag{2.5}$$

where P^K is written as a $n \times 1$ vector, and $I\!I$ is the identity matrix.

So, calculating the Katz Prestige associated with the nodes of a given network reduces to finding the unit eigenvector of $\widehat{g}$, which is a standard calculation (see Section 2.4 for background on eigenvectors). Note that the Katz Prestige is only determined up to a scale factor, so that if $P^K(g)$ solves (2.4) and (2.5) then so does cP^K for any scalar c.

Katz Prestige turns out to be more novel in directed networks than undirected ones. If indegree is the same as outdegree for every node, then it is easy to check that the solution to (2.4) is the list of nodes' degrees (or any rescaling of them), so that $[P^K(g)]_i = d_i(g)$. This provides a justification of degree centrality but not a new measure. In the case of a directed network, the normalization in $\widehat{g}_{ij} = g_{ij}/d_j(g)$ is generally by indegree, so that columns still sum to 1, with the interpretation that directed links to a given node have equal access to that node. In that case, the measure of Katz prestige differs from indegree and outdegree.[26]

When applied to the network in Figure 2.2.4, the Katz Prestige is the degree $P_4^K(g) = 2$, $P_3^K(g) = 3$, and $P_1^K(g) = 2$. This gives more "prestige" to the nodes 3 and 5 than to the middle node 4, which ends up with the same prestige as nodes 1,2,6 and 7. Here we see the importance of the weighting in the Katz-Prestige calculation. The middle node 4 is linked to two prestigious nodes, but only gets 1/3 of their time each. So its prestige is $(3)/3 + (3)/3 = 2$. Nodes 3 and 5 are linked to three nodes each. Although each of these three nodes is less prestigious, 3 and 5 get 1/2 of each of their weight (so $2/2 + 2/2 + 2/2 = 3$).

A variation on this idea that avoids boiling down to degree centrality is where one does not normalize the network of relations g, is what is known as *eigenvector*

[25] Let 0/0=0, so that if $d_j(g) = 0$, then set $\widehat{g}_{ij} = 0$.

[26] However, if one normalizes by outdegree, then the measure will be outdegree.

centrality,[27] and was proposed by Bonacich [83]. Letting $C^e(g)$ denote the eigenvector centrality associated with a network g, the idea is that the centrality of a node is proportional to the sum of the centrality of its neighbors. Thus, we write $\lambda C_i^e(g) = \sum_j g_{ij} C_j^e(g)$. In terms of matrix notation,

$$\lambda C^e(g) = gC^e(g), \tag{2.6}$$

where λ is a proportionality factor. Thus, $C^e(g)$ is an eigenvector of g, and λ is its corresponding eigenvalue. Given that it generally makes sense to look for a measure where these are nonnegative, the standard convention is to look for the eigenvector associated with the largest eigenvalue, which is nonnegative here.[28]

Note that the definition of eigenvector centrality also works for weighted and/or directed networks, without any changes to the expressions. Thus, one can think of the Katz Prestige as a form of eigenvector centrality when we have adjusted the network adjacency matrix to be weighted.

Katz [361] also introduced another way of keeping track of the power or prestige of a node. The idea is based on presuming that the power or prestige of a node is simply a weighted sum of the walks that it has emanating from it. A walk of length 1 is worth a, a walk of length 2 is worth a^2, and so forth, for some parameter $0 < a < 1$. This gives higher weights to walks of shorter distance, in a similar way as in the connections model. So, it is a way of looking at all of the walks from some given node to other nodes in the network and weighting them by distance.

Note that $g\ \mathbb{1}$ (where $\mathbb{1}$ is the $n \times 1$ vector of 1's) is the vector of degrees of nodes, which tells us how many walks of length 1 emanate from each node. Based on what we saw in Section **??**, $g^k\ \mathbb{1}$ is the vector where each entry is the total number of walks of length k that emanate from each node. Thus, the vector of the power of nodes, or prestige of nodes, can be written as

$$P^{K2}(g,a) = ag\ \mathbb{1} + a^2g^2\ \mathbb{1} + a^3g^3\ \mathbb{1} \cdots \tag{2.7}$$

We can rewrite this as

$$P^{K2}(g,a) = \left(1 + ag + a^2g^2 \cdots\right) ag\ \mathbb{1}. \tag{2.8}$$

For small enough $a > 0$, this is finite and then can be expressed as[29]

$$P^{K2}(g,a) = (\mathbb{I} - ag)^{-1}\, ag\ \mathbb{1}. \tag{2.9}$$

[27] Again, see Section 2.4 for background on eigenvectors.

[28] See Section 2.4.

[29] From (2.8), if $P^{K2}(g,a)$ is finite then it follows that $P^{K2}(g,a) - agP^{K2}(g,a) = ag\ \mathbb{1}$ or $(\mathbb{I} -$

Another way to interpret (2.8) is to note that we can start by assigning some base value of $ad_i(g)$ to node i. This is expressed as the vector $ag\ \mathbb{1}$. Then a given node gets its base value, plus a times the base value of each node it has a direct link to, plus a^2 times the base value of each node that it has a walk of length 2 to and weighted by the number of walks to the given node, plus a^3 times the base value of each node it has a walk of length 3 to, and so forth.

The measure introduced by Bonacich can be thought of as a direct extension of the above measure of power or prestige. This is often called "Bonacich Centrality," and can be expressed as

$$Ce^B(g, a, b) = (\mathbb{I} - bg)^{-1} ag\ \mathbb{1}, \tag{2.10}$$

where $a > 0$ and $b > 0$ are scalars, and b is sufficiently small so that (2.10) is well defined. [30]

Bonacich centrality can be thought of as a variation on the second prestige measure of Katz, where again we start with base values of $ad_i(g)$ for each node, but then we evaluate walks of length k to other nodes by a factor of b^k times the base value of the end node, allowing b to differ from a. So b is a factor that captures how the value of being connected to someone decays with distance, while a captures the base value on each node. In the case where $b = a$, the two measures clearly coincide.

Normalizing $a = 1$, we can calculate the Bonacich centrality of the network in Figure 2.2.4 for a couple of values of b, which are listed in Table 2.1 along with other centrality measures for the same network.

Degree centrality favors nodes 3 and 5, but treats nodes 1,2,6,7 and 4 similarly, and so seems to miss some aspects of the structure of the network. Closeness provides differences among the three types of nodes, favoring node 4, which is similar to Betweenness centrality, but with less spread. Decay centrality treats nodes 3, 4, and 5 as being more central than 1,2,6, and 7 for any δ, but the relative rankings of 3 and 5 relative to 4 depends on δ. With a lower δ it looks more like degree centrality and favors nodes 3 and 5, while for higher δ it looks more like closeness or betweenness and favors node 4. The eigenvector centalities and self-referential defintions of Bonacich

$ag)P^{K2}(g, a) = ag\ \mathbb{1}$. A sufficient condition for this to be finite is that a be smaller than 1 over the norm of the largest eigenvalue of g; and for this it is sufficient that a be smaller than 1 over the maximum degree of any agent.

[30] Note that the scalar a is no longer relevant, as it simply multiplies all of the terms. It is only useful in comparing back to the corresponding Katz measure. This is not to say that the Bonacich measure is the same as that of Katz, as being able to change b without forcing a to adjust in the same manner can lead to important differences.

Table 2.1: Centrality Comparisons for Figure 2.2.4

	Nodes 1,2,6,7	Nodes 3 and 5	Node 4
Degree (and Katz Prestige P^K)	.33	.50	.33
Closeness	.40	.55	.60
Decay Centrality ($\delta = .5$)	1.5	2.0	2.0
Decay Centrality ($\delta = .75$)	3.1	3.7	3.8
Decay Centrality ($\delta = .25$)	.59	.84	.75
Betweenness	0.0	.53	.60
Eigenvector Centrality	.47	.63	.54
Katz Prestige-2 P^{K2}, $a = 1/3$	3.1	4.3	3.5
Bonacich Centrality $b = 1/3$, $a = 1$	9.4	13	11
Bonacich Centrality $b = 1/4$, $a = 1$	4.9	6.8	5.4

and Katz Prestige-2 all favor nodes 3 and 5, to varying extents. As b gets lower it favors closer connections and favors higher degree nodes, while for higher b longer paths become more important.

While these are some measures of centrality, and ones that I sometimes refer to in what follows, they are certainly not the only measures of centrality, and it is clear from the above that the measures capture different aspects of the positioning of the nodes. Given how complex networks can be, it is not surprising that there are many different ways of viewing position, centrality, or power within a network.

2.3 Appendix: Some Basic Graph Theory

Here I present some basic results in graph theory that will be useful in other chapters.[31]

2.3.1 Hall's theorem and Bipartite Graphs

A *bipartite* network (N, g) is one where one can partition the set of nodes N into two sets A and B, such that if a link ij is in g then one of the nodes comes from A and the other comes from B. A bipartite networ is pictured in Figure 2.3.1.

[31] Excellent texts on graph theory are Bollobás [79] and Diestel [**?**].

Figure 2.3.1 A Bipartite Network

This is often referred to as a "matching" setting (and in some cases a "marriage market"), where one group is referred to as "women" and the other as "men." It has applications to markets, where for instance one of the sets consists of buyers and the other of sellers, as well as things such as the assignment of students to schools, researchers to labs, and so forth. (See Roth and Sotomayor [**?**] for an overview of the matching literature.)

One interpretation of a bipartite graph in a matching setting is that it represents the potential relationships that might occur. The object is then often to determine a matching for some set of nodes, say $S \subset A$, which is a pairing of the nodes in S with nodes in B, such that each node in S is assigned to a distinct node of B and the pairings are feasible as defined by g. That is, a matching for $S \subset A$ relative to g is a mapping $\mu : S \to B$ such that $i\mu(i) \in g$ for each $i \in S$ and $j \neq i$ implies $\mu(j) \neq \mu(i)$.

It is clear that if we wish to assign each element of $S \subset A$ to a distinct element of B then the number of neighbors of S in B must be at least as large as the size of S. Moreover, this must be true for any subset of S, since we wish to match each element

Figure 2.3.2. ***Indepdendent Sets: {1}; {2};{3}; {1,3}; Maximal Independent Sets: {1,3}, {2}.***

to a different element from B. What Hall's Theorem [300] states is that this is not only a necessary condition, but also a sufficient condition for such a matching to exist.

THEOREM **2.3.1** *[Hall's Theorem] Consider a bipartite graph (N, g) with an associated bipartition of nodes $\{A, B\}$. There exists a matching of a set $S \subset A$ if and only if $|N_{S'}(g)| \geq |S'|$ for all $S' \subset S$.*

As we shall see in Chapter 10, this will be a useful theorem when it comes to working with networked models of markets, which are often bipartite in structure.

2.3.2 Set Coverings and Independent Sets

Given a network (N, g), an *independent* set of nodes $A \subset N$ is a set such that if $i \in A$ and $j \in A$ and $i \neq j$ then $ij \notin g$.

An independent set of nodes A is maximal if it is not a proper subset of any other independent set of nodes.

The following observation (from Galeotti et al [256]) is straightforward, but useful when characterizing equilibria of games played on networks.

OBSERVATION **2.3.1** *Consider a network (N, g) and a network (N, g') such that $g \subset g'$. Any independent set A of g' is an independent set of g, but if $g' \neq g$ then there exist (maximal) independent sets of g that are not (maximal) independent sets in g'.*

The proof of this is Exercise 2.8.

Independent sets are closely related to the equilibria of some games played on networks, as first pointed out by Bramoullé and Kranton [95]. To see how independent sets relate to equilibria, consider the following game played on a network.[32] Each player

[32] For more detailed definitions of game theoretic concepts and discussion of games played on networks see Chapter **??**.

chooses whether to buy a product (say a book) or not. If a player does not buy the book, then he or she can freely borrow the book from any of its neighbors who bought it.[33] Indirect borrowing is not permitted, so a player cannot borrow the book from a neighbor of a neighbor. If none of a player's neighbors have bought the book, then the player would prefer to pay the cost of buying the book himself or herself, rather than not having any access to the book at all. This is what is known as a classic "free-rider" problem, but on a network. Each player would prefer have some neighbor buy the book and then "free-ride" by borrowing the book, rather than having to buy the book himself or herself. A (pure strategy) equilibrium in this game is simply a specification of which players buy the book such that: (i) no player who buys the book regrets it, and (ii) no player who did not buy the book would rather buy the book. It is easy to see that the (pure strategy) equilibria of this game are precisely the situations where the players who buy the book form a maximal independent set. This follows from the observations that (i) implies that if some player buys a book then it must be that none of his or her neighbors buy the book, and (ii) implies that any player who does not buy a book must have at least one neighbor who bought the book. Thus the first part implies that the set of people who buy the book must be independent, and the second part implies that the set must be maximal.

2.3.3 Colorings

Related to the concept of independent sets is that of colorings. One of the basic applications is to scheduling problems. For example, consider a network where the nodes are researchers who will attend a conference.[34] A link indicates that the two researchers wish to attend each other's presentations. The conference organizer wishes to know how many different time slots are needed (running parallel sessions within time slots) in order to make sure that each researcher can attend all of the presentations he or she would like to, and also present his or her own work. This problem is equivalent to coloring the associated graph. Suppose we have a different color to code each time slot of the conference. We want to color the nodes so that no two neighboring nodes have the same color. What is the minimum number of colors that we need? That

[33] Assume that if some player buys the book, and several neighbors wish to borrow it, then they can coordinate on when they borrow it so that they can each borrow it without rivalry.

[34] This example is from Bollobás [79].

Figure 2.3.3 A Planar Network on Six Nodes with Chromatic Number 4

number is called the *chromatic number* of the graph.[35]

If we color the nodes of a network in k colors, then we have produced k independent sets. The coloring problem can then be thought of as finding the minimum number of independent sets needed to partition the set of nodes.[36] This is a challenging problem that has resulted in some celebrated results. The most famous is probably the four-color theorem. That theorem concerns *planar* graphs. Without providing a formal topological definition, a planar graph is one that can be drawn on a piece of paper

[35]This is what is known as the vertex coloring problem. There are also edge coloring problems, and a recent generalization called list coloring problems. The edge coloring problem is to color the edges so that no two adjacent edges have the same color. The minimal number of colors needed has application, for instance, to having enough time slots for scheduling bilateral meetings of neighboring nodes, so that no node needs to be in more than one meeting at once. For an introduction to these problems, see Bollobás [79] or Diestel [**?**].

[36]But note that the sets need not be maximal independent sets. For instance, node 1 is in its own element of the partition in Figure 2.3.3, but it is not a maximal independent set as it is not connected to 6. If we change the partition and color 6 to be green along with 1, then we have another 4-coloring. But then 2 is in its own element of the partition and does not form a maximal independent set.

without having any two links cross each other (so that links can only intersect at one of their involved nodes). The four color theorem is that every planar graph has a chromatic number of no more than four. This theorem was conjectured in the middle 1800's, and some false proofs were provided before it was proven in 1977 by Appel and Haken [**?**].[37] An overview of coloring problems would take us beyond the scope of this text, but the problems are so central to graph theory and important in their applications that they at least deserve mention.

2.3.4 Eulerian Tours and Hamilton Cycles

The mathematician Leonhard Euler asked (and answered) a question that concerns paths in a graph. The puzzle traces back to a question concerning the old Prussian city of Königsberg, which lay on the Pregel river. The city was cut into four pieces by the river and had seven bridges. The question was whether it was possible to design a walk that started at some point in the city, crossed each bridge exactly once, and returned to the starting point. The four parts of the city can be thought of as the vertices or nodes of a graph, and the seven bridges as edges or links of the graph. The question then amounts to asking whether their exists a walk in the graph that contains each link in the graph exactly once and starts and ends at the same node.[38] Such a closed walk is said to be a Eulerian tour or circuit.

A walk is said to be *closed* if it starts and ends at the same node. It is clear that in order to have a closed walk that involves every link of a network exactly once it must be that each node in the network has an even degree.[39] This follows since each time a node is "entered" by one link on the walk it must be "exited" by a different link, and each time the node is visited, it must be by a link that has not appeared previously on the walk. Euler's [**?**] simple but remarkable theorem is that this condition is necessary *and sufficient* for there to exist such a closed walk.

[37] That proof involved a computer verification that a series of 1482 cases each reduce to being 4-colorable. Shorter proofs have since been provided.

[38] The graph here is actually a "multigraph", as there is more than one link between some pairs of nodes. The general problem of finding Eulerian tours can be stated in either context.

[39] Note that a closed walk is not necessarily a cycle (as it may visit some of the intermediate nodes more than once), but a cycle is a closed walk.

Figure 2.3.4 The Multi-Graph for the Königsberg Bridge Problem

THEOREM **2.3.2** *A connected network g has a closed walk that involves each link exactly once if and only if the degree of each node is even.*

The proof is straightforward and appears as Exercise 2.9.

One can ask a related question for nodes rather than links: when is it possible to find a closed walk that involves each node in the network exactly once? Such a closed walk must be a cycle, and is referred to as a Hamilton Cycle or a Hamiltonian. A related question is whether there exists a "Hamilton path" that hits each node exactly once. Clearly a network that has a Hamilton cycle has a Hamilton path, while the converse is not true (consider a line).

Discovering whether or not a network has a Hamilton cycle is a much more challenging question than whether it has a Euler tour; and this has been an active area of research in graph theory for some time. It has direct applications to the "traveling salesman problem," where a salesman must visit each city on a trip exactly once, cities are nodes on a network, and the path must follow the links.

The seminal theorem on Hamilton cycles is due to Dirac [**?**]. Stronger theorems have since been developed, as we shall shortly see, but it is worth stating on its own, as it has an intuitive proof that helps one see the paths to proving some of the later

results.

THEOREM **2.3.3** *If a network has $n \geq 3$ nodes and each node has degree of at least $n/2$, then the network has a Hamilton cycle.*

The proof is as follows. First, let us argue that the network must be connected. This follows since if the minimum degree is $n/2$ then the smallest component has more than half the nodes, and so the network cannot consist of more than one component. Next, consider a longest path in this network, and if there is more than one longest path then pick any one. Let i be the node that the path starts at and j be the node it ends at. It must be that each of i's neighbors lies on the path, and so at least $n/2$ of the nodes in the path are neighbors of i. To see this, note that if this were not the case, then by starting with an omitted neighbor of i and then moving to i, we could find a longer path. Similarly, we know that j has at least $n/2$ neighbors on the path. It is then easy to check that since i and j each have at least $n/2$ neighbors on the path, at least one of the nodes on the path that is a neighbor of i, say k, must have the previous node on the path be a neighbor of j. Thus, consider the cycle formed as follows: ik, $k+1 \ldots j$, j $k-1$, $k-2 \ldots i$ (where the $\ldots$ correspond to the original path). The claim is that this is a Hamilton cycle. If this cycle does not include all nodes, then since the network is connected there is some node outside of the cycle connected to some node in the cycle. Then it is possible to make a path including that node and all nodes in the cycle, which contradicts the fact that the original path was of maximal length.

An example of a strengthening of the Dirac Theorem, is the following theorem due to Chvátal [**?**].

THEOREM **2.3.4** *Order the nodes of a network of $n \geq 3$ nodes in increasing order of their degrees, so that node 1 has the lowest degree and node n has the highest degree. If the degrees are such that $d_i \leq i$ for some $i < n/2$ implies $d_{n-i} \geq n - i$, then the network has a Hamilton cycle.*

This theorem also has a converse. If a degree sequence does not have this property, then one can find a network that has a degree sequence with at least as high a degree in each entry that does not have a Hamilton cycle. While it is clear that there are networks that have low average degree and have Hamilton cycles (e.g., simply arrange nodes in a circle), this converse shows that guaranteeing the existence of Hamilton cycles either requires strong conditions on basic characteristics like degree sequences, or else one needs much more information about the structure of the network.

2.4 Appendix: Eigenvectors and Eigenvalues

Given an $n \times n$ matrix T, an *eigenvector* v is a nonzero vector such that

$$Tv = \lambda v, \tag{2.11}$$

for some scalar λ, which is called the *eigenvalue* of v. Generally, we are interested in non-zero solutions to this equation (noting that a vector of 0's always solves (2.11)).

Eigenvectors come in two flavors: *left-hand eigenvectors* and *right-hand eigenvectors*, which are also known as *row eigenvectors* and *column eigenvectors*, respectively. This refers to whether the eigenvector multiplies the matrix T from the left-hand or right-hand side, and correspondingly whether it is a row or column vector. So, a left-hand (row) eigenvector is an $1 \times n$ vector v such that

$$vT = \lambda v, \tag{2.12}$$

whereas, a right-hand (column) eigenvector is an $n \times 1$ vector v that satisfies (2.11) for some eigenvalue λ. As the definition at the start of this section suggests, "eigenvector" without a modifier usually refers to a right-hand eigenvector.

Basically, eigenvectors are vectors that, when acted upon by the matrix T, give back some rescaling of themselves, rather than being distorted to some new vector or new direction. So they serve as a sort of fixed-point, and for many matrices, but not all, there will be as many eigenvector-eigenvalue pairs as there are dimensions, n.[40]

The usefulness of eigenvectors can be seen in terms of some of their applications. We have already seen one important application, in terms of calculating centrality or power, and in particular in terms of calculating Katz-Prestige (and also the eigenvector-centrality). The idea is that a given agent's prestige is a weighted average of his or her neighbors' prestige, where the weights correspond to weights from a social network. This then provides a self-referential problem, as the prestige has to be derived from the prestige. In that case, we look for an eigenvector with an eigenvalue of 1. The existence of an eigenvector with an eigenvalue of 1 in this context is implied by the Perron-Frobenius Theorem.

The Perron-Frobenius Theorem implies that if T is a nonnegative *(column) stochastic* matrix, so that the entries of each of its columns sum to 1, then there will exist

[40] We have to be careful here to restrict attention to some normalization of each eigenvector, so it has norm 1, for instance. Otherwise, note that if v is an eigenvector of T, then so is kv for any scalar k, as (2.11), as well as (2.12), are satisfied if we rescale v.

a nonnegative right-hand eigenvector v that solves (**??**) and has a corresponding eigenvalue $\lambda = 1$. The same is true of row stochastic matrices and left-hand eigenvectors. If in addition T^t has all positive entries for some t, then all other eigenvalues have a magnitude less than 1.[41]

Another type of application where eigenvectors are quite useful is in examining the steady state or limit point of some system. Here we might think of T as a transition matrix. So, starting with some column vector v, the system transitions to some new vector Tv. A steady state of such a system, or a convergence point, will often be a point such that $v = Tv$, so that once one reaches v, one stays there. Again, this is an eigenvector of T, which has a unit eigenvalue. These play a central role in Markov chains (see Section 4.5.8), where the v's represent probabilities of being in different states of a system, and the T represents probabilities of transferring from one state to another. This is again a stochastic matrix (as probabilities sum to 1), and has a unit eigenvector.

Calculating the eigenvalues and corresponding eigenvectors of a matrix can be done using different methods, as the eigenvector calculation is basically a set of linear equations in a set of unkowns. If one knows λ, then (2.11) and (2.12) are systems of n equations in n unknowns. A useful way to solve for the eigenvalues associated with T is to rewrite (2.11) as

$$(T - \lambda I)v = 0$$

where I is the identity matrix (with 1's on the diagonal and 0's elsewhere). In order for this equation to have a nonzero solution v, it must be that $T - \lambda I$ is a singular (non-invertible) matrix.[42] Thus, the *characteristic equation* of T is that

$$det(T - \lambda I) = 0$$

where $det(\cdot)$ indicates determinant. The solutions to this equation are the eigenvalues of T.

[41] The Perron-Frobenius Theorem implies that the largest eigenvalue of any nonnegative matrix is real-valued, and its corresponding eigenvector is nonnegative. Other eigenvalues can be complex-valued.

[42] This is a matrix where some rows are linear combinations of other rows, or similarly for columns, and this corresponds to having a determinant that is 0.

2.4.1 Diagonal Decompositions

There are some particularly useful ways to rewrite a matrix T. To begin, let V be the matrix of left-hand eigenvectors - so that each row is one of the eigenvectors of T. Then we can write

$$VT = \Lambda V, \tag{2.13}$$

where Λ is the matrix with the eigenvalues corresponding to each row of V on its diagonal:

$$\Lambda = \begin{pmatrix} \lambda_1 & 0 & 0 & 0 \\ 0 & \lambda_2 & 0 & 0 \\ \vdots & 0 & \ddots & \vdots \\ 0 & 0 & \dots & \lambda_n \end{pmatrix}.$$

From (2.13) it follows that if V is invertible, then

$$T = V^{-1}\Lambda V, \tag{2.14}$$

This is the *diagonal decomposition* of T, if it exists, and then T is said to be *diagonalizable*.

It is sometimes useful to note that V^{-1}, if it is well-defined, is the matrix of right-hand (column) eigenvectors of T, and that they have the same matrix of eigenvalues as V. To see this, note that from (2.13) it follows that $VTV^{-1} = \Lambda VV^{-1} = \Lambda$. Thus $V^{-1}VTV^{-1} = V^{-1}\Lambda$ and so $TV^{-1} = V^{-1}\Lambda = \Lambda V^{-1}$, and V^{-1} is the vector of right hand eigenvectors.

This is useful in calculating higher powers of T (which, for instance recalling Section **??**, is useful in calculating the walks of T if T has 0,1 entries). From (**??**) it follows that

$$T^2 = V^{-1}\Lambda VV^{-1}\Lambda V = V^{-1}\Lambda^2 V,$$

and more generally that

$$T^t = V^{-1}\Lambda^t V.$$

This helps in calculating speeds of convergence, as in Section **??**.[43]

[43] It is worth noting that this can help substantially from a computational perspective as well. Raising T to a power directly, for a large matrix, can be computationally intensive. Instead, raising Λ to a power is much easier since it just involves raising the diagonal entries to a power.

2.5 Exercises

EXERCISE **2.1** *Paths and Connectedness*

Given a network (N, g) define its complement to be the network (N, g') such that $ij \in g'$ if and only if $ij \notin g$. Show that if a network is not connected then its complement is. Provide an example of a four node network that is connected and such that its complement is also connected.

EXERCISE **2.2** *Facts about Trees.*

Show the following:

- A connected network is a tree if and only if it has $n - 1$ links.
- A tree has at least two leaves, where leaves are nodes that have exactly one link.
- In a tree, there is a unique path between any two nodes.

EXERCISE **2.3** *Diameter and Degree*

Consider a sequence of networks such that each network in the sequence is connected and involves more nodes than the previous network. Show that if the diameter of the networks is bounded, then the maximal degree of the networks is unbounded. That is, show that if there exists a finite number M such that the diameter of every network in the sequence is less than M, then for any integer K there exists a network in the sequence and a node in that network that has more than K neighbors.

EXERCISE **2.4** *Centrality Measures*

Consider a two link network among three nodes. That is let the network consist of links 12 and 23.

Calculate the Katz-prestige (based on (2.5)) of each node, and compare this to the degree centrality and betweenness centrality for this network.

Calculate the second measure due to Katz (based on (2.9)) for each node, when a=1/2, which is the Bonacich centrality of each node when $b = 1/2$ and $a = 1/2$.

How does this compare to Bonacich centrality when $b = 1/4$ and $a = 1/2$?

Which nodes are relatively favored when b increases and why?

What happens as we continue to increase b to $b = 3/4$?

EXERCISE **2.5** *Average versus Overall Clustering*

Consider a network (g, N) such that each node has at least two neighbors ($n_i(g) \geq 2$ for each $i \in N$). Compare the average clustering measure of a network to the overall clustering measure in the following two cases:

a. $Cl_i(g) \geq Cl_j(g)$ whenever $d_i(g) \geq d_j(g)$, and

b. $Cl_i(g) \leq Cl_j(g)$ whenever $d_i(g) \geq d_j(g)$.

Hint: Write average clustering as $\sum_i Cl_i(g)\left(\frac{1}{n}\right)$ and argue that overall clustering can be written as $\sum_i Cl_i(g)\left(\frac{d_i(g)(d_i(g)-1)/2}{\sum_j d_j(g)(d_j(g)-1)/2}\right)$. Then compare these different weighted sums.

EXERCISE **2.6** *Cohesiveness and Close-Knittedness*

There are various measures of how introspective or cohesive a given set of nodes is.

Consider a set of nodes $S \subset N$. Given $1 \geq r \geq 0$ Morris [464] defines the set of nodes S to be *r-cohesive* with respect to a network g if each node in S has at least r of its neighbors in S. That is, S is r-cohesive relative to g if

$$\min_{i \in S} \frac{|N_i(g) \cap S|}{d_i(g)} \geq r, \tag{2.15}$$

where $0/0$ is set to 1.

Young [632] defines the set of nodes S to be *r-close-knit* with respect to a network g if each subset of S has at least r of its links staying in S. Given S' and S, let $d(S', S, g) = |\{ij | i \in S', j \in S\}|$ be the number of links between members of S' and members of S. Then S is r-close-knit relative to g if

$$\min_{S' \subset S} \frac{d(S', S, g)}{\sum_{i \in S'} d_i(g)} \geq r, \tag{2.16}$$

where $0/0$ is set to 1.

Show that if a set of nodes S is r-close-knit relative to g then it is r-cohesive. Provide an example showing that the converse is false.

EXERCISE **2.7** *Independent Sets*

Show that there is a unique network on n nodes that is connected and such that a maximal independent set of that network involves all nodes except node i. Show that there are two maximal independent sets of that network.

EXERCISE **2.8** *Independent Sets and Equilibria*

Prove Observation 2.3.1.

EXERCISE **2.9** *Euler Tours*

Prove Theorem 2.3.2. (Hint: First argue that any longest walk that does not involve any link more than once must be closed.)

Chapter 3

Empirical Background on Social and Economic Networks

There are numerous and extensive case studies of a variety of social and economic networks. Through such studies we have learned an immense amount about the structure of networks. In this chapter, I discuss some of the basic stylized facts and hypotheses that have come out of decades of empirical research on social and economic networks. As this literature is much too large to survey here, I focus on the fundamental characteristics of networks, mainly dealing with the structural aspects of networks, and some of the hypotheses that we return to in later chapters.

I begin with two cautions regarding some of the stylized facts from the literature. First, examining the structure of any given social network is a formidable task that faces significant hurdles associated with how to define and measure links or relationships. For instance, a primary tool for estimating social networks is to use various sorts of surveys or interviews of involved parties. Given that individuals have hundreds or even thousands of social relationships, getting them to recall the relevant ones with any desired accuracy is difficult.[1] In addition, it may be impossible to contact or observe all nodes in the network, and when contacted they may have reasons to distort or conceal relationships. Even recent studies of web pages, co-authorship, email, and citation networks, where data are more easily obtained, have other measurement idiosyncrasies. Beyond this, networks change over time and overlap in various ways. Close friends may fail to interact for long periods. Much of the information that we have about

[1] There is a sizeable literature on techniques for measuring social networks, as well as dealing with other measurement issues such missing data, biases in responses, etc. For instance, see Marsden [427], Bernard [52], and Bernard et al [53].

the structure of social networks comes from limited measurements of links that often take a static and discrete view of something that is inherently dynamic and volatile. Second, as there are biases and idiosyncrasies associated with each data set, and data are often collected and encoded in different ways, little has been done to systematically determine the prevalence of characteristics across ranges of social settings.[2] Thus, much of what is discussed below is based on what might be termed anecdotal evidence gleaned from various case studies, and the stylized facts reported below should be interpreted with the appropriate caution, and there is a need for broader systematic studies and comparisons of networks across social settings.

3.1 The Prevalence of Social Networks

Social relationships play a critical role not only in day-to-day life and behavior, but also in determining long run welfare. They affect the opinions that we hold and the information that we see, and are also often the key to accessing resources. While this is self-evident and gives sociology its foundation, quantifying the extent to which social relationships play roles in various aspects of life is an illuminating exercise.

One of the most robust and well-studied roles of social networks is in obtaining employment. There have been a number of studies of how social contacts matter in obtaining information about job openings. Such studies began in the late 1940's and there is now a rich base of information on this subject.[3] One of the earliest studies, by Myers and Shultz [472], was based on interviews with textile workers. They found that 62 percent had found out about and applied to their first job through a social contact, in contrast with only 23 percent who applied by direct application, and the remaining 15 percent who found their job through an agency, ads, etc. A study by Rees and Shultz [531] showed that these numbers were not particular to textile workers, but applied very broadly. For instance, the percentage of those interviewed who found their jobs through the use of social contacts as a function of their profession was: typist 37.3 percent, accountant 23.5 percent, material handler 73.8 percent, janitor 65.5 percent, and electrician 57.4 percent. Moreover, the prevalent use of social contacts in finding jobs is robust across race and gender.[4]

[2] There are authors, such as Watts [620] and Newman [480], who have looked across (a few) case studies to suggest some common features.

[3] For a recent overview of research on social networks in labor markets see Ioannides and Loury [**?**].

[4] See Corcoran, Datcher, and Duncan [**?**] for comparisons across race and gender, and Pellizzari [510] for data across countries.

The role of social networks is not unique to labor markets, but has been documented much more extensively. For example, networks and social interactions play a role in crime: Reiss [533], [534] finds that two thirds of criminals commit crimes with others, and Glaeser, Sacerdote and Scheinkman [**?**] find that social interaction is important in determining criminal activity, especially with respect to petty crime, youth activity in crime, and in areas with less intact households. Networks have also been studied with regards to various markets: Uzzi [598] finds that relation specific knowledge is critical in the garment industry and he documents how social networks play a key role in that industry; and Weisbuch, Kirman, Herreiner [626] study repeated interactions in the Marseille fish market and discuss the importance of the network structure. Social networks also serve a vital role in the provision of social insurance. For instance, Fafchamps and Lund [221] show that social networks are critical to the understanding of risk-sharing in rural Philippines, and De Weerdt [176] analyzes risk-sharing in parts of Africa. The set of case studies is much more extensive than this list indicates, and also includes extensive analyses of networks in disease transmission, in the diffusion of language and culture, in the collaboration on scientific research and invention, in the citation of articles, in the formation of opinions, in political activity, in choices of products to buy, and interactions of boards of firms - just to name a few other applications.[5]

I now turn to discuss some of the regularities and stylized facts about social networks that some of these studies have revealed.

3.2 Observations about the Structure of Networks

The following are characteristics that have been exhibited by a variety of social networks.

3.2.1 Diameter and Small Worlds

The stylized fact that large social networks exhibit features of "small worlds" (see Milgram [444]) is one of the earliest, best-known, and most extensively studied aspects of social networks. The term "small worlds" embodies the idea that that large networks

[5] The analysis also moves beyond social networks per se, to include things like analyses of the co-appearance of literary (comic-book) superheroes.

tend to have small diameter and small average path length.[6]

Stanley Milgram [444] pioneered the study of path length through a clever experiment where people had to route a letter to another person who was not directly known to them. Letters were distributed to subjects in Kansas and Nebraska, who were told the name, profession, and some approximate residential details about a "target" person who lived in Massachusetts. The subjects were asked to pass the letter on to someone whom they knew well and would be likely to know the target or to be able to pass it on to someone else, etc., with the objective of getting the letter to the target. While roughly a quarter of the letters reached their targets, the median number of hops for a letter to reach a target was 5 and the maximum was 12. Given that the letters should not be expected to have taken the shortest path, this is a startlingly small number. In addition, given the chains of interactions needed to get a letter from an initial subject to the target, the fact that a quarter of the letters reached their targets is also an impressive figure, especially in light of the fact that response rates in many voluntary surveys are on the order of twenty to thirty percent.[7]

To get some feeling for why many social networks exhibit small diameters, it is useful to think about neighborhood sizes. Most people have thousands of acquaintances. Depending on whether one keeps track of strong relationships or casual acquaintances, this might vary from the order of tens or hundreds to the order of thousands for a typical adult in a developed country (e.g., see Pool and Kochen [518], which is a key early study of small worlds). If we take a conservative estimate that a given individual has 100 relatives, friends, colleagues, and acquaintances with whom they are in somewhat regular contact, then we end up with a very rough calculation (ignoring clustering and treating the network as if it were a tree) of 100^2 or 10,000 friends of friends, and 1 million friends of friends of friends. By the time we move out four links, we have covered a nontrivial portion of most countries. While this overestimates the reach of a network since it treats the network like a tree and ignores the clustering exhibited in most networks, it still provides a feeling for orders of magnitude. If we count more casual acquaintances, and use a figure on the order of 1000 acquaintances per person, then a tree network reaches a million nodes within a path distance of two and reaches

[6] See Watts [620] for more discussion. This stylized fact is captured in the famous "six degrees of separation" of John Gaure's play, and actually dates to a 1929 play called "Chains" by Frigyes Karinthy.

[7] This study has been replicated and extended a number of times. A recent example is research by Watts [**?**], who used email messages in a study involving nearly 50000 subjects in 157 countries and found similar sized chains.

a billion within a path distance of three.

Other examples provide similar impressions of path length and diameter measurements of observed networks. Watts and Strogatz [623] report a mean distance of 3.7 in a network among actors where a link indicates that two actors have been in a movie together. Studies of networks of co-authorship in scientific journals also report relatively small path lengths and diameters on larger numbers of nodes. Here a link represents the co-authorship of a paper during some time period covered by the study. The well-known and prolific mathematician Paul Erdös had many co-authors, and as a fun distraction many mathematicians (and economists for that matter) have found the shortest path(s) from themselves to Erdös. For example, an author who co-authored a paper with Erdös has an Erdös number of 1. An author who never directly co-authored a paper with Erdös, but who co-authored with a co-author of Erdös has an Erdös number of 2, and so forth. There are also some interesting patterns that emerge in such networks in terms of how they grow. [8] These networks are of scientific interest themselves, as they tell us something about how research is conducted and also how information and innovation might be disseminated. Similar studies have now been conducted in various fields, including mathematics (Grossman and Ion [**?**], de Castro and Grossman [**?**]), biology and physics (Newman [**?**], [**?**]), and economics (Goyal, van der Leij and Moraga-González [286]). Various statistics from these studies give us some impression of the network structure, as shown in Table 3.1.[9]

Here we see that despite the non-comparabilities of the networks along some dimensions (e.g., average degree, clustering, and size of the largest component), the average path length and diameters of each of the networks are very comparable. Moreover, these are of an order substantially smaller than the number of nodes in the network. This gives us an impression of the "small-world" nature of social networks.

To see how dramatic this effect can be, consider the average number of links it

[8] A web site (www.oakland.edu/enp/) maintained by Jerry Grossman, Patrick Ion, and Rodrigo de Castro provides a part of that graph. The American Mathematical Society website also provides platform that gives a shortest path between two authors. A similar analysis is of the "Kevin Bacon" network (see the web site at the computer science department at the University of Virginia, www.cs.virginia.edu/oracle/), where a link indicates that two actors appeared in the same movie. In 2004, William Tozier auctioned (on eBay) a promise to co-author an article, as that would provide the purchaser with an Erdös number of 5 as Tozier's is 4. This led to a winning bid of over one thousand dollars and a resulting controversy, as well as a number of other such auctions (see *Science News Online*, June 12, 2004, vol. 165, no. 24).

[9] As these networks are not connected (there are many isolated authors), the figures for average path length and diameter are reported for the largest component.

Table 3.1: Co-Authorship Networks

	Biology	Economics	Math	Physics
number of nodes	1520521	81217	253339	52909
average degree	15.5	1.7	3.9	9.3
average path length	4.9	9.5	7.6	6.2
diameter of the largest component	24	29	27	20
overall clustering	.09	.16	.15	.45
fraction of nodes in the largest component	.92	.41	.82	.85

takes to get from one web page to another on the world wide web. Lada Adamic [1] analyzed a sample of 153,127 web sites.[10] She found that there existed a (undirected) path starting at one page and ending at another in 85.4 percent of the possible cases; and that in those cases the average minimum path length was only 3.1. In looking for directed paths, she found that of the 153,127 web sites, there was a strongly connected component of 64,826 sites (so that any web site in that component could be reached via a directed path from any other web site in that component). The average minimum directed path length in that component was 4.2. Again, while not all pairs of sites are path-connected, the fact that it takes so few clicks to get from many of the sites to many others is impressive.[11]

3.2.2 Clustering

Another interesting observation about social networks is that they tend to have high clustering coefficients relative to what would emerge if the links were simply determined by an independent random process. Ideas behind clustering have been important in sociology since Simmel [560] who pointed out the interest in triads (triples of mutually connected nodes). A variety of large socially generated networks exhibit clustering

[10] This was based on a data set collected by Jim Pitkow of Xerox PARC. The initial data set contained 259,794 web sites and consisting of over 50 million pages. The network was trimmed of any "leaf nodes".

[11] It is worth noting that the data were collected via an algorithm that followed links in order to locate nodes, and such web-crawling algorithms necessarily introduce some bias in the portion of the overall network that they identify and particularly with respect to path structure.

measures much larger than would arise if the network were generated at random. For instance, let us re-consider the networks of researchers that have been analyzed in various fields of study. For instance, Newman [480] reports overall clustering coefficients of 0.496 for computer science, and 0.45 for physics, while Grossman [298] reports an overall coefficient of 0.15 in mathematics. To get an idea of how this compares with the clustering that would appear in a purely random network, let us consider the physics network which has 52,909 nodes and an average degree of 9.27. A purely random network that had this average degree would have a probability of any given link forming of 9.27/52908, or roughly .00018. For such a purely random network, the chance that link ik is present when ij and jk are present is simply the probability that ik is present, which is then .00018. This tells us that the clustering of .45 is roughly 2500 times greater than the clustering we would see in a random network of the same size and connectivity. We can also examine analogous numbers for a similar network constructed for researchers in economics. The data of Goyal, van der Leij, and Moroga-Gonzalez [286] covering papers published in economics journals in the 1970's has a total of 33770 nodes and an average degree of .894.[12] The clustering they report for that network is .193, whereas the corresponding clustering for a purely random network of the same degree is on the order of .894/33770 or .000026. Here the observed clustering is almost 10000 times larger than in the random network.[13]

Similarly high clustering has been observed in a variety of other contexts. For example, Watts [620] reports a clustering coefficient of 0.79 for the network consisting of movie actors linked by movies in which they have co-starred. Several studies have also analyzed clustering in the world wide web. Adamic [1] gives a clustering measure of 0.1078 on the world wide web data set mentioned in Section **??**. To get a feeling for how large this clustering measure is, note that we expect a purely random graph with the same number of links to have a clustering coefficient of 0.00023, so that the observed network has about 469 times more clustering than if links were formed independently.

[12] The data in Table **??** are from the 1990's rather than 1970's, and have more nodes, higher average degree and slightly lower clustering.

[13] Note in such collaboration networks, as there may be many co-authors on any given paper, clustering in this particular application partly reflects the fact that a multi-co-authored paper provides a complete set of connections between the authors. Given large numbers of co-authors per paper in physics, this partly explains the high clustering number there. The economics data exhibits less of this, as there less than 4 percent of all papers involved more than two co-authors, while roughly 25 percent of all papers had two co-authors.

Figure 3.2.3. Comparison of the Degree Distributions of a Co-Authorship Network and a Poisson Random Network with the same Average Degree

3.2.3 Degree Distributions

As we saw in Table 3.1, networks differ in their average numbers of links. For instance, in Table 3.1, the number of co-authors per paper varies dramatically across fields, and there are other differences in social structure across fields. For instance, in the economics data set, there are on average 1.6 authors per paper (and only 12 percent of papers have more than two authors), while in the biology data there are on average 3.8 authors per paper. Although the average degree of a network provides a rough feeling for connectivity, there is much more information that we would like to know. For instance, how variable is the degree across the nodes of the network? We get a much richer feeling for the structure of a social network by examining the full distribution of node degrees rather than just looking at the average.

To see an example of such a distribution, consider Figure 3.2.3 below, which provides a log-log plot of the frequency distribution of degrees from the economics co-authorship data from Goyal, van der Leij, Moraga-Gonzalez [286].

The degrees of economists in the data set range from 0 to over 50. The distribution

also has an interesting shape. It clearly exhibits some curvature. However it also shows "less" curvature than the distribution of degrees generated from a network with the same number of links, but where the links are chosen independently with identical probability (a Poisson random graph, as discussed in Section **??**). What this indicates is that there are more economists with very high degree and more with very low degree than we would see in a network where links were generated uniformly at random.

This "fat-tailed" property is not unique to this network, as discussed already in Section 2.2.1. There has been a good deal of attention paid to the observation that the degree distributions of many observed large networks tend to exhibit "fat tails." Price [521] was the first to document such distributions in a network setting, observing that citation networks among scientific articles seemed to follow a power law (both in terms of in and out degree). It has been loosely said that these distributions approximate a "scale-free" or "power-law" distribution, at least in the upper tail. This refers to a frequency of a given degree being proportional to the degree raised to a power, so that the probability or frequency of a given degree can be expressed as

$$P(d) = cd^{-\gamma}, \tag{3.1}$$

where $c > 0$ and $\gamma > 1$ are parameters of the distribution, and hence the term "power-law." The "scale-free" aspect refers to the fact that if we consider the probability of a degree d and compare that to a degree d', then the ratio of $P(d)/P(d') = (d/d')^{-\gamma}$. Now suppose that we double the size of each of these degrees. We find that $P(2d)/P(2d') = (d/d')^{-\gamma}$. It is easy to see that rescaling d and d' by any factor will still give us this same ratio of probabilities, and hence the relative probabilities of different degrees just depends on their ratio and not on their absolute size. This explains the term "scale-free."[14]

For example, Figure 3.2.3 shows the degree distribution from the data set of Albert, Jeong and Barabási [8], which is the distribution of in-degrees from the network of links

[14] A discrete distribution, such as above where d can only take on values $\{0, 1, 2, \ldots\}$, is sometimes hard to work with in terms of estimating expected values and conditional expectations, and so in some cases it is useful to use an approximation in the form of a continuous distribution where d can take on non-integer values. The canonical continuous distribution satisfying a power law is a Pareto distribution, named for Vilfredo Pareto [501] who studied the distribution of wealth across individuals, among other things. The cumulative distribution function for a Pareto distribution with support $[1, \infty)$ and where $\gamma > 1$ is $F(d) = 1 - d^{-\gamma+1}$. The corresponding density is then $f(d) = (\gamma - 1)d^{-\gamma}$, which is of a similar form to the probability given in (3.1). If one tries to estimate the cumulative distribution function corresponding to (3.1), one would end up with $Prob[d \leq d'] = \sum_0^{d'} cd^{-\gamma}$, which does not have a nice closed form, but is approximately $1 - c'd^{-\gamma+1}$, where $c' > 0$ is a constant.

Figure 3.2.3. Distribution of In-Degrees of Notre Dame WWW from Albert, Jeong, and Barabasi [8] compared to a Poisson Random Network

among web pages on the Notre Dame world-wide-web in the late 1990s.

If we estimate the γ for a scale-free distribution of the type $P(d) = cd^{-\gamma}$ from a log-log regression on these data, we find an estimate of -2.56.[15]

Such scale-free distributions and fat tails appear well beyond network applications, such as word usage (Estoup [**?**] and Zipf [639]), plant classifications (Willis [629] and Yule [636]), city size (Auerbach [**?**] and Zipf [639]), and article citations (Price [521]).[16] There is a natural explanation for them (discussed in detail in Section **??**).

There is a very important caution to be mentioned here. It is clear that many network degree distributions exhibit "fat tails" when compared to a Poisson random graph, and that many of the other mentioned applications also have such fat tails. However, it is not so clear that these distributions are really power distributions. Most of these claims are made simply by examining log-log plots that appear approximately linear, and then fitting a regression and finding a coefficient. On a plot of log of

[15] This is as estimated by Jackson and Rogers [337].

[16] See Mitzenmacher [446] for an overview of some of the literature on power laws.

frequency versus log of degree, most of the data can end up occupying only a small portion of the figure. For example, in Figure 3.2.3, *less than ten percent* of the data fall in the range below -4 on the vertical scale.[17] The few studies that have fit more than one distribution to a network have found that the degree distribution that best fit tended *not* to be a power distribution (e.g., Pennock et al [513] and Jackson and Rogers [337]).

Table 3.2 from Jackson and Rogers [337] provides a look at how close to scale-free versus independently random a network is. They examine a class of degree distributions where the cumulative distribution function F is given by

$$F(d) = 1 - (rm)^{1+r} (d + rm)^{-(1+r)}, \tag{3.2}$$

where $m > 0$ is the average in-degree and r is a parameter that varies between 0 and ∞ and captures how randomly the links are formed. (See Section **??** for details.) In the extreme where r tends to 0 this converges to a scale free distribution, and in the extreme where r tends to ∞ this converges to a negative exponential distribution, which is the proper analog of the degree distribution of a purely random network that is growing over time.[18]

The following figures show how the degree distribution changes as r is varied, changing from a scale-free distribution with fat-tails to one with uniformly random attachment.

[17] Here the points on the graph seem misleading, as here are more points below -4 on the scale. However, the frequency on the vertical scale provides the log weights, and so points higher on the scale represent orders of magnitude more data points. The point with log(degree) equal to 0 corresponds to more than 20 percent of the data!

[18] Instead of starting with a fixed number of nodes and randomly putting in links all at once, consider a process where at each time a new node is born. That new node forms some links randomly with the existing nodes. As nodes age, they will gain links as more nodes are added, while newborn nodes will have only their initial number of links. Rather than a Poisson distribution, this leads to a negative exponential distribution of degrees, which fits some networks very well. This is discussed in more detail in Chapter **??**.

Figure 3.2.3. Degree Distribution with low r - Essentially Preferential Attachment

Figure 3.2.3. Degree Distribution with medium r - A Mixture of Uniform and Preferential Attachment

Figure 3.2.3. Degree Distribution with high r - A Growing Random Network

Fits to a few networks[19] give us an idea of the variation across applications.[20] In Chapter **??**, the derivation of a variation on this degree distribution as well as techniques for fitting it to data are detailed.

[19] The www data are from an analysis of the links between web pages on the Notre Dame domain of the world wide web from Albert, Jeong, and Barabási [**?**]. The co-authorship data are from the above cited study by Goyal, van der Leij, and Moraga-González [286]. The citation network consists of the network of citations among all papers that have cited Milgram's [444] paper or have the phrase "small worlds" in the title, and is from Garfield [258]. The prison data record friendships among inmates in a study by MacRae [422], the ham radio data record interactions between ham radio operators from Killworth and Bernard [372], and the high school romance data collected romantic relationships between high school students over a period of a year and a half in a US high school and is from Bearman, Moody, and Stovel [47]. The number of nodes, average degree, and clustering numbers are as reported by the studies. The estimates on randomness are from Jackson and Rogers [337]. The fits on these estimated r's are high, with R^2's ranging between 93 and 99 percent.

[20] The clustering figure for the co-author data is actually for overall clustering, as the average number is not available but is likely to be higher given that the clustering is decreasing in degree. The clustering for the high school romance network is special because that network is mainly heterosexual in its relationships, and so completed triads do not appear. Even if one looks for larger cycles, there are only five present in the whole network, which would be characteristic of a large network formed at random between two groups.

Table 3.2: Comparisons Across Applications

	WWW	Citations	Co-author	Ham Radio	Prison	High School Romance
Number of Nodes	325729	396	81217	44	67	572
Randomness: r	0.57	0.63	4.7	5.0	∞	∞
Avg. In-Degree: m	4.6	5.0	.84	3.5	2.7	.83
Avg. Clustering	.11	.07	.16	.47	.31	-

In all cases, the degree distribution fits the data quite closely (the R^2's on the corresponding regressions vary from .94 to .99).

We see even in the data of Albert, Jeong and Barabási [8] for the Notre Dame web sites, that although the degree distribution appears to be scale-free to the naked eye, when we fit a model to the data, it is best fit by a mixture of more than 1/3 parts uniformly random to 2/3 parts scale-free ($r = .57$ has random/scale-free of more than 1/2).[21] When we get to some of the more purely social networks, we see parameters that indicate much higher levels of random link formation, which are very far from satisfying a power law. In fact, the degree distribution of the romance network among high school students is essentially the same as that of a purely random network.

So there are two lessons here. The first is that many social networks exhibit "fat tails" in that there are more nodes with relatively high and low degrees than would tend to arise if links were formed independently. The second is that it is hard to find networks that actually follow a strict power law. Even networks that are often cited as exhibiting power laws (e.g., the world wide web) are better fit by distributions that differ significantly from a power distribution.

3.2.4 Correlations and Assortativity

Beyond the degree distribution of a network, we can also ask questions about the correlation patterns in the degrees of connected nodes. For instance, do relatively high degree nodes have a higher tendency to be connected to other high degree nodes? This

[21] In terms of a comparison, the statistical fit of this model (in terms of R^2) with $r = .57$ is .99 while the fit of a scale-free distribution is only .86.

is termed positive assortativity.[22]

While there is little systematic study of assortativity, there is a hypothesis that positive assortativity is a property of many socially generated networks, and contrasts with the opposite relationship that is more prevalent in technological and biological networks. This hypothesis is put forth by Newman [480] (see p. 314) who examines the correlation in degree across linked nodes.[23] Newman [480] reports the following correlations among degrees in seven different applications:

Table 3.3: Correlations in Degrees

	math co-authorship	physics co-authorship	email network	film actors	internet wiring	electric power grid	neural network
Correlation	.12	.36	.09	.21	-.19	-.003	-.23

Newman refers to the first four networks as social networks and the latter three as technological networks, and remarks the pattern of the positive correlations for the social networks and the negative correlations in the technological networks.

The network of reported friendships among prison inmates of MacRae [422] shows a similar positive assortative relationship as the social networks above. It has a correlation between a node's in-degree and the average in-degree of its neighbors of .58 (as reported by Jackson and Rogers [337]). However, one can also find exceptions. For example, the Ham radio network of interactions between amateur radio operators studied by Killworth and Bernard [372], has a negative correlation. There, the correlation between a node's in-degree and the average in-degree of its neighbors is -.26 (as reported by Jackson and Rogers [337]); although since it is a small network the correlation is not statistically significant. Once one examines networks such as a network of trading

[22] Even a finite network where links are formed completely independently, there can be correlation in degrees. For instance, consider the simplest possible setting with just two nodes, and where the probability of a link is 1/2. Here the degree of the two nodes is perfectly correlated, as they either both have degree 1 or both have degree 0. So, even when links are formed independently, the fact that a node has a high degree tells us something about which other nodes it is likely to be connected to based on their degrees. That correlation tends to disappear in a Poisson random network as the number of nodes grows, but this gives us an idea that such correlations will be delicate.

[23] Thus, the calculation for a network g is simply $\frac{\sum_{ij \in g}(d_i - m)(d_j - m)}{\sum_{i \in N}(d_i - m)^2}$, where m is average degree and d_i is the degree of a node i.

relationships among countries, one ends up with structures that can be thought of as primarily economic in nature, and having some aspects of both social and technological relationships. For example, Serrano and Boguñá [557] find a negative correlation among the degrees of countries that trade with each other and suggest that the average degree of the neighbors of a given node is proportional to the inverse of the square root of that node's degree.[24] They describe the network as a "hub-and-spoke" system, where smaller countries (the spokes) have few partners and trade with larger countries (the hubs) which tend to have many more partners. While many larger countries trade with each other, one still sees a negative relationship overall.

Related to assortativity, studies of some social networks have also suggested "core-periphery" patterns (e.g., see Brass [**?**]), where there is a core of highly connected and interconnected nodes, and then a periphery of less connected nodes. Moreover, theories of structural similarity posit that people tend to use other people who are similar to themselves as a reference group (Festinger [**?**]). Studies building from this hypothesis (e.g., Burt [105]) have found that people with similar structural positions tend to have similar issues to deal with and that leads them to communicate with each other.

As the patterns of connections in a network can have a profound impact on things like the diffusion of behavior, information, or disease, it is important to develop a better understanding of assortativity and other characteristics that describe who tends to be connected to whom in a network.

3.2.5 Patterns of Clustering

There are other patterns in networks that help characterize overall structure. Beyond degree distributions and correlations in degrees, one can also examine how clustering is distributed across a network. Clustering measures such as average or overall clustering are simple summary statistics. While they give some insight, we can look at much more detailed information about how clustering varies throughout a network.

For instance, in the example of the Florentine marriages, we can keep track of the full distribution of individual clustering coefficients across nodes. In that network there are nine nodes with clustering coefficients of 0, five nodes with clustering coefficients of 1/3, one node with a clustering coefficient of 2/3, and one with a clustering coefficient

[24] Their network has a directed link from one country to another if the first exports to the second. The relationship they examine is similar whether or not one examines outdegree, indegree, an undirected version (with a link if there is a directed link in either direction), and a different undirected version where one only examines reciprocal links (where there are directed links both ways).

of 1/15. It is perhaps even more informative to see how the clustering relates to the degree of a node. In the Florentine Marriage example, all nodes with degree two or less have individual clustering coefficients of 0. Degree three nodes have on average a clustering of 4/15 (one has 0 and four have 1/3), degree four nodes have on average a clustering of 1/6 (one has 2/6 and the other 0), and the degree six node has a clustering of 1/15. Here there is some pattern. First, the low degree nodes have clusterings of 0, most simply by convention. But more interestingly, the rate of clustering among the higher degree nodes is decreasing in the degree. This sort of pattern has been noted in other applications as well. That is, the neighbors of a higher degree node are less likely to be linked to each other as compared to the neighbors of a lower degree node. For example, Goyal, van der Leij, and Moraga-González [286] observe that a network of co-authorship among 81217 economists in the 1990's had an overall clustering coefficient of .157, while averaging over the one hundred nodes with the highest degrees only yielded an average clustering of .043. Thus, the highest degree nodes tend to exhibit lower clustering than one sees on average across the whole network. A very simple way to see if a network might exhibit such a pattern is to compare the overall clustering to the average clustering. Overall clustering can be thought of a weighted averaging of clustering across nodes with weights proportional to the number of pairs of neighbors that the nodes have (so the weight on node i is $d_i(d_i - 1)/2)$), while average clustering weights all nodes equally. Thus, overall clustering is weighting the higher degree nodes much more than average clustering is, and so if the overall clustering is significantly lower than the average clustering, then there is a sense in which the clustering is relatively lower for higher degree nodes. We can see this by comparing the overall clustering numbers for the networks reported in Table **??** to the average clustering numbers for the same networks. For instance, the ratios of overall clustering to average clustering are .09/.60 for biology, .15/.34 for math, and .45/.56 physics.[25] We can also simply examine the correlation between degree and the clustering in a node's neighborhood. Jackson and Rogers [337] calculate such correlations for the prison and ham radio networks mentioned above. They find a correlation of -.05 between a node's in-degree and the clustering in its neighborhood for MacRae's [422] friendship network among prison inmates, and a correlation of -.27 between a node's degree and the clustering in its neighborhood for Killworth and Bernard's [372] Ham radio network. However, these are both small networks and so

[25] The number is not reported in the economics co- authorship data set, but we already saw some aspect of this relationship in that network, as discussed above.

neither of these figures is statistically significant and are thus only suggestive.

It is not obvious whether this is a general pattern of social and/or other forms of networks, but it is at least exhibited in some observed networks, and is something that we will see exhibited by some models of network formation.

3.2.6 Homophily

Many social networks exhibit what is was named "homophily" by Lazarsfeld and Merton [404]. As we saw in Section 1.2.2, this refers to the fact that people are more prone to maintain relationships with people who are similar to themselves. This applies very broadly, as measured by age, race, gender, religion, profession and is generally a quite strong and robust observation (see McPherson, Smith-Lovin and Cook [439] for an overview of research on homophily). It was first noted by Burton [108] who coined the phrase "birds of a feather." For example, based on a national survey Marsden [429] finds that only 8 percent of people have *any* people of another race with whom they "discuss important matters." Homophily is an important aspect of social networks since it means that some social networks may be largely segregated. This, for instance, has profound implications in the access to job information (e.g., see Calvó-Armengol and Jackson [119]). It can also have profound implications for the spread of other sorts of information, behaviors, and so forth.

There is an important distinction between different forms of homophily. One is due solely to opportunity, while the other is due to choice. For instance, it is not surprising that most children have closest friends who are of a similar age as themselves. Much of this is due to the fact that they form friendships with other children with whom they regularly interact at school. This is the aspect that it is due to opportunity, which is constrained by the structure of classes within schools, among other things. Beyond this, even when presented with opportunities to form ties across age, there is still a tendency to form a disproportionate fraction with own-age individuals. This has been attributed to a number of factors including maturity and interests. One also sees this with respect to other factors such as race. For example, in middle school, less than 10 percent of "expected" cross-race friendships exist (Shrum et al [**?**]). That is, given the composition of schools in terms of race, if individuals form relationships in proportion to the relative numbers of people of various races that they encounter, there should be ten times more cross-race relationships than are observed. Thus, in addition to the substantial homophily one would expect due to the fact that most schools are biased in their racial composition and thus there is a bias in opportunity towards own-race

relationships, one also sees a very strong own-race bias in the relationships formed beyond that governed by relative population sizes.

To get a better impression of homophily, consider Table 3.4, which describes the frequency of friendships across different ethnicities in a Dutch high school. The data were collected by Baerveldt, Van Duijn, Vermeij, and Van Hemert [24].

	Ethnicity of Students				
Percent of Friends by Ethnicity:	Dutch n=850	Moroccan n=62	Turkish n= 75	Surinamese n=100	Others n=230
Dutch	79	24	11	21	47
Moroccan	2	27	8	4	5
Turkish	2	19	59	8	6
Surinamese	3	8	8	44	12
Others	13	22	14	23	30

Table 3.4: Friendship Frequencies (in percent) by Ethnicities in a Dutch High School; from Baerveldt et al [24].

For instance, the first column indicates that Dutch students form 79 percent of their friendships with other Dutch students, 2 percent of their friendships with Moroccan students, etc. Here we see "inbreeding" homophily through the high percentages occurring on the diagonals, which are higher than the relative percentages in population. This inbreeding can be due to biases in the interactions within the school that provide the opportunities to form friendships, and can also be influenced by the choices made by the students.[26] There are other factors influencing these tendencies, such as religious and economic background.[27]

3.2.7 The Strength of Weak Ties

The role of social networks in finding jobs was at the heart of some of the most influential research in the social networks area, which was conducted by Granovetter [289],

[26] See Currarini, Jackson and Pin [171] for evidence that both effects are present.

[27] See Baerveldt et al [24], Moody [458], Fong and Isajiw [234], Adamic and Adar [2], Fryer [244], and Currarini, Jackson and Pin [171] for more discussion and background on the factors influencing friendship formation.

[290]. He interviewed people in Amherst Massachusetts, across a variety of professions to determine how they found out about their jobs. He recorded not only whether they used social contacts in their employment searches, but also the strength of the social relationships as measured by frequency of interaction. He found that a surprising proportion of jobs were obtained through "weak ties" (as opposed to "strong" ones). There are various ways to measure the strength of a tie, but Granovetter's basic idea is that strength is related to the "amount of time, the emotional intensity, the intimacy (mutual confiding), and the reciprocal services which characterize the tie," (Granovetter [289] p. 1361). His measure of the strength of a tie was by the number of times that individuals had interacted in a past year (strong = at least twice a week, medium = less than twice a week but more than once a year, and weak = once a year or less). Out of the 54 people that Granovetter had detailed interviews with and who had found their most recent job through a social contact, he found that 16.7 percent had found their job through a strong tie, 55.7 percent through a medium tie, and 27.6 percent through a weak tie.[28]

Granovetter's idea was that individuals involved in a weak tie were less likely to have overlap in their neighborhoods than individuals involved in a strong tie. Such ties then are more likely to form bridges across groups that have fewer connections to each other, and can thus play critical roles in the dissemination of information. Granovetter concludes that weak ties are the glue that holds communities together, and in paradoxical contrast, strong ties lead to more local cohesion but then to more overall fragmentation.

There are numerous follow-up studies, including direct tests of some of the hypotheses put forth by Granovetter (e.g., see Friedkin [240]), as well studies of the roles of weak ties hypotheses in a variety of settings, from the diffusion of technological information to patterns of immigration. There remain many interesting and basic questions about the relative use of weak ties that are not fully answered or such that the answers vary across applications. For instance, given that individuals tend to have many weak ties (and for employed adults in large societies, conceivably orders of magnitude more weak ties than strong ties), how active should we expect weak ties to be in diffusing vital information? Are weak ties important solely because of their bridging behavior and information that they diffuse, or more generally because of other features they embody? And even more fundamentally, is it even generally true that individuals in-

[28] These are raw numbers and to keep these in perspective it is worth noting that we tend to have far more weak ties than strong ones.

volved in stronger ties are more likely to have strong overlap in their neighborhoods? Regardless of the answers to these and other related questions, Granovetter's work on the strength of weak ties makes it clear that the abstraction to simple 0-1 networks is a crude approximation of interaction structures, and that developing richer models capturing additional nuances of interaction frequency, duration, and heterogeneity, is important.

3.2.8 Structural Holes

Another important concept regarding the structure of networks is due to Burt [105] and concerns what he named "structural holes". A structural hole is a void in a social structure, and in terms of social networks refers to an absence of connections between groups. As Burt points out, this does not mean that the groups are unaware of each other, but instead that the lack of links between the groups leads to non-redundancies in the information between the groups and can also lead to a failure of diffusion between the groups. One of Burt's main points is that individuals who fill structural holes, by offering connections between otherwise separated or sparsely inter-connected groups, end up with power and control over the flow of information and favors between groups. For instance, Burt [106] offers evidence that filling structural holes leads to benefits in the form of promotion, bonuses, and other measures of performance networks of managers.

3.2.9 Social Capital

The term social capital has come to embody a number of different concepts related to how social relationships lead to individual or aggregate benefits in a society. The concept has been defined in many ways and applied many contexts, so that there is no tight and encompassing definition of social capital. For instance, in some incarnations it refers to the relationships that an individual has and the potential benefits that those relationships can bestow (e.g., Bourdieu [**?**]) and in others it refers to the aspects of broader social interaction (relationships, norms, trust,...) that facilitate cooperation (e.g., see Putnam [**?**]).[29] Although there is resonance in the idea that social networks and social relationships can translate into individual and societal benefits, and although various definitions of social capital can be useful in identifying the relationship

[29] Sobel [**?**] provides an insightful overview of the objectives, as well as the shortcomings, of the literature including some of the difficulties with various definitions.

between social structure and welfare, it is important to be precise in the definition and application of social capital, as the term has been so broadly and differentially used that it is not always clear what it means. While I will avoid the term social capital in most of what follows, many of the models that appear in this book, especially ones that directly relate social network structure to individual behavior and welfare, can be interpreted as capturing various aspects of social capital, operationally defined. There is much that remains to be done in terms of providing definitions and models of social capital that are incisive and yet still portable across applications.

3.2.10 Diffusion

One important role of social networks is as conduits of information. People often learn from each other, and this has important implications not only for how they find employment, but also about what movies they see, which products they purchase, how technology becomes adopted, whether or not they participate in government programs, whether they protest, and so forth. Many studies on the diffusion of innovation, including some classic early ones such as Ryan and Gross's [544] study of the diffusion of hybrid corn seed among Iowa farmers, and Hagerstrand's [**?**] examination of the diffusion of the telephone, have shown how important social contacts are in determining behavior.[30]

A classic study in this area that illustrates the relation between social structure and adoption of a new technology is that of Coleman, Katz, and Menzel [154]. They examined the adoption of a new drug by doctors in four cities over a period of fifteen months.[31] The adoption of the drug means that it was prescribed to a patient by the doctor, as found through pharmacists' records. The drug was first used in trials by a few "innovators" and subsequently was adopted by almost all of the doctors by the end of the study. Along with the information about adoption times, Coleman, Katz and Menzel interviewed the doctors to collect other information, including the type of each doctor's practice, his or her age, general prescription habits, etc.; as well as information about the doctor's social interaction. To get at the social network, Coleman, Katz and Menzel asked each doctor questions which, quoting Coleman, Katz, and Menzel [154], were: "To whom did he most often turn for advice and information?", "With whom did he most often discuss his cases in the course of an ordinary week?", and "Who were

[30] Rogers [536] provides a detailed overview of much of the research on diffusion.

[31] The data cover a period of seventeen months.

the friends, among his colleagues, whom he saw most often socially?". The interviewed doctors were asked to provide three names in response to each question.

Using the answers to these questions, and the time series data about adoption rates, Coleman, Katz and Menzel were able to deduce some things about how the time of adoption related to the social structure. For instance, they examined how the proportion of doctors who had adopted the drug depended on how many social contacts the doctors had.[32]

As summarized in the table below, after six months, among the 36 doctors who were not named as "friends" by any of the other doctors in their survey only one third had adopted the drug, while this ratio was just over one half for the 56 doctors named as friends by one or two of the other doctors, and the adoption ratio was over seventy percent for the 33 doctors names as friends by three or more other doctors. By ten months, the adoption rate among the doctors not named as friends was still just below fifty percent, while it as roughly seventy percent among doctors named as friends by one or two others, and ninety-four percent for the doctors named as friends by three or more others.

Table 3.5: Diffusion of Drug Among Doctors

	Named as Friend:		
Fraction adopting by:	by 0 others (36 subjects)	by 1 or 2 others (56 subjects)	by 3 or more others (33 subjects)
6 months	.31	.52	.70
8 months	.42	.66	.91
10 months	.47	.70	.94
17 months	.83	.84	.97

As with any data, one has to be careful about inferring causation from correlations; but the differences in adoption rates do indicate that the level of social integration as measured through this survey is related to the speed of adoption. As we shall

[32] The particular explanation for this relationship is not obvious. It appears from the study that there was information about the drug widely available, and so one must rely on other sorts of explanations for such a peer effect, for example, such as some sort of validation: one is more willing to prescribe if one knows a colleague that has prescribed, or that experience from colleagues is more trusted than studies and marketing information, etc. See Section **??** for more discussion.

see in Chapters 7 and 8, this is to be expected for a variety of reasons relating to position in a network. As one should intuitively expect, nodes with greater numbers of connections are more likely to hear information more quickly and can serve as conduits of information. In terms of empirical work, in order to determine the role of social structure in influencing behavior, one has to carefully sort out other factors which might be correlated with position in a network and influence behavior. This is often a challenge, as in any sort of empirical work where critical variables are endogenous.

Just as an indicator of how wide the variety of applications is where diffusion is important, consider a recent study by Cristakis and Fowler [**?**]. They examined a network of 12,067 people during a period from 1971 to 2003, based on data including both social relationships and health outcomes. Given that the data included weight at different times for the same individuals, they were able to examine whether weight gain by one individual correlated with weight gains of that individual's friends, while controlling for other factors that might have influenced weight gain. They reported a significant increase in the probability of a weight gain due to a friend's weight gain, which is not present when looking at close geographic proximity. While this leaves many questions of causation and interpretation open, it does suggest that network structure is important in understanding various forms of diffusion.

With some definitions and empirical background in hand, let us now turn to modeling network formation.

Chapter 4

Random Graph-Based Models of Networks

In this chapter, I discuss some of the workhorse models of static random networks and some of the properties that they exhibit. As we saw in the introductory chapter, randomly generated networks exhibit a variety of features that we see in the data, and through examining the properties of these models we can begin to trace traits of observed networks to characteristics of the formation process.

Models of random networks find their origin in the studies of random graphs by Solomonoff and Rapoport [576], Rapoport [526] and Erdös and Rényi [211], [212], [213]. The canonical version of such a model, a Poisson random graph, was discussed in Section **??**. The next chapter is a "sister" to this one, where I discuss a series of recent models of growing random networks that have arisen in an attempt match more of the properties, such as those discussed in Chapter 3, that are exhibited by many observed networks. Indeed, random-graph-based models of networks have been a primary tool in analyzing various observed networks. For example the network of high school romances described in Section 1.2.2 has a number of features that are well-described by a random network model, such as having a single giant component and then a large number of much smaller components and a few isolated nodes. Such random models of network formation help tie observed social patterns back to the structure of the inherent randomness and the process of link formation.

Beyond their direct use in analyzing observed networks, random network models also serve as a platform for modeling how behaviors diffuse through a network. For instance, the spread of a disease depends on the contact that various individuals have with each other. That spread can be very different depending on how much interaction

there is on average (e.g., do people interact with a few others or hundreds of others) as well as how it is distributed throughout the population (e.g., does everyone interact with roughly the same number of people, or are there some people who have contact with very large numbers while others have contact with very few). In order to understand how such diffusion works, one has to have a tractable model of what the link structure within a society looks like, and random graph models provide such a base. These models are not only be useful in understanding the diffusion of a disease, but also in modeling things like the spread of information, or decisions that are heavily influenced by one's peers (e.g., whether or not to go to college), as we shall see in more detail in Chapters 7 and 8.

Let me reiterate that random models of network formation are largely context-free, in that the nodes and processes for link formation are often simply governed by some given probabilistic rules. Some of these probabilistic rules have stories behind them, but this is not true of all such models. As such, these models are generally missing the social and economic incentives and pressures that underlie network formation, as discussed more fully in Chapter **??**. Nevertheless, these models are still quite useful for the reasons mentioned above, and they also serve as useful benchmarks. By keeping track of the properties that random-graph models of networks exhibit, and which ones they fail to exhibit, we end up with a useful reference point for building richer models, and also for understanding the strengths and weaknesses of models of networks that are tied to social and economic forces influencing individual decisions to form and maintain relationships.

The chapter starts with the presentation of a series of fundamental random graph models that have been useful in various aspects of network analyis. This includes variations on the basic Poisson random graph model that include correlations between links and allow richer degree distributions to be generated. Once these models have been described, I turn to presenting some of the properties of the resulting networks. This includes understanding how small changes in underlying parameters can lead to large changes in the properties of the resulting graphs (thresholds and "phase transitions"), as well as understanding when it is that resulting networks are connected, have a giant component, and other properties such as their diameter and clustering. The chapter concludes with an illustration of how random networks can be used as a basis for understanding the spread of contagious diseases or behaviors in a society.

4.1 Static Random-Graph Models of Random Networks

The term "static" refers to the fact that a model can be thought of as having all nodes present at the same time and then having links drawn according to some probabilistic rule. Poisson random graphs constitute one such static model. This class of "static" models contrasts with processes where networks "grow" over time. In such models new nodes are introduced over time, and form links with existing nodes as they enter. Such growing processes can result in properties that are different from those of static networks, and allow different tools for analysis. They are also naturally suited to different applications, and are discussed in detail in Chapters 4 and **??**.

4.1.1 Poisson and Related Random Network Models

The Poisson random graph model is one of the most extensively studied models in the static family. Closely related models are the ones mentioned in Section **??**, where a network is randomly chosen from some set of networks. For instance, out of the all the possible networks on n nodes, one could simply pick one completely at random, with each network having an equal probability. Alternatively, one could simply specify that the network should have M links, and then pick one of those networks at random with equal probability (that is, with each M link network having probability $\binom{N}{M}^{-1}$, where $N = \binom{n}{2}$ is the number of potential links among n nodes). Some of these different models of random networks turn out to have remarkably similar properties. On an intuitive level, if we examine a network where each link is formed with an independent probability p, we expect to have $pn(n-1)/2$ links formed (where $n(n-1)/2$ is the potential number of links). While we might end up with more or fewer links, with a large number of nodes, an application of the law of large numbers tells us that we will not deviate too much from this expected number of links in terms of the percentage formed. This turns out to be enough to guarantee that a model where links are formed independently has many things in common with a model where we force the network to have the expected number of links.[1]

[1] Let $G(n,p)$ denote the Poisson random graph model on n nodes with probability p of any given link, and $G(n,M)$ denote the model where a network with M links is chosen with a uniform probability over all networks of M links on n nodes. The properties of $G(n,p)$ and $G(n,M)$ are closely related for large n when M is near $pn(n-1)/2$. In particular, if $n^2p(1-p) \to \infty$, and a property holds for each sequence of M's that lie within $\sqrt{p(1-p)n}$ of $pn(n-1)/2$, then it holds for $G(n,p)$. The

While these networks are static in the way that they are generated, much of the analysis of such random networks concerns what happens when n becomes large. It is easy to understand why most results for random graphs are stated for large numbers of nodes. For example, in the Poisson random graph model, if we fix the number of nodes and some probability of a link forming, then every conceivable network has some positive probability of appearing. In order to talk sensibly about what might emerge, we want to make statements of the sort that networks exhibiting some property are (much) more likely to appear than networks that fail to exhibit that property. As such, most results in random graph theory concern the probability with which a network generated by one of these processes will have a given property as n goes to infinity. For instance, what is the probability that a network will be connected and how does this depend on how p behaves as a function of n? Many such results are proven by finding some lower or upper bound on the probability that a given property will hold, and then seeing if the bounds can be shown to converge to 0 or 1 as n becomes large.

We shall examine some of these properties for a general class of static random networks below.

Let me begin, however, by describing some variations of static random graph models other than the Poisson model that provide a feeling for the variety of such models and the motivations behind their development.

4.1.2 "Small World" Networks

While random graphs can exhibit some of the features of observed social networks, (e.g., diameters that are small relative to the size of the network when average degree grows sufficiently quickly), it is clear that random graphs lack some of the features that are prevalent among social networks, such as the high clustering discussed in Sections **??** and **??**. To see this, consider the Poisson random network model, and let us ask what its clustering will be. Suppose that i and j are linked and j and k are linked. What is the frequency with which i and k will be linked? Since link formation is completely independent, it is simply p. Thus, as n becomes large, if the average degree grows more slowly than n (which would be true in most "large" social and economic networks where there are some bounds on the number of links that agents can maintain) then it must be that p tends to 0 and so the clustering (both average and overall) will tend to 0.

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converse holds for a rich class of properties (called convex properties). See Chapter 2 in Bollobas [80] for detailed definitions and results along these lines.

Figure 4.1.2. A Ring Lattice on 25 Nodes with 50 Links

With this in mind, Watts and Strogatz [623] developed a variation of a random network that showed that it only takes a small number of randomly placed links in a network to generate a small diameter. They combined this with a highly regular and clustered starting network in order to generate networks that simultaneously exhibit high clustering and low diameter, a combination observed in many social networks. Their point is easy to see. Suppose we start with a very structured network that exhibits a high degree of clustering. For instance, let us construct a large circle, but then connect a given node to the nearest four nodes rather than just its nearest two neighbors, as in Figure 4.1.2.

In such a network, each node's individual clustering coefficient will be 1/2. To see this, consider some set of consecutive nodes 1, 2, 3, 4, 5, that are part of such a network for a large n. Consider node 3, which is connected to each of nodes 1,2, 4 and 5. Out of all the pairs of 3's neighbors $(\{1,2\},\{1,4\},\{1,5\},\{2,4\},\{2,5\},\{4,5\})$, we see that half of them are connected $(\{1,2\},\{2,4\},\{4,5\})$. Here, as we let n grow, the clustering (both overall and average) will stay at 1/2. By adjusting the structure of the local connections we can also adjust the clustering.

While this sort of regular network exhibits high clustering, it fails to exhibit some

Figure 4.1.2. A Ring Lattice on 25 Nodes Starting with 50 Links and Rewiring 6

of the other features of many observed networks, such as a small diameteter and at least some variance in the degree distribution. The diameter of such a network is on the order of $n/4$. The main point of Watts and Strogatz [623] is that by randomly re-wiring relatively few links, we can end up with a network that has a much smaller diameter but still has substantial clustering. The re-wiring can be done by randomly selecting some link ij and disconnecting it and then randomly connecting i to another node k chosen uniformly at random from nodes which are not already neighbors of i. Of course, as more such re-wiring is done, the clustering will eventually vanish. The interesting region is where enough re-wiring has been done to substantially reduce (average and maximal) path length, but not so much that clustering vanishes.

Here we see that after having rewired just six links the diameter of the network has decreased from 6 in the network pictured in Figure 4.1.2 to 5 in the network pictured in Figure 4.1.2, with minimal impact on the clustering. Note also that in the network in Figure 4.1.2 every node is at distance 6 from three other nodes (e.g., node 1 and nodes 13, 14, and 15), so it is not simply that the rewiring has shortened a few long paths, but rather that these new links shorten many paths in the network, as there are 39 pairs of nodes at a distance of 6 from each other in the original network, which are

all moved closer to each other by the rewiring. This example is suggestive, and Watts and Strogatz perform simulations to provide an idea of how this works for ranges of parameters.

This model of networks makes an interesting point in showing how clustering can be maintained in the presence of enough random link formation to produce a low diameter. The model also has obvious shortcomings, in particular in that the degree distribution is essentially a convex combination of a degenerate distribution with all weight on a single degree and a Poisson distribution. Such a degree distribution is fairly particular, and not often observed in social networks. I return to discuss alternative models that better match observed degree distributions in Sections **??** and **??**.

4.1.3 Markov Graphs and p* networks

Next, I describe a generalization of Poisson random graphs that has been useful in statistical analysis of observed networks and was introduced by Frank and Strauss [236]. They called this class of graphs "Markov graphs", and such random graph models were later imported to the social networks literature by Wasserman and Pattison [616] under the name of p* networks, and further studied and extended in various directions.[2] The basic motivation is to provide a model that can be statistically estimated, and still allows for specific dependencies between the probabilities with which different links form.

Again, one important aspect of introducing dependencies is related to clustering, since Poisson random networks with average degrees growing more slowly than the number of nodes have clustering ratios tending to zero, which are too low to match many observed networks. Having dependences in the model can produce nontrivial clustering.

Conditional dependencies can be introduced so that the probability of a link ik depends on whether ij and jk are present. The obvious challenge is that such dependencies will tend to interact with each other in ways that could make it impossible to specify the probability of different graphs in a tractable manner. For instance, if the conditional probability of a link ik depends on whether ij and jk are present, but also on any other adjacent pairs being present, and the conditional probability of jk depends on other adjacent pairs being present, etc.; we end up with a complicated set

[2] For instance, see Pattison and Wasserman [509] for an extension to multiple interdependent networks on a common set of nodes.

of dependencies. The important contribution of Frank and Strauss [236] is to make use of a theorem by Hammersley and Clifford (see Besag [55]) to derive a simple log-linear expression for the probability of any given network in the presence of arbitrary dependencies.

One of the more useful results of Frank and Strauss [236] can be expressed as follows. Consider n nodes, and keep track of the dependencies between links by another graph, D, which is a graph among all of the $n(n-1)/2$ possible links.[3] So, D is not a graph on the original nodes, but a graph whose nodes are all the possible links. The idea is that if ij and jk are neighbors in D, then there is some sort of conditional dependency between them, possibly in combination with other links. Thus, D captures which links are dependent on which others, possibly in quite complicated combinations. For example, the Poisson random graph model is one where D is empty, as all links are independent. If instead, we wish to capture the idea that there might be clustering, then we would like the link ik to depend on the presence of ij and kj for each possible j. Thus, D would have ik connected to each other link that contains either i or k.

Let $C(D)$ be all the cliques of D; that is, all of the completely connected subgraphs of D (where the singleton nodes are considered connected subgraphs). So, in the case of a Poisson random graph $C(D)$ would simply be the set of all links ij. In the case of the clustering dependence just mentioned above, the set $C(D)$ would include all individual links and also all of the triads (sets of the form $\{ij, jk, ik\}$). Given a generic element $A \in C(D)$, let $I_A(g) = 1$ if $A \subset g$ (viewing g as a set of links), and $I_A(g) = 0$ otherwise. So, if A is a triad $\{ij, jk, ik\}$, then $I_A(g) = 1$ if each of the links ij, jk and ik are in g, and $I_A(g) = 0$ otherwise. Then, Frank and Strauss show that Hammersley and Clifford's theorem implies that the probability of a given network g depends only on which cliques of D it contains, and that it can be written as

$$log(\Pr[g]) = \sum_{A \in C(D)} \alpha_A I_A(g) - c, \tag{4.1}$$

where c is a normalizing constant, and the α_A's are other free parameters.

In general, given that D can be very rich and that the α_A's can be chosen at will, this allows for an almost arbitrary probability specification. The difficulty and art in applying this type of model in practice is in specifying the dependencies sparingly and imposing restrictions on the α_A's so that the resulting probabilities are simple and

[3] This is easily adapted to directed links, by having D be a graph on the $n(n-1)$ possible directed links.

practical. For certain kinds of dependencies, the expressions can be quite simple and useful (e.g., see Anderson, Wasserman and Crouch (1998)).

To see how the expressions can simplify, let us consider the clustering dependency we mentioned above. This means that $C(D)$ is just the set of all links and all triads (triplets of the form $\{ij, jk, ik\}$). To simplify things further, let us also suppose that there is a symmetry among nodes, so that the probability of any two networks that have the same architecture but possibly different labels on the nodes is identical. This means that the α_A's are the same across all A's that correspond to single links, and the same across all A's that correspond to triads. Thus, the expression in 4.1 simplifies substantially. Let $n_1(g)$ be the total number of links in g, and let $n_3(g)$ be the total number of completed triads in g. Then there exist α_1, α_3 and c such that (4.1) becomes

$$log(\Pr[g]) = \alpha_1 n_1(g) + \alpha_3 n_3(g) - c.$$

This then provides us with a simple generalization of Poisson random graphs (which are the special case where $\alpha_3 = 0$), which will allow us to control the frequency of clusters. That is, we can adjust the parameters so that graphs that have more substantial clustering will be relatively more likely than graphs that have less clustering (for instance, by increasing α_3).[4]

While such a model can be cumbersome as we try to capture more complicated dependencies, it still provides a powerful statistical tool for testing for the presence of some specific dependency.[5] One can test for significant differences between fits of a model where such dependencies are present and a model where such dependencies are absent. Obviously, the validity of the test depends on the appropriateness of the basic specification of the model, as it could be that the model is not a very good fit with or without the dependencies, and so the comparison is invalidated.[6]

4.1.4 The Configuration Model

While the Markov model of random networks allows for general forms of dependencies, it is hard to keep track of the degree distribution that it will generate, and to adjust

[4] See Park and Newman (2004) for some derivations of clustering probabilities for this example.

[5] There are other such models designed for statistical analysis, as well as associated Monte Carlo estimation techniques, as for instance in Handcock and Morris [303].

[6] There are some challenges in estimating such models. A useful technique is proposed by Snijders [572], based on a Monte Carlo style simulation of the model and sampling of those simulations and then using an algorithm to approximate the maximum likelihood fit.

that to match observed networks. In order to generate random networks with a given degree distribution, various methods have been proposed. One of the most widely used is what is referred to as the "configuration model," as developed by Bender and Canfield [49]. The model has been further elaborated on and used by Bollobás [80], Wormwald [**?**], Molloy and Reed [449], Newman et al [**?**], among others.

To see how the configuration model works, it is useful to work with degree sequences rather than degree distributions. That is, given a network on n nodes, we end up with a list of the degrees of different nodes: $(d_1, d_2, \ldots, d_n)$, which is the *degree sequence*.

Now suppose that we have an idea of the degree sequence $(d_1, d_2, \ldots, d_n)$ that we wish to generate in a network of n nodes. This is directly tied to the degree distribution, so that the proportion of nodes that have degree d in this sequence is $P^n(d) = \#\{i : d_i = d\}/n$.

Construct a sequence where node 1 is listed d_1 times, node 2 is listed d_2 times, etc.:

$$\underbrace{1,1,1,1,1,1,1,1,1,1,1,1,1}_{d_1 \text{ entries}} \quad \underbrace{2,2,2,2,2,2}_{d_2 \text{ entries}} \quad \ldots \quad \underbrace{n,n,n,n,n,n,n,n,n,n,n,n}_{d_n \text{ entries}}$$

Now randomly pick two elements of the sequence and form a link between the two nodes corresponding to those entries. Delete those entries from the sequence in 4.1.4 and repeat.

There are a few things to note about this procedure. First, it is possible to have more than one link between two nodes. As such, it generates what is called a multi-graph (allowing for multiple links) instead of a graph. Second, self links are possible and may even occur multiple times, while we have generally been ignoring self links in our discussion of networks up to this point. Third, as a more minor point, the sum of the degrees needs to be even or else there will be a leftover entry at the end of the process.

Despite these difficulties, this process still has nice properties for large n. There are two different ways in which we can work with this from our perspective of understanding randomly generated networks. One is to work directly with multi-graphs instead of graphs, and then try to show that multi-graphs generated (under suitable assumptions on the degree sequence) will have essentially the same properties as a randomly selected graph with the same degree sequence. Another is to generate a multigraph, and then from it delete self-links and duplicate links between two nodes. This is then a graph, and if the proportion of links we needed to delete is suitably small, then we end up with a graph with a degree distribution close to what we started with.

With this in mind, let us make the idea of growing the sequence more explicit. We can begin with an infinite degree sequence $(d_1, d_2, d_3, \ldots)$ and then dicuss increasing portions of the sequence. Let q_i^n denote the number of links that node i ends up with that are either self-links or duplicate links when the configuration model is operated on the first n nodes. Then let Q_i^n denote the probability that under the configuration model node $i \leq n$ ends up with at least one self-link or duplicate link, so that $Q_i^n = \Pr[q_i^n > 0]$. We can then show the following.

PROPOSITION **4.1.1** *If a degree sequence* $(d_1, d_2, d_3, \ldots)$ *is such that* $\max_{i \leq n} d_i/n^{1/3} \to 0$*, then* $\max_{i \leq n} Q_i^n \to 0$.

This proposition is not true if we drop the restriction that $\max_{i \leq n} d_i/n^{1/3} \to 0$ (see Exercise **??**). The reason is that if some nodes have degrees that are too large relative to n then nontrivial portions of the links involve these nodes, and then the probability of self-links and/or multiple links can be nontrivial. Thus, while the configuration model is a useful network model when the degrees of nodes are not growing too large relative to the number of nodes, one has to be careful about the degree sequences that are admitted in order to have the resulting multi-graph be "close" to a graph.

The proposition establishes that if $\frac{\max_{i \leq n} d_i}{(n\langle d \rangle)^{1/3}}$ tends to 0, then the chance that any given node (including the largest ones) has a duplicate or self-link tends to 0. From this proposition, we can deduce that if we delete multiple links and self-links from the resulting multi-graph, we end up with a network where the proportion of nodes having the correct degree approaches 1 as the number of nodes grows, and the resulting degree distribution converges to the desired degree distribution (pointwise, if there is an upper bound on degrees). However, this does not imply that the multigraph will be a graph. When one aggregates across many nodes, there will tend to be some duplicate and self-links in this process, except under more extreme assumptions on the degree sequences; but there will not be many of them relative to the total number of links. To explore this in more detail, let us consider different statements that we could envision about the probability of self-links or multiple links under the configuration model:

(1) Fixing a node and its degree, as the the number of nodes grows the probability that the given node has any self or multiple links vanishes. That is, $Q_i^n \to 0$.

(2) The maximum probability across the nodes of having any self or multiple links vanishes. That is, $\max_{i \leq n} Q_i^n \to 0$.

(3) The fraction of nodes that have self-links or duplicate links goes to 0. That is, for any $\varepsilon > 0$, $\Pr\left[\#\{i \leq n : q_i^n > 0\}/n > \varepsilon\right] < \varepsilon$ for large enough n.

(4) The fraction of links that are self-links or duplicate links goes to 0. That is, for any $\varepsilon > 0$, $\Pr\left[\sum_{i \leq n} q_i^n / \sum_{i \leq n} d_i > \varepsilon\right] < \varepsilon$ for large enough n.

(5) The probability of seeing any self or multiple links vanishes. That is, $\Pr\left[\sum_{i \leq n} q_i^n > 0\right] \to 0$.

It is easy to see that (1) is true for any degree sequence, presuming that the sequence includes an infinite number of nodes with positive degree. (2) is what is shown in this proposition, and this then implies (3) based on an argument that the when the probability across nodes of having self or duplicate links goes to 0 uniformly across nodes, then it is impossible to expect a nontrivial fraction of nodes to have self or multiple links (see Exercise **??**). A similar argument establishes (4) (see Exercise **??**). The statement that would make our lives easiest in terms of ending up with a graph instead of a multigraph, (5), is only true under extreme conditions. To see why this (5) will generally fail, consider a degree sequence of $(2, 2, 2, \ldots)$, which is about as well-behaved as one could want in terms of having a good chance of avoiding self and duplicate links. Let us argue that even for this regular degree sequence there is still a nontrivial limiting probability of having at least one self-link. Here the probability that any given link is not a self link is $1 - \frac{1}{2n-1}$. To see this, think of starting by connecting one end of the link to some node, and then there are $2n - 1$ equally likely entries in the full sequence of points where we can attach the other end of this link to under the configuration model (see diagram **??**). Only one of these leads to a self-link. As we form links, continue to think of them as being formed in this way: randomly pick an entry to be one end of the link, and then pick a second entry for the other end. Now, as we proceed, regardless of how things work out, there will be at least $n/2$ links where the initial node that we picked for the first end of the link does not yet have any link attached to it. For each of these links, an upper bound on the probability of not ending up with a self-link is $1 - \frac{1}{2n-1}$. So, we have an upper bound on the probability of not ending up with any self-links in the whole process which is $\left(1 - \frac{1}{2n}\right)^{n/2}$ which converges to $e^{-1/4}$.

The nice implication of (3) is that we work with a degree sequence that has a nice limiting degree distribution $P(d)$,[7] if we generate a network through the configuration

[7] There are various definitions of a limiting distribution that we could work with. For instance, it

model and delete duplicate and self links, then proportion of nodes that have degree d converges almost surely to $P(d)$ (so $\Pr[\lim_n |p^n(d) - P(d)| = 0] = 1$, where $p^n(d)$ is the realized proportion of nodes with degree d after the deletion of duplicate and self-links).

Proof of Proposition 4.1.1: Let $\widehat{d^n} = \max_{i \leq n} d_i$ be the maximum degree up to node n and $\langle d \rangle^n = \frac{\sum_{i \leq n} d_i}{n}$ be the average degree through node n. We can find a bound for the probability that any given node ends up with a self-link or a duplicate link. First, instead of thinking of the configuration process as picking two entries at random and matching them and then iterating, imagine instead that we start by picking the first entry of the first element and randomly choosing a match for it, and then movie on to the second remaining entry, and so forth. It is not hard to see that this leads to the same distribution over matchings and thus of links. Consider the first node and its first link (isolated nodes can be discarded). The chance that the link is not a self-link or duplicate link (so far) is $1 - \frac{d_1 - 1}{n\langle d \rangle^n - 1}$, as we only need to worry about self-links. This is greater than $1 - \frac{\widehat{d^n}}{n\langle d \rangle^n - \widehat{d^n}}$. The chance that the second link (if it has degree above 1) is not a self-link or duplicate link (so far), presuming the first one is not a self-link, is then $1 - \frac{d_1 - 2}{n\langle d \rangle^n - 2} - \frac{d_i - 1}{n\langle d \rangle^n - 2}$, where d_i is the degree of the node that the first link went to. This is greater than $1 - \frac{2\widehat{d^n}}{n\langle d \rangle^n - \widehat{d^n}}$. Continuing in this manner, we end up with a lower bound on the probability of self or duplicate links of

$$\prod_{j=1,\ldots,\widehat{d^n}} \left(1 - \frac{j\widehat{d^n}}{n\langle d \rangle^n - \widehat{d^n}}\right).$$

This is larger than

$$\left(1 - \frac{(\widehat{d^n})^2}{n\langle d \rangle^n - \widehat{d^n}}\right)^{\widehat{d^n}}.$$

If $\frac{\widehat{d^n}}{(n\langle d \rangle^n - \widehat{d^n})^{1/3}}$ tends to 0, then we can approximate the above expression by[8]

$$e^{-(\widehat{d^n})^3/(n\langle d \rangle^n - \widehat{d^n})}$$

which tends to 1 if (and only if) $\frac{\widehat{d^n}}{(n\langle d \rangle^n)^{1/3}}$ tends to 0. ∎

could be that $P_n(d)$ converges to $P(d)$ for each d, but that it takes much longer to get to the limit for some d's compared to others. To make the above statement precise, consider a form of uniform convergence where $\max_d |P^n(d) - P(d)| \to 0$. We can also work with other (weaker) definitions of convergence, such as pointwise convergence and also to what is known as weak convergence, or convergence in distribution (e.g., see Billingsley [63]).

[8] We can approximate $(1 - \frac{r}{x})^x$, when $r \to 0$ and x does not decrease, by e^{-r}. See Section **??** for approximating expressions.

4.1.5 An Expected Degree Model

Chung and Lu [145] [146] provide a different random model that also approximates a given desired degree sequence. The advantage of this process is that it forms a graph instead of a multigraph, although it still allows for self loops and does not result in the exact degree sequence, even asymptotically.

Once more, start with n nodes and a desired degree sequence $\{d_1, \ldots, d_n\}$. Form a link between nodes i and j with probability $d_i d_j / (\sum_k d_k)$, where the degree sequence is such that that $(\max_i d_i)^2 < \sum_k d_k$, so that each of these probabilities is less than 1.

It is clear that any node i's expected degree is indeed d_i (when a self-link ii is allowed to form with probability $d_i^2 / \sum_k d_k$).

To get a better feeling for the differences between the configuration model and the Chung-Lu process, consider a degree sequence where all nodes have the same number of links $k = \langle d \rangle$. Let us first consider the configuration model, where we delete self and duplicate links. As we argued above, the probability that any given node has no duplicate links or self links, and hence degree exactly k, converges to 1. From here it is not difficult to conclude that with a probability going to 1, the proportion of nodes with degree k will also converge to 1. Under the Chung-Lu process, although the expected degree of any given node is k (and approaches this if we exclude self links), the chance that it ends up with exactly k links is bounded away from 1, regardless of whether we allow self links. To see this, note that the number of links to other nodes for any node follows a binomial distribution on $n-1$ draws with a probability of k/n. As the probability of self links vanishes, the probability that the degree is the same as the number of links excluding self links approaches 1. However, even as n becomes large, a binomial distribution of $n-1$ draws with probability k/n places a probability bounded away from 1 on having exactly k links. In fact, this is effectively the same as having a Poisson random network! The probability of having exactly k links can be approximated from a Poisson approximation (recall (1.4)), and we find a probability on the order of $\frac{e^{-k}(k)^k}{k!}$, which is maximized at $k = 1$ and always less than $1/2$. This tells us that the realized degree distribution will differ significantly from the distribution of the expected degree sequence, which places full weight on degree k.

While the configuration process (under suitable conditions) leads to a degree distribution more closely tied to the starting one, the Chung-Lu expected degree process is still of interest and more naturally relates to the Poisson random networks. Both are useful.

4.1.6 Some Thoughts about Static Random Network Models

The configuration model and the expected degree model are effectively algorithms for generating random networks with desired properties in terms of their degree sequences. They will generally lack the observed clustering and correlation patterns that were discussed in Chapter 3, as the links are formed without paying attention to anything except relative degrees. A node forms links to two other nodes who are connected to each other purely by chance, and not because of their relation to each other. They are also severely limited as models of how social and economic networks form, since they miss the incentives and forces that influence the formation of relationships; as the models describe a world governed completely and uniformly by chance. So, why study such random graph models? One of the biggest challenges in network analysis is developing tractable models. The combinatorial nature of networks that exhibit any heterogeneity makes them complex animals. Much of the theory starts by building up from simple models and techniques, and seeing what can be carried further. These two models represent important steps in generalizing Poisson random graphs, and we can see that some of the basic properties of Poisson random graphs do generalize to some richer degree distributions, and we get a better understanding of how degree distributions relate to other properties of networks. Although there are more things that we will introduce to the models, but there is still much to be learned from looking at these relatively simple generalizations of the Poisson model. As we shall see, these models will be workhorses in providing foundations for understanding diffusion in a network, among other things.

4.2 Properties of Random Networks

If we fix some number of nodes n, and then try to analyze the properties of a resulting random network, we run into some difficulties. For instance, if we examine the Poisson random network model, then each possible network has a postive probability of being formed. While some are much more likely than others, it is difficult to talk about what properties the resulting network will exhibit since everything is possible. We could try to sort out which properties are "likely" to hold and how this depends on the probability with which links are formed, but for a fixed n the likelihood of a given property holding will often be a complicated expression that will be difficult to interpret. One technique for dealing with this issue is to resort to computer simulations where a large number of

random networks are generated according to some model to estimate probabilities of different properties being exhibited on some fixed number of nodes. Another technique is to examine the properties of the network at some limit, for instance as the number of nodes tends to infinity. If one can show that a property does (or does not hold) at the limit, then one can often conclude that the probability of it holding for a large network is close to 1 (or 0). Simulations are useful in a number of ways. For instance, it can be that even limiting properties are hard to ascertain analytically, and then simulations provide the only real tool for examining a property. It could also be that we are interested in a relatively small network, or that we want to see how the probability of a given property being exhibited varies with parameters and the size of the population. As simulation techniques are more straightforward, I illustrate them at different points in what follows. The alternative approach of examining the limiting properties of large networks requires the development of some tools and concepts which I now discuss.

4.2.1 The Distribution of the Degree of a Neighboring Node

In a variety of applications, one is faced with the following sort of calculation. Start at some node i with degree d_i. Consider a neighbor j. How many neighbors do we expect j to have? This is important in estimating the size of i's expanding neighborhoods, in keeping track of contagion and transmission of beliefs, in estimating diameters, and many other calculations. Basically, any time that we consider some process that moves through the network and we wish to keep track of how many lins it expects to have to be able to follow at a next step, this is an important sort of calculation.

To understand such calculations, let us start by examining the following related calculation. Suppose that we randomly select a link from a network and then randomly pick one of the nodes at either end of the link. What is the conditional probability that describes that node's degree? If the network has a degree distribution described by P, the answer is *not* simply P. To understand this, let us start with a simple case where the network is such that $P(1) = \frac{1}{2} = P(2)$. So, one half of the nodes have degree 1 and one have have degree 2. For instance, a network on four nodes with links: $\{12, 23, 34\}$. While the degree distribution is $P(1) = \frac{1}{2} = P(2)$, it is easy to see that if we randomly pick a link and then randomly pick an end of it, there is a $\frac{2}{3}$ chance that we find a node of degree 2 and a $\frac{1}{3}$ chance that we find a node of degree 1. This just reflects the fact that higher degree nodes are involved in a proportionately higher percentage of the links. In fact, their degree determines relatively how many more links they are involved with. In particular, if we randomly pick a link and a node at the end of it,

and we consider two nodes of degrees d_j and d_k, then node k is relatively d_k/d_j times more likely to be the one we find than node j. Extrapolating, it is easy to see that the distribution of degrees of a node found by choosing a link uniformly at random from a network that has degree distribution P and then picking either one of the end nodes with equal probability is

$$\widetilde{P}(d) = \frac{P(d)d}{\langle d \rangle} \tag{4.2}$$

where $\langle d \rangle = E_P[d] = \sum_d P(d)d$ is the expected degree under the distribution P.

This means that simply randomly picking a node from a network, and finding nodes by randomly following the end of a link, are two very different exercises. One is much more likely to find high degree nodes by following the links in a network than by randomly picking a node.

Now let us return to the question we started with: let us start at a node i with degree d_i and examine the distribution of the degree of one of its randomly selected neighbors. If we consider either the configuration or expected degree models, and we let the number of nodes grow large and have the degree distribution converge (uniformly) to P, then the answer will converge to the $\widetilde{P}$ described in (4.2). This is true since the degrees of two neighbors are approximately independently distributed for large networks provided the largest nodes are not too large.[9] This is also true in the Poisson random networks of Erdös and Rényi. We can also directly deduce that the distribution of the *expected* degree of the node at a given end of any given link (including self-links) under the Chung-Lu process is exactly given by $\widetilde{P}$. However, this might not match the distribution of degree of the node at a given end of any given link. As an example, under the Chung-Lu process if we have $P(2) = 1$, so that all nodes have an expected degree of 2, some nodes will end up with more than two links and some with less. There, $\widetilde{P}$ places probability 1 on having degree 2. If we rewrite P to be the realized degree distribution, then for large n, (4.2) provides a good approximation of the degree of a neighbor.

However, it is important to note that (4.2) does not provide the right calculation for many prominent models of growing random networks (such as those coming from preferential attachment) that are discussed in Chapter **??**. In those random networks there is nonvanishing correlation between the degrees of nodes, so that higher degree

[9] To see why this is only approximate, consider any given degree sequence and for the expected degree model. Say that there are n_d nodes with degree d. One of those nodes can only be connected to $n_d - 1$ nodes with degree d, while a node with degree $d' \neq d$ can be connected to n_d nodes with degree d. So, here we actually see a (slight) negative correlation in the degrees of neighboring nodes.

nodes tend to have neighbors with higher degrees than do lower degree nodes.

To see how correlation can change the calculations, consider two different methods of generating a network with a degree distribution such that half of the nodes have degree 1 and half have degree 2. First, generate such a network by operating the configuration model on a degree sequence of $(1, 1, 2, 2, 1, 1, 2, 2, 1, 1, 2, 2, 1, 1, 2, 2 \ldots)$.[10] In this case, it is clear that picking any node and asking what the degree of a randomly selected neighbor is has an answer that converges to a $\frac{2}{3}$ chance that it is a node of degree 2 and a $\frac{1}{3}$ chance that it is a node of degree 1.

Second, consider the following very different way of generating a network with the same degree distribution. Start with eight nodes. Connect four of them in a square, so that they each have degree 2 and have two neighbors each with degree 2. Connect the other four of them in two pairs, so that each has degree 1 and has a neighbor with degree 1, as in Figure 4.2.1. Now replicate this process. We end up with the same degree distribution, so that half of the nodes are of degree 1 and half of degree 2, but nodes are segregated so that nodes with degree 1 are only connected to nodes of degree 1, and similarly nodes of degree 2 are only connected to nodes of degree 2. Here, the degree of a node's neighbor is perfectly correlated with that node's degree. Note also that if we examine the degree of a neighbor of a randomly picked node in Figure 4.2.1, we end up with an equal probability that it will have degree 1 or degree 2! That is, if we examine nodes 1 to 4, then any randomly selected neighbor will have degree 2, while if we examine nodes 5 to 8, then any randomly selected neighbor will have degree 1. So, the distribution of a node's neighbor's degree is quite different from $\widetilde{P}$, regardless of whether we condition on the starting node's degree or whether we simply pick a node uniformly at random and then examine one of its neighbors' degrees.

While this example is stark, it illustrates that we do need to be careful in keeping track of how a network was generated, and not only its degree distribution, in order to properly calculate things like the distribution of degrees of neighboring nodes.[11]

[10] For this calculation, let us work with the resulting multigraph, so that we allow for self-links and duplicate links, and so that the degree distribution is exactly realized when the number of nodes is a multiple of four.

[11] A caution here is that some of the literature proceeds with calculations as if there were no correlation between neighboring nodes, even though some of the models (like preferential attachment discussed in Chapter **??**) used to motivate the analysis generate significant correlation. Using a variation on the configuration model is one approach to avoiding such problems, but it does limit the scope of the analysis.

Figure 4.2.1. Forming Networks with Perfect Correlation in Degrees

4.2.2 Thresholds and Phase Transitions

When we examine random networks on a growing set of nodes and for some given parameters or structure, often properties hold with either a probability approaching 1 or a probability approaching 0 in the limit. So, while it may be difficult to figure out the precise probability that some property holds for some fixed n, it is often much easier to discern whether that probability is tending to 1 or 0 as we let n approach infinity.

To see how this works, let us consider the Poisson random network model on a growing set of nodes n, where we index the probability of a link forming as a function of n, denoted $p(n)$. It is quite natural to have the probability of a link forming between two nodes vary with the size of the population. For example, if we imagine that people have on average several thousand acquaintances, then we might need p to be on the order of one percent if we are dealing with an n that includes a few hundred thousand nodes, but more on the order of a fraction of a percent if we are dealing with a population of millions of nodes. So, for instance if we want to keep average degree constant as the number of nodes grows then we need $p(n)$ to be proportional to $1/n$. With a $p(n)$ in hand, we can ask what the probability is that a given property holds as

$n \to \infty$. Interestingly, many properties hold with a probability that approaches either 0 or 1 as the number of nodes grows, and the probability that a property holds can shift sharply between these as we change the underlying random network process. For example, we can ask what the probability is that a network will have some isolated nodes. For some random network formation processes if the network is large then it will be almost certain that there will exist some isolated nodes, while for other network formation processes it will be almost certain that the resulting network will not have any isolated node. We will see that this sharp dichotomy will be true of a variety of properties such as whether the network has a giant component, or has a path between any two nodes, or has at least one cycle, etc. There are also many exceptions, in terms of properties that do not exhibit such convergence patterns. For instance, consider the property that a network has an even number of links. For many random network processes, the probability of this property holding will be bounded away from 0 and 1.

There are different ways of specifying a property, but an easy way is just to list the networks that satisfy it. Thus, properties are generally specified as a set of networks for each n, and then a property is satisfied if the realized network is in the set. Thus a property is a list of $A(N) \subset G(N)$ listing the networks that have the property when the set of nodes is N. So, for instance, the property that a network has no isolated nodes is

$$A(N) = \{g \mid N_i(g) \neq \emptyset \forall i \in N\}.$$

Most properties that are studied are referred to as *monotone or increasing properties*. Those are properties such that if a given network satisfies the property, then any supernetwork (in the sense of set inclusion) satisfies it. So a property $A(\cdot)$ is monotone if $g \in A(N)$ and $g \subset g'$ implies that $g' in A(N)$. The property of having an even number of links is obviously not a monotone property, while the property of being connected is a monotone property.

If we work in the Poisson model, then the model is completely specified by $p(n)$ where n is the cardinality of the set of nodes N. In that case, a *threshold function* for some given property is a function $t(n)$ such that the property holds with a probability approaching 1 (i.e., $\Pr[A(N)|p(n)] \to 1$) if $p(n)/t(n) \to \infty$, while the property holds with a probability approaching 0 (i.e., $\Pr[A(N)|p(n)] \to 0$) if $p(n)/t(n) \to 0$. When such a threshold function exists, it is said that a *phase transition* occurs at that threshold.[12] Even when there are not sharp threshold functions, we can still often produce

[12] There are different sorts of probabilistic statements that one can make, analogous to differences between the weak and strong laws of large numbers. That is, it can be that the as n grows the

lower or upper bounds so that we know that a given property holds for $p(n)$'s above or below those bounds.

This definition of a threshold function is tailored to the Erdös-Rényi or Poisson random network setting, as it is based on having a function $p(n)$ describe the network formation process. We can also define threshold functions for other sorts of random network models, but they will be relative to some other description of the random process, generally characterized by some parameter(s).

To get a better feeling for a threshold function, let us consider a relatively simple one. Let us consider the property that node 1 has at least one link; that is the property described by $A(N) = \{g \,|d_1(g) \geq 1\}$. In the Poisson model, the probability that node 1 has no links is $(1-p(n))^{n-1}$ and so the probability that $A(N)$ holds is $1-(1-p(n))^{n-1}$. To derive a threshold function, we just need to see for which $p(n)$ this tends to 0 and for which $p(n)$ this tends to 1. If we consider $t(n) = \frac{r}{n-1}$, then by a definition of the exponential function (see Section **??**), the limit of the probability that node 1 has no links is

$$\lim_n (1 - t(n))^{n-1} = \lim_n \left(1 - \frac{r}{n-1}\right)^{n-1} = e^{-r}. \tag{4.3}$$

So, if $p(n)$ is proportional to $\frac{1}{n-1}$, then there will be a probability that node 1 has at least one link that is bounded away from 0 and 1 in the limit. Thus, $t^*(n) = \frac{1}{n-1}$ is a function that could potentially serve as a threshold function. Let us check that $t^*(n) = \frac{1}{n-1}$ is in fact a threshold function. Suppose that $p(n)/t^*(n) \to \infty$. This implies that $p(n) \geq \frac{r}{n-1}$ for any r and large enough n. Therefore, from (4.3) it follows that $\lim_n (1 - p(n))^{n-1} \leq e^{-r}$ for all r, and so $\lim_n (1 - p(n))^{n-1} = 0$. Similarly, if $p(n)/t^*(n) \to 0$, then an analogous comparison implies that $\lim_n (1 - p(n))^{n-1} = 1$. Thus, $t^*(n) = \frac{1}{n-1}$ is a threshold function for a given node having neighbors in the Poisson random network model.

Note that the threshold function is not unique here, as $t(n) = an + b$ for any fixed a and b will also provide the same conclusion. Moreover, threshold functions provide

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probability of a property holding goes to one. This is the "weak" form of the statment. The stronger form of the statement reverses the order between the probability and the limit, stating that the probability that the property holds in the limit is one. This is also stated as having something hold *almost surely*. For many applications this difference is irrelevant, but in some cases it can be an important distinction. In most instances in this text, I will claim or use the weaker form, as that is generally much easier to prove and one can work with a series of probabilities, which keeps the exposition relatively clear, rather than having a probability defined over sequences. Nevertheless, many of these claims hold in their stronger form.

only conclusions about the how large or small $p(n)$ has to be in terms of its limiting order and only provide limiting conclusions. How large n has to be in order for the property to hold with a high probability depends on more detailed information. For instance, $p(n) = e^{-n}$ and $p(n) = \frac{1}{n^{1.0001}}$ both lead to probabilities of 0 that node 1 will have any neighbors in the limit, but the second function gets there much more slowly. Determining smaller n properties requires examining the probabilities directly, which is feasible in this example, but more generally may require simulations.

With regards to the Poisson random network model, there is much that is known about properties and thresholds. A very brief summary is as follows.

- At the threshold of $\frac{1}{n^2}$ the first links emerge, so that the network is likely to have no links in the limit for $p(n)$'s of order less than $\frac{1}{n^2}$, while for $p(n)$'s of order larger than $\frac{1}{n^2}$ the network has at least one link with a probability going to one.[13] (The proof of this is Exercise **??**.)

- Once $p(n)$ is at least $\frac{1}{n^{3/2}}$ there is a probability converging to one that the network has at least one component with at least three nodes.

- At the threshold of $\frac{1}{n}$ we see cycles emerge, and we also see the emergence of a "giant component," which is a unique largest component which contains a nontrivial fraction of all nodes.

- The giant component grows in size until the threshold of $\frac{\log(n)}{n}$, where the network becomes connected.

These various thresholds are illustrated in the following series of figures from randomly drawn networks. These are Poisson random networks generated on fifty nodes (using the program Ucinet). With $n = 50$, we have the first links emerging at $p = \frac{1}{n^2} = .0004$. The threshold where we see the first component emerge with more than two nodes is at $p = n^{-3/2} = .003$. Indeed, we see in the first network with $p = .01$ that we have a component with three nodes, but still the network is very sparse.

[13] Note that this does not contradict the calculations above, which were for the property that single node did/did not have any neighbors. The property here is that none of the nodes have any neighbors.

Figure 4.2.2. A First Component with More than Two Nodes: A Random Network on 50 Nodes with p=.01

At the threshold of $p = \frac{1}{n} = .02$ we should see cycles start to emerge. We see this in that the first network with $p = .01$ has no cycles, while the networks with $p = .03$ (or more) all have cycles. Moreover, this is also where we see the first signs of a giant component.

Figure 4.2.2. The Emergence of Cycles: A Random Network on 50 Nodes with p=.03

As we increase p we see that the giant component starts to swallow more and more nodes.

Figure 4.2.2. The Giant Component: A Random Network on 50 Nodes with p=.05

Eventually, at the threshold of $p = \frac{log(n)}{n} = .08$ we should see the network become connected. Again, this is seen in the random networks, as the networks generated with $p = .01$, $p = .03$, and $p = .05$ all have at least two components, while the network generated with $p = .10$ is connected.

To get a deeper understanding of how some of these thresholds work, let us start by examining the connectedness of a random network.

4.2.3 Connectedness

Whether or not a network is connected, and more generally what its component structure looks like, is important in the transmission and diffusion of information, behaviors, and diseases, as we shall see in Section **??**. Thus, it is important to understand how these properties relate to the network formation process.

The phase transition from a disconnected to a connected network was one of the many important discoveries of Erdös and Rényi [211] about random networks. Exploring this phase transition in detail is not only useful for its own sake, but also because

Figure 4.2.2. Emergence of Connectedness: A Random Network on 50 Nodes with p=.10

it helps illustrate the idea of phase transitions and provides some basis for extensions to other random network models.

THEOREM **4.2.1** [Erdös and Rényi] *A threshold function for the connectedness of the Poisson random network is* $t(n) = log(n)/n$.

The theorem thus shows that if the probability of a link is larger than $log(n)/n$, then the network is connected with a probability tending to one, while if it is smaller than $log(n)/n$ then the probability that it is not connected tends to one. This threshold corresponds to an expected degree of $log(n)$.

The ideas behind Theorem 4.2.1 are relatively easy to understand, and a complete proof is not too long, even though the conclusion of the theorem is profound. In order to show that a network is not connected, it is enough to show that there is some isolated node. It turns out that $t(n) = log(n)/n$ is not only the threshold for a network being connected, but also for there not to be any isolated nodes. To see why this is true, note that the probability that a given node is completely isolated is $(1 - p(n))^{n-1}$ or roughly $(1 - p(n))^n$. When working with a $p(n)$ near the threshold, $p(n)/n$ converges

to 0, and so we can approximate $(1-p(n))^n$ by $e^{-np(n)}$. Thus, the probability that any given node is isolated goes to $e^{-p(n)n}$, which evaluated at the threshold is $1/n$. When we have n nodes, it is then not too hard to show that this is the threshold of having some of them be isolated, as below the threshold the chance of any node being isolated is significantly less than $1/n$ while above the threshold it is significantly above $1/n$. The proof then shows that above this threshold it is not only that there are no isolated nodes, but also no components of size less than $n/2$. The intuition behind this is that the probability of having a component of some small finite size is similar (asymptotically) to having an isolated node: there need to be no connections between any of the nodes in the component and any of the other nodes. Thus, one either has some isolated nodes, or else the smallest components must be approaching infinite size. However, the chance of having more than one component of substantial size goes to 0, as there are many nodes in each component and there cannot be any links between separate components, which is then a very low probability event. So, components roughly come in two flavors: very small or very large.

I now offer a full proof of the Theorem in order to give a rough idea of how some of the many results in random graph theory have been proven: basically by bounding probabilities and expectations and showing that the bounds have the claimed properties.

Proof of Theorem 4.2.1:[14]

Let us start by showing that $t(n) = log(n)/n$ is the threshold for having isolated nodes. First, we show that if $p(n)/t(n) \to 0$, then the probability that there are isolated nodes is tending to 1. This clearly implies that the network is not connected.

The probability that a given node is completely isolated is $(1-p(n))^{n-1}$ or roughly $(1-p(n))^n$ if $p(n)$ is converging to 0. Given that $p(n)/n$ converges to 0, we can approximate $(1-p(n))^n$ by $e^{-np(n)}$. Thus, the probability that any given node is isolated goes to

$$e^{-p(n)n}.$$

We can write $p(n) = \frac{log(n)-f(n)}{n}$, where $f(n) \to \infty$ and $f(n) < log(n)$, and then $e^{-p(n)n}$ becomes

$$\frac{e^{f(n)}}{n}.$$

The expected number of isolated nodes is then $e^{f(n)}$, which tends to infinity.

[14] This proof is adapted from two different proofs by Bollobas (Theorem 7.3 in [80] and Theorem 9 on page 233 of [79]).

While expecting a divergent number of isolated nodes in the limit is suggestive that there will be some isolated nodes, it does not prove that the probability of there being at least one isolated node converges to 1. We show this via Chebychev's inequality.[15] Let X^n denote the number of isolated nodes. We have shown that $E[X^n] \to \infty$. If we can show that the variance of X^n, $E[(X^n)^2] - E[X^n]^2$, is no more than twice $\mu = E[X^n]$, then we establish the claim by applying Chebychev's inequality. In particular, we then can conclude that $\Pr[X^n < \mu - r\sqrt{2\mu}] < 1/r^2$ for all $r > 0$, which since $\mu \to \infty$ implies that the probability converges to 1 that X^n will be arbitrarily large and so there will be an arbitrarily large number of isolated nodes. To obtain an upper bound on $E[(X^n)^2] - E[X^n]^2$, note that $E[X^n(X^n - 1)]$ is the expected number of ordered pairs of isolated nodes, which is $n(n-1)(1-p)^{2n-3}$ since a pair of nodes is isolated from the other nodes if none of the $2(n-2)$ links from either of them is present and the link between them is not present. Thus,

$$\begin{aligned}
E\left[(X^n)^2\right] - E\left[X^n\right]^2 &= n(n-1)(1-p)^{2n-3} + E[X^n] - E[X^n]^2 \\
&= n(n-1)(1-p)^{2n-3} + E\left[X^n\right] - n^2(1-p)^{2n-2} \\
&\leq E\left[X^n\right] + pn^2(1-p)^{2n-3} \\
&= E\left[X^n\right]\left(1 + pn(1-p)^{n-2}\right) \\
&\leq E\left[X^n\right]\left(1 + (log(n) - f(n))e^{-log(n)+f(n)}(1-p)^{-2}\right) \\
&\leq 2E\left[X^n\right].
\end{aligned}$$

To complete the proof that $t(n) = log(n)/n$ is the threshold for having isolated nodes, we need to show that if $p(n)/t(n) \to \infty$, then the probability that there are isolated nodes is tending to 0. It is enough to show this for $p(n) = \frac{log(n)+f(n)}{n}$, where $f(n) \to \infty$ but $f(n)/n \to 0$.[16] By a similar argument to the one above, we conclude that the expected number of isolated nodes is tending to $e^{-f(n)}$, which tends to 0. The probability of having X^n be at least one then has to tend to 0 as well in order for $E[X^n] \to 0$.

To complete the proof of the Theorem, we need to show that if $p(n)/t(n) \to \infty$, then the chance of having any components of size 2 to size $n/2$ tends to 0. Let X_k denote

[15] Chebychev's inequality (see Section 4.5.3) says that for a random variable X with mean μ and standard deviation σ, $\Pr[|X - \mu| > r\sigma] < 1/r^2$ for every $r > 0$.

[16] Having no isolated nodes is clearly an increasing property, so that it holds for larger $p(n)$. The reason for working with $f(n)/n \to 0$ is to ensure that the approximation of $(1 - p(n))^n$ by $e^{-np(n)}$ is valid asymptotically.

the number of components of size k, and write $p(n) = \frac{log(n)+f(n)}{n}$, where $f(n) \to \infty$ and $f(n)/n \to 0$.[17] It is enough to show that $E[\sum_{k=2}^{n/2} X_k] \to 0$.

$$\begin{aligned}
E\left[\sum_{k=2}^{n/2} X_k\right] &= E\left[\sum_{k=2}^{n/2} X_k\right] \\
&\leq \sum_{k=2}^{n/2} \binom{n}{k}(1-p)^{k(n-k)} \\
&= \sum_{k=2}^{n^{3/4}} \binom{n}{k}(1-p)^{k(n-k)} + \sum_{k=n^{3/4}}^{n/2} \binom{n}{k}(1-p)^{k(n-k)} \\
&\leq \sum_{k=2}^{n^{3/4}} \left(\frac{en}{k}\right)^k e^{-knp} e^{k^2 p} + \sum_{k=n^{3/4}}^{n/2} \left(\frac{en}{k}\right)^k e^{-knp/2} \\
&\leq \sum_{k=2}^{n^{3/4}} e^{k(1-f(n))} k^{-k} e^{2k^2 log(n)/n} + \sum_{k=n^{3/4}}^{n/2} \left(\frac{en}{k}\right)^k e^{-knp/2} \\
&\leq 3e^{-f(n)} + n^{-n^{3/4}/5},
\end{aligned}$$

which tends to 0 in n. ∎

The above proof used the specific structure of the Poisson random networks model fairly extensively. How far can we extend it to other random network models?

It is fairly clear that the argument we used to prove the above theorem is not well suited to the configuration model. Under the configuration model, under some reasonable bounds on degrees, each node will end up with its specified degree with a probability approaching 1. This renders the approach above inapplicable. It is clear that if the limiting degree distribution has a positive mass on nodes of degree 0 in the limit then it will not be connected, but otherwise it is not so clear what will happen. For instance, if the associated $\widetilde{P}$ has mass on nodes of some bounded degree in the limit, then there will be a non-vanishing probability that the network will be not be connected. However, requiring that the mass on nodes of some bounded degree vanish is not enough, as it is still possible to have the network have a nontrivial probability of being disconnected.

[17] Here again, we work with $p(n)$ "near" the threshold, as this will establish that the resulting network is connected with a probability going to one for such p's, and then it holds for larger p's.

The expected-degree model of Chung and Lu **??** is better suited for an analysis with regard to being connected, or at least we can make some progress with regard to the threshold for the existence of isolated nodes. This follows since it is essentially a generalization of the Poisson random network model that allows for different expected degrees across nodes (with the possibility of self loops).

Recall that in the expected-degree model, we work with degree sequences of an expected degree for each node $d_1, \ldots, d_n$. Let

$$Vol^n = \sum_{i=1}^{n} d_i, \tag{4.4}$$

denote the total expected degree of the network on n nodes. The probability of a link between nodes i and j is then $\frac{d_i d_j}{Vol^n}$, and so the probability that node i is isolated is

$$\prod_j (1 - \frac{d_i d_j}{Vol^n}).$$

The probability that a given node i is isolated is then approximately $e^{-d_i \sum_j d_j / Vol^n} = e^{-d_i}$ for large n (under the assumption that $max_i \frac{d_i^2}{Vol^n}$ converges to 0, which is maintained under the expected-degree model). The probability that no node is isolated is then

$$\prod_i (1 - e^{-d_i})$$

or approximately

$$e^{-\sum_i e^{-d_i}}.$$

This suggests a threshold such that if $\sum_i e^{-d_i} \to 0$ then there will be no isolated nodes, while if $\sum_i e^{-d_i} \to \infty$ then there will be isolated nodes.[18] As a double-check of this, let $d_i = d(n) = log(n) + f(n)$ for each i the Poisson random network setting (where $p(n) = d(n)/n$). This leads to $\sum_i e^{-d_i} = e^{-f(n)}$, so if $f(n) \to \infty$ we end up with no isolated nodes (and a connected network) and if $f(n) \to -\infty$ then with a probability going to 1 there are isolated nodes. Indeed, this corresponds to the threshold we found in the Poisson random network model.

[18] I am not aware of results on this question or the connectedness of the network under the expected degree model. While it seems natural to conjecture that the threshold for the existence of isolated nodes will again be the same as the threshold for connectedness, the details need to be checked.

4.2.4 Giant Components

indexgiant component

In cases where the network is not connected, it will be interesting to know something about the component structure as there will generally be many components. In fact, we have already shown that if the network is not connected in the Poisson random network model then there should be an arbitrarily large number of components. We also know from Section **??**, that in this case there may still exist a giant component. Let us examine this in more detail and for a wider class of degree distributions.

In defining the size of a component, a convention is to call a component "small" if it has fewer than $\frac{n^{2/3}}{2}$ nodes, and "large" if it has at least $n^{2/3}$ nodes (e.g., see Chapter 6 in Bollobas **??**). The term "giant component" refers to the unique largest component if there is one. This may turn out to be a small component in some networks but we will generally be interested in giant components that involve non-vanishing fractions of nodes, which will necessarily be "large" components.

The idea of there being a unique largest component is fairly easy to understand, in the case where these are large components. It relates back to what we saw in the proof of Theorem 4.2.1: for any two large sets of nodes (each containing at least $n^{2/3}$ nodes) it is very unlikely that there will be no links between them, unless the overall probability of links is very small. For instance, in the Poisson random network model the probability of having no links between two given large sets of nodes is no more than $(1-p)^{n^{4/3}}$. If $pn^{4/3} \to 0$, then this expression is positive, but otherwise it tends to 0. Proving that the probability of not having two separate large components goes to 0 involves a bit more proof, but is relatively straightforward (see Exercise 4.7).

4.2.5 Size of the Giant Component in Poisson Random Networks

As we have already seen, it is not even clear whether each node will reach every other node. Unless p is high enough relative to n, it is likely there will be pairs of nodes that are not path-connected. As such, diameter is often measured with respect to the largest component of a network.[19] But this also raises a question as to what the network looks like in terms of components. The answer is one of the deeper and more elegant results of Erdös and Rényi's work.

[19] This can result in some distortions, as, for instance, a network where each node has exactly one link has a diameter much smaller than a network that has many more links.

To get some impression as to the size of the largest component, generally referred to as the "giant component," let us do a simple heuristic calculation.[20] Form a Poisson random network on $n-1$ nodes with a probability of any given link being $p > 1/n$. Now let us add a last node, and again connect this node to each other node with an independent probability p. Let q be the fraction of nodes in the largest component of the $n-1$ node network. As a fairly accurate approximation for large n, this will also be the fraction of nodes in the largest component of the n node network. [The only possible exception to this is if the added node ends up connecting two large components that were not connected before. As argued above, the chance of having two components with large numbers of nodes that are not connected to each other goes to 0 in n, given that $p > 1/n$.] Now, the chance that this added node ends up outside of the giant component is the probability that none of its neighbors are in the giant component. If the new node has degree d_i this probability is converging to $(1-q)^{d_i}$, as we let n become large. As we can think of any node as having been added in this way, in a large network the expected frequency of nodes of degree d_i that end up outside of the giant component is approximately $(1-q)^{d_i}$.[21] So, the overall fraction of nodes outside of the giant component, $1-q$, can then be found by averaging $(1-q)^{d_i}$ across nodes. This leads to[22]

$$1 - q = \sum_d (1-q)^d P(d). \tag{4.5}$$

When we apply this to the Poisson degree distribution described by (1.4), the fraction of nodes outside of the giant component is then approximated by the solution of

$$1 - q = \sum_d \frac{e^{-(n-1)p}((n-1)p)^d}{d!}(1-q)^d.$$

[20] The heuristic argument is based on Newman [480], but a very different and complete proof of the characterizing equation above the threshold for the emergence of the giant component can be found in Bollobas [80].

[21] There are steps omitted from this argument, as for any finite n the degrees of nodes in the network are correlated, as are their chances of being in the largest component conditional on their degree. For example, for a node of degree 1, it is in the giant component if and only if its neighbor is. Then, if that neighbor has degree d, then it has $d-1$ chances to be connected to a node in the giant component. So, now the calculation begins to look like $(1-q)^{d-1}$ for the neighbor to be in the giant component. To see a fuller proof of this derivation, see Bollobás [80].

[22] Here take the convention that $0^0 = 1$, so that if $q = 1$, then the right hand side of this equation is $P(0)$.

Since $\sum_d \frac{((n-1)p(1-q))^d}{d!} = e^{(n-1)p(1-q)}$, an approximation is described by the solution to

$$q = 1 - e^{-q(n-1)p}. \tag{4.6}$$

There is always a solution of $q = 0$ to this equation. In the case where the average degree is larger than 1 (i.e., $p > 1/(n-1)$), and only then, there is also a solution for q that lies between 0 and 1.[23] This corresponds to phase transition, in that the appearance of such a giant component comes above the threshold of $(n-1)p = 1$. That is, there is a marked difference in the structure of the resulting network depending on whether average degree is bigger or smaller than one. If the average degree is less than one, then there is essentially no giant component, but instead the network consists of many components which are all of small size relative to the number of nodes. If the average degree exceeds one, then there is a giant component which contains a non-trivial fraction of all nodes (approximately described by (4.6)).

Note that if we let $p(n-1)$ grow (so that the average degree is unbounded as n grows), then the solution for q tends towards 1. Of course, that requires the average degree to become large. In a random network where there is some bound on average degree, so that $p(n-1)$ is bounded, then q will be somewhere between 0 and 1. If we look for a solution to $q = 1 - e^{-q(n-1)p}$ when $n = 50$ and $p = .08$, we are looking for a q that roughly satisfies $q = 1 - e^{-4q}$, and such a q is about .98. So, an estimate for the size of the giant component is 49 nodes out of 50 - which happens to match the realized network in Figure 1.2.3 exactly.

4.2.6 Giant Components in the Configuration Model

Understanding giant components more generally is especially important as they play a central role in various problems of diffusion, and a giant component gives an idea of the most nodes that one might possibly reach starting from a single node. With this in mind, let us examine giant components for more general random networks, using

[23] To see this let $f(q) = 1 - e^{-q(n-1)p}$. We are looking for points q such that $f(q) = q$; known as a "fixed-point". Since $f(0) = 1 - e^0 = 0$, $q = 0$ is always a fixed point. Next, note that f is increasing in q with derivative $f'(q) = (n-1)pe^{-q(n-1)p}$ and strictly concave (as the second derivative is negative: $f''(q) = -((n-1)p)^2 e^{-q(n-1)p}$). Since $f(1) = 1 - e^{-(n-1)p} < 1$, we have a function that starts at 0 ends up with a value below 1 and which is increasing and strictly concave. The only way in which it can ever cross the 45 degree line is if it has a slope greater than 1 when it starts, otherwise it will always lie below the 45 degree line and 0 will be the only fixed-point. The slope at 0 is $f'(0) = (n-1)p$, and so there is a $q > 0$ such that $q = f(q)$ if and only if $(n-1)p$ is greater than 1.

the configuration model as a basis.[24] We will work with randomly formed networks according to the configuration model on n nodes; and will then be looking at the limiting probability the resulting networks have a giant component when we let n grow to be large. Consider a sequence of degree sequences, ordered by the number of nodes n, with corresponding degree distributions described by $P^n(d)$. Assume that these satisfy some conditions:

(i) the degree distributions converge uniformly to a limiting degree distribution P that has a finite mean,

(ii) there exists ε such that $P^n(d) = 0$ for all $d > n^{\frac{1}{4}-\varepsilon}$,

(iii) $(d^2 - 2d)P^n(d)$ converges uniformly to $(d^2 - 2d)P(d)$, and

(iv) $E_{P^n}[d^2 - 2d]$ converges uniformly to its limit (which may be infinite).

An important aspect of such sequences is that the probability of having cycles in any small component is tending to 0. Let us examine properties of the degree distribution that tell us when such networks exhibit a giant component. The following is a simple and informal derivation. A somewhat more complete derivation appears in Section 4.3.1.

The idea is to look for the threshold where starting at a random node there is some chance of finding a nontrivial number of other nodes through tracing out expanding neighborhoods. Indeed, if a node is in a giant component then exploring longer paths from the node should lead to the discovery of more and more nodes, while if it is in a small component then expanding neighborhoods will not result in finding many more nodes.

When we are looking for the threshold where the giant component just emerges, then at or below this threshold we will be working with components that are essentially trees, and so each time we search along a link that we have not traced before, we will find a node that we have not visited before. This allows us to analyze component structure up to the point where the giant component emerges as if the network were a collection of trees. The following argument (due to Cohen et al [151]) provides the idea behind there being negligible numbers of cycles below the threshold.[25] Consider

[24] Similar results hold for the expected degree model of Chung and Lu (see [145]), and under weaker restrictions on the set of admissible degree distributions, but follow a less intuitive argument.

[25] This is part of the informality of the derivation, and I refer the interested reader to Molloy and Reed [449] for a more complete proof.

any link in the configuration model on n nodes. The probability that the link connects two nodes that were already connected in a component with s nodes (where s is the size of some component ignoring that link) is the probability that both of its end nodes lie in that component, which is proportional to $\left(\frac{s}{n}\right)^2$. Thus, the fraction of links that end up on cycles is on the order of $\sum_i \left(\frac{s_i}{n}\right)^2$, where the s_i's are to the sizes of each of the components in the network. This is less than $\sum_i \frac{s_i S}{n^2}$, where S is the size of the largest component. Thus, since $\sum_i s_i = n$, we find that the proportion of links than lie on cycles is of an order no more than S/n. If we are at or below the threshold where the giant component is just emerging, then with probability one, S/n is vanishing for large n.

Thus, when we consider a sequence of degree disributions at or below the threshold of the emergence of the giant component, the components are essentially trees.[26]

To develop an estimate of component size as the network grows, then let ϕ denote the limiting number of nodes that can be found on average by picking a link uniformly at random, picking with equal chance one of its end nodes, and then exploring all of the nodes that can be found via expanding neighborhoods from that end nodes. Given an absence of cycles, the number of new nodes reached by a link is the first node reached plus that node's degree minus one (as one of its links points back to the original node) times ϕ, which indicates how many new nodes are expected to be reached from each of the first node's neighbors. Thus,

$$\phi = 1 + \sum_{d=1}^{\infty}(d-1)\widetilde{P}(d)\phi = 1 + \sum_{d=1}^{\infty}\frac{P(d)d}{\langle d\rangle}(d-1)\phi.$$

We can rewrite this as

$$\phi = 1 + \frac{(\langle d^2\rangle - \langle d\rangle)\phi}{\langle d\rangle}$$

or

$$\phi = \frac{1}{2 - \frac{\langle d^2\rangle}{\langle d\rangle}}. \tag{4.7}$$

Now we deduce the threshold for where a giant component emerges. If ϕ has a finite solution, then when we start from a node picked uniformly at random in the network and examine a the number of nodes we can reach from one of its links, we expect to find a finite number of nodes. This places the node in a finite component. If ϕ does not have a finite solution, then we expect at least some nodes that we find uniformly

[26] The more rigorous result proven by Molloy and Reed [449] establishes that almost surely, no component has more than one cycle.

at random to be in components that are growing without bound, which should be happening right at the threshold for the emergence of a giant component. In order for ϕ to have a finite solution it must be that $0 > \langle d^2 \rangle - 2\langle d \rangle$. Thus, if

$$\left\langle d^2 \right\rangle - 2\langle d \rangle > 0. \tag{4.8}$$

we end up with a giant component, and so the threshold is where $\langle d^2 \rangle = 2\langle d \rangle$.

In the case of a Poisson distribution $\langle d^2 \rangle = \langle d \rangle + \langle d \rangle^2$, and so the giant component emerges when $\langle d \rangle^2 > \langle d \rangle$, or $\langle d \rangle > 1$. Indeed the threshold for the existence of a giant component under the Poisson random network model is $t(n) = 1/n$, which corresponds to an average degree of 1.

In the case of a regular network, were the degree sequences have full weight on some degree k, if we solve for $\langle d^2 \rangle = 2\langle d \rangle$ we end up with $k^2 = 2k$ and so a threshold for a giant component at $k = 2$. Clearly, with $k = 1$ we just end up with a set of dyads (paired nodes) and no giant component.

In the case of a scale-free network, where the probability of degree d is of the form $P_n(d) = cd^{-\gamma}$, we find that $\langle d^2 \rangle$ diverges, whenever $\gamma < 3$, and so there will generally be a giant component regardless of the specifics of the distribution.

In order to estimate the size of the giant component, the arguments underlying the derivation of (4.5) were not specific to a Poisson distribution, and so for the configuration model where the probability of loops is still negligible, we still have the approximation for the size of the giant component to be the largest q that solves

$$1 - q = \sum_d (1-q)^d P(d). \tag{4.9}$$

Using this expression, there is much that we can deduce about how the size of the giant component changes with the degree distribution. For instance, if we increase the distribution in terms of putting more weight on higher nodes (in the sense of first order stochastic dominance, and see Section 4.5.5 for definitions of stochastic dominance), then the right hand side expectation goes down for any value of q, and then the new value of $1 - q$ that solves (4.9) has to decrease as well, which corresponds to a larger giant component, as detailed in Exercise 4.11. This makes sense, since we can think of such a modification as effectively adding links to the network, which should increase the size of the giant component. Interestingly, providing a mean-preserving spread in the degree distribution has the opposite effect, decreasing the size of the giant component. This is a bit more subtle, but has to do with the fact that $(1-q)^d$ is a convex function of d. So, spreading out the distribution leads to some higher degree nodes which have

a higher chance of being in a giant component, but also some lower degree nodes which have a much lower chance of being in the giant component. The key is that the convexity implies that there is more loss in probability from moving to lower degree nodes than gain in probability from the high degree nodes.

4.2.7 Diameter Estimation

Another important feature of a network is its diameter. This, as well as other related measures of distances between nodes, are important in understanding how quickly behavior or information can spread through a network, among other things.

To explore the diameter of a network, let us start by calculating the diameter of a network which makes such calculations relatively easy. Suppose that we examine a component that we know to be a tree so that there are no cycles. A method of obtaining an upper bound on diameter is to pick some node and then successively expanding its neighborhood by following paths of length ℓ, where we increase ℓ until the paths are long enough so that we reach all nodes. Then we know that every node is at distance at most ℓ from our starting node and that no two nodes can be at a distance of more than 2ℓ from each other; and so the diameter is bounded below by ℓ and above by 2ℓ.[27] What this diameter works out to be will depend on the shape of the tree.

Let us explore a particularly nicely behaved class of trees. Consider a tree such that every node either has degree k or degree 1 (the "leaves"), and such that there is a "root" node that is equidistant from all of the leaves. Let us start from that "root" node.[28] If we then move out by a path of 1, we have reached k nodes. Now, by traveling on all paths of length 2, we will have reached all of the nodes in the immediate neighborhoods of the nodes in the original node's neighborhood. We will have reached $k + k(k-1)$ or k^2 nodes. Extending this reasoning, by traveling on all paths of length ℓ, we will have reached

$$k + k(k-1) + k(k-1)^2 + \ldots + k(k-1)^{\ell-1}$$

This can be rewritten (see the appendix) as

$$k\frac{(k-1)^\ell - 1}{k-1-1} = \left(\frac{k}{k-2}\right)\left((k-1)^\ell - 1\right).$$

[27] Note that we can easily see that both of these bounds could be reached. If the network is a "line" with an odd number of nodes and we do this calculation from the middle node then the diameter is exactly 2ℓ, while if we start at one of the end nodes, then the diameter is exactly ℓ.

[28] Trees where all nodes have either degree k or degree 1 are known as *Cayley trees*.

We can thus find the neighborhood size needed to reach all nodes by finding the smallest ℓ such that

$$\left(\frac{k}{k-2}\right)\left((k-1)^{\ell}-1\right) \geq n-1.$$

Approximating this equation provides us with a fairly accurate estimate of the neighborhood size needed to reach all nodes of

$$(k-1)^{\ell} = n-1,$$

or

$$\ell = \frac{log(n-1)}{log(k-1)},$$

and then the estimated diameter for this network is $2\frac{log(n-1)}{log(k-1)}$.

Newman, Watts and Strogatz [**?**] follow a reasoning similar to this to develop a very rough estimate of the diameter of more general sorts of random networks by examining the expansion in the neighborhoods. The calculation presumes a tree structure, which in the Poisson random network setting we know not to be valid beyond the threshold where the giant component emerges, and so it only gives us an order of magnitude approximation near the threshold. Generally, obtaining bounds on diameters is a very challenging problem. We will see a number of other points where there are potential problems with the calculation as we proceed.

A randomly picked node i has an expected number of neighbors of $\langle d \rangle$ (recalling the $\langle \cdot \rangle$ notation for the expectation operator). If we presume that nodes' degrees are approximately independent, then each of these nodes has a degree described by the distribution $\widetilde{P}(d)$ from (4.2). Thus, each of these nodes has an expected number of neighbors (besides i) of $\sum_d (d-1)\widetilde{P}(d)$ or $\frac{\langle d^2 \rangle - \langle d \rangle}{\langle d \rangle}$. So, the expected number of i's second neighbors (who are at a distance of 2 from i) is *very* roughly $\langle d \rangle \frac{\langle d^2 \rangle - \langle d \rangle}{\langle d \rangle}$.[29] Iterating, the expected number of k-th neighbors is estimated by

$$\langle d \rangle \left(\frac{\langle d^2 \rangle - \langle d \rangle}{\langle d \rangle}\right)^{k-1}.$$

[29] So, we see several approximations. The tree structure is implicit in the assumption that each of these "second neighbors" are not already first neighbors. There is an assumption about the correlation in neighbors' degrees implicit in the use of $\widetilde{P}$ to calculate neighbors' degrees. Next, the expected number of second neighbors is found by multiplying first neighbors times expected number of their neighbors, again embodying some independence to have the expectation of a product equal the product of the expectations.

This means that expanding out to a ℓ-th neighborhood reaches:

$$\sum_{k=1}^{\ell} \langle d \rangle \left(\frac{\langle d^2 \rangle - \langle d \rangle}{\langle d \rangle} \right)^{k-1} \tag{4.10}$$

nodes. When this sum is equal to $n-1$, then we have an idea of how far we need to go from a randomly picked node to hit all other nodes. This gives us a *very* rough estimate of the diameter of the largest component. Substituting for the sum of the series in (4.10) (see Section 4.5 for some facts about sums of series), we obtain an estimate of diameter as the ℓ that solves

$$\langle d \rangle \left(\frac{\left(\frac{\langle d^2 \rangle - \langle d \rangle}{\langle d \rangle} \right)^{\ell} - 1}{\left(\frac{\langle d^2 \rangle - \langle d \rangle}{\langle d \rangle} \right) - 1} \right) = n - 1,$$

or

$$\ell = \frac{\log\left[(n-1)\left(\langle d^2 \rangle - 2\langle d \rangle\right) + \langle d \rangle^2\right] - \log\left[\langle d \rangle^2\right]}{\log\left[\langle d^2 \rangle - \langle d \rangle\right] - \log\left[\langle d \rangle\right]} \tag{4.11}$$

In cases where $\langle d^2 \rangle$ is much larger than $\langle d \rangle$, this is approximately

$$\ell = \frac{\log[n] + log\left[\langle d^2 \rangle\right] - 2\log\left[\langle d \rangle\right]}{\log\left[\langle d^2 \rangle\right] - \log\left[\langle d \rangle\right]} = \frac{\log\left[n/\langle d \rangle\right]}{\log\left[\langle d^2 \rangle / \langle d \rangle\right]} + 1. \tag{4.12}$$

although here we have to be careful, as we are ignoring any cycles and when we are above the threshold for a giant component to exist and include many nodes (e.g., when $\langle d^2 \rangle$ is much larger than $2\langle d \rangle$), then there can be nontrivial clustering for some degree sequences.

If we examine (**??**) for the case of a Poisson random network, then $\langle d^2 \rangle / \langle d \rangle = 1 + \langle d \rangle = 1 + (n-1)p$, and then

$$\ell = \frac{\log\left((n-1)\frac{\langle d \rangle - 1}{\langle d \rangle} + 1\right)}{\log(\langle d \rangle)}.$$

In cases where $\langle d \rangle$ is subsantially above 1, this is roughly $\log(n)/\log(\rangle d \langle)$, which is very similar to the regular the tree example. If p is held constant, then as we increase n, ℓ decreases and converges to 1 from above. In that case we would estimate the diameter to be 2. In fact, it can be shown that for a constant p, this crude approximation is right on the mark in that the diameter of a large random graph with such a p is 2 with a probability tending to one (see Corollary 10.11 Bollobás [80]). Next, let us consider the case where average degree is not exploding, but instead average degree is

held constant so that $p(n-1) = \langle d \rangle > 1$. Then our estimate for diameter is on the order of $log(n)/log(\langle d \rangle)$. Here the estimate is not as accurate.[30] Applying this to the network generated in Figure 1.2.3 where $n = 50$, $p = .08$ and average degree is roughly $\langle d \rangle = 4$, we get an estimated diameter of 2.8. While this is not precise, it is not far off for the largest component in Figure 1.2.3.

Developing accurate estimates for diameters, even for such completely random networks, turns out to be a formidable task that has been an active area of study in graph theory for the past four decades.[31] Nevertheless, the above approximations reflect the fact that the diameter of a random network is likely to be "small" in the sense that it is significantly smaller than the number of nodes.

4.3 An Application: Contagion and Diffusion

To get a feeling for how some of the derivations from random networks might be useful, consider the following application. There is a society of n individuals. One of them is initially infected with a contagious virus (possibly even a computer virus). Let the network of interactions in the society be described by a Poisson random network with link probability p.

The initially infected person interacts with each of his or her neighbors. Some of the neighbors are immune to the virus, while others are not. Let any given individual be immune with a probability π. For instance, this might represent a natural immunity, a percentage of people who have been vaccinated, or the percentage of people whose computers are not susceptible to the given disease. This is a variation on what has is known as the Reed-Frost model in the epidemiology literature (see Bailey [25], as the work of Reed and Frost was never published), and is is discussed in more detail in Section **??**.

The eventual spread of the disease can then be modeled by:

- generating a Poisson random network on n nodes with link probability p,
- deleting πn of the nodes (uniformly at random) and considering the remaining network,

[30] In this range of p, the network will generally have a giant component, but will most likely not even be completely connected.

[31] See Chapter 10 in Bollobás [80] for a report on some of the results and references to the literature.

- identifying the component that the initially infected individual lies in on this subnetwork.

This calculation is equivalent to examining a network on $(1-\pi)n$ nodes with a link probability of p, and then examining the size of the component containing a randomly chosen node. Thus, given that the threshold for the emergence of a giant component is at $p(1-\pi)n = 1$, then if $p(1-\pi)n < 1$, we expect the disease to die out and only infect a negligible fraction of the population. In contrast, if $p(1-\pi)n > 1$, then we there is a nontrivial probability that it will spread to a some fraction of the originally susceptible population. In particular, from (4.6) we know that for large n, if an agent in the giant component of the susceptible population is infected, then the expected size of the epidemic as a percentage of the nodes that are susceptible is approximated by the nonzero q which solves

$$q = 1 - e^{-q(1-\pi)np}. \tag{4.13}$$

Furthermore, from Theorem 4.2.1 we also know that if $p > \frac{log((1-\pi)n)}{(1-\pi)n}$, then with a probability approaching 1 (as n grows) the network of susceptible agents will be connected and so all of the susceptible population will be infected.

While the equation above is difficult to solve directly for q, we can rewrite the equation as

$$(1-\pi)np = \frac{\log(1-q)}{q}. \tag{4.14}$$

Then putting in different values of q, we find the corresponding levels of $(1-\pi)np$ that lead to those q's. This leads to the following figure:

The figure provides us with an initial threshold of $(1-\pi)np = 1$, and then we see that nearly the entire population of susceptible individuals is connected once we approach $(1-\pi)np = 5$. So, for instance, if half the population is susceptible, and average degree is above 10, then nearly all of the susceptible agents are interconnected, and so the probability of them all becoming infected from a tiny initial seed is quite high.

It is also worth emphasizing that this can also capture diffusion of various behaviors. For instance, let susceptible indicate someone who would buy a certain product if made aware of it. Then $(1-\pi)$ can be interpreted as the percentage of the population who would buy the product if everyone was aware of it. The size of the giant component from these calculations indicates the potential impact of the reach of informing a few agents in the population about the product, when they communicate by word of mouth with others and are sure to learn about the product from any neighbor who buys it.

Figure 4.3. Fraction of the Susceptible Population in the Largest Component of a Poisson Random Network, as a Function of the Proportion of Susceptible Nodes (1-π) times the Link Probability, p, times the Population Size, n.

This analysis is built on contagion taking place with certainty between any infected and susceptible neighbors. When the transmission is probabilistic, which is the case in some applications, then the analysis needs to account for that. Such diffusion is discussed in greater detail in Chapter **??**.

4.3.1 Distribution of Component Sizes*

The derivations in Section 4.2.6 provide an idea of when a giant component will emerge, and its size, but we might be interested in more information about the distribution of component sizes that emerge in a network. Again, we will see how important this is when we examine network-based diffusion in more detail in Chapter **??**. Following Newman, Watts and Strogatz [**?**], we can use probability generating functions to examine the component structure in more detail. (For those not familiar with generating functions, it will be useful to read the appendix in Section 4.5.9 before preceding with this section.)

This analysis presumes that adjacent nodes have independent degrees, and so it is best to fix ideas with respect to the Configuration Model, where approximate independence holds for large n. Let the degree distribution be described by P.

Consider the following question. What is the size of the component of a node picked uniformly at random from the network? We find this by starting at a node, picking one of its edges and examining the neighboring node, and then following the edges from that neighboring node and seeing how many additional nodes we find. Then summing across edges leaving the initial node, we have an idea of the expected size of the component. This method presumes a tree structure, and is thus only a good approximation when the degree distribution is such that the number of cycles in the network is negligible.

So, let us first examine how many nodes we find when pick a link at random from the network, and then follow one of its nodes and count all of its further neighbors and so forth. In particular, let Q denote the distribution of the number of nodes that can be found by picking an edge uniformly at random from the network, then picking one of its nodes uniformly at random, and then counting that node plus all of the nodes that are found by following all paths from that node that do not use the original link. Let $G_Q(x)$ denote the generating function associated with this distribution.

Note that Q can be thought of in the following way. There is a probability of $\widetilde{P}(d)$ that the node at the end of the randomly selected edge will have degree d. In that case, it will have $d-1$ edges emanating from it. The number of additional nodes that can be

found by starting from each such edge is a random variable Q.[32] We now use some facts about generating functions to deduce the generating function of Q. In Section 4.5.9 (see (4.25)) it is shown that the generating function of the sum of $d-1$ independent draws from the distribution of Q is the the generating function of Q raised to the power $d-1$, so the generating function of additional nodes found through the node if it happens to have degree d is $[G_Q(x)]^{d-1}$. The overall distribution of the number of nodes found through the additional node, is then given by a mixture of distributions in the following sense, firt pick some random d according to $\widetilde{P}(d)$, and then draw a random variable from a distribution having generating function $[G_Q(x)]^{d-1}$ (see (4.26)). So, the generating function of the distribution of the additional nodes found past the first one is $\sum_d \widetilde{P}(d)\,[G(q)]^{d-1}$. Finally, we need to add one node for the first one found, and the generating function of a distribution of a random variable plus one is just x times the generating function of the random variable discussed above (see (4.27)). So, the distribution function of the number of nodes found from one side of an edge picked uniformly at random is

$$G_Q(x) = x \sum_d \widetilde{P}(d)[G_Q(x)]^{d-1}.$$

Noting that $G_{\widetilde{P}}\left(G_Q(x)\right) = \sum_d \widetilde{P}(d)[G_Q(x)]^d$, we rewrite the above as[33]

$$G_Q(x) = x\frac{G_{\widetilde{P}}\left(G_Q(x)\right)}{G_Q(x)}.$$

or

$$G_Q(x) = \left(xG_{\widetilde{P}}\left(G_Q(x)\right)\right)^{1/2}. \tag{4.15}$$

As Newman, Strogatz, and Watts [**?**] point out, finding a solution to (4.15) is in general impossible with knowing something more about the structure of P. However, we can solve for the expectation of Q, as that is simply $G'_Q(1)$.

$$G'_Q(x) = \frac{1}{2}\left(xG_{\widetilde{P}}\left(G_Q(x)\right)\right)^{-1/2}\left(G_{\widetilde{P}}\left(G_Q(x)\right) + xG'_{\widetilde{P}}\left(G_Q(x)\right)G'_Q(x)\right).$$

Thus, recalling that $G(1) = 1$ for any generating function we find that:

$$G'_Q(1) = \frac{1}{2}\left(1 + G'_{\widetilde{P}}(1)\,G'_Q(1)\right). \tag{4.16}$$

[32] Here, we need to be working with a large number of nodes to have this be an accurate approximation, as otherwise with a small n we are working with fewer potential nodes to explore.

[33] This appears different from (25) in Newman, Strogatz, and Watts [**?**], but in fact $\frac{G_{\widetilde{P}}(\cdot)}{G_Q(x)}$ is the same as their G_1, and allows for an easy derivation of (4.15).

Then since $G'_{\widetilde{P}}(1) = E_{\widetilde{P}}[d] = \frac{\langle d^2 \rangle}{\langle d \rangle}$ it follows from (4.16) that in cases where the expectation of Q does not diverge it must be that

$$G'_Q(1) = \frac{1}{2 - \frac{\langle d^2 \rangle}{\langle d \rangle}}. \tag{4.17}$$

If $\langle d^2 \rangle \geq 2\langle d \rangle$, then the expectation of Q diverges and so (4.17) is no longer valid, and indeed we see that this expression grows as $\langle d^2 \rangle$ approaches $2\langle d \rangle$. This is consistent with our earlier calculation in (4.7).

Now, we can calculate the average size of a component. Let H be the distribution of the size of the component of a node picked uniformly at random. Then, starting from a node picked uniformly at random, the degree is governed by $P(d)$, the extended neighborhood size has generating function $[G_Q(x)]^d$, and we have to account for the initial node as well.[34] Thus, the generating function for H is:

$$G_H(x) = x \sum_d P(d)[G_Q(x)]^d = xG_P\left(G_Q(x)\right). \tag{4.18}$$

Thus, the average size of the component that a randomly selected node lies in is (in situations where the average under Q does not diverge):

$$G'_H(1) = 1 + G'_P(1)G'_Q(1) = 1 + \frac{\langle d \rangle^2}{2\langle d \rangle - \langle d^2 \rangle}. \tag{4.19}$$

If we examine Poisson random networks, we know that it must be that $\langle d \rangle = (n-1)p < 1$ in order for the network not to become connected, and so this must also hold in order to have the average size of the component not diverge. Indeed, in the Poisson random network model substituting for $\langle d \rangle = (n-1)p$, and $\langle d^2 \rangle = \langle d \rangle^2 + \langle d \rangle$, we find that average component size of a node picked uniformly at random is

$$G'_H(1) = 1 + \frac{1}{1 - (n-1)p}.$$

So, for instance, if $(n-1)p = 1/2$ then the average component size is 3, if $(n-1)p = 9/10$ then the average is 11.

If we examine scale-free networks, then $\langle d^2 \rangle$ is generally large relative to $\langle d \rangle$, and diverges as we let n grow. In that case, the expected component size diverges. The

[34] The derivation of the distribution for Q was based on randomly picking a node at either end of an edge. Here, we are working out from a given node, but given (approximate) independence in degrees, the calculation is ok.

intuition behind this is as follows. Even though average degree might be low, when we examine a given node, if it has a neighbor, that neighbor is very likely to have a large degree (as $\widetilde{P}(d) = P(d)d/\langle d\rangle$, which in a scale free network places very high weight on the highest degree nodes), and then it is even more likely to have additional high degree neighbors, and so forth.

4.4 Exercises

EXERCISE **4.1** *Self and Multiple Links in the Configuration Model**

Show that in the Configuration model that if $\max_{i\leq n} Q_i^n \to 0$, then the fraction of nodes that experience self- or multi-links is vanishing as the population size n grows; or more specifically, for any $\varepsilon > 0$, $\Pr\left[\#\{i \leq n : q_i^n > 0\}/n > \varepsilon\right] < \varepsilon$ for large enough n.

EXERCISE **4.2** *A Degree Sequence that always has Large Nodes.*

Consider the degree sequence (1,1,2,4,8,16,...). Show that in the Configuration model any fixed node has a probability of having any self-link or multiple links going to 0 as n becomes large, but for each $n \geq 2$ there is some node with a significant probability of having a self-link or multiple links. That is, show that $Q_i^n \to 0$; but that $Q_n^n \to 1$ for all n.

EXERCISE **4.3** *A Degree Sequence for the Power Distribution in the Configuration Model*

Find a degree sequence that converges to a power distribution and has $\frac{\widehat{d}^n}{(n\langle d\rangle)^{1/3}}$ tend to 0.

EXERCISE **4.4** *The Distribution of Neighbors' Degrees in the Configuration Model and Expected Degree Model*

Consider a constant degree sequence $(d, d, d \ldots)$. Form a random network by operating the configuration model and form another random network by operating the expected degree model. Provide an expression for the resulting degree distributions in the limit as n grows (working with a resulting multigraph in the configuration model). Provide an expression for the limiting distribution $\widetilde{P}$ of the degree of a node found at either end of a uniformly randomly chosen link.

EXERCISE **4.5** *The Distribution of Neighbors' Degrees*

Consider the Poisson random network model on n nodes with a link probability of p. Consider a node i and a node j, which are fixed in advance. Conditional on the link ij being present, what is the distribution of j's degree?

Consider a node i. Conditional on it having at least one link, randomly pick one of its neighbors (with equal probability on each neighbor). Argue that the conditional distribution of the node's degree is different from the conditional distribution for j's degree that you found above. What does this distribution converge to as we let n grow if p is set to keep average degree constant (so that $p = m/(n-1)$ for some fixed $m > 0$)?

Explain the difference between these two distributions.

EXERCISE **4.6** *A Threshold for Links in the Poisson Random Network Model*

Show that $t(n) = 1/n^2$ is a threshold function for there being at least one link a network relative to the Poisson random network model.

EXERCISE **4.7** *There is at Most One Giant Component in the Poisson Random Network Model**

Consider the Poisson random network model when p (as a function of n) is such that there exists $m > 0$ such that $pn \geq m$ for all n. Show that the probability of having more than one giant component vanishes as n grows.

EXERCISE **4.8** *The size of the Giant Component.*

Show that there is a solution to (4.9) of $q = 1$ if and only if $P(0) = 0$.

Find a nonzero solution to (4.9) when $P(0) = 1/3$ and $P(2) = 2/3$.

EXERCISE **4.9** *Estimating the Extent of an Infection in an Exponential Random Network Model**

Consider a degree distribution given by $P(d) = \frac{e^{\frac{-d}{(1-\pi)m}+1}}{m}$ with support from $(1-\pi)m$ to ∞, which has a mean of $2(1-\pi)m$ (which is derived in Section **??** as the distribution corresponding to a uniformly random network where the number of nodes grows over time). Use (4.9) to estimate the percent of susceptible nodes that will be infected when a random selection π of nodes are immune. Hint: See the Section 4.5 for helpful formulas of sums of series.

EXERCISE **4.10** *Estimating the Diameter in an Exponential Random Network Model*

Consider a degree distribution given by $P(d) = \frac{e^{\frac{-d}{m}}+1}{m}$ with support from m to ∞, Use (**??**) to estimate the diameter.

EXERCISE **4.11** *First Order Stochastic Dominance and Increasing Giant Components*

Consider two degree distributions $\widehat{P}$ and P, such that P first order stochastically dominates $\widehat{P}$ (see Section 4.5.5 of the appendix if this definition is unfamiliar). Show that if q' and q are interior solutions to (4.9) relative to $\widehat{P}$ and P, respectively, then $q \geq q'$.[35]

If $\widehat{P}$ is a mean-preserving spread of P and q' and q are interior solutions to (4.9) relative to $\widehat{P}$ and P, respectively, how are q' and q ordered?

EXERCISE **4.12** *Mean Preserving Spreads and Decreasing Diameters*

Consider two degree distributions $\widehat{P}$ and P, such that $\widehat{P}$ is a mean preserving spread of P (see Section 4.5.5 of the appendix if this definition is unfamiliar). Show that the solution to (**??**) under $\widehat{P}$ is lower than that under P. Show that if we change "is a mean preserving spread of" to "first order stochastically dominates" then we cannot order the solutions to (**??**).

EXERCISE **4.13** *First Order Stochastic Dominance and Decreasing Diameters**

Consider two degree finite degree sequences in the expected degree model of Section **??**, with corresponding distributions $\widehat{P}$ and P, such that P first order stochastically dominates $\widehat{P}$. Show that the diameters of the random networks associated with $\widehat{P}$ have higher diameters in the sense of first order stochastic dominance of the realized network diameters compare to those associated with P.

EXERCISE **4.14** *Component Sizes for A Family of Degree Disributions**

Calculate $\langle d^2 \rangle$ under the degree distribution that has a distribution function of

$$F(d) = 1 - (rm)^{1+r} (d + rm)^{-(1+r)},$$

[35] To offer a complete answer to this, note that (4.9) can be written as a function $1 - q = H(1 - q)$, where you can show that $H(\cdot)$ is increasing and strictly convex and is such that $H(1) = 1$. Thus, you can show that it has at most one solution other than $q = 0$. Drawing a picture will help.

from (3.2), using this continuous distribution as an approximation for distributions with large n.

Show that $\langle d^2 \rangle$ diverges when $r < 1$. Use the expression for $\langle d^2 \rangle$ and (4.19) to estimate the expected component size in large networks with such a degree distribution when $r > 1$ and for $m = \langle d \rangle$ such that $\langle d^2 \rangle < 2\langle d \rangle$.

4.5 Appendix: Useful Facts, Tools, and Theorems

This appendix contains a few mathematical definitions, formulas, theorems, and approximations that are useful in working with random networks.

4.5.1 Sums of Series

A geometric series is one where we sum a series of powers of x where $x \neq 1$:

$$\sum_{i=m}^{n} ax^i = a\frac{x^m - x^{n+1}}{1-x}.$$

Thus,

$$\sum_{i=0}^{n} ax^i = a\frac{1 - x^{n+1}}{1-x}.$$

For $x < 1$ it follows that

$$\sum_{i=1}^{\infty} ax^i = \frac{ax}{1-x}$$

and

$$\sum_{i=0}^{\infty} ax^i = \frac{a}{1-x}.$$

Another series of interest (especially for scale-free degree distributions) is

$$\sum_{i=1}^{\infty} a\frac{1}{i^\gamma}.$$

This is the Riemann Zeta Function, $z(\gamma) = \sum_1^\infty \frac{1}{\gamma}$, which is convergent whenever γ is greater than 1.

A special case of this occurs if $\gamma = 1$, when we can look at a truncated series

$$\sum_{i=1}^{n} \frac{1}{i} = H_n \tag{4.20}$$

is known as a *harmonic number* and has various approximations. For large n, an approximation of H_n is $\gamma + log(n)$, where the γ of roughly .577 is the Euler-Mascheroni constant; and the difference between this approximation and H_n tends to 0. This is useful in approximating some sequences such as

$$\frac{1}{i+1} + \frac{1}{i+2} + \cdots + \frac{1}{t}, \tag{4.21}$$

which can be written as $H_t - H_i$. For large t, this is approximately $log(t) - log(i)$, or $log\left(\frac{t}{i}\right)$.

4.5.2 e and Stirling's Formula

The exponential function can be defined in various ways that provides useful formulas. Fixing x (at any positive, negative or complex value)

$$\lim_{n\to\infty}\left(1+\frac{x}{n}\right)^n = e^x.$$

Another definition of e is given by

$$e^x = \sum_{i=0}^{\infty} \frac{x^n}{n!}.$$

Stirling's formula for large n is that

$$n! \sim \sqrt{2\pi n}\left(\frac{n}{e}\right)^n.$$

4.5.3 Chebyshev's Inequality and the Law of Large Numbers

Chebyshev's inequality says that for a random variable X with mean μ and standard deviation σ,

$$\Pr[|X-\mu| > r\sigma] < 1/r^2$$

for every $r > 0$. This is easy to prove directly from the definition of standard deviation. Letting $r = \frac{x}{\sigma}$, we can also write this as

$$\Pr[|X-\mu| > x] < \sigma^2/x^2$$

for every $x > 0$.

Chebyshev's inequality leads to a very easy proof of a version of the Weak Law of Large Numbers:

THEOREM **4.5.1** *[The Weak Law of Large Numbers] Let $(X_1, X_2, \ldots)$ be a sequence of independently distributed random variables such that $E[X_i] = \mu$ for all i and there is a finite bound B so that $Var(X_i) \leq B$ for all i. Then*

$$\Pr\left[\left|\frac{\sum_{i=1}^n X_i}{n} - \mu\right| > \varepsilon\right] \to_n 0$$

for all $\varepsilon > 0$.

Proof of Theorem 4.5.1: Let $S_n = \sum_{i=1}^n \frac{X_i}{n}$. Then $Var(S_n) = \sum_i \frac{Var(X_i)}{n^2} \leq \frac{B}{n}$. Thus, $Var(S_n) \to 0$. By Chebyshev's inequality, fixing any $\varepsilon > 0$

$$\Pr\left[\left|\sum_{i=1}^n \frac{X_i}{n} - \mu\right| > \varepsilon\right] \leq \frac{Var(S_n)}{\varepsilon^2} \to 0,$$

which establishes the claim. ∎

There is also a stronger conclusion that is possible. The weak law of large numbers just states that the probability that a sequence of observed sample means deviates from the true mean of the process tends to 0. This does not directly imply that there is a probability 1 that the sequence will converge. The strong law of large numbers provides this stronger conclusion. For a proof, see Billingsley [64].

THEOREM **4.5.2** *[The Strong Law of Large Numbers] Let $(X_1, X_2, \ldots)$ be a sequence of independently and identically distributed random variables such that $E[X_i] = \mu$ for all i. Then*

$$\Pr\left[\lim \frac{\sum_{i=1}^n X_i}{n} = \mu\right] = 1.$$

4.5.4 The Binomial Distribution

There are many situations where we need to make use of the binomial distribution, and this also provides us with an illustration of the law of large numbers.

Consider flipping a coin repeatedly, but in a situation where the coin is not a "fair" coin, but instead has a probability of p of coming up heads and a probability of $1 - p$ of coming up tails. A single flip is called a "Bernoulli trial." In many instances we are interested in a whole set of flips. If we ask the probability of a particular sequence of heads and tails being realized, say heads, tails, tails, heads, heads, ..., where there are m heads out of n flips, then its probability is $p^m(1-p)^{n-m}$. Noting that there are $\binom{n}{m}$

(read "n choose m," where $\binom{n}{m} = \frac{n!}{m!(n-m)!}$) different orderings that have m heads out of n flips of the coin, the probability that there are m heads if we flip it n times is

$$\binom{n}{m} p^m (1-p)^{n-m}.$$

The expected number of heads out of n flips is simply pn, while the standard deviation is $\sqrt{np(1-p)}$.

Note also that the expected fraction of flips of the coin that come up heads is simply p, and the standard deviation of this fraction out of n flips is $\sqrt{\frac{p(1-p)}{n}}$.

Then applying Chebyshev's inequality, letting X be the realized fraction of flips that come up heads,

$$\Pr\left[|X-p| > r\sqrt{\frac{p(1-p)}{n}}\right] < \frac{1}{r^2}.$$

So, if we let $r = n^{1/4}$, then we see that

$$\Pr\left[|X-p| > \frac{\sqrt{p(1-p)}}{n^{1/4}}\right] < \frac{1}{n^{1/2}},$$

and so with a large number of flips of the coin it is very unlikely that the realized fraction of heads will differ from p by very much, just as the law of large numbers tells us.

4.5.5 Stochastic Dominance and Mean-Preserving Spreads

Consider discrete distributions $\widehat{P}$ and P with support on $\{0, 1, 2, \dots\}$.[36]

The concept of first order stochastic dominance captures the idea that P is obtained by shifting mass from $\widehat{P}$ to place it on higher values. The following are equivalent

- $\sum f(d)P(d) \geq \sum f(d)\widehat{P}(d)$ for all nondecreasing functions f,
- $\sum_0^x P(d) \leq \sum_0^x \widehat{P}(d)$ for all x,
- $\sum_x^\infty P(d) \geq \sum_x^\infty \widehat{P}(d)$ for all x

and if they hold we say that
P first order stochastically dominates $\widehat{P}$.

[36] The extension of these definitions is straightforward to the case of more general probability measures, simply substituting $\int \cdot dP$ in the place of sums with respect to P.

We say that the dominance is strict if the inequalities above hold strictly for some x (or f). Note that if strict dominance holds, then it must be that $\sum f(d)P(d) > \sum f(d)\widehat{P}(d)$ for any strictly increasing f.

An example of a degree distribution that (strictly) first order stochastic dominates another is pictured in Figure 7.2.5.

The last two items above are clearly equivalent and capture the idea that P places less weight on low values, and thus more weight on higher values than $\widehat{P}$. The idea that stochastic dominance provides higher expectations for all nondecreasing functions is not difficult to prove as P is shifting weight to higher values of the function f, and the converse is easily seen using the last item above and a simple step function that has value 0 up to x and then 1 from x onwards.

Often when people refer to first order stochastic dominance, the "first order" is omitted and it is simply said that P stochastically dominates $\widehat{P}$.

The idea of second order stochastic dominance is a less demanding relationship than first order stochastic dominance and so it orders more pairs of distributions. It is implied by first order stochastic dominance. Instead of requiring a higher expectation relative to all nondecreasing functions, it only requires a higher expectation relative to all nondecreasing functions that are also concave. This has deep roots in foundations of decision making and risk aversion, although for us it quite useful in comparing degree distributions of different networks.

THEOREM **4.5.3 (Rothschild and Stiglitz [541])** *The following are equivalent*

- $\sum f(d)P(d) \geq \sum f(d)\widehat{P}(d)$ *for all nondecreasing, concave functions* f,
- $\sum f(d)P(d) \leq \sum f(d)\widehat{P}(d)$ *for all nonincreasing, convex functions* f,
- $\sum_{z=0}^{x}\sum_{d=0}^{z} P(d) \leq \sum_{z=0}^{x}\sum_{d=0}^{z} \widehat{P}(d)$ *for all* x,

and when they hold we say that P second order stochastically dominates $\widehat{P}$. *If* P *and* $\widehat{P}$ *have the same mean then the above are also equivalent to*

- $\widehat{P}$ *is a* mean-preserving spread *of* P,[37]
- $\sum f(d)P(d) \geq \sum f(d)\widehat{P}(d)$ *for all concave* f.

[37] This indicates that the random variable described by $\widehat{P}$ can be written as the random variable described by P plus a zero mean random variable.

Again, the dominance (or mean-preserving spread) is strict if the inequalities listed above hold strictly for some f (or x). In that case, $\sum f(d)P(d) > \sum f(d)\widehat{P}(d)$ for any strictly increasing and strictly concave functions f.

So, if P and $\widehat{P}$ have the same average, then P second order stochastically dominates $\widehat{P}$ if and only if $\widehat{P}$ is a mean preserving spread of P. This implies that $\widehat{P}$ has a (weakly) higher variance than P, but also requires a more structured relationship between the two. Having a higher variance and identical mean is not sufficient for one distribution to be a mean preserving spread of another.

4.5.6 Domination

There are also definitions of domination for distributions on several dimensions.

Consider two probability distributions μ and ν on $\mathbb{R}^n$.

μ *dominates* ν if

$$E_\mu[f] \geq E_\nu[f]$$

for every non-decreasing function $f : \mathbb{R}^n \to \mathbb{R}$. The domination is *strict* if strict inequality holds for some non-decreasing f.

Domination captures the idea that "higher" realizations are more likely under μ than under ν. In the case where $n = 1$, domination reduces to first order stochastic dominance.

4.5.7 Association

Beyond comparing two different distributions, we will also be interested in knowing when it is that a joint distribution of a set of random variables exhibits relationships between the variables. Concepts like correlation and covariance can address two random variables, but when working with networks we will often work with groups of variables at the same time. A notion that captures such relationships is association, a definition due to Esary, Proschan, and Walkup [**?**].

Let μ be a joint probability distribution describing a random vector $S = (S_1, \ldots S_n)$, where each S_i is real-valued.

μ is *associated* if

$$\mathrm{Cov}_\mu(f, g) = E_\mu[f(\mathbf{S})g(\mathbf{S})] - E_\mu[f(\mathbf{S})]E_\mu[g(\mathbf{S})] \geq 0,$$

for all pairs of non-decreasing functions $f : \mathbb{R}^n \to \mathbb{R}$ and $g : \mathbb{R}^n \to \mathbb{R}$.

If $S_1, \ldots, S_n$ are the random variables described by a measure μ that is associated, then we say that $S_1, \ldots, S_n$ are associated.

Association of μ implies that S_i and S_j are non-negatively correlated for any i and j, and it entails that all dimensions of $\mathbf{S}$ are non-negatively interrelated.[38]

To establish strictly positive relationships, as opposed to non-negative ones, Calvó-Armengol and Jackson [119] define a strong version of association.

A partition Π of $\{1, \ldots, n\}$ captures which random variables are positively related (for instance, the components of nodes in a network).

A probability distribution μ describing the random variables $(S_1, \ldots S_n)$ is *strongly associated* relative to the partition Π if it is associated, and for any $\pi \in \Pi$ and nondecreasing functions f and g

$$\mathrm{Cov}_\mu (f, g) > 0$$

whenever f is increasing in s_i for all s_{-i}, g is increasing in s_j for all s_{-j}, and i and j are in π.

An implication of strong association is that S_i and S_j are positively correlated for any i and j in π.

4.5.8 Markov Chains

There are many settings where one considers a random process over time, the world can be described by a state, and the transition from one state to another depends only on the current state of the system and not how we got there. For the applications in this book, we will mainly be concerned with finite-state systems. For instance, states could be the network that is presently in the society. Alternatively, a state might instead describe something that the agents in a network are doing.

Let the finite set of states be denoted S. If the state of the system is $s_t = s$ at time t, then there is a well-defined probability that the system will be in state $s_{t+1} = s'$ at time $t + 1$. What is critical is that are well-defined probabilities of being in each state tomorrow as a function only of the state today. Let Π be the $n \times n$ matrix describing these *transition probabilities* with entries

$$\Pi_{ss'} = \Pr(s_{t+1} = s' \mid s_t = s).$$

[38] This is a weaker concept than "affiliation," which requires association for when conditioning on various events. The weaker concept is useful in many network settings where the states of nodes of a network will be associated, but are not affiliated. See Calvó-Armengol and Jackson [119] for an example and discussion.

This results in what is known as a (finite state) Markov chain, where "Markov" refers to the property that the ditribution of what will happen in the future of the system only depends on the current state, and not how we got to the current state. Markov chains have a number of applications and very nice properties, so that they have been studied extensively.

There are some basic facts about Markov chains that are quite useful.

The Markov chain is said to be *irreducible* when for any two states s' and s, if the system starts in state s' in some period, then there is a positive probability that it will reach s at some future date.

Irreducibility corresponds to the strong connectedness of sthe associated directed graph where the nodes are the states and s points to s' if $\Pi_{s's} > 0$.

An irreducible Markov chain is *aperiodic* if the greatest common divisor of its cycle lengths is one, where the cycles are in the associated directed graph just described. Checking whether a system is aperiodic is equivalent to asking the following. Start in some state s at time 0 and list all the future dates where there is a positive probability of being in this state again. If the answer for a state s a list of dates with a greatest common divisor greater than 1 then that state is said to be periodic. If no state is periodic, then the Markov chain is aperiodic.[39]

Noting that the probability of starting in state s and ending in state s' in two periods is simply Π^2, we see by similar reasoning that the probability of starting in state s and ending in state s' in t periods is Π^t. If Π^t has all entries greater than 0 for some t, then it is clearly both irreducible and aperiodic as it will then have all positive entries for all times thereafter. In contrast, if it never has all positive entries, then it either fails to be irreducible, or it is periodic for some states.

An important theorem about Markov chains states that an irreducible and aperiodic finite-state Markov chain has what is known as a *steady-state* distribution (e.g., see Billingsley [64]). The steady-state of the Markov process is described by a vector μ with dimension equal to the number of states, where μ_s is the probability of state s. The steady-state condition is that if the process is started at time 0 by randomly drawing the state according to the steady state distribution, then the distribution over

[39] For those who want to be sure to master all of the definitions, verify that if a Markov chain has a finite number of states and is irreducible, then one state is periodic if and only if all states are periodic, and in that case they all have the same period (greatest common divisor of dates at which they have a probability of recurring).

the state at time 1 will be given by the same distribution. That is,

$$\mu_{s'} = \sum_s \mu_s \Pi_{ss'},$$

or

$$\mu = \mu\Pi.$$

We can find the steady-state distribution as a left-hand unit eigenvector, noting that Π is a row-stochastic matrix (that is, the elements of each row sum to 1).

Other useful facts about the steady-state distribution of a finite-state, irreducible, and aperiodic Markov chain include that it provides the long-run limiting average fraction of periods that the process will spend in each state regardless of the starting state; and regardless of where we start the system the probability of being in state s at time t as t grows goes to μ_s.

Thus, in situations where behavior can be described by a Markov chain, we have sharp predictions about behavior over the long run.

4.5.9 Generating Functions

Generating functions (also known as probability generating functions[40]) are useful tools for encapsulating the information about a discrete probability distribution and also for calculating moments of the distribution and various other statistics associated with the distribution.

Let $\pi(\cdot)$ be a discrete probability distribution, which for our purposes has support in $\{0, 1, 2 \ldots\}$. The *generating function* associated with π, denoted G_π, is defined by

$$G_\pi(x) = \sum_{k=0}^{\infty} \pi(k) x^k = E_\pi \left[x^k\right]. \tag{4.22}$$

Note that since $\pi(\cdot)$ is a probability distribution, $G_\pi(1) = 1$.

Moreover, G_π has a number of useful properties. Taking various derivatives of it helps us to recover the various expectations with respect to π.

$$G'_\pi(x) = \sum_{k=0}^{\infty} \pi(k) k x^{k-1}. \tag{4.23}$$

[40] These are distinct from moment generating functions, which are defined by $\sum_{k=0}^{\infty} \pi(k) e^{xk} = E_\pi \left[e^{xk}\right]$.

Thus,

$$G'_\pi(1) = \sum_{k=1}^{\infty} \pi(k)k = E_\pi[k] = \langle k \rangle.$$

More generally,[41]

$$\left(x\frac{d}{dx}\right)^m G_\pi = \sum_{k=1}^{\infty} \pi(k)k^m x^k, \tag{4.24}$$

and so

$$E\left[k^m\right] = \langle k^m \rangle = \left(x\frac{d}{dx}\right)^m G_\pi \mid_{x=1}$$

Next, suppose that we consider two independent draws of the random variable k and we want to know the sum of them. The probability that the sum is k is given by $\sum_{i=0}^{k} \pi(i)\pi(k-i)$. This new distribution of the sum, denoted π_2, is then such that $\pi_2(k) = \sum_{k=0}^{k} \pi(i)\pi(k-i)$. It has an associated generating function

$$G_{\pi_2}(x) = \sum_{k=0}^{\infty} \pi_2(k)x^k = \sum_{k=0}^{\infty}\sum_{i=0}^{k} \pi(i)\pi(k-i)x^k.$$

Note that

$$[G_\pi(x)]^2 = \left[\sum_{k=0}^{\infty} \pi(k)x^k\right]^2 = \sum_{i,j} \pi(i)\pi(j)x^{i+j} = G_{\pi_2}(x).$$

This extends easily to higher powers (simply iterating gives even powers) and so the generating function associated with the distribution π_m of a sum of m independent draws of k from π is given by

$$G_{\pi_m}(x) = [G_\pi(x)]^m. \tag{4.25}$$

Another useful observation is the following. Consider a distribution π which is derived by first randomly picking a distribution from a series of distributions $\pi_1, \pi_2, \ldots, \pi_i, \ldots$, picking each with corresponding probability γ_k, and then drawing from the chosen distribution. Then it follows almost directly that

$$G_\pi = \sum_i \gamma_i G_{\pi_i}. \tag{4.26}$$

[41] The notation $\left(x\frac{d}{dx}\right)^m G_\pi$ indicates taking the derivative of G_π with respect to x and then multiplying the result by x, and then taking the derivative of the new expression and multiplying it by x, and so forth for m iterations.

Finally, there are many situations where we have a variable k with distribution P and we want to work with the distribution of $k+1$. The distribution $\overline{P}$ of $k+1$ is described by $\overline{P}(k) = P(k-1)$, where $k \geq 1$. Thus, it has a generating function of

$$G_{\overline{P}}(x) = \sum_{k=1}^{\infty} P(k-1)x^k = xG_P(x). \tag{4.27}$$

To use generating functions in the context of degree distributions, let us begin with a degree distribution P. Let it have an associated generating function G_P, defined as under (4.22). Suppose that we are also interested in the generating function $G_{\widetilde{P}}$ associated with the distribution of neighboring degrees under the configuration model, denoted $\widetilde{P}$. Recalling from (**??**) that $\widetilde{P}(d) = \frac{d\ P(d)}{\langle d \rangle}$, it follows that

$$G_{\widetilde{P}}(x) = \sum_{k=0}^{\infty} \widetilde{P}(d)x^d = \sum_{k=0}^{\infty} \frac{P(d)d}{\langle d \rangle} x^d = \frac{xG'_P(x)}{G'_P(1)}. \tag{4.28}$$

Chapter 5

Growing Random Networks

Another prominent class of models of random networks consists of those where new nodes are born over time and form attachments to existing nodes when they are born. As an example, consider the creation of a new web page. When the web page is designed, it will often include links to existing web pages. The web page might be updated over time; but nonetheless, a nontrivial portion of its links will have been included when the web page is first created. Over time, an existing page will be linked to by new web pages. The same is true of people entering a school, or a new job or new neighborhood. This means that there is a fundamental difference between a growing network and a static one. Time introduces a natural heterogeneity to nodes based on their age in a growing network. This heterogeneity is important for two reasons. First, it is present in many applications where individuals or nodes enter (and leave) networks over time. This includes the web page example mentioned above, as well as many networks of friendships, acquaintances, citations, and professional relationships. People enter and leave networks and accumulate connections over time. Second, the added heterogeneity comes in a simple form that allows the model to move beyond the Poisson random networks of Erdös and Rényi and to have extra layers of richness; but still be manageable to analyze.

In this chapter, I discuss growing random network models and show some of the properties that emerge. The first aspect that will be important is that the resulting degree distributions will be richer than that of Poisson random networks, and at one extreme will provide an explanation for how scale-free distributions might naturally emerge. This contrasts with models such as the configuration model, where we essentially program in the degree distribution that we want and then generate a network. The configuration model is a workhorse for studying diffusion and other properties on

a random network, but precisely because it is simple and lacks the full richness of more foundational or grounded models of networks. Growing networks will allow for several key factors that generate network characteristics that match some of the observations about social networks discussed in Chapter 3. First, when nodes are born we can consider different ways in which they attach to existing nodes. At one extreme, where newborn nodes pick nodes to link to uniformly at random, we will just have a growing variation on an Erdös-Rényi random network. At the other extreme, where they pick nodes in proportion to the current degrees of the existing nodes (something named "preferential attachment" by Barabasi and Albert [40]), nodes that are older and have had a chance to grow in degree will grow faster than younger nodes who have lower degrees. This sort of rich-get-richer process leads to scale-free distributions. Preferential attachment has a nice interpretation in that if we randomly pick a node and then start searching through the network, we will end up finding nodes in proportion to their degree. We can also consider hybrid models, where the attachment probabilities vary between these extremes. Despite claims in the literature that many social networks exihibit power-laws (having scale-free degree distributions), by fitting such hybrid models it becomes clear that most social networks lie between these extremes.

Beyond degree distributions, growing random networks provide insight into other observed characteristics. By the nature of the process, older nodes will have higher degrees on average, and, since older nodes have a greater proportion of their connections to older nodes than do younger nodes, a natural positive correlation in degrees emerge. Actually, not only do we see correlation in degrees, but also age-based homophily which is also consistent with many observed social networks. To the extent that the process involves some form of preferential attachment, we also see large hub nodes emerge in the networks, and this will produce a lower diameter than in a Poisson random network. Finally, certain variations of hybrid models produce the high clustering observed in many social networks. This comes out in hybrid models where newborn nodes find the nodes that they link to by navigating the network itself. That is, to the extent that people are introduced to someone who becomes their friend through a friend, then we see natural clustering emerge. The same is true in citation networks where one finds new articles to cite by examining the bibliography of other relevant articles; and similarly in finding new web pages to link to by following links of pages one is already linked to, and so forth. In short, the growing random networks introduce new aspects to network formation that generate structures exhibiting networks that more closely match many observed characteristics of social networks.

5.1 Uniform Randomness: an Exponential Degree Distribution

To get a feeling for a process where a network grows over time, I start by discussing a dynamic variation on the Poisson random network model, where nodes are born over time and form links with existing nodes at the time of their birth.[1]

As nodes are born over time, index them by the order of their birth. Thus, node i is born at date i, where $i \in \{0, 1, 2 \ldots\}$. I postpone the question of how we should interpret the scale of time until we investigate situations in which nodes are born in clusters. For now, think of each period of time as indicating that a new node has been born, regardless of how much physical time has passed since the last node entered the system.

A node forms links to existing nodes when the new node is born. To start, examine the case where links are undirected. Let $d_i(t)$ be the degree of node i (born at time i) at a time t. So, $d_i(i)$ is the number of links formed at a node's birth, and then $d_i(t) - d_i(i)$ will be the number of links that node i gets from the new nodes that were born between time i and time t.

Consider a variation of the Poisson random setting, where each newborn node randomly selects m of the existing nodes and links to them. To have things well defined, start the network with $m+1$ nodes born at times $\{0, 1, \ldots, m\}$, each connected to each other. The specifics of this will not be of great consequence when we look at limiting properties of the system, but it is helpful in order to be able to properly analyze the system. Thus, the first newborn node that we consider is the one born at time $m + 1$.

At the end of time $m + 1$, m of the older nodes will have new links and one older node will not; while the newest node will have m links. Each of the pre-existing nodes expects to gain $m/(m + 1)$ links (or one link with a probability of $m/(m + 1)$). At the end of time $m + 2$, there are different possibilities: m of the $m + 2$ pre-existing nodes will have gained a new link, while 2 of them will not have. Depending on which 2 do not gain a link we have different possibilities for degree distributions that could be realized. As we continue, the number of possible realizations of the degree distribution grows. While it is hard to keep track of the potential realizations and their relative probabilities, we can do some more direct calculations. If we look at time t, a node i

[1] Here, we already see one of the deficiencies of such models, as the only links formed over time are between a new node and an existing node. There are no new links formed between existing nodes over time. We can return to this feature later.

born at time $m \leq i < t$ has an *expected* degree at time t of

$$m + \frac{m}{i+1} + \frac{m}{i+2} + \cdots + \frac{m}{t},$$

or

$$m\left(1 + \frac{1}{i+1} + \frac{1}{i+2} + \cdots + \frac{1}{t}\right). \tag{5.1}$$

For large t, this is approximately[2]

$$m\left(1 + log\left(\frac{t}{i}\right)\right). \tag{5.2}$$

Therefore, although it is difficult to deduce the actual degree distribution of this network formation process, it is relatively straightforward to deduce the distribution of *expected* degrees. For a large t, the nodes that have expected degree less than d are (using the approximation) those such that

$$m\left(1 + log\left(\frac{t}{i}\right)\right) < d. \tag{5.3}$$

We rewrite this as the nodes i such that

$$i > te^{1-\frac{d}{m}}.$$

Thus, the nodes with expected degree less than d (where $d < m\left(1 + log\left(\frac{t}{m}\right)\right)$) are those born after time $te^{1-\frac{d}{m}}$. This is a fraction of $1 - e^{1-\frac{d}{m}}$. Thus we have deduced an approximation of the distribution function of the expected degrees at time t. For $d < m\left(1 + log\left(\frac{t}{m}\right)\right)$, the fraction of nodes with expected degrees less than than d is

$$F_t(d) = 1 - e^{-\frac{d-m}{m}}. \tag{5.4}$$

This is a variation of an exponential distribution. In particular, each node starts out with m links, and then the expected links that a random node expects to gain over time has an exponential distribution with expected value m.

Note that the distribution is in fact independent of time t. This is because the faction of nodes with no more than some degree d is actually the same over time. As more nodes are being born, more of them are also below any given level. This can be seen in that the expected degree of a given node in (5.2) is dependent on t/i, so it depends on when i was born relative to the overall set of nodes, and not on i's absolute date of birth. This is true of some processes and not others.

[2] $\sum_{k=1}^{n} \frac{1}{k} = H_n$ is a Harmonic Number and has various approximations, as discussed in Section **??**. For large n, an approximation of H_n is $\gamma + log(n)$, where γ is the Euler-Mascheroni constant which is roughly .577; and the difference between this approximation and H_n tends to 0. Thus, we can rewrite (5.1) as $m(1 + H^t - H^i)$, which then leads to the stated approximation.

5.1.1 Mean-Field Approximations

Above, we calculated the distribution of *expected degrees* after time t. How close is this to the distribution of *actual degrees* after time t? This turns out to be a good approximation in this particular model. While proving that this is a good approximation of the actual degree distribution is beyond the scope of this text, let me outline the issues. First, the distribution we derived can easily be shown to be an accurate approximation of the distribution of expected degrees for large t. Our only approximations in this respect came in the rounding the sum of the Harmonic Series, and in not worrying about the differences between the first m nodes and other nodes, which is only an issue for a vanishing fraction of nodes and would only enter the calculation if we examined the very high tail of the distribution. Thus, the place where the approximation might face difficulties is in the difference between a distribution of expected degrees and actual degrees. Here we benefit from the fact that the relative distance of the degree of a node from the expected degree (actual degree minus expected degree divided by expected degree) is going to 0 for this process. The degree of a given node can be seen as the realization of a sum of independent random variables (whether or not each newborn node happens to link to it). While these independent random variables have different probabilities and expectations, their summed expectation relative to the expected value of any given one tends to infinity, and so by a variation on the law of large numbers, (e.g., see Landers and Rogge [400]) we can deduce that the *ratio* of the actual degree relative to the expected degree of any given node tends to 1. There is still much work to be done to establish that the distribution over nodes then converges, as one has to aggregate across nodes. If we fix some degree d, and then ask how many nodes end up on the other side of it compared to the nodes degree, this probability vanishes for any given node, since its expected degree only increases and its ratio over the expected degree goes to one. The key to aggregating, is then showing that this convergence has some uniformity in it, so that the fraction of nodes whose ratios of realized to expected degrees are off by more than a given amount is going to 0.

When we compare the network that emerges from this growing system to a Poisson random network there are two differences. First, in this process, each node starts with a given number m of links. Then it is only the additional links that are random. Thus, an appropriate benchmark random network would not be the Poisson random network of Erdös and Rényi, but instead a variation where there are t nodes, and each picks m

others at random to link to.[3] There each node would approximately have a degree of m plus a Poisson random variable with expectation m. The main difference between the distribution for a Poisson random network and exponential distribution from the growing random network is that the exponential distribution has more of a spread to it: The older nodes tend to have higher degrees and the younger nodes have lower degrees.

The previous section gave us a first exposure to what is known as a *mean-field approximation*. The full randomness of the process was quite complex, and so rather than try to deduce the degree distribution of the process directly, we found an approximation of the distribution of expected degrees. We then argued why, at least in that specific case, the distribution of expected degrees is a valid approximation of the actual degree distribution.

Random graph processes tend to be complex; especially ones where heterogeneity enters the system through time so that nodes are facing different distributions on how connected they will be. As such, deriving the degree distribution at any point in time can be quite difficult. A standard technique, borrowed from the statistical-physics literature, for solving such complex dynamic systems is to use a mean field approximation. That is, one assumes that the system evolves so that things occur at the average level rather than randomly. For instance, let us suppose that there are already 100 nodes and a new node appears and is supposed to form links to existing nodes independently with probability 1/10. Under such an approximation, we instead suppose that the node forms exactly 10 links. This, coupled with a continuous time approximation, allows us to model the change in time of a given node's degree at a fixed rather than a stochastic rate. All of the variation that comes into the system under such an approximation is not due to the stochastics, but rather through other forms of heterogeneity in starting conditions - for instance, here the heterogeneity is in terms of dates of birth. While there are many obvious departures from reality in such an approximation, in many situations these techniques provide remarkably accurate estimates.

There is still distressingly little that we know analytically about when such approximations are good and when they are not. The analysis above provides an argument for why this is an accurate approximation for large growing networks with uniform probabilities on attachment; but such arguments become more difficult with more complex

[3] Here we would have to either admit duplicate links between pairs of nodes, or ignore them.

processes and generally are overlooked entirely.[4] A standard (but not fully satisfactory) technique to verify the accuracy of the approximation is to compare the approximations to simulations of the actual process for some range of parameter values. While we might prefer to be able to calculate things like degree distributions directly, this usually turns out to be intractable for all but the starkest of models, and hence turning to mean-field approximations is a next-best alternative.

5.1.2 Continuous Time Approximations of Degree Distributions

Let us now re-examine the growing random network analyzed in Section 5.1, but do so with an alternative technique, working with a continuous time mean-field approximation.

A new node is born at time t. It forms m links by uniformly randomly picking m out of the t existing nodes.

Node i's degree is thus described by a starting condition of $d_i(i) = m$ and an approximate change over time of

$$\frac{dd_i(t)}{dt} = \frac{m}{t},$$

for each $t > i$. This is due to the new node born at each time spreading it's m new links randomly over the t existing nodes at time t.

This differential equation has a solution

$$d_i(t) = m + m \log\left(\frac{t}{i}\right).$$

Now, from this we can derive an approximation of the degree distribution. We again note that the degrees of nodes are increasing over time. So for instance, if we ask how many nodes have degree of no more than 100, and we see that a node born at time τ has degree of exactly 100, then we are equivalently asking how many nodes were born on or after time τ. So, if it is currently time t, then the fraction of nodes having degree of no more than 100 would be $(t - \tau)/t$. In this manner we derive a degree distribution.

Thus, for any d and time t, we find the node $i(d)$ such that $d_{i(d)}(t) = d$. The nodes that have degree of less than d are then those born after $i(d)$. The resulting cumulative distribution function is then $F_t(d) = 1 - \frac{i(d)}{t}$.

[4] For one such analysis, see Benaïm and Weibull [50].

Applying this technique to this random network process, we solve for $i(d)$ such that

$$d = m + m \log\left(\frac{t}{i(d)}\right).$$

This implies that

$$\frac{i(d)}{t} = e^{-\frac{d-m}{m}}$$

Thus, such a network would have distribution function described by

$$F_t(d) = 1 - e^{-\frac{d-m}{m}}$$

This is a negative exponential distribution with support from m to infinity and a mean degree of $2m$ (as it intuitively should be, as each link involves two nodes and each new node brings m links with it).

Note that this matches what we found in Section **??**, where we worked with the discrete time system, rather than the continuous time approximation. Once we are working with a mean-field approximation, the continuous time approximation is relatively minor, smoothing things out and allowing us to use differential equations, which can substantially simplify calculations. The main approximation to worry about is working with expected rather than realized values.

5.2 Preferential Attachment

With some understanding of techniques for tackling growing processes, let us enrich the process a bit.

As discussed in Section **??**, degree distributions of a number of observed networks exhibit "fat tails." Price [521], [522] pioneered the study of power distributions in networks. He adapted ideas of Simon [561] to scale-free degree distributions in a setting of growing networks. His empirical focus was on networks of citations among scientific papers. His idea was that an article would gain citations over time in a manner proportional to the number of citations the paper already had. This goes along with a story where researchers randomly find some article (e.g., via searching for key words on the internet) and then search for additional papers by tracing through the references of the first article. The more citations an article has, the larger the likelihood that it will be found and cited again. So, ignoring other issues guiding citation decisions,[5] the

[5] We will come back to discuss this in Section **??**.

probability that an article gets cited is proportional to the number of citations it already has. In the recent literature, such a link formation process was named "preferential attachment" by Barabasi and Albert [40].[6]

It is important to note that fat-tailed distributions have been found in a wide variety of applications, and so the basic ideas behind generating such distributions has a long history. Some of the first work on this was by Pareto [501], for whom the canonical power distribution is named. In the 1890's, Pareto was looking at wealth distributions across a society, and noticed that the distribution had scale-free features, where there were many more individuals who had large or small amounts of wealth than would appear in a normal or other purely random distribution. Such features were also observed in the frequency of word usage by Zipf [639] and city sizes (also known as "Zipf's law").[] Explanations for why systems should exhibit such a distribution were first put forth by Yule in 1925 [636] and Simon in 1955 [561]. Most processes that generate scale-free distributions are essentially (and sometimes unknowingly) variations on the ideas first formalized by Simon, with roots tracing back to Yule. The two basic ingredients that lead to scale-free distributions are (i) that the system grows over time so that new objects continue to enter (e.g., nodes in network applications, people in wealth applications, and cities in city-size applications) and (ii) that existing objects grow at rates that are proportional to their size. This second feature has the effect that the rich get richer (faster than the poor), and is essential to obtaining such a distribution. This proportional growth feature is also central to a close cousin of scale-free distributions: lognormal distributions. It is the specifics of the growth of the system that results in the scale-free features rather than the lognormal nature of the distribution.

Let us explore a basic preferential-attachment model in more detail. Nodes are born over time and indexed by their date of birth $i \in \{0, 1, 2..., t, ...\}$. Just as in the model above, upon birth each new node forms m links with pre-existing nodes. The difference is that way in which a new node selects which existing nodes it links to.

[6] Barabasi and Albert [40] developed a similar model to that of Price [522] except it is undirected, while Price's was directed. There are a number of studies generating power or scale-free degree distributions based on variations of preferential attachment. These include, for example, Kumar et al [**?**], whose copying method is akin to preferential attachment, as well as Dorogovtsev and Mendes [191], Levene et al [**?**], and Cooper and Frieze [163]. See Newman [480] and Mitzenmacher [446] for more discussion of such processes and their development. There are also other models generating scale-free distributions by appealing directly to the fitness of nodes and proposing that links depend on fitness and that fitness has a power distribution (e.g., see Caldarelli et al [111]).

Instead of selecting m of the nodes uniformly at random, it attaches to nodes with probabilities proportional to their degrees. For example, if one existing node has three times as many links as some other existing node, then it is three times as likely to get a given link from the newborn node. Thus, the probability that an existing node i gets a new link from the newborn node at time t is m times i's degree relative to the overall degree of all existing nodes at time t, or

$$m\frac{d_i(t)}{\sum_{j=1}^{t} d_j(t)}.$$

As there are tm total links in the system at time t, it follows that $\sum_{j=1}^{t} d_j(t) = 2tm$. Therefore, the probability that node i gets a new link in period t is

$$\frac{d_i(t)}{2t}.$$

Again, there are some details to worry about in starting such a process. So, start with a pre-existing group of m nodes each connected to each other. Now we have well-defined stochastic process. Following our discussion above, we examine the "mean-field" approximation. The mean-field, continuous-time approximation of this process is described by

$$\frac{dd_i(t)}{dt} = \frac{d_i(t)}{2t},$$

with initial condition $d_i(i) = m$. This has a solution of

$$d_i(t) = m\left(\frac{t}{i}\right)^{1/2}. \tag{5.5}$$

Thus, nodes are born over time and then grow. Just as before, the degrees of nodes can be ordered by their ages, with oldest nodes being the largest. To find the fraction of nodes with degrees that exceed some given level d at some time t, we just need to identify which node is at exactly level d at time t, and then we know that all nodes born before then are the nodes that are larger. Let $i_t(d)$ be the node which has degree d at time t, or such that $d_{i_t(d)}(t) = d$. From (5.5) it follows that

$$\frac{i_t(d)}{t} = \left(\frac{m}{d}\right)^2.$$

The fraction of nodes that have degree smaller than d at time t is the proportion born after node $i_t(d) = t\left(\frac{m}{d}\right)^2$. At time t, this is a fraction of $\frac{m^2}{d^2}$. Thus, the distribution function is

$$F_t(d) = 1 - m^2 d^{-2}.$$

This has a corresponding density or frequency distribution (for $d \geq m$) of

$$f_t(d) = 2m^2 d^{-3}.$$

Thus, the degree distribution (of expected degrees) is a power distribution with an exponent of -3.

This has the same time independence that we saw with the exponential distribution coming from a growing random network where new links were formed to existing nodes uniformly at random. This again follows since the relative degrees of nodes are determined by their relative birth dates.

To understand why this came out as an exponent of -3, and not some other exponent, let us examine the growth process. Recall from equation (5.5) that the degree of a node i as a function of time can be written as $d_i(t) = m\left(\frac{t}{i}\right)^{1/2}$. So, nodes are growing over time at a rate that is proportional to the square root of the time measured relative to their birthdate. It is this square root that translates into the -2 in the distribution function (and then the -3 in the density or frequency distribution). So, why is it a square root here? It was a particular aspect of process that led nodes to grow at a specific rate. To get a better feeling for this, suppose a node's degree grows at a rate of $\frac{dd_i(t)}{dt} = \frac{d_i(t)}{\gamma t}$. Then, following the same steps as we did before a node's degree would be $d_i(t) = m\left(\frac{t}{i}\right)^{1/\gamma}$ and the degree distribution would be described by $F_t(d) = 1 - m^\gamma d^{-\gamma}$, or a freqency of

$$f_t(d) = \gamma m^\gamma d^{-\gamma-1}.$$

A slower growth rate of any given node's degree over time (corresponding to a higher γ), leads to a distribution of degrees with a steeper fall-off in its frequency. That is, degrees get relatively more bunched at lower levels as we increase γ. How would one interpret γ? In the model we examined, m links were formed at each date and to nodes in proportion to their relative degrees. So, we had a sum of degrees of $2mt$ in the network at time t, and a chance $md_i/(2mt)$ of a node i getting a new link in period t. The γ was 2.

How could one justify a probability of $md_i/(\gamma mt)$ for node i getting a new link in period t? The γ here is not an easy parameter to justify altering. One possibility is as follows. Suppose that instead of a single node being born at time t, a group of new nodes comes in at time t. They form a fraction of links among themselves and the remaining fraction to existing links. So, for instance if they form a fraction α of links to existing nodes and $1 - \alpha$ amongst themselves, then the probability of node i (born before t) getting a new link in period t would be $\alpha md_i/(2mt)$. Therefore, $\gamma = 2/\alpha$.

So, if $\alpha = 1$ and new nodes form all of their links with pre-existing nodes then this is exactly the preferential attachment model we saw before with $\gamma = 2$. As α decreases, and new nodes form more of their link amongst themselves, then γ increases, which corresponds to slower growth in the degrees of pre-existing nodes, and a distribution with more concentration on relatively lower degrees.

In terms of an approximation, we have again looked at expectations and a continuous time approximation. Here there is an added complication. In the case where links were uniformly random, as in Section **??**, the realization of links was independent across time. Here, if a node happens to get more links at an early stage, that can snowball into more links at later stages. Moreover, this is a nonlinear effect. Thus, it is not only that it is difficult to see whether the approximation above is a good approximation for the degree distribution, but in fact it is not even clear that it is a good approximation of the distribution of expected degrees. The fact that a preferential attachment process does lead to the stated degree distribution has been verified by Bollabas, Riordan, Spencer, and Tusnady, [**?**], but by using an approach to keep track of the degree distribution directly (explicitly keeping track of the possible degree sequences that we could see emerging over time), rather than showing that mean-field approximations are accurate.

To get some feeling for such a network, and how it might differ from the previous random graph models, consider the following figure of a 25 node network which was generated using such a preferential-attachment process where each new node forms two links. To get this process started, Node 1 formed no links at birth, Node 2 formed only a link to 1, and the process was well defined from then on.

This network looks very different from the earlier models which had approximately the same average degree (Figures **??** and **??**). As the nodes are indexed by their birth dates, we see that the older nodes tend to have much higher degrees. For instance, node 2 has degree 11 while nodes 22 to 25 have only degree 2, or the links they form at birth. In the mean-field approximation, this is taken to an extreme where older nodes always have higher degrees. Even observed networks that display higher degrees for older nodes (e.g., citation networks, co-authorship networks, etc.) have degree distributions that are not so purely age dependent. Some older nodes might have few links, and some young ones might have more links. By adding a weighting parameter or "fitness," it is easy to extend the model so that some younger nodes can overtake older nodes because they are more attractive to link to, as outlined by Bianconi and Barabasi **??**. Just to get a feeling for that, suppose one changes the probability of a node getting a new link

Figure 5.2. A Network of 25 nodes Formed by Preferential Attachment

via preferential attachment from $d_i/(2t)$ to $d_i v_i/(2tv)$, where v_i is a node's inherent attractiveness or fitness, and v is the average fitness in the population. Here a node can grow more quickly because of having a large d_i or a large v_i.

5.3 Hybrid Models

While network formation via preferential attachment leads to a degree distribution that is scale-free and is consistent with a power-law, many observed degree distributions match neither the exponential process we saw in Section **??** nor the preferential attachment process we saw in Section **??**. For example, consider the following degree distribution from the co-authorship network that was pictured in Figure **??**.

Here we see a degree distribution that lies somewhere between the two extremes of uniformly random link formation and preferential attachment. This suggests that a more general network formation model is needed to match observed degree distributions.

Figure 5.3. A Degree Distribution of A Co-Authorship Network that Fits Between a Uniformly Random Network and One formed via Preferential Attachment

5.3.1 Mean-Field Analyses of Growing Network Processes

There is a variety of models that are hybrids of random and preferential attachment (e.g., Kleinberg et al [**?**], Kumar et al [397] , Dorogovtsev and Mendes [191], Levene et al [**?**], and Cooper and Frieze [163], Vazquez [603], Pennock et al [513], and Jackson and Rogers [337]). Interestingly, most of these ignore the fact that the resulting degree distributions are not scale-free, but instead try to show that the distribution is at least approximately scale-free for large degrees. The explicit interest in examining the full aspects of the degree distribution and the interest in matching the features that are not scale-free first appears in Pennock et al [513], and is also a feature of Jackson and Rogers [337]. Let us examine this in more detail.

In order to work with more general processes, I start by noting the basic techniques underlying the mean-field analyses in the previous sections.

Consider any growing network such that nodes are indexed in the order of their birth and a node i's degree at time t can be represented as

$$d_i(t) = \phi_t(i),$$

where $\phi_t(i)$ is a decreasing function of i. The fact that ϕ_t is an decreasing function of i

indicates that younger nodes have lower degrees. It also means that ϕ_t is an invertible function, so that if we specify some degree d, then we can see which node has degree d at time t. The fact that degree increases with age means that the fraction of nodes with degree at least d are precisely those which are older than the node i which satisfies $\phi_i(t) = d$; that is, those nodes older than $\phi_t^{-1}(d)$. Thus, the degree distribution at time t is

$$F_t(d) = 1 - \frac{\phi_t^{-1}(d)}{t}. \tag{5.6}$$

So, whenever we can derive an expression for $d_i(t)$ that is decreasing in i, so that older nodes have more links, then we can easily derive the associated degree distribution.

5.3.2 Mixing Random and Preferential Attachment

So, now let us examine a hybrid model of link formation. Suppose for instance, that a newborn node meets existing nodes via two different processes, where we combine the formation of links uniformly at random with preferential attachment. Each newborn node forms m links, with a fraction of $\alpha < 1$ of them formed to existing nodes selected uniformly at random, and a fraction $1 - \alpha$ of them formed to existing nodes via preferential attachment.

In that case, the mean-field expression for the change in the degree of a node over time can be written as

$$\frac{dd_i(t)}{dt} = \frac{\alpha m}{t} + \frac{(1-\alpha)md_i(t)}{2mt} = \frac{\alpha m}{t} + \frac{(1-\alpha)d_i(t)}{2t}, \tag{5.7}$$

where the second expression has $(1-\alpha)m$ links being formed via preferential attachment and node i having a probability of $\frac{d_i(t)}{2mt}$ of receiving any one of them, and the first expression representing the chance of receiving one of the αm links being formed by picking uniformly at random from the t existing nodes.

(5.7) is a differential equation that has as its solution

$$d_i(t) = \phi_t(i) = \left(d_0 + \frac{2\alpha m}{1-\alpha}\right)\left(\frac{t}{i}\right)^{(1-\alpha)/2} - \frac{2\alpha m}{1-\alpha}, \tag{5.8}$$

Where d_0 is the initial number of links that a node has when it is born. From (5.8) we deduce that

$$\phi_t^{-1}(d) = t\left(\frac{d_0 + \frac{2\alpha m}{1-\alpha}}{d + \frac{2\alpha m}{1-\alpha}}\right)^{\frac{2}{1-\alpha}}. \tag{5.9}$$

Thus, from (5.6) and setting $d_0 = m$ we conclude that

$$F_t(d) = 1 - \left(\frac{m + \frac{2\alpha m}{1-\alpha}}{d + \frac{2\alpha m}{1-\alpha}} \right)^{2/(1-\alpha)} . \tag{5.10}$$

When $\alpha = 0$ this is the degree distribution $1 - \left(\frac{m}{d}\right)^2$ which is the power distribution that we found in the case of pure preferential attachment. When $\alpha \to 1$, then the limit is harder to see directly, but it approaches the exponential distribution of $F(d) = 1 - e^{-\frac{d-m}{m}}$ that we found in Section **??** for the model where links were formed uniformly at random. To see this, let $x = \frac{2\alpha}{1-\alpha}$ and then note that $\left(\frac{m+xm}{d+xm}\right)^x = \left(1 + \frac{m-d}{d+xm}\right)^x$, which for large x is approximately $\left(1 + \frac{m-d}{xm}\right)^x$, which tends to $e^{\frac{m-d}{m}}$.

5.3.3 Simulations as a Check on the Degree Distribution

We are again faced with the difficulty that we have not shown that the continuous-time mean-field process where nodes grow deterministically over time will match the actual distribution of degrees in a large random network. While this is a challenging open problem, we can perform a rough check that has become a standard technique when faced with such problems. That is, we can simulate the process for some parameter choices and check that the resulting degree distribution is well-approximated by the analysis above. While this is clearly not a guarantee, it provides some reassurance that the process is not too far off for some parameter values.

Simulating such a process is actually quite easy, especially to the extent that we just want to keep track of the resulting degree distribution and not the whole network. We can do this as follows. Let $D(t)$ be the sequence such that if node i has $d_i(t)$ links at time t, then the label i appears $d_i(t)$ times in the entries of the vector $D(t)$, as in the following figure:

$$D(t) = \underbrace{1,1,1,1,1,1,1,1,1,1,1,1}_{d_1(t) \text{ entries}} \quad \ldots \quad \underbrace{i,i,i,i}_{d_i(t) \text{ entries}} \quad \ldots$$

If each new node is forming m links then this is of length $2mt + m^2$, since each link counts for two different nodes, plus whatever we started the system with (say m^2 additional entries).

Now, let us consider what happens at time $t+1$. The new node forms αm links uniformly at random, and $(1-\alpha)m$ links via preferential attachment. Let us take these to be integers. The αm links can be found simply by drawing αm numbers out of 1 to

t. The $(1-\alpha)m$ links via preferential attachment can be chosen by picking an entry out of $D(t)$ with equal weight on each entry. If we happen to form more than one link to an existing node, we can do three possible things: keep duplicate links, delete a duplicate link (and not redraw), or redraw according to the appropriate part of the process until the link is not a duplicate. The third option is most in the spirit of the network formation process, at least for cases where links keep track of whether two individuals have some social or economic relationship or not.[7] To be sure that this is fully specified, let us add the uniformly random links first (without replacement, so redrawing until we have αm links to distinct nodes) and then the preferential attachment links, again redrawing if any links are duplicated.

Below are some results from a set of such simulations.

[[fill in]]

5.3.4 Fitting Hybrid Degree Distributions to Data

The degree distribution described by (5.10) is useful for fitting to data because when α varies we span between the extremes of uniformly random attachment and preferential attachment. By estimating α from fitting the hybrid model to an observed network, we can get some feeling for how links might have been formed.

Such analyses have been carried out by Pennock et al [**?**] and Jackson and Rogers [337] for different variations on such a process. Let us examine a couple of examples to see how this works.

Here is a degree distribution from a network of amateur radio operators, where a link represents the fact that two operators had a radio conversation during a one month

[7] Although we might be tempted to proclaim that the other two options should lead, asymptotically, to the same distribution, by appealing to arguments such as those in Section **??** for the configuration model, we must be careful here. That argument worked with a pre-specified degree sequence that was already on a large number of nodes. Here, one of the main reasons for running simulations is to check how the process evolves when we are careful to keep track of the full evolution of the system and not to work with an approximation or with a limiting argument starting from some late point. It is conceivable, at least with pure preferential attachment, that some node will come to grow so large, that it completely dominates the system, having almost all of the links and thus gaining more and more links. Here if we do not redraw, this puts lower degree nodes at a relative disadvantage with regards to gaining new links, compared to a situation where we redraw and are forced to form new links to different nodes in each iteration. Thus, without a careful argument that applies to the full evolution of the system and takes into account starting conditions, we cannot be sure whether these details will matter.

period. These data were collected by Killworth and Bernard [372].

[[insert histogram, move table to an appendix]]

degree	ham radio
0	3
1	11
2	5
3	2
4	1
5	0
6	2
7	2
8	3
9	3
10	2
11	2
12	1
13	1
14	0
15	0
16	1
17	0
18	0
19	0
20	1
21	1
22	1
23	0
24	0
25	1
26	0
27	1

First, we directly calculate m. Since m is the number of new links formed each period, it is half of the added degree in each period. The overall degree is $2tm$, and so m is half of the average degree. In this network the average degree is 6.95, and so m

is roughly 3.5.

Next, we need to derive the parameter α which gives us the proportion of links that are formed uniformly at random versus via preferential attachment. Recall that the continuous time mean-field approximation to the degree distribution was described in (5.10) as

$$F(d) = 1 - \left(\frac{m + \frac{2\alpha m}{1-\alpha}}{d + \frac{2\alpha m}{1-\alpha}} \right)^{2/(1-\alpha)}.$$

This is non-linear in α. While there are different approaches to estimating α in such a situation, let us take a simple iterative least squares regression approach that provides fairly accurate estimates.[8] We can rewrite things in the following form:

$$\log(1 - F(d)) = \frac{2}{1-\alpha} \log\left(m + \frac{2\alpha m}{1-\alpha} \right) - \frac{2}{1-\alpha} \log\left(d + \frac{2\alpha m}{1-\alpha} \right). \tag{5.11}$$

If we now start with an initial guess of α, say α_0, we can regress $\log(1 - F(d))$ on $\log\left(d + \frac{2\alpha_0 m}{1-\alpha_0}\right)$ to estimate $\frac{2}{1-\alpha}$, and hence get an estimate α_1. We can either iterate this process until our estimate converges to some α^*, or simply examine a grid of values for α_0. Let us see what estimates that come out for a grid of values of α_0.

Table for ham radio operator fits:

α_0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	0.99	.999	.9999
α_1	-0.63	-0.40	-0.21	-0.04	0.12	0.28	0.44	0.61	0.79	0.89	0.98	0.9998

Here our estimate is that α is nearly 1, and so it appears that the ham radio operator network's degree distribution is best fit in the hybrid model by the extreme where links are formed uniformly at random.

To compare this to another application, we can also fit such a hybrid distribution to a data set of co-authorship relationships among economists from Goyal, van der Liej, and Moraga-Gonzalez [286]. This data set consists of researchers who published an article in a journal listed in EconLit during the 1990's. A link indicates that two researchers were co-authors on at least one article during this period.

[[insert histogram, move table to an appendix]]

[8] As discussed by Jackson and Rogers [337], one could hypothetically do a maximum likelihood estimation here. However, that requires deriving the probability of observing any given degree distribution as a function of the parameters of the model, which appears to be difficult analytically.

degree	co-author
0	24578
1	25078
2	17139
3	5069
4	3089
5	1853
6	1232
7	815
8	631
9	443
10	329
11	226
12	156
13	134
14	87
15	73
16	60
17	51
18	35
19	19
20	27
21	16
22	9
23	11
24	15
25	7
26	7
27	6
28	7
29	1
30	2
31	3
32	1
33	2
34	2
35	0
36	0
37	0
38	0

Table for co-author fits:

α_0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	0.56
α_1	0.43	0.45	0.48	0.51	0.54	0.58	0.62	0.69	0.79	0.56

So here, we estimate α to be about .56. This corresponds to a ratio of links formed uniformly at random to links formed via preferential attachment of about 1.27.[9]

5.4 Small Worlds, Clustering, and Assortativity

Let us now examine how growing random networks relate to other observed aspects of social networks.

5.4.1 Diameter

The diameter of a growing random network can be quite different than that of say a Poisson random network, to the extent that the growing network has very large degree nodes emerge which can serve as hubs and decrease distances. Generally, diameters and average path lengths are very difficult to calculate in neworks beyond Poisson random networks and variations on the configuration model, where the independence of the randomness provides somewhat of a toehold.

A result has been worked out by Bollobás and Riordan [81] for the special case of a preferential attachment network formation process where each node forms a single link (see also Reed [529]). They show that the network consists of a single component with diameter proportional to $\log(n)$ almost surely, while if more than one link is formed by each new node then the diameter is proportional to $\frac{\log(t)}{\log\log(t)}$. The proof of the following theorem is quite long and omitted.

PROPOSITION **5.4.1** *[Bollobás and Riordan [81]] In a preferential attachment model where each newborn node forms $m \geq 2$ links, as n grows the resulting network will consist of a single component with diameter proportional to $\frac{\log(n)}{\log\log(n)}$, almost surely.*

Thus, the diameter of a pure preferential attachment process is lower than that of a Poisson random network (which is proportional to $\log(n)$ when average degree is held

[9] This differs significantly from the Jackson and Rogers [337] estimates reported in Table **??** as they worked with a directed process and this is an undirected one. In their setting, the preferential attachment aspect is dependent on in-degree and they estimate in-degree from total degree to be 1/2 of the total degree. Here, the preferential attachment is based on the total degree. Dividing the degree by two changes the size of the degrees in the upper tail so that less preferential attachment is needed (roughly by a factor of four less).

constant), and as pointed out above, the intuition for this comes from the precess of high degree nodes which serve as hubs in the network.

One might conjecture that such a result provides an upper bound on more general growing network processes, where at least two links are formed via preferential attachment. The validity of such a conjecture is not clear, and one cannot simply extend the Bollobás and Riordan [81] argument, which is particular to pure preferential attachment. The difficulty is that as we alter the process, we change the mix of the degrees at any date, which then alters the probabilities of attachment and how quickly different nodes grow.

5.4.2 Positive Assortativity and Degree Correlation

As mentioned in Section **??**, a number of social networks have positive correlation in their degree distribution. Such correlation is absent in the Poisson random networks model, and generally in the configuration model by design. It emerges quite naturally in growing random networks, and the growth of the network might help explain why we see such correlation in social networks, a point first made by Krapivsky and Redner [393].[10] The following result is a variation on a result from Jackson and Rogers [337]. It shows a very strong form of correlation in that older nodes have distribution of neighbor's degrees that first order stochastically dominates that of younger nodes. This is a stronger conclusion than positive correlation in degree, showing that the whole distribution of neighbors' degrees is shifted up for higher degree nodes, and not just the mean of the distribution.

Let $F_i^t(d)$ denote the fraction of node i's neighbors at time t who have degree d or less.

PROPOSITION **5.4.2** *[Jackson and Rogers [337]] Consider a growing hybrid random network formation process as described in Section* **??**. *Under the mean-field estimate, a node i's degree is larger than a node j's degree at time t after both are born if and only if i is older than j. In that case, the estimated distribution of i's neighbors' degrees strictly first order stochastically dominates that of j's at each time $t > j$, and in particular $F_i^t(d) < F_j^t(d)$ for all $d < d_i(t)$.*

The first part of the proposition is obvious under the mean-field estimate, as degrees

[10] For an alternative explanation, relating to relevance of nodes, see Capocci, Caldarelli and De Los Rios [126].

grow deterministically and faster for higher degrees. The second part of the condition follows from the form of the distribution functions, as shown in the proof that follows.

It is worth stressing that the extent to which networks exhibit positive degree correlation, or have degree correlated with age depends on the application, and seem more typical of social networks than other forms.[11]

Proof of Proposition 5.4.2: Under the mean field approximation, by (5.8) the degree of node i at time t is described by

$$d_i(t) = \left(d_0 + \frac{2\alpha m}{1-\alpha}\right)\left(\frac{t}{i}\right)^{(1-\alpha)/2} - \frac{2\alpha m}{1-\alpha}. \tag{5.12}$$

If $d_i(t) > d_j(t)$, then since the above is decreasing in i, it must be that $i < j < t$. For $d < d_i(t)$,

$$F_i^t(d) = 1 - \frac{d_i(t^*(d,t))}{d_i(t)},$$

where $t^*(d,t)$ is the date of birth of a node that has degree d at time t; and for $d \geq d_i(t)$

$$1 - F_i^t(d) = \frac{0}{d_i(t)}.$$

So consider $d < d_j(t)$, as the result is clear for d such that $d_j(t) \leq d < d_i(t)$). It is thus enough to show that for any $i < j < t' < t$

$$\frac{d_i(t')}{d_i(t)} > \frac{d_j(t')}{d_j(t)}. \tag{5.13}$$

Then (5.12) implies that

$$\frac{d_i(t')}{d_i(t)} = \frac{\left(d_0 + \frac{2\alpha m}{1-\alpha}\right)(t')^{(1-\alpha)/2} - \left(\frac{2\alpha m}{1-\alpha}\right) i^{(1-\alpha)/2}}{\left(d_0 + \frac{2\alpha m}{1-\alpha}\right) t^{(1-\alpha)/2} - \left(\frac{2\alpha m}{1-\alpha}\right) i^{(1-\alpha)/2}}.$$

This expression is decreasing in i, which establishes the result. ∎

As is clear from the proof, the result also holds for many other growing processes, including exponential random networks (see Exercise **??**. However, the result will not hold if the rate of growth of degree accelerates substantially beyond being proportional to degree, as then older nodes would grow so fast that (5.13) would no longer hold.

[11] See, for instance, Adamic and Huberman [3] for evidence against the correlation of age and degree on the world wide web.

5.4.3 Clustering in Growing Random Networks

As discussed in Chapter 3, a distinguishing feature of observed networks is that they exhibit high clustering, as well as low diameters and and a positive correlation between neighbors' degrees. While the above hybrid model does a good job of matching observed degree distributions, and degree assortativity, it lacks some of the other properties, as do the extremes of preferential attachment and uniform random attachment. In particular, regardless of the choices of α and m, as the network grows the average and overall clustering will both converge to 0.

To get some feeling for this, consider the exponential random network model where links are formed to existing nodes uniformly at random. The only way a cluster can form is when a newborn node links to both ends of an existing link. Consider a node born at time $t+1$, and consider two of its newly formed links. What is the chance that a link will be present? Given that it picked the two nodes uniformly at random, and there are $t(t-1)/2$ such pairs to pick from and tm existing links in the network, it is a probability of $2m/(t-1)$, which converges to 0 as t grows. When we consider the hybrid model, or pure preferential attachment, this calculation is a bit more complicated, as now the attachment probability favors high degree nodes, and as we have just seen, they are more likely to be connected to each other than to lower degree nodes. Nevertheless, the process still has a clustering going to 0, as the likelihood that any two high degree nodes are connected to each other is still vanishing, as the number of high-degree nodes is growing rapidly enough (the fat tail of the power distribution). This is difficult to show, but has been established in a mean-field analysis as we shall see below.

There are several simple processes of network formation that are hybrid processes and that will tend to have some clustering in the limit. The simplest of these is described in Vazquez [603] in the context of finding web pages to link to. A new node first randomly chooses some node. Next, with a probability q it follows a link out from that node, and with probability $1-q$ jumps to a new node chosen uniformly at random. It continues this process until it has it has formed some set number of links. First, note that if $q=0$, then this simply reduces to the growing network formed via uniformly random attachment. In the other extreme, where $q=1$, only the first node is identified uniformly at random, while the other nodes are found via the network structure itself. Nodes that have higher degrees are more likely to be neighbors of the first node, and thus more likely to be found as the second node. This gives a sort of preferential attachment aspect to the network formation. If node i has degree d_i, then it can be found via this network-based search process if any d_i of its neighbors

are found in the first step. Having a higher degree, holding all else constant, leads to a proportionately higher chance of being found via this search process, just as in preferential attachment. Here we now see a reason for clustering to emerge, as nodes are finding other nodes to link to precisely by following the existing link structure of the network and are thus linking to neighboring nodes on a regular basis.

To work out the details, it helps to work with a directed version of this, for reasons explained below. With this in mind, consider a variation on a network formation process proposed and analyzed by Jackson and Rogers [337], for which it is easy to estimate clustering expressions for.

5.4.4 A Meetings-Based Network Formation Model

Consider the following meetings-based network formation process. Each new node some meets $m_r > 0$ nodes uniformly at random and forms directed links to them. Then, the new node randomly chooses m_n of the out-links of the first group of nodes, and follows those links and then forms links to each of the nodes it finds via these links. We start this process with some initial network in place with enough nodes so that any group of m_r nodes has at least m_n additional neighbors (but beyond this, the precise form of the initial network does not matter for asymptotic behavior). Let $m = m_r + m_n$ be the total number of out-links formed by each newborn node and let $d_i^{in}(t)$ be a node's indegree at date t. Let m, m_r, and m_n be integers. According to this process, for a large time t, an approximation is that a node has a probability of $\frac{m_r}{t}$ of being linked to uniformly at random, and a probability of $\frac{m_n d_i^{in}(t)}{mt}$ of being found through the search along links of the first group of nodes. In this second expression, i can potentially be found if any of its d_i^{in} neighbors are found in the first step, which occurs with probability $\frac{m_r d_i^{in}(t)}{t}$, and then conditional on one of its neighbors being found it is found with probability $\frac{m_n}{m_r m}$ where m_n is the number of out-links followed out of $m_r m$ total out-links to search.[12]

Thus, the expected change in the number of links at time t for a node with indegree $d_i^{in}(t)$ is

$$\frac{dd_i^{in}(t)}{dt} = \frac{m_r}{t} + \frac{m_n d_i^{in}(t)}{mt} \tag{5.14}$$

If we compare this to the hybrid process (5.7) it is as if we are working with $\alpha = \frac{m_r}{m}$ and $1 - \alpha = \frac{m_n}{m}$, *except* that we are missing a figure of 2 in the denominator of the

[12] These calculations ignore the chance of finding more than one neighbor, or being found via multiple paths, which are second order effects and of relatively negligible probability for large t.

second expression which comes from the difference between the directed and undirected version. This is a minor change and following the same steps as we did before leads to continuous time mean-field approximation of the distribution of in-degrees described by

$$F(d^{in}) = 1 - (rm)^{1+r} \left(d^{in} + rm\right)^{-(1+r)}, \tag{5.15}$$

where $r = \frac{m_r}{m_n}$, which matches (3.2).[13]

The above described processes are a good match for network formation in cases such that the network has a natural direction to it, such as in following links among web pages or locating scientific articles and then locating articles that are cited by those articles, etc. However, if we think of more purely social processes, where an individual meets the friends of a new friend, then it would be more natural to examine an undirected process, as friendships tend to be reciprocal. If we analyze an undirected version of the above process, we run into a complication. In an undirected version, the probability that a node with degree $d_i(t)$ is linked to by a new node at time t is more complicated. There is still a probability of $\frac{m_r}{t}$ of being linked to uniformly at random. It is also true that i can potentially be found if any of its $d_i(t)$ neighbors are found in the first step, which occurs with probability $\frac{m_r d_i(t)}{t}$. But then conditional on one of its neighbors being found, the probability that i ends up with a new link is more complicated. It depends on the total degrees of its neighbors rather than just the outdegrees of the neighbors. In the above process we knew the outdegrees of any neighbor of i to be m. However, in the undirected case, the degree of a neighbor of i is actually positively correlated with $d_i(t)$ and this correlation is time-varying. Now a node with a higher degree has a higher chance of one of its neighbors being found than a node with a lower degree; but then conditional on a neighbor being found, the higher degree node actually has a lower chance of being met through the network search process as its neighbors will tend to have more neighbors than the neighbors of a lower degree node. The first effect still dominates, but the second correction can be substantial.

5.4.5 Clustering

Let us examine the clustering in this meetings-based network formation model. Given the directed nature of the process, let us begin by examinining the percentage of

[13] This sets $d_0 = 0$ so that new nodes have no in-degree.

transitive triples defined in Section **??**. Recall that this measure is

$$Cl^{TT}(g) = \frac{\sum_{i;j\neq i;k\neq j} g_{ij}g_{jk}g_{ik}}{\sum_{i;j\neq i;k\neq j} g_{ij}g_{jk}}.$$

This transitive triple measure is examining directed links ij jk, and counting the fraction of these where the link ik is present.

We immediately see why this process leads to nontrivial clustering, since if node i finds j at random, and j has a directed link to k, then there is a nontrivial chance that i will find k through the search of j's out-links and then i will form a directed link to k. Thus, it is precisely because some nodes are met through meeting the "friends of friends" that we see clustering in the process. We can easily derive a lower bound for this clustering. First, note that the denominator of the fraction of transitive triples is simply the m^2 potential triples that are generated for each distinct i (counting across its outdegree m of j's and then each j's outdegree m of k's), and so at time t the denominator is tm^2. The numerator has the cardinality t times the number of situations for each i such that i connects to both j and k and then those two are linked to each other. Each any newborn node i will have at least m_n situations where i found k by following a link from j. Thus, a lower bound on Cl^{TT} is $\frac{tm_n}{tm^2} = \frac{m_n}{m^2} = \frac{1}{(r+1)m}$. This turns out to be the correct expression for the fraction of transitive triples when $r \geq 1$, but is only lower bound otherwise, as there are also possibilities that j and k are neighbors of each other and both found via the network search process when $r < 1$ (as then $m_n > m_r$. Let us explore this in more detail.

To develop clustering estimates, consider a special case of the process such that when $r \geq 1$ then at most one link is formed in each node found uniformly at random's neighborhood, and otherwise let $\frac{m_n}{m_r}$ be a positive integer and that exactly $\frac{m_n}{m_r}$ links are formed in each node found uniformly at random's neighborhood.

PROPOSITION **5.4.3** *[Jackson and Rogers [337]] Under a mean-field approximation the fraction of transitive triples, Cl^{TT}, tends to*

$$\begin{cases} \frac{1}{(r+1)m} & \text{if } r \geq 1, \text{ and} \\ \frac{(m-1)r}{m(m-1)(1+r)r-m(1-r)} & \text{if } r < 1. \end{cases}$$

Let us examine how the fraction of transitive triples behaves as a function of r, the relative weight on uniformly random versus network-based meetings. As r grows, then the fraction of transitive triples tends to 0, just as we should expect given that the model then operates almost uniformly at random and we know that clustering in

such models goes to 0. At the other extreme, as r becomes small we have to be a bit careful. There is a lower bound on r here, since there is always at least one node found uniformly at random so that the newborn can search its neighborhoods. So, in order to run r to be low, m must be large. For instance, fixing $m_r = 1$ implies that $r = 1/m_n = 1/(m-1)$. Then Cl^{TT} simplifies to $\frac{m-1}{2m}$ which tends to $\frac{1}{2}$ as m grows (and r shrinks).[14] To see this explicitly, recall from the lower-bound discussion above, that the denominator of the fraction of transitive triples is tm^2. Then the numerator is t times the number of ij, ik pairs that a typical i has that end up with a link between j and k. In the case where $m_r = 1$, the newborn i finds one other node j at random, attaches to it, and then attaches to all but one of its neighbors. So, i has $m-1$ completed triples of the form ij and jk. Then out of the $(m-1)(m-2)/2$ pairs of j''s and k's in j's neighborhood that i has linked to, those are linked at the rate that j's neighbors are linked to each other. That happens with a rate of $\frac{Cl^{TT}m^2}{m(m-1)/2}$. [15] So we end up with

$$Cl^{TT} = \frac{(m-1) + \frac{Cl^{TT}m^2}{m(m-1)/2}(m-1)(m-2)/2}{m^2},$$

This simplifies to $Cl^{TT} = \frac{m-1}{2m}$. The proof of the overall proposition proceeds similarly.

With the estimate of transitive triples in hand, then overall clustering (ignoring the direction of links) in the meetings-based network formation model can be estimated to tend to (see Exercise 5.8):[16]

$$\begin{cases} 0 & \text{if } r \leq 1, \text{ and} \\ \frac{6(r-1)}{(1+r)[3(m-1)(r-1)+4mr]} & \text{if } r > 1. \end{cases}$$

Here the expression is 0 at or below $r = 1$ and then tends to 0 again as r gets to be very large, and so clustering is only significantly positive in an intermediate range where $r > 1$ but r is not too large. The critical aspect that requires $r > 1$ is that total clustering does not account for the direction of links in the same way that transitive triples do. When $r < 1$, then very high degree nodes start to appear, as the preferential aspect of the attachment becomes prevalent. High degree nodes have large numbers

[14] This differs from the Jackson and Rogers [337] process, where they allow a probability of linking to nodes found. In that case, one can lower the probability of linking to the uniformly randomly found node, without having to let m grow. There at the extreme of preferential attachment, the fraction of transitive triples, overall clustering, and average clustering all go to 0.

[15] $Cl^{TT}m^2$ provides the total number of pairs of linked neighbors that a typical node will have, and then $m(m-1)/2$ is the number of such pairs.

[16] Average clustering is more cumbersome and the interested reader is referred to Jackson and Rogers [337] for details.

of pairs of neighbors and a vanishing fraction of them are connected to each other, because many of them are nodes that found the high degree node via different paths. These dominate the calculation. These do not end up dominating the calculation if we account for directions of links (as in the transitive triples calculation) or average across nodes so that then the effect of low clustering that is seen among the high degree nodes is offset by the non-vanishing clustering among low degree nodes who have many fewer pairs of neighbors and were the initiator of the links to a nontrivial fraction of them. This model thus also illustrates how careful one has to be in terms of which definition of clustering one uses.

Sketch of a Proof of Proposition 5.4.3: To derive the expression for $C^{TT}(g)$, we note that the denominator is tm^2, and then consider that the numerator is then t times the expected number of situations where some i has links ij and ik and it also turns out that there is a link between j and k. So, we need to find this expectation for a given i, and then divide by m^2. The situations where there is a pair of links ij and ik for which either jk or kj is present, break into three cases relative to how node i found j and k:

1. Both j and k were found at random.
2. One of j and k (say j) was found at random and the other by a network-based meeting.
3. Both j and k were found by network-based meetings.

Under 1, the probability of j and k being connected tends to 0 as t becomes large, just as in the uniformly random case. Under 2, j and k will tend to be connected if k was found through j, but not if k was found by search of some $j' \neq j$'s neighborhood. There are a total of m_n situations where k was found via j's neighborhood. Under 3, if j and k were found by the search of different nodes' neighborhoods, then the probability that they will be linked tends to 0. It is only in the case where they were found by search of the same node's neighborhood that they will have a nonvanishing probability of being linked. Under the process described above, this can only occur when $m_n \geq m_r$; and so let us examine that case. There are $\frac{m_n}{m_r}$ links formed by a new node in the neighborhood of any one of the nodes that were found uniformly at random, and there are m_r such neighborhoods, and so there are $m_r \frac{m_n}{m_r}(\frac{m_n}{m_r} - 1)/2$ such pairs in total. As the initial node and these links are independently and uniformly chosen, these potential clusters are completed with probability $\frac{Cl^{TT}m^2}{m(m-1)/2}$, since the initial node

i' has approximately $Cl^{TT}m^2$ completed triples of $m(m-1)/2$ possible pairs of outward links. This leads to approximately

$$\frac{Cl^{TT}mm_n}{m-1}\left(\frac{1}{r}-1\right) \tag{5.16}$$

completed triples from case 3 if $m_n \geq m_r$, and 0 otherwise. Summing across the three cases we expect a given newborn node to have

$$m_n + \frac{Cl^{TT}mm_n}{m-1}\left(\frac{m_n}{m_r}-1\right)$$

clusters out of m^2 possibilities if $m_n \geq m_r$, and m_n clusters otherwise. Thus,

$$Cl^{TT} = \frac{m_n}{m^2} + Cl^{TT}\frac{m_n}{m(m-1)}\left(\frac{m_n}{m_r}-1\right), \tag{5.17}$$

if $m_n \geq m_r$, and

$$Cl^{TT} = \frac{m_n}{m^2}$$

otherwise. Solving for C^{TT} in (5.17) yields the claimed expression. ∎

While a meetings-based model offers one explanation for how clustering might emerge, there are at least two other reasons for it. One is that nodes might be connected based on some cost and benefit structure, and we then expect clustering among groups of nodes that share low connection costs due to geographical or other characteristics. This is explored in Section **??**. Another is that groups of nodes might be born in waves. For example, Klemm and Eguíluz [383] have a variation of a preferential attachment model where nodes are declared either "active" or "inactive." A new node enters as "active" and then one existing active node is randomly de-activated (with a probability inversely proportional to its degree). New nodes attach to each active node. Then with a probability μ, each of these links is rewired to a random node in the population chosen according to preferential attachment. This process thus has a fixed number of "active" nodes and each entering node ends up linked to a proportion $1-\mu$ of the active nodes when they are born. This, coupled with the fact that the list of active nodes only changes by one each period, results in significant clustering.

5.5 Exercises

EXERCISE **5.1** *Growing Objects and Degree Distributions*

Suppose we start with a population of an object of size 1. Suppose also that a new object of size 1 is born at each date, and that existing objects double in size in each period. Over time, the sequence of populations as listed by their sizes will look like (1), (1,2), (1,2,4), (1,2,4,8), (1,2,4,8,16), and so forth.

Show that fraction of objects that have size less than d at date t is $log(d)/(t-1)$ for $d \in \{1, 2, 4, \ldots, 2^{t-1}\}$.

What is different between this and the preferential attachment system described in Section **??**? (How many "links" are added each period if we interpret this as a system where the sizes are degrees?)

EXERCISE **5.2** *Three types of Link Formation*

In the appendix of Jackson and Rogers [337] the following sort of growing network formation process is considered. Newborn nodes form links to existing nodes. An existing node gets links from a newborn in three different ways:

- some links are formed with a probability relative to the size of the existing node (as in preferential attachment),
- some links are formed with a probability depending on the total time that has already evolved (as in the growing variation of the purely random network), and
- some links are formed with a constant probability.

We can think of the second and third ways of forming links as different extensions of the idea of purely random Poisson networks to a growing set of nodes. The difference between these two is only in terms of how the probability of a link scales with the size of the society. In both cases, each existing node at some time has an equal chance of getting a new link from a newborn node. The difference is in terms of what the probability of a link is. Is it that we are keeping the average degree of newborn nodes constant - which necessitates a probability of link formation that decreases with the size of the society; or is it that we are holding the probability of a link between any two nodes constant - which necessitates a growing average degree. The analysis in Section **??** worked by holding average degree constant, but the other approach is also natural in some applications.

Allowing for an arbitrary combination of all three of these different methods of forming links leads to the following expression for the change in a node i's degree over time at a time t:

$$\frac{dd_i(t)}{dt} = \frac{ad_i(t)}{t} + \frac{b}{t} + c, \tag{5.18}$$

where a b, and c are scalars.

Solve for the degree distribution under a continuous time mean-field approximation of the process under the condition that $a > 0$ and either $c = 0$ or $a \neq 1$, and with an initial condition of $d_i(i) = d_0$. Note that in those cases, the solution to (5.18) is

$$d_i(t) = \phi_t(i) = \left(d_0 + \frac{b}{a} - \frac{c}{1-a}\right)\left(\frac{t}{i}\right)^a - \frac{b}{a} + \frac{ct}{1-a}. \tag{5.19}$$

EXERCISE **5.3** *Dying Links*

Consider a growing network process such that a newborn node forms m links with a portion α (with $1 > \alpha > 0$) uniformly at random and a portion $(1-\alpha)$ via preferential attachment. Also, in any given period qm links are destroyed, where $1 - \alpha \geq q \geq 0$ and the links are selected uniformly at random out of all links that exist at the end of the period. Solve for the degree distribution under a continuous time mean-field approximation.

EXERCISE **5.4** *Degree Distributions with Groups of Self-Attaching Newborn Nodes*

Suppose that newborn nodes come in groups of n in each period. Suppose that they attach a fraction f of their links uniformly at random to other newborn nodes, and a fraction $1 - f$ to older nodes via preferential attachment. Using a continuous time mean-field approximation, develop an expression for the degree distribution.

EXERCISE **5.5** *Stochastic Dominance in Hybrid Growing Network Models**

Consider the distribution function given in (**??**) corresponding the the hybrid growing random network model, which has support for degrees of m and above. Show that for any fixed α, the distribution associated with m strictly first order stochastically dominates an alternative distribution with $m' < m$. Show that for any fixed m, the distribution associated with α strictly second order stochastically dominates an alternative distribution with $\alpha' > \alpha$.

EXERCISE **5.6** *Degree Distributions with Growth in the Numbers of Newborn Nodes over Time*

The models we worked with in this chapter generally had a single node born at each point in time. The systems are generally unchanged if we had a fixed number of nodes come in at each date. However, if the number of newborn nodes grows over time, then

that changes the degree distribution. Consider an extension of the hybrid model to a where the number of nodes entering at each date grows over time. Let the number of new nodes entering at time t be gn_t, where n_t is the number of nodes at time t and $g > 0$ is a growth rate.

Derive an estimated degree distribution under a continuous time mean-field approximation.

EXERCISE **5.7** *Positive Assortativity in Exponential Growing Random Networks*

Show that the statement of Proposition 5.4.2 also holds for exponential growing random networks of the sort described in Section 5.1.

EXERCISE **5.8** *Overall Clustering in the Meeting-Based Network Formation Model**

Building from the proof of Proposition 5.4.3, show that overall clustering in the meetings-based network formation model, treating directed links as if they were undirected, tends to

$$\begin{cases} 0 & \text{if } r \leq 1, \text{ and} \\ \frac{6(r-1)}{(1+r)[3(m-1)(r-1)+4mr]} & \text{if } r > 1. \end{cases}$$

Hint: First argue that the overall clustering at time t can be approximated by

$$\frac{3m^2 C^{TT}}{m(m-1)/2 + m^2 + \frac{1}{t}\sum_i d_i(d_i-1)/2}, \tag{5.20}$$

and then calculate $\frac{1}{t}\sum_{i=1}^{t} d_i(d_i-1)/2$ under the mean-field approximation.

EXERCISE **5.9** *Fitting a Degree Distribution from a Hybrid Model*

Consider the following degree distribution for a network of friendships among prison inmates as collected by MacRae [422].

degree	number of prisoners
0	7
1	17
2	11
3	9
4	12
5	3
6	4
7	3
8	1

Using the techniques described in Section 5.3.4, fit the degree distribution described by (5.10) to the above data.

Chapter 6

Strategic Network Formation

While the random network models discussed in Chapters **??** and **??** are useful in growing large and complex networks that exhibit certain features, they are still lacking along some important dimensions. In particular, there are many settings where not only chance but also choice plays a central role in determining relationships. Social settings by definition involve sentient actors who have discretion in which relationships they form and maintain, and generally have discretion in how much effort, time, or resources that they devote to different relationships. Examples of this include trading relationships, political alliances, employer-employee relationships, marriages, professional collaborations, citations, emails, friendships, and so forth.

There are two central aspects to modeling networks from a "strategic" point of view. The first is that we must explicitly model the costs and benefits that arise from various networks. Doing this not only enables us to model how networks form in the face of individual incentives to form or sever links, but also provides well-defined measures of overall societal welfare. Thus, we not only have predictions about which networks might form, but we also have measures of which networks are "best" from society's point of view. The second aspect of modeling strategic network formation is making a prediction of how individual incentives translate into network outcomes. In this chapter I focus on an equilibrium method, and come back to discuss a variety of possible methods as well as dynamic models in Chapter **??**.

From the outset, it is important to emphasize what is or is not embodied in a "strategic" model. Individuals need not be Machiavellian and calculate their potential benefits and costs from each potential relationship. What is critical is that they have a tendency to form relationships that are (mutually) beneficial and to drop relationships that are not. The forces behind such incentives can be quite strong and can operate

with people even being aware that they are influenced in this way. The term strategic thus carries with it connotations that are not necessary to its application.

Some of the important conclusions from the literature on strategic network formation regard the comparison between the networks that form based on individual incentives and those networks that maximize overall societal welfare. There is often some disparity and generally a tension between the individual incentives and societal welfare. This is not surprising given that there are externalities present. For example, one of my trading partners in a market might care whom I choose as my other trading partners as that could affect the prices or other terms of trade that he or she ends up with, even though he or she may have little direct influence over my choice of whom else I trade with. The interesting aspect of this tension is how extensive and resilient it is. In particular, as we shall see, even if there are transfers present so that individuals can be subsidized to maintain relationships that would be in society's interest but are not in their own interests, it can still be impossible to maintain the socially efficient networks, under some reasonable restrictions on transfers.

Another important aspect of strategic models of network formation is that they provide answers as to *why* networks take particular forms, rather than just *how* they take particular forms. For example, growing random network models allowed us to trace certain aspects of networks, such as the shape of the degree distribution and clustering, to specific types of network formation, such as the extent to which nodes are formed uniformly at random versus via preferential attachment and whether new nodes are met by navigating the network or searching at random. While such analyses relate features of the network to features of the formation process, they do not provide an understanding of why people would tend towards preferential attachment in some settings and not others. The strategic approach ties explanations back to fundamental aspects of the setting. For example, as discussed below, the explanation behind the combination of high clustering and low diameter comes out of a strategic analysis which relates high clustering to low costs of connecting to nodes that are close in social or geographical distance, and low diameter to the benefits of accessing the information held by distant nodes. This brings us to a related point. In a situation where there is diffusion of information through a network, agents payoffs will depend on the access to information that they have. As a result, this will shape their incentives regarding which relationships to form or maintain, and ultimately will affect the network structure.

6.1 Pairwise Stability

In order to model network formation in a way that accounts for individual incentives, we first need to model the net payoffs or utility that each agent receives as a function of the network.

In this setting, the nodes of the network $N = \{1, \ldots, n\}$ will often be referred to as "players."

The overall benefit net of costs that a player enjoys from a network is modeled via a *utility function* or *payoff function*. That is, the payoff to a player i is represented by a function $u_i : G(N) \to I\!R$, where $u_i(g)$ represents the net benefit that i receives if network g is in place.[1]

The utility function captures all of the benefits net of costs that a given player experiences as a function of the network in place. Depending on the setting these can include very different things, such as the value of trading opportunities if this is a trading network or the value of information that might be obtained if this is a job-contact network. The extent to which the players in a network would "know" their own or other people's utility functions is very much context-dependent. What is most critical for the approach described here is that they be aware of changes in their own utility as they add or delete links, or at least react in terms of adding relationships that increase payoffs and delete relationships that decrease payoffs.

In order to capture the fact that forming a relationship or link between two players usually involves mutual consent, while severing a relationship only involves the consent of one player, we need an equilibrium or stability concept that differs from an off-the-shelf adaptation of a non-cooperative game theoretic solution such as Nash equilibrium (see Section 9.10 for a primer on game theory). Nash equilibrium-based solution concepts fail to capture the possibility that if two players each want to engage in a relationship then we should expect them to.

To get a feeling for this issue, let us consider a basic example (see Chapter 11 for a more detailed discussion). Consider just two individuals and a choice of whether or not to form a link. A natural inclination is to model this as a game where players (simultaneously) announce whether or not they wish to be linked to each other. If they both announce that they wish to form the link, then it is formed, while if either says that they do not wish to form the link does then the link is not formed. Thus,

[1] This can be viewed as a special case of a richer object called an allocation rule, as defined in Jackson and Wolinsky [343], which is described in more detail in Chapter **??**.

it takes mutual consent to form a relationship. Suppose the link is beneficial to both players. One might try to use the concept of Nash equilibrium. A Nash equilibrium is a choice of action by each player, such that no player would benefit by changing his or her action, given the actions of the other player(s). Unfortunately, that is not a very useful concept here. There are two equilibria: one where both players say they wish to form the link and it is formed, and another where both players say they do not wish to form the link and it is not formed. The second pair of actions form a Nash equilibrium since neither player has an incentive to change his or her action, given the (correct) anticipation that the other player will say that he or she does not want to form the link. This second equilibrium does not make much sense in a social setting, where we would expect the players to talk to each other and form the link if it is in their mutual interest. However, standard game theoretic concepts do not take this into account.[2] This is an indication of the fact that some standard game theoretic equilibrium notions are not well-suited for the study of network formation, as they do not properly account for the communication and coordination that is important in the formation of social relationships in networks.

A die-hard game theorist might respond that this is simply because the game has not been properly defined. We could explicitly model all of the communication that is available between the individuals, and then the actions that they might take in response, etc. While on the face of it this might seem reasonable, it is impractical for at least two reasons. One is that modeling the possible communication is very cumbersome. A game that incorporates all of the back and forth that might go on in forming a social relationship is complex, and yet all of the added complexity only captures a very simple idea: that two individuals should be able to coordinate on forming a link when it is in their mutual interest. Moreover, even once such a game is modeled, it might have multiple equilibria and need special refinements on beliefs and other aspects of equilibrium in order to make fairly obvious predictions. An alternative to all of this modeling is to directly define an equilibrium notion on networks that incorporates mutual consent.

A very simple stability concept that captures mutual consent is pairwise stability, as defined by Jackson and Wolinsky [343],[3] which we previewed in Section **??**.

[2] There are some refinements of Nash equilibrium (such as undominated Nash or trembling hand perfect equilibrium) that select the "natural" equilibrium of forming the link in this particular example, but fail to handle other examples. This is discussed in more detail in Chapter 11.

[3] This should not be confused with a similarly named concept that has been used in the "marriage market" literature following Gale and Shapley [**?**]. Although related, there are distinctions as the Gale

A network g is *pairwise stable* if

(i) for all $ij \in g$, $u_i(g) \geq u_i(g - ij)$ and $u_j(g) \geq u_j(g - ij)$, and

(ii) for all $ij \notin g$, if $u_i(g + ij) > u_i(g)$ then $u_j(g + ij) < u_j(g)$.

A network is pairwise stable if no player wants to sever a link and no two players both want to add a link. This comes in two parts in the definition. The requirement that no player wishes to delete a link that he or she is involved in implies that a player has the discretion to unilaterally terminate relationships that he or she is involved in. The second part of the definition can be stated in various ways. In order for a network to be pairwise stable, it is required that if some link is not in the network and one of the involved players would benefit from adding it, then the other player would suffer from the addition of the link. Another way to state this is that if a network g is such that the creation of some link would benefit both players involved (with at least one of them strictly benefiting), then g is not stable.

While pairwise stability is natural and easy to work with, there are limitations to the concept that deserve discussion (and are discussed at more length in Chapter 11). First, pairwise stability is a weak notion in that it only considers deviations on a single link at a time. Although this makes it easy to apply, if other sorts of deviations are viable and attractive, then pairwise stability could be too weak a concept. For instance, it could be that a player would not benefit from severing any single link but would benefit from severing several links simultaneously, and yet the network could still be pairwise stable. Second, pairwise stability considers only deviations by at most a pair of players at a time. It might be that some group of players could all be made better off by some more complicated reorganization of their links, which is not accounted for under pairwise stability. To the extent that larger groups can coordinate their actions in making changes in a network, a stronger solution concept might be needed. While this might sound artificial, such group actions can capture things like the expulsion or ostracism of an individual. In both of these regards, pairwise stability might be thought of as a necessary but not sufficient requirement for a network to be stable over time. Nevertheless, pairwise stability still turns out to be quite useful and often provides tight predictions about the set of stable networks without the need to consider richer deviations.

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and Shapley notion allows a pair of individuals to simultaneously divorce their previous partners and marry each other. The pairwise stability notion defined on networks only considers one link at a time.

6.2 Efficient Networks

Next, let us turn our attention to the evaluation of the overall benefits that society sees from a given network. Payoffs not only provide an individual's perspective on the network, but also enable us to at least partially order networks with regards to the overall societal benefits that they generate.

6.2.1 Efficiency

Given that we have well-defined payoffs to players as a function of the network, there are two obvious and standard notions of welfare that we can apply.

One way of evaluating societal welfare is via a utilitarian principle, which is to say the "best" network is the one which maximizes the total utility of the society. This notion was referred to as "strong efficiency" by Jackson and Wolinsky [343], but I will simply refer to it as efficiency as in much of the subsequent literature.

A network g is *efficient* relative to a profile of utility functions $(u_1, \ldots, u_n)$ if $\sum_i u_i(g) \geq \sum_i u_i(g')$ for all $g' \in G(N)$.

It is clear that there will always exist at least one efficient network, given that there are only finitely many networks.

6.2.2 Pareto Efficiency

Another very standard tool used by economists for examining overall societal welfare is that of Pareto efficiency, as first defined by Pareto [501].

A network g is *Pareto efficient* relative to $(u_1, \ldots, u_n)$ if there does not exist any $g' \in G$ such that $u_i(g') \geq u_i(g)$ for all i with strict inequality for some i.

We say that one network *Pareto dominates* another if it leads to a weakly higher payoff for all individuals, and a strictly higher payoff for at least one. A network is then Pareto efficient if it is not Pareto dominated by any other network.

Pareto domination indicates unanimity in the ordering between two netwroks, and thus is a quite compelling argument in favor of the dominating network compared to the dominated network, at least from a purely welfaristic perspective. The difficulty, is of course, that such a unanimous ordering can be quite rare, and so while Pareto domination can help us rule out some networks, we are often faced with a very large set of Pareto efficient networks, and so it may not be very prescriptive or discriminating.

Figure 6.2.2. An Example of Efficient, Pareto Efficient, and Pairwise Stable Networks in a Four Person Society

Figure 6.2.2 illustrates these definitions in the context of a four player setting. The numbers next to the nodes are the payoffs to the respective player for each network.

There are many networks that are not pictured in Figure 6.2.2. Let any permutation of the pictured networks have correspondingly permuted payoffs to the players, and any networks that are not permutations of the pictured ones lead to payoffs of 0 for all players. The arrows in the figure indicate that the network that the arrow points away from is unstable in that some player would benefit by deleting a link, or two players would each benefit by adding a link. The network the arrow points to indicates which network would result if the player(s) who benefit from the action take the action. In this figure there is just one efficient network, marked in red, which is to have match the players into two pairs and have each player have one link. This is also a Pareto efficient network, as any other network leads to lower payoffs for some player. The efficient network here is not pairwise stable, as two disconnected players would benefit from adding a link. If such an action is taken, then the new network is the green one. The players who have formed the link have increased their payoffs from 3 to 3.25, while this has led to a lowering of the payoffs of the other two players. The green network is also Pareto efficient, as there is no other network that gives all players a weakly higher

payoff with some a strictly higher payoff. However, the green network is not pairwise stable. Here, the two players who have only one link would benefit by adding a link to each other. This then leads to the dark blue network, which is the only pairwise stable network out of those pictured. No player would gain by adding or severing a link here. We already see a conflict between stability and efficiency here, as the only pairwise stable network (or networks, if we count the permutations) is Pareto dominated by the efficient (red) network.

To better understand the relationship between efficiency and Pareto efficiency, note that if g is efficient relative to $(u_1, \ldots, u_n)$ then it must also be Pareto efficient relative to $(u_1, \ldots, u_n)$. However, the converse is not true, as we already see from Figure 6.2.2. What is true is that g is efficient relative to $(u_1, \ldots, u_n)$ if and only if is Pareto efficient relative to all payoff functions $(\widehat{u}_1, \ldots, \widehat{u}_n)$ such that $\sum_i \widehat{u}_i = \sum_i u_i$.

Thus, efficiency is a more discriminating notion and is the more natural notion in situations where there is some freedom to change the way in which utility is allocated throughout the network, for instance by reallocating value through transfers (e.g., taxes and subsidies). It can also be justified in settings where the utility functions are fixed, but where one is willing to make interpersonal comparisons of utility and take a utilitarian perspective on welfare. Pareto efficiency is a much less decisive notion, often admitting many networks, but it might be more reasonable in contexts where the payoff functions are fixed and no transfers are possible, and noting the inherent difficulties in comparing utilities across individuals.

Beyond these notions of efficiency, one may want to consider others. For instance it may be that some reallocation of value is possible, but only under the constraints that the allocations are balanced on each component. Such constraints lead to definitions of constrained efficiency, as considered in Exercises **??** and **??**.

With definitions of efficiency in hand, we can start to take a longer look at the relationship between stability and efficiency of networks.

6.3 Distance-Based Utility

I begin with a generalization from Bloch and Jackson [74] of the symmetric connections model discussed in Section **??**. The basic idea is that players get utility from their direct connections and also from their indirect connections; and the utility deteriorates with the distance between individuals. So, all else held equal, being closer to another player brings higher benefits. The rate at which is happens is captured by a benefit function.

Let $b : \{1, \ldots, n-1\} \to I\!R$ denote the net benefit that a player gets from (indirect) connections as a function of the distance between the players. The *distance-based utility model* is one where a player's utility can be written as

$$u_i(g) = \sum_{j \neq i : j \in N^{n-1}(g)} b(\ell_{ij}(g)) - d_i(g)c,$$

where $\ell_{ij}(g)$ is the shortest path length between i and j. Let $b(k) > b(k+1) > 0$ for any k and $c \geq 0$. This embodies the idea that a player sees higher benefits for having a lower distance to other players.

The benefit function is fairly general, allowing the benefits to vary with distance in a wide variety of ways. It could be that being at a distance of two links rather than one is almost as beneficial as being directly connected; or it might be that the benefits fall off dramatically. This would depend on the application and what generates the benefits. The symmetric connections model is a special case of this model, where the benefits fall off exponentially with distance, so that $b(k) = \delta^k$.

This distance-based utility model has two critical aspects: similar utility functions for different players, and benefits from indirect connections that only depend on minimum path length. While these are clearly special, it is still a setting that captures some basic aspects of the costs and benefits of many social and economic situations. It also serves as a useful benchmark, so that as we add heterogeneity or benefits that depend on other aspects of the network structure, we can understand how they change the analysis.

The following proposition shows that efficient networks in the distance-based utility model share the same features as the special case of the symmetric connections model.

PROPOSITION **6.3.1** *The unique efficient network structure in the distance-based utility model is*

(i) the complete network if $b(2) < b(1) - c$,

(ii) a star encompassing all nodes if $b(1) - b(2) < c < b(1) + \frac{(n-2)}{2} b(2)$, *and*

(iii) the empty network if $b(1) + \frac{(n-2)}{2} b(2) < c$.

So, efficient networks take simple and intuitive forms in a broad class of settings. If link costs are high relative to benefits, then it does not make sense to form any links, and so the empty network is the only efficient network (iii). If link costs are sufficiently

low ($c < b(1) - b(2)$), then it makes sense to form all links as the cost of adding a link is less then the gain from shortening a a geodesic of length at least two into a path of length one, and so the unique efficient network is the complete network (i). The more interesting case arises for intermediate costs of links relative to benefits, such that the only efficient network structure is a star (ii).

Proof of Proposition 6.3.1: To see (i), note that adding a link ij cannot decrease the utility of any $k \notin \{i, j\}$, and so if the utility to i and j increases as the result of adding a link, then total utility increases. Thus, it suffices to show that adding any link benefits the two nodes involved in the link regardless of the starting network. Note that adding a link ij cannot increase distances between them and any other nodes, and it decreases the distance between i and j. Thus, adding a link between any i and j increases each of their utilities by at least $b(1) - c - b(2)$, which is greater than 0 in case (i). Thus, adding the link increases total utility and the unique efficient network is the complete network.

Next, let us verify (ii) and (iii). To connect any k nodes involves at least $k-1$ links. A star network involves exactly $k-1$ links. A star network with $k-1$ links leads to a total utility of

$$2(k-1)(b(1)-c) + (k-1)(k-2)b(2). \tag{6.1}$$

Next, note that if a component has k nodes and $m \geq k-1$ links, then the value of the direct connections due to the links is $2m(b(1)-c)$. This leaves $\frac{k(k-1)}{2} - m$ pairs of players who are at a distance of at least 2 from each other. The value of each such indirect connection is at most $b(2)$. Therefore, the overall value of the component is at most

$$2m(b(1)-c) + (k(k-1) - 2m)\, b(2). \tag{6.2}$$

The difference between (6.1) and (6.2) is

$$2(m-(k-1))(b(2)-(b(1)-c)).$$

Since $b(2) > b(1) - c$, this is greater than 0 whenever $m > k-1$. So the value can only equal the value of the star when $m = k-1$. Any network other than a star with $k-1$ links connecting k nodes leads to a total utility that is

$$2(k-1)(b(1)-c) + X,$$

where $X < (k-1)(k-2)b(2)$, since if it is not a star and has only $k-1$ links among k nodes then some of the nodes are at a distance of more than two and at most $k-1$

pairs of nodes are directly connected. Thus, if one chooses to involve k nodes and have exactly $k-1$ links, then a star is the most efficient architecture. This implies that when $b(2) > b(1) - c$, efficient networks must involve some combinations of stars and disconnected nodes.

Next, let us show that if two stars, involving $k_1 \geq 1$ and $k_2 \geq 2$ nodes respectively, each lead to nonnegative utility, then a single star among $k_1 + k_2$ nodes leads to strictly higher total utility. This follows from (6.1), noting that the total utility from a star of $k_1 + k_2$ nodes is

$$(k_1 + k_2 - 1)[2(b(1) - c) + (k_1 + k_2 - 2)b(2)],$$

which is larger than

$$(k_1 - 1)[2(b(1) - c) + (k_1 - 2)b(2)] + (k_2 - 1)[2(b(1) - c) + (k_2 - 2)b(2)],$$

when both terms in this latter expression are nonnegative.

Thus, we can conclude that if $b(2) > b(1) - c$, then an efficient network is either a star involving all nodes or an empty network. The condition differentiating between (ii) and (iii) is exactly the calculation of whether the value of a star involving all n players is positive or negative (which is given in (6.1), setting $k = n$). ∎

We can now compare the efficient networks with those that arise if players form links in a self-interested manner. The pairwise stable networks in the distance-based utility model have similar properties to those in the symmetric connections model.

PROPOSITION **6.3.2** *In the distance-based utility model :*

(i) A pairwise stable network has at most one (non-empty) component.

(ii) For $b(2) < b(1) - c$, the unique pairwise stable network is the complete network.

(iii) For $b(1) - b(2) < c < b(1)$, a star encompassing all players is pairwise stable, but for some n and parameter values in this range is not the unique pairwise stable network.

(iv) For $b(1) < c$, in any pairwise stable network each node has either no links or else at least two links (and thus every pairwise stable network is inefficient when $b(1) < c < b(1) + \frac{(n-2)}{2} b(2)$).

The proof appears as Exercise 6.2.

As one might expect, for high and low costs to links, efficient networks coincide with pairwise stable networks. Disparities occur with intermediate link costs relative to benefits. In the range of costs and benefits such that $b(1) - b(2) < c < b(1) + \frac{(n-2)}{2} b(2)$, a star involving all players is the unique efficient network architecture, but is only sometimes pairwise stable and even then not uniquely so.

Moreover, there are situations where all pairwise stable networks are *Pareto inefficient*. To see this, consider a situation where $n = 4$ and $b(1) < c < b(1) + \frac{b(2)}{2}$, and so a star network is the unique efficient structure. Here, the only pairwise stable network is the empty network. We can argue this as follows. If a player has three links, then severing one leads to a increase in payoff of $c - b(1)$. If a player has two links, there are two possibilities: the player is in a component of all the players, or the player is in a component of just three players. In the second case, severing one of the links leads to an increase in payoff of $c - b(1)$. In the first case, the player is directly connected to two players, and then at a path length of 2 to the third player. One of the two links can be severed without increasing the path length to the third player. this leads to an increase in payoff of $c - b(1)$. Thus, it must be that each player in the network has at most one link. In that case, any player who has one link would increase his or her payoff by severing the link since it does not lead to any indirect payoffs. Although the empty network is the unique pairwise stable network, *it is not even Pareto efficient*. The empty network is Pareto dominated by a line (e.g., $g = \{12, 23, 34\}$). To see this, note that under the line, the payoff to the end players (1 and 4) is $b(1) + b(2) + b(3) - c$ which is greater than 0, and to the middle two players (2 and 3) the payoff is $2b(1) + b(2) - 2c$ which is also greater than 0 since $c < b(1) + \frac{b(2)}{2}$.

Thus, there exist cost ranges for the distance-based utility model (and hence the symmetric connections model) for which all pairwise stable networks are *Pareto inefficient*, and other cost ranges where all pairwise stable networks are efficient. There are also some cost ranges where some pairwise stable networks are efficient and some other pairwise stable networks are not even Pareto efficient.

6.3.1 Externalities

The inefficiency of pairwise stable networks in the distance-based utility model stems from the externalities that are present. Externalities refer to situations where the utility or payoffs to one individual are affected by the actions of others, where those actions do not directly involve the individual in question. In the distance-based utility

model, beyond one's own links, a player in this setting can have an increase in payoffs (hence the "positive") as his or her neighbors form more links or even if indirectly connected players form more links.

Let us say that there are *nonnegative externalities* under $u = (u_1, \ldots, u_n)$ if

$$u_i(g + jk) \geq u_i(g)$$

for all $i \in N$, $g \in G(N)$ and jk such that $j \neq i \neq k$. There are *positive externalities* under $u = (u_1, \ldots, u_n)$ if there are nonnegative externalities under $u = (u_1, \ldots, u_n)$ and the inequality above is strict in some instances.

It is easy to see that the distance-based utility model is one of positive externalities, as added links can only bring players closer together.

Let us say that there are *nonpositive externalities* under $u = (u_1, \ldots, u_n)$ if

$$u_i(g + jk) \leq u_i(g)$$

for all $i \in N$, $g \in G(N)$ and jk such that $j \neq i \neq k$. There are *negative externalities* under $u = (u_1, \ldots, u_n)$ if there are nonpositive externalities under $u = (u_1, \ldots, u_n)$ and the inequality above is strict in some instances.

We shall see an example of a model with negative externalities shortly.

6.3.2 Growing Networks and Inefficiency

As there can be many pairwise stable networks, even when some are efficient we might not expect that those would be the ones to arise. How can we predict which networks are likely to emerge from a multitude of pairwise stable networks? There are a variety of approaches focusing either on refining the equilibrium concept or examining some dynamic process. To get an impression of one such dynamic, let us examine a natural and intuitive process that was introduced by Alison Watts [618], and is described as follows.

Consider a random ordering over links, where at any point in time any link is as likely as any other to be identified. If the link has not yet been added to the network, and at least one of the two players involved would benefit from adding it and the other would be at least as well off given the current network in place (and not accounting for what might happen in the future), then the link is added. If the identified link has already been added, then it is deleted if either player would (myopically) benefit from its deletion, and it is kept otherwise. If this process comes to rest, then it must be at a

pairwise stable network. It is also possible for the process to cycle. (I discuss the full range of possibilities in more detail in Chapter 11.)

Based on this process, we can deduce which pairwise stable networks will be reached in the symmetric distance-based utility model. If the empty network is the only pairwise stable network, then the process will get stuck there.[4] This happens whenever $c > b(1)$, even in cases where there are nonempty networks that are strictly preferred by all players to the empty network. In cases where $b(1) - c > b(2)$, then it is clear that all links will form and the efficient complete network will be reached. More subtle cases arise where $b(2) > b(1) - c > 0$. In this range a star is the efficient network, but players are willing to add a link to players with whom they do not have any indirect connection (or have only a sufficiently distant one). In order for a star to form, it must be that the links are identified in an order that always includes some particular player (who becomes the center) until all of the possible $n-1$ links to that player have been formed. So, for instance, if the first link that pops up is ij, then the next one (other than ij) has to be of the form ik or jk. If ik is the next one that arises, then the subsequent links that are identified to be added all have to involve i until the star forms. If any other link pops up first, the star network will not be formed (this takes some proof, which is given below). As n grows, the chance that this happens is clearly going to 0.

While Alison Watts' [618] result was stated for the symmetric connections model, it extends to the symmetric distance-based utility model.

PROPOSITION **6.3.3** *Consider the symmetric distance-based utility model in the case where $b(1) - b(2) < c < b(1)$. As the number of players grows, the probability that the above described dynamic process leads to an efficient network (star) converges to 0.*

Proof of Proposition 6.3.3: First, note that if a player forms a link at some point in the process, then that player will always be linked to at least one player from that point on. This follows from the observation that in a case where $b(1) > c$ no player would ever sever a link to a player who has no other connections (nor would that player sever his or her only link).

With this observation in hand, let us show that forming a star involves specific orders of links being identified, and that the probability of such an order being realized goes to 0. Consider a star forming with some center player, without loss of generality

[4] Here it is clear that the myopic nature of the process is critical. If players anticipate further additions to the network, they may form links that are initially costly but could later lead to net benefits. For discussion of forward looking behavior, see Chapter 11.

labeled as 1. Order the other players in terms of the last time that they end up linked to 1, and without loss of generality, label them as $2, \ldots, n$.

Note that 1 will only link to n if n is not linked to any other player when they meet as otherwise 1 is already at a distance of two links to n, and $b(2) > b(1) - c$. By the first observation above, for 1 to link to n it must be that n has not met any other players before meeting 1. Similar reasoning then implies that when 1 meets $n-1$, it must be that $n-1$ has not met any other player previously. Based on this reasoning, the only way for a star to form is for some link ij to form, then ik or jk to form, and then the center player to meet each other player before any other two players meet each other. So, suppose that ij meet first. The chance that the next two players who meet and have not met before are other than ij is $(n-2)(n-3)/[n(n-1)-2]$[5] This probability goes to 1, and so the probability that the star results goes to 0. ∎

6.3.3 The Price of Anarchy and the Price of Stability

[?] [?]

Beyond simply knowing that the network formation might lead to inefficiencies, we might also be interested in the extent to which the emergent networks are inefficient. That is, the situation is somehow worse if the stable networks are "very" inefficient compared to if they are "nearly" efficient. This issue of quantifying the social inefficiency that results from selfish individuals acting in a system is not just an issue in network settings, but is critical to a variety of settings and this has become known as the "price of anarchy."[6]

To get an idea of the price of anarchy, let us consider a special case of the distance-based utility model, where preferences are directly proportional to distance. That is, let

$$u_i(g) = \sum_{j \neq i} -\ell_{ij}(g) - d_i(g)c, \tag{6.3}$$

where ℓ_{ij} is set to ∞ if i and j are not in the same component. Such a model was considered by Fabrikant et al [216].

The way these payoffs are written they are always negative, and they can be interpreted as a sort of cost of communication.

[5] There are $(n-2)(n-3)/2$ such (unordered) pairs. The total number of possible pairs is $n(n-1)/2$, and one has already formed. So the probability is $(n-2)(n-3)/2$ divided by $[n(n-1)/2]-1$.

[6] For example, this was studied in selfish-routing settings by Roughgarden and Tardos [542], and was named the price of anarchy by Papadimitriou [500].

Here, the *price of anarchy* is the ratio *largest* total cost (in absolute value) generated by any pairwise stable network compared to the cost of the efficient network. A ratio of 1 indicates that all pairwise stable networks are efficient, while a ratio above 1 indicates that there are higher costs (lower payoffs) associated with some pairwise stable networks than the efficient network.

We can distinguish between the best possible pairwise stable network and the worst possible pairwise stable network. This is the distinction between the "price of stability" and the "price of anarchy" (e.g., see Tardos and Wexler [585]). The *price of stability* is the ratio of the *lowest* total cost (in absolute value) generated any pairwise stable network to the cost of the efficient network. Clearly the price of anarchy will always exceed the price of stability, as one is a worst-case scenario and the other is the best-case scenario. A price of stability of 1 indicates that the efficient network will be stable, while a price of anarchy of 1 indicates that the all stable networks are efficient. A price of stability greater than 1 indicates that all stable networks are inefficient, while a price of stability of 1 and a price of anarchy greater than 1 indicates that some stable networks are efficient while others are not. These prices can differ substantially, and we can keep track of a *anarchy-stability gap*.

An easy variation on Proposition **??** shows that in this setting the unique efficient network structure is

(i) the complete network if $c < 1$, and

(ii) a star encompassing all nodes if $c > 1$.

We also see that a pairwise stable network here will have all players in one component, given that there is an infinite cost of not being connected to some other player. If $c < 1$ then it is clear that the unique pairwise (Nash) stable network is the complete network, and so there the price of anarchy and the price of stability are both 1. When $c \geq 1$, in this model a star is pairwise (Nash) stable, and so the price of stability remains 1. However, for these higher costs, there are other pairwise (Nash) stable networks and so the price of anarchy increases to be above 1. Fabrikant et al [216] provide an upper bound on this price of anarchy. The bound is fairly easy to derive by bounding the diameter of a pairwise stable network and the number of links it can contain.

PROPOSITION **6.3.4** *[Fabrikant et al [216]] The diameter of any pairwise stable network in the model described by (6.3) is at most* $2\sqrt{c}+1$ *and such a network contains at most* $n-1+\frac{2n^2}{\sqrt{c}}$ *links. Thus, the price of anarchy is no more than* $17\sqrt{c}$.

Proof of Proposition 6.3.4: First, let us bound the diameter of a pairwise stable network. Suppose that the diameter is at least $2D$ and no more than $2D+1$, where D is a positive integer. If we show that D cannot exceed $\sqrt{c}$, then it follows that the diameter cannot exceed $2\sqrt{c}+1$. Consider players i and j at a maximal distance from each other, which is at least $2D$. If they link to each other, the gain in payoff for each one will be at least

$$(2D-1)+(2D-3)+\cdots+1=D^2,$$

since they reduce the distance between them from at least $2D$ to 1 and the distance from the next closest player on the path between them from $2D-1$ to 2 (a gain of $2D-3$), and so forth. Thus, given pairwise stability, they cannot gain from adding this link and so $D^2 \leq c$ and so $D \leq \sqrt{c}$ as claimed.

Next, let us argue that the number of links in a pairwise stable network is at most $n-1+\frac{3n^2}{\sqrt{c}}$. First, there are at most $n-1$ edges which are bridges (so that the network would have more than one component if the link were removed).[7] So, we need to argue that there are at most $\frac{3n^2}{\sqrt{c}}$ links that are not bridges. Consider a link ij that is not a bridge. Let A_{ij} be the set of nodes (including j) for which the shortest path to i goes through j. If ij is deleted, the distance between i and a node in A_{ij} can become at most double the diameter of the network (denoted by d). Thus, deleting the link increases the distance costs by at most $2d|A_{ij}|$ and so this must be at least c as otherwise i should sever the link, Thus $|A_{ij}| \geq \frac{c}{2d}$. This implies that any given node i can have at most $2dn/c$ non-bridge links, so there are at most dn^2/c non-bridge links in total. Since $d \leq 3\sqrt{c}$, it follows that there are at most $3n^2/\sqrt{c}$ non-bridge links.

Finally, to derive the price of anarchy, we simply need to bound the cost of pairwise stable networks. A crude upper bound on the cost is $n(n-1)$ times the diameter plus two times c times the number of links. We also know that the cost of the efficient network when $c>1$ is that of a star, which is $2(n-1)[n-1+c]$. Therefore the price of anarchy is at most

$$\frac{(2\sqrt{c}+1)\,n(n-1)+2(n-1)c+6n^2\sqrt{c}}{2(n-1)[n-1+c]},$$

which (noting that $1<\sqrt{c}$ and $n \geq 2$) is less than $17\sqrt{c}$. ∎

This is a very loose bound, but it shows that the price of anarchy is no more than the order of the $\sqrt{c}$ in this setting, and so is the price of stability and anarchy gap.

[7] Each bridge that is removed breaks the network into one more component than we start with, and we can end up with at most n components, so there can be at most $n-1$ bridges (noting that the fact that one link is a bridge is not affected by the removal of another bridge).

In this extreme model, the price of stability is one as there is always some pairwise stable and efficient network, but there is a price of anarchy as there are some inefficient pairwise stable networks. We know more generally in the distance-based utility model that all stable networks can be inefficient.

Such price of anarchy and stability calculations are important as they provide a magnitude to the inefficiency of selfish network formation. As such calculations can be challenging outside of simple settings, the prices of stability and anarchy are still unknown for most models, especially with any heterogeneity across players.

6.4 A Co-Author Model and Negative Externalities

The analyses above for the distance-based model show us that self-centered incentives can lead to inefficient networks forming. That model has a specific form of positive externality in it: individuals benefit from indirect connections. That is, one individual can benefit because another individual has connections. The tension arising between stability and efficiency results because individuals do not account for the indirect benefits that their connections will bring to their neighbors. That is, an individual considers whether or not his or her payoff will increase when forming a link, but does not pay attention to whether the link would increase the payoffs of other players in the network.

Let us now consider another simple model of network payoffs that has a different sort of externality. Consider a situation where there are negative externalities due to links. That is, consider a situation where a given individual would rather that his or her neighbors have fewer connections rather than more. This corresponds to a situation where an individual is in competition with other indirect connections for access to the individual's neighbors. This contrasts with the connections and distance-based model where individuals draw benefits from indirect connections.[8]

This model is called the "co-author model", as introduced by Jackson and Wolinsky [343]. The story that accompanies the payoff structure is that individuals benefit from

[8] There are also models where either positive or negative externalities can result from indirect links depending on the network configuration and the players in question. This is true, for instance, if the payoff of a player is related to a centrality measure such as betweenness centrality as in Buechel and Buskens [104]. Adding a link to a network could increase some player's centrality by placing him or her between new pairs of players, even if that player is not involved in the link. So there could be positive externalities in some cases. Adding a link could also decrease some player's centrality, as it could result new paths, between other players in the network, that circumvent the given player. Thus, adding a link could exhibit negative externalities.

interacting with others, for instance, in collaborating on a research project. Beyond the benefit of having the other player put time into the project, there is also a form of synergy. The synergy is proportional to the product of times that the two researchers devote to the project. If they spend more time together, they generate more synergy. This leads to the negative externality. If an individual's collaborator increases the time spent on other projects, then the individual sees less synergy with that collaborator. Effectively, each player has a fixed amount of time to spend on projects and the time that researcher i spends on a given project is inversely related to the number of projects, $d_i(g)$, that he or she is involved in. The synergy between two researchers depends on how much time they spend together, and is captured by a term $\frac{1}{d_i(g)d_j(g)}$. Here the more projects a researcher is involved with, the lower the synergy that is obtained per project. Player i's payoff is represented by

$$u_i(g) = \sum_{j:ij\in g} \left(\frac{1}{d_i(g)} + \frac{1}{d_j(g)} + \frac{1}{d_i(g)d_j(g)} \right)$$

for $d_i(g) > 0$, and $u_i(g) = 1$ if $d_i(g) = 0$. So, the value generated by any given research project is proportional to the sum of the time that i puts into the project, the time that j puts into it, and a synergy that is dependent on an interaction between the time that the two researchers put into the project.

Note that in the co-author model there are no directly modeled costs to links. Costs are implicit in the diluted synergy as efforts are spread among more co-authors.

PROPOSITION **6.4.1** *[Jackson and Wolinsky [343]] If n is even, then the efficient network structure consists of $n/2$ separate pairs. If a network is pairwise stable and $n \geq 4$, then it is inefficient and can be partitioned into fully intra-connected components, each of which has a different number of members. Moreover, if m is the number of members of one component of a pairwise stable network and $\widehat{m}$ is the number of members of a different component that is no larger than the first, then $m > \widehat{m}^2$.*

Proof of Proposition 6.4.1:

To verify efficiency, note that

$$\sum_{i\in N} u_i(g) = \sum_{i:d_i(g)>0} \sum_{j:ij\in g} \left[\frac{1}{d_i(g)} + \frac{1}{d_j(g)} + \frac{1}{d_i(g)d_j(g)} \right],$$

so that

$$\sum_{i\in N} u_i(g) \leq 2N + \sum_{i:d_i(g)>0} \sum_{j:ij\in g} \frac{1}{d_i(g)d_j(g)},$$

and equality can only hold if $d_i(g) > 0$ for all i. Then the result follows since $\sum_{i:d_i(g)>0}\sum_{j:ij\in g}\frac{1}{d_i(g)d_j(g)} \leq n$, with equality only if $d_i(g) = 1 = d_j(g)$ for all i and j, and $3n$ is the value of $n/2$ separate pairs.

To characterize the pairwise stable networks, consider i and j who are not linked. It follows from the formula for $u_i(g)$ that i will strictly want to link to j at a given network g if and only if

$$\frac{1}{d_j(g)+1}(1+\frac{1}{d_i(g)+1}) > [\frac{1}{d_i(g)} - \frac{1}{d_i(g)+1}]\sum_{k:k\neq j,ik\in g}\frac{1}{d_k(g)},$$

(substitute 0 on the right hand side if $d_i(g) = 0$) which simplifies to

$$\frac{d_i(g)+2}{d_j(g)+1} > \frac{1}{d_i(g)}\sum_{k:k\neq j,ik\in g}\frac{1}{d_k(g)}. \tag{6.4}$$

The following facts are then true of a pairwise stable network.

1. If $d_i(g) = d_j(g)$, then $ij \in g$.

To see 1, it is enough to show that if $d_j(g) \leq d_i(g)$, then i would benefit from linking to j. Note that if $d_j(g) \leq d_i(g)$, then $\frac{d_i(g)+2}{d_j(g)+1} > 1$ while the right hand side of (6.4) is at most 1 (the average of d_i fractions). Therefore, i benefit from linking to j.

2. If $d_h(g) \leq \max\{d_k(g)|ik \in g\}$, then i benefits from a link to h.

To see 2, let j be such that $ij \in g$ and $d_j(g) = \max\{d_k(g)|ik \in g\}$. If $d_i(g) \geq d_j(g) - 1$ then $\frac{d_i(g)+2}{d_h(g)+1} \geq 1$. If $\frac{d_i(g)+2}{d_h(g)+1} > 1$ then (6.4) clearly holds for i's link to h. If $\frac{d_i(g)+2}{d_h(g)+1} = 1$, then it must be that $d_h(g) \geq 2$ and so $d_j(g) \geq 2$. This means that the right hand side of (6.4) when calculated for adding the link h will be strictly less than 1. Thus (6.4) will hold. If $d_i(g) < d_j(g) - 1$, then $\frac{d_i(g)+1}{d_j(g)} < \frac{d_i(g)+2}{d_j(g)+1} \leq \frac{d_i(g)+2}{d_h(g)+1}$. Since $ij \in g$ and g is pairwise stable, it follows from (6.4) that

$$\frac{d_i(g)+1}{d_j(g)} \geq \frac{1}{d_i(g)-1}\sum_{k:k\neq j,ik\in g}\frac{1}{d_k(g)}.$$

Also,

$$\frac{1}{d_i(g)-1}\sum_{k:k\neq j,ik\in g}\frac{1}{d_k(g)} \geq \frac{1}{d_i(g)}\sum_{k:ik\in g}\frac{1}{d_k(g)}$$

since the extra element on the right hand side is $1/d_j(g)$ which is smaller than (or equal to) all terms in the sum. Thus $\frac{d_i(g)+2}{d_h(g)+1} > \frac{1}{d_i(g)}\sum_{k:ik\in g}\frac{1}{d_k(g)}$.

Facts 1 and 2 imply that all players with the maximal number of links are connected to each other and nobody else. [By 1, they must all be connected to each other. By

2, anyone connected to a player with a maximal number of links would like to connect to all players with no more than that number of links, and hence all those with that number of links.] Similarly, all players with the next to maximal number of links are connected to each other and nobody else, and so on.

The only thing which remains to be shown is that if m is the number of members of one (fully intra-connected) component and $\widehat{m}$ is the next largest in size, then $m > \widehat{m}^2$. Notice that for i in the next largest component not to be willing to link to j in the largest component it must be that $\frac{d_i(g)+2}{d_j(g)+1} \leq \frac{1}{d_i(g)}$ (using (6.4), since all nodes to which i is connected also have $d_i(g)$ connections). Thus $d_j(g) + 1 \geq d_i(g)(d_i(g) + 2)$. It follows that $d_j(g) > d_i(g)^2$. ∎

The co-authorship model, while very different in structure from the distance-based utility model, exhibits similar features in the sense that it has a simple structure to its efficient networks, and yet the pairwise stable networks tend to be inefficient. In both models the inefficiencies are tied to externalities, but of different sorts. In the distance-based settings, when stars are efficient the center may not have an incentive to maintain links with solitary players. The externality is that when the center forms a link it benefits other players since it brings them valuable indirect connections. The failure, or tension between efficiency and stability, is due to the fact that the indirect value that the center generates is not adequately reflected in the payoffs that the center sees from a direct connection. In the co-authorship model, by forming additional connections, a player dilutes the time he or she spends with his original partners, which harms them. Here the inefficiency of stable networks stems from the fact that (up to a point) a given player sees more benefit from adding a new link than harm in terms of dilution of value from existing partnerships, while those existing partners only see harm. In both models, social and private incentives are not aligned, but for different reasons stemming from opposite sorts of externalities.

6.5 Small Worlds in an Islands-Connections Model

Before moving on to discuss the tension between stability and efficiency more generally, let us examine one more model. This is another variation on the connections model. This model shows how some of the observed features of real-world networks, such as small-world properties, can be explained from a strategic point of view. This provides a very different perspective on why we observe small-worlds than what we saw from the random networks perspective.

The reasoning behind small worlds in this model is that high clustering stems from a distance-based cost structure. Nodes that are closer (or more similar) find it cheaper to maintain links to each other and this generates high clustering. Short overall path length then comes from the fact that if there were no short enough paths between two given nodes, then even if there were a high cost to adding a link, that link would bridge distant parts of the network and bring high benefits to that pair of nodes.

This highlights an important distinction between strategic models and purely random models. The random models can identify processes which generate certain features, but do not explain why those processes might arise. In a strategic model, the explanation for a specific characteristic of a network is instead traced back to more primitive elements such as costs and benefits from social relationships. Thus, in a sense, the strategic model can be thought of as explaining "why," whereas the random-graph models can be thought of as explaining "how". This is not to say that strategic models are "better." Each modeling technique has its strengths and weaknesses, and they are quite complementary. For instance, with random graph models it is easy to produce processes which match arbitrary given degree distributions, something which is difficult (at least analytically) with a fully strategic model. Yet strategic models allow us to evaluate networks in terms of overall welfare, and trace structure back to underlying primitives.

6.5.1 The Islands-Connections Model

Consider a simple "islands" version of a truncated version of the connections model from Jackson and Rogers [335]. There are two modifications to the symmetric connections model discussed in Section **??**. First, if the minimum path length between two players is more than D links, then they do not receive any value from each other. Next, there is a "geographic" structure to costs. That is, there are K islands, each of which has J players on it. Forming a link between players i and j costs i and j each c if they are on the same island, and C otherwise, where $C > c > 0$. So, it is cheaper to link to nearby players.

This geography provides a very simple way of introducing heterogeneity among players or nodes. It is important to emphasize that the geographic structure need not be interpreted literally, but instead can also describe differences among players in terms of social or political attributes, research interests, compatibility of R&D programs, etc. In a richer model, players would be coded by whole lists of attributes and linking costs

would depend on the vectors of attributes.[9] However, this simple formulation already captures some essential aspects of social interaction and provides substantial insight into small-worlds phenomena.

The overall utility to a player i in network g is

$$u_i(g) = \sum_{j \neq i : \ell(i,j) \leq D} \delta^{\ell(i,j)} - \sum_{j : ij \in g} c_{ij},$$

where $c_{ij} = c$ if i and j are on the same island and C otherwise.[10]

For large enough D, the truncation is irrelevant. For smaller D, truncation captures the idea that benefits fall off quite dramatically beyond some threshold connection distance. So for instance, it is impossible to ask for favors from the friend of a friend of a friend of a friend. The results in this model extend to the distance-based utility model under a suitable formulation, but the truncation makes things particularly transparent.

Recall from Chapter 3 that many social networks exhibit so-called small-world characteristics embodied by a relatively low diameter and average path length, and a high clustering (compared to an independent random network). The following proposition from Jackson and Rogers [335] shows that for suitable parameter values, an islands version of the truncated connections model exhibits small-worlds characteristics. This makes clear how costs and benefits can explain small-worlds phenomena, a point first made by Carayol and Roux [127].

PROPOSITION **6.5.1** *If $c < \delta - \delta^2$ and $C < \delta + (J-1)\delta^2$, then any network that is pairwise stable or efficient is such that*

1. *the players on any given island are completely connected to each other,*
2. *the diameter and average path length are no greater than $D+1$, and*
3. *and if $\delta - \delta^3 < C$, then a lower bound on individual, average, and overall clustering is $\frac{(J-1)(J-2)}{J^2K^2}$.*[11]

[9] See Johnson and Gilles [349], as discussed in Exercise 6.13, for an alternative geographic cost structure based on distance on a line.

[10] This cost structure is the similar that of the insiders-outsiders model of Galeotti, Goyal, and Kamphorst [254], while the benefits structure is quite different: the insiders-outsiders model has almost no decay in value to distance, while this islands model matches the truncated version of the connections model (see Jackson and Wolinsky [343]). The difference in benefit structure between the islands connections model and the insider-outsider model leads to very different conclusions regarding clustering.

[11] For the bounds on clustering it is assumed that $\delta - \delta^2 \neq C$. If $\delta - \delta^2 = C$ then there is a great deal of indifference over links, and the set of pairwise stable networks explodes.

Figure 6.5.1. A Pairwise Stable "Small World" in an Islands Version of the Connections Model

The intuition behind the proposition is relatively straightforward. Low costs of connections to nearby players (those on the same island) lead to high clustering. The high value to linking to other islands (accessing many other players) leads to low average path length. The high cost to linking across islands means that there are only a few links across islands.

These properties are illustrated in Figure 6.5.1. Figure 6.5.1 is for a case where $c < .04$, $1 < C < 4.5$, $\delta = .95$. players are grouped in sets of five who are completely connected to and lie on the same island, and there are five separate islands.

This economic analysis of small worlds gives complementary insights to those of rewiring analysis of Watts and Strogatz [623] discussed in Section **??**. The random rewiring analyzed by Watts and Strogatz shows that it is possible to have both high clustering and short path length at the same time, whereas the above model gives more insight into why we should expect this to be exhibited by social networks.

Another feature distinguishing an economic modeling and a random modeling of these network characteristics concerns "shortcut" links (i.e., those which link distant parts of the network and if deleted would substantially alter the distance between the connected nodes). In a random rewiring model shortcut links would at least occasion-

ally occur in close proximity to each other. Under the strategic approach, the cost of building a second shortcut link next to an existing one would outweigh the benefit.[12]

Proof of Proposition 6.5.1: Let us first show 1. If two players on the same island are not connected in some network, then they would each gain at least $\delta - \delta^2 - c > 0$ by adding the link, and this would only help other players, and so the network cannot be pairwise stable or efficient.

Let us next show 2. Suppose that there are two players (on distinct islands), say i and j, such that $\ell(i,j) \geq D+2$. As just argued, in any pairwise stable or efficient network, j is directly connected to all members of his island and so is i. Thus i is at a distance of at least $D+1$ from each member of j's island and so enjoys no benefit from any of these players; the same is true for j from i's island. Thus, by linking to j, i would gain at least $\delta + (J-1)\delta^2 - C > 0$ (and vice versa), so this cannot be pairwise stable or efficient.

Next, let us derive a lower bound for an individual's clustering (and thus average clustering). Consider an individual with L inter-island links. All of the player's pairs of intra-island neighbors are themselves neighbors in either an efficient or pairwise stable network. Thus there are at least $(J-1)(J-2)/2$ pairs of i's neighbors that are linked out of a maximal total of $(J+L-1)(J+L-2)/2$ pairs of neighbors. This leads to a lower bound of $(J-1)(J-2)/[(J+L-1)(J+L-2)]$. Since $L \leq J(K-1)$, we have a loose lower bound of $(J-1)(J-2)/(J+J(K-1))^2$, resulting in the claimed expression.

The lower bound on the overall clustering coefficient is established as follows. For a given network, write i's clustering coefficient as a_i/b_i, where a_i is the number of links among neighbors in i's neighborhood and b_i is the number of pairs of neighbors in i's neighborhood. We have established a lower bound for a_i/b_i. Note that overall clustering is $(\sum_i a_i)/(\sum_i b_i)$ and that this is clearly greater than $\min_i(a_i/b_i)$.[13] ∎

Proposition 6.5.1 identifies small-world properties in a strong sense. The diameter is bounded above by $D+1$, and average path lengths will be smaller since each island is fully connected. Next observe that average clustering is approximated by K^{-2}. Thus, clustering can remain large when n is very large, provided that per-island population is not too small. In cases where C is large enough so that the number of inter-island

[12] I thank Yann Bramoullé for pointing this out. This does depend on the structure of the strategic model. It might be that including links which are close substitutes is valuable in changing bargaining power and payoffs. This is something discussed at more length in Section **??**.

[13] It is straightforward to check that $(a_1+a_2)/(b_1+b_2) \geq \min(a_1/b_1, a_2/b_2)$. The result then follows by induction.

links is lower (bounded by KJ), then the lower bound for clustering is even higher (on the order of $(J/(J+K))^2$); and then even for large K relative to J, the clustering is much larger than one would observe in a independent random network (which goes to 0 as the population grows, holding the probability of links constant, as discussed in Section **??**).

Proposition **??** applies to networks that are either pairwise stable or efficient, and thus it shows that there are some similarities between these sets of networks. Understanding the exact relationship between pairwise stable networks and efficient networks is complex in this model. Jackson and Rogers [335] characterize the efficient networks when the intra-island costs are low. From that they conclude that for some range of inter-island costs the pairwise stable and efficient networks coincide, whereas for other cost ranges the set of pairwise stable networks, though always exhibiting small-world features, can be quite varied. This is discussed in Exercises 6.10 and 6.11.

These results apply to cases where the intra-island cost of connections is low enough that players are completely connected within their own islands. The analysis becomes more complex when the intra-island connection cost rises, so that not all players within an island are connected. Exercise 6.12 concerns diameters in such a situation.

6.6 A General Tension Between Stability and Efficiency

In the above models, we have seen that there are settings where all pairwise stable networks are inefficient and sometimes all pairwise stable networks are even Pareto inefficient. This raises a number of interesting issues that we shall examine here, and more in Chapters **??** and **??**.

6.6.1 Transfers: Taxing and Subsidizing Links

One question is to what extent this problem can be dealt with via some transfers among the players. This might take different forms. It could be that a government or other entity intervenes to tax and subsidize different links (for example, subsidizing research and development partnerships) if it feels that there are positive externalities and individual players might form too few partnerships. It might instead be that the players themselves bargain over some payments to maintain links. For instance, the center of the star could negotiate with the other players to receive some payments

or favors for maintaining her links with the other players. In fact, intuition from the sociology literature would suggest that a player in such a central position should receive a high payoff (e.g., see Burt [105]), which could come from the implicit power that the player gets from the implicit threat of severing links, or the favors and benefits that come along with the indirect connections that the player provides. If we start to account for such reallocations, can efficiency and stability be reconciled? And, more generally, what characterizes the settings where there is a tension and when can some sort of transfers help?

Let us start with the basic question of whether or not it is possible to make some transfer payments among the players so that at least some efficient network ends up being stable. It turns out, as Jackson and Wolinsky [343] showed, that there are some very simple and natural settings where it is not possible to make transfers to align incentives and efficiency, without violating some basic principles about how transfers should or would be structured. To make this precise, we need a few definitions.

A *transfer rule* is a function $t : G \to I\!R^N$ such that $\sum_i t_i(g) = 0$ for all g.

A transfer rule can thus capture any reallocation of payoff at a given network. These payments could subsidize or tax certain links or collections of links, and could be due to intervention by some outside authority or due to bargaining by the players. What matters to players is the net payoff they receive as a function of the network. The requirement that transfers sum to 0 is usually termed a "balance" condition, and embodies the idea that the system neither depends on any outside infusion of capital in order to operate, nor does it destroy value.

In the presence of transfers, player i's net payoff becomes $u_i(g) + t_i(g)$, and this is used by the player in decisions regarding the addition or deletion of links. That is, pairwise stability is then applied where the payoffs to the players from a network g are $u_i(g) + t_i(g)$ rather than $u_i(g)$.

A first thing to note is that there is a transfer rule that aligns individual and societal incentives. That is the *egalitarian transfer rule* (denoted t^e) such that

$$u_i(g) + t_i^e(g) = \frac{\sum_j u_j(g)}{n}$$

or

$$t_i^e(g) = \frac{\sum_j u_j(g)}{n} - u_i(g).$$

This transfer rule is the one that completely equalizes all players' payoffs on any given network. Under this rule, any network that is efficient will also maximize each

individual's net payoff, as each individual equally shares in the overall societal value. While this is one way to realign individual incentives, there are reasons that such rules would not tend to arise. These are captured in the following conditions.

6.6.2 Component Balance

One condition that we would expect transfers to satisfy when they arise from a bargaining or voluntary process, and also in situations where a society worries about secession, is the following.

A transfer rule t is *component balanced* if there are no net transfers across components of the network; that is, $\sum_{i \in S} t_i(g) = 0$ for each network g and component of players $S \in \Pi(N, g)$.

Component balance requires that the value of a given component of a network is allocated to the members of that component. This is a condition that a planner or government would like to respect if they wish to avoid secession by components of the network, or if they wish to only reallocate value among the individuals who generated it.

Whether or not component balance of the transfers is a compelling condition depends on the context, and in particular on the utility functions. If the utility functions exhibit externalities across components, so that the payoffs in one component depend on how other components are organized, then it may be important to make transfers across components. This is the case, for instance, when links are cooperative ventures between firms and firms are in competition with each other. For example, if links refer to code-sharing between airlines, then a given group of airlines might care to what extent airlines whom they are not linked to are linked to each other. Applications where component balance makes more sense are those where, for instance, links represent friendships and it does not matter to a given player how players in completely separate components are organized. Component balance is also a condition that one might expect to arise naturally if the transfers are coming out of some bargaining process. For example, individuals in one component might not be willing to make transfers to another component of individuals *provided the second component's organization has no effect on the first component.*

It is important to emphasize that the result below only requires that component balance be applied in situations where there are absolutely no externalities across

components.[14] In particular, there are no externalities across components when u is component-decomposable, which is defined as follows.

A profile of utility functions u is *component-decomposable* if $u_i(g) = u_i(g|_{N_i^n(g)})$ for all i and g.[15]

6.6.3 Equal Treatment of Equals

Another basic condition regarding transfers is an equal treatment condition. The condition of equal treatment has a rich tradition in social choice (e.g., see Thomson [**?**]). It requires that two players who are completely identical according to all criteria should end up with the same transfers or allocations. It is one of the most basic fairness criteria.

In the context of social networks, the condition can be formulated as follows. Given two players i and j and a network g, let g^{ij} denote the network derived from switching the positions of i and j (and switching each of their connections).[16]

Two players i and j are *complete equals* relative to a profile of utility functions u and a network g if the following holds.

- $ik \in g$ if and only if $jk \in g$
- $u_k(\widehat{g}) = u_k(\widehat{g}^{ij})$ for all $k \notin \{i, j\}$ and for all $\widehat{g} \in G(N)$,
- $u_i(\widehat{g}) = u_j(\widehat{g}^{ij})$ and $u_j(\widehat{g}) = u_i(\widehat{g}^{ij})$ for all $\widehat{g} \in G(N)$.

Thus, two players are complete equals relative to a network and a profile of utility functions if they sit in a completely symmetric position relative to all players in the network, all other players see them as completely interchangeable in forming a network, and the two players have the same utility function as a function of the structure of the network.

A transfer rule satisfies *equal treatment of equals* relative to a profile of utility functions u if $t_i(g) = t_j(g)$ whenever i and j are complete equals relative to u and g.

[14] The definition here is adapted from a condition defined on allocation rules, where it can be made explicit in the actual definition that it only be applied when the allocation rule is component additive. For more on that formulation, see Chapter 12.

[15] Recall that $N_i^n(g)$ is the set of all players at a distance of no more than n from i, where n is the number of players, and so is the set of all players in i's component.

[16] Thus, $g_{kh} = g_{kh}^{ij}$ when $k \notin \{i, j\}$ and $h \notin \{i, j\}$; and $g_{jk} = g_{ik}^{ij}$ and $g_{ik} = g_{jk}^{ij}$ for all k.

Equal treatment is the weakest possible anonymity condition, stating that two players should get the same transfers when they are completely identical in terms of their position in the network and completely interchangeable in the eyes of all players, including themselves.

This condition has several justifications. From the normative side, if one is designing transfers, it captures the most basic fairness principle that one should treat identical people equally. From the positive side, in cases where one might think of the transfers arising endogenously, it captures the idea that identical people would have similar bargaining positions which would lead them to similar outcomes.

6.6.4 Incompatibility of Pairwise Stability and Efficiency

The following proposition is a variation on a result of Jackson and Wolinsky [343].[17] The proposition can be strengthened to replace efficiency with a weaker form of efficiency, as outlined in Exercise **??**.

PROPOSITION **6.6.1** *There exist component-decomposable utility functions such that every pairwise stable network relative to any component balanced transfer rule satisfying equal treatment of equals is inefficient.*

The proof is by example. It is presented for $n = 3$, but is easily adapted to any n. The utility of each player in the complete network is 4. The utility of each connected player in a linked pair is 6. The utility of players who are disconnected is 0. The efficient networks are those with two links, which have a total utility of 13, with the central player getting a utility of 4.5 and the other two players getting a utility of 4.25 each. this is pictured in Figure 6.6.4

In the absence of any transfers, the pairwise stable networks all fail to be efficient. The pairwise stable networks are only those involving a single link. In any other network some player(s) have an incentive to sever a link (every player has such an incentive in the complete network, and the center player has an incentive to do so in each of the two link networks).

Consider introducing transfers to ensure that at least one efficient network is pairwise stable. Equal treatment of equals implies that the transfers on the complete

[17] Their formulation was stated in terms of allocation rules rather than transfer rules, which is essentially equivalent (see the discussion in Chapter 12). They also required a stronger anonymity condition rather than the equal treatment condition, but their proof works with the equal treatment condition.

Figure 6.6.4. Payoffs such that No Pairwise Stable Network is Efficient Regardless of Transfers

network must be 0, and equal treatment plus component balance implies the same for the single link and empty networks. So, consider the middle network out of the two link networks, and let us try to introduce transfers to make it pairwise stable. Payoffs with transfers are $4.25+t_1$, $4.5+t_2$ and $4.25+t_3$, where t_1, t_2, t_3 are the transfers on this network to the three players. Given the complete symmetry between the first and third players, equal treatment implies that their transfers must be equal so that $t_1 = t_3$. For the middle two-link network to be pairwise stable, it must be that the first and third players would not gain from adding the missing link. So $t_1 = t_3 \geq -.25$. However, in order to have the network be pairwise stable we also need the second player, or center player, to be willing to keep both of the links that are in place. As that player gets a payoff of 6 if either link is deleted, it must be that $t_2 \geq 1.5$. However, now the sum of the transfers exceeds 0 and hence component balance is violated (in fact, even a basic feasibility condition is violated).

This example extends for weaker notions of efficiency and a variety of notions of stability, as for example, in Exercises 6.8 and 6.9.

While this is only an example, it has natural properties in that some intermediate sized network is efficient. It is clear that this holds for a range of examples and that this is easily modified to hold for larger societies.

Both of the conditions of component balance and equal treatment of equals are required for the result to hold. The importance of component balance is easily seen. The egalitarian transfer rule satisfied equal treatment of equals and is such that all efficient networks are pairwise stable. Individuals only have incentives to form or sever links when that increases total utility. If we drop equal treatment of equals, but keep component balance, then a careful and clever construction of transfers by Dutta and Mutuswami [200] ensures that some efficient network is strongly stable for a class of utility functions. This is stated in the following proposition, from Dutta and Mutuswami [200].

PROPOSITION **6.6.2** *[Dutta and Mutuswami [200]] If the profile of utility functions is component-decomposable and all nonempty networks generate positive total utility, then there exists a component balanced transfer rule such that some efficient network is pairwise stable. Moreover, while transfers will sometimes fail to satisfy equal treatment of equals, they can be structured so as treat completely equal players equally on at least one network that is both efficient and pairwise stable.*[18]

[18] Dutta and Mutuswami work with a variation of strong stability that is not quite a strengthening

While the details of the proof of Proposition 6.6.2 are involved, we can see some of the intuition by seeing how it would work in Example **??**. Here, we set transfers so that if player 2 is involved in a single link network, then he or she pays the other player at least 1.5. Under such transfers, the two link network with player 2 in the middle is pairwise stable, as he or she no longer gets a higher utility from severing one of the links.

Next, note that if we weaken efficiency to Pareto efficiency, Proposition 6.6.1 no longer holds. This takes a bit of proof to show generally, as one needs to work with specific transfers and then to find an algorithm to identify pairwise stable networks that are Pareto efficient. That method is described in Exercise 6.14. It is easy to see why this is true in the network in Figure **??** above, as without any transfers the single link networks are pairwise stable and Pareto efficient. Although this is of some interest, when admitting transfers Pareto efficiency is arguably not the right notion of efficiency. Instead, an efficiency notion that considers the admitted transfers is more appropriate, and then the result of Proposition 6.6.1 extends as there is an incompatibility of stability and efficiency allowing for component-balanced transfers that satisfy equal treatment of equals (as outlined in Exercise 6.8).

So, reconciling the tension between stability and efficiency requires giving something up in terms of our desired conditions of equal treatment of equals, component balance, and (constrained) efficiency; and this tension is characteristic of many network games.

There are many related questions associated with this tension that we address in the coming chapters. For instance, which settings (in terms of the structure of costs and benefits) naturally lead efficient networks to be stable? In which settings can transfers help reconcile efficiency and stability? How efficient or ineffectient are the networks that form if players bargain over payoffs during the network formation process?

6.7 Exercises

EXERCISE **6.1** *Efficiency versus Pareto Efficiency*

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of pairwise stability, as it only considers one network to defeat another if there is a deviation by a coalition that makes all of its members strictly better off; while pairwise stability allows one of the two players adding a link to be indifferent. However, one can check that the construction of Dutta and Mutuswami extends to pairwise stability as well.

Provide an example of a society of three individuals and corresponding utility functions such that there are several Pareto efficient networks and yet only a single efficient network.

EXERCISE **6.2** *Pairwise Stability in the Distance-Based Utility Model.*

Prove Proposition 6.3.2.

EXERCISE **6.3** *Diameters in Large Pairwise Stable Networks in the Connections Model**

Consider the symmetric connections model when $c > \delta$. Show that as n grows, the diameter of any nontrivial pairwise stable network is bounded above.

Show that the same is true in the distance-based utility model for any specification of $c > b(1) > b(2) > b(3) > \cdots > b(k) > b(k+1) > \cdots$, provided that these are fixed and independent of n.

EXERCISE **6.4** *An Asymmetric Connections Model*

Consider an asymmetric version of the connections model, where players all have a common δ parameter where $0 < \delta < 1$ and the only asymmetry is that individuals might have different costs per link. In particular, suppose that each individual's cost for a link is the same for all links, so that individual i has a cost c_i for each link that i is involved with; but where it is possible that these costs differ across players.

Provide an example where the unique efficient network is not a star network, nor a complete network, nor the empty network.

Show that every efficient network has a subnetwork that is a star network (possibly only involving a subset of the players) and such that the center player in that star has a minimal cost (that is $c_i \leq c_j$ for all j).

Show that if individuals have different δ_i's, then it is possible to have an efficient network that is not empty and does not have a star network as a subnetwork.

EXERCISE **6.5** *Growing Strategic Networks*

Consider the network growth process in the distance-based utility model described in Section 6.3.2 when $n = 4$. Suppose that $b(1) - b(2) < c < b(1)$. Find the probability that an efficient network forms.

EXERCISE **6.6** *Pareto Inefficiency in the Co-Author Model.*

Show that if $n \geq 4$ is even, then any pairwise stable network in the co-author model of Section 6.4 is not only inefficient but is, in fact, Pareto dominated by some efficient network. (Hint: show that any player in any component of a pairwise stable network (including being alone) that does not involve exactly two players, receives a lower payoff than he or she would in any efficient network.)

EXERCISE **6.7** *Constrained Efficiency.*

The following notion of efficiency (from Jackson [329]) falls between efficiency and Pareto efficiency.

A network g is *constrained efficient* relative to a profile of component-based utility functions u if there does not exist any $g' \in G(N)$ and a component balanced t satisfying equal treatment of equals relative to u such that $u_i(g') + t_i(g') \geq u_i(g) + t_i(g)$ for all i with strict inequality for some i.

- Show that for any profile of component-based utility functions u, the set of efficient networks is a subset of the constrained efficient networks.

- Let $n = 5$ and consider a component based utility where all individuals are interchangeable such that the complete network generates utility of 2 per player, a component consisting of pair of individuals with one link gives each of the pair a payoff of 1, and a completely connected component among three individuals gives each player in the component a payoff of 3. All other networks generate utility of 0.

  Identify the efficient networks, and show that the completely connected network is constrained efficient but not efficient.

- Let $n = 3$. Consider a profile of utility functions u such that the complete network has a payoff of 3 for each player, any network with two links leads to a payoff of 4 to the center player and 2 to each of the other players, and all other networks lead to payoffs of 0 to all players.

  Find a Pareto efficient network relative to this u and that is not constrained efficient.

EXERCISE **6.8** *Constrained Efficiency*

Show that Proposition 6.6.1 holds when efficiency is replace by constrained efficiency.

EXERCISE **6.9** *Side Payments and the Incompatibility of Efficiency and Stability*

Consider a stronger definition of stability than pairwise stability due to Jackson and Wolinsky [343].

A network g' *defeats* a network g *allowing for side payments* if either

- $g' = g - ij$ and $u_i(g) < u_i(g')$ or $u_j(g) < u_j(g')$, or
- $g' = g + ij$ and $u_i(g') + u_j(g') > u_i(g) + u_j(g)$.

The network g is *stable relative to side payments* if it is not defeated by another network allowing for side payments.

Show that Proposition 6.6.1 holds with stability relative to side payments replacing pairwise stability, and without need for the equal treatments of equals condition.

EXERCISE **6.10** *Efficient Networks in the Islands Model*

Jackson and Rogers [335] provide the following partial characterization of efficient networks in the islands model:

Let $c < \delta - \delta^2$. In any efficient network, each island is internally completely connected and inter-island links are as follows.

1. If $C < \delta - \delta^2$ then the unique efficient network is the completely connected network.
2. If $\delta - \delta^2 < C < \delta - \delta^3$ and $K = 2$, then the efficient networks are those such that there are exactly J links between the two islands, and on at least one island each player is involved in exactly one of the J links.
3. If $\delta - \delta^3 + 2(J - L - 1)(\delta^2 - \delta^3) < C < \delta - \delta^3 + 2(J - L)(\delta^2 - \delta^3)$ and $K = 2$, then the efficient networks are those such that there are exactly $1 \leq L < J$ links between the two islands and no player is involved in more than one of these links.
4. If $\delta - \delta^3 + 2(J - 2)(\delta^2 - \delta^3) < C$ and $K = 2$, then the efficient networks have at most one link between the two islands.

Provide proof for these claims. Show also that when K is very large and $C < \delta - \delta^3$, completely connecting all players within each island, and then connecting every player on every island other than island 1 directly to the same player on island 1 can be more efficient than having intra-island links that don't all pass through the same island.

Hint for the proof of the proposition: Suppose there are just two islands and call the number of links between them L. Use the fact that

$$V(x_1, x_2, L) = 2L\delta + 2\left[Jx_1 + Jx_2 - x_1x_2\right]\left(\delta^2 - \delta^3\right) - 2L\delta^2 + 2J^2\delta^3,$$

is the utility obtained by the members of island 1 from connections to island 2 plus the reverse, where $x_i \leq L$ is the number of players on island i having links to the other island.

EXERCISE **6.11** *Inefficiency of Pairwise Stable Networks in the Islands model.*

Consider the islands model when $c < \delta - \delta^2$ and show an example with at least three islands and three players per island, such that all pairwise stable networks are nonempty and distinct from all efficient networks.

EXERCISE **6.12** *Diameter in the Islands Model.*

Consider the islands model when $\delta - \delta^2 < c < \delta$ and $C < \delta + (J-1)\delta^D$. Show that the diameter of all pairwise stable networks is no greater than $2D$.

EXERCISE **6.13** *The Spatial Connections Model*

A version of the connections model is studied by Johnson and Gilles [349] introduces geography to costs. Let there be more than three players.

The benefits take the same form as in the symmetric connection model, but there is a geography to player locations and the cost of forming a link between players i and j, c_{ij}, is related to physical distance. Let players be spaced equally on a line and i's location be at the point i, and have c_{ij} be proportional to $|i - j|$.

Provide an example where all efficient networks are nonempty, incomplete, and not stars.

Provide an example where all pairwise stable networks are ineffcient.

EXERCISE **6.14** *Pairwise Stable and Pareto Efficient Networks*

There are component balanced transfer rules, satisfying equal treatment of equals relative to utility functions that are component-based, relative to which there always exists at least one pairwise stable network that is Pareto Efficient.[19]

[19] This is a variation of a result due to Banerjee [36], based on an algorithm that is adapted to work for pairwise stability by Jackson **??**.

Given a profile of component-based utility functions u and a set of nodes $S \subset N$, let

$$g(u, S) = \text{argmax}_{g \in G(S)} \frac{\sum_{i \in S} u_i(g)}{\#N(g)}$$

denote the network with the highest per capita value to those who have links in the network out of those that can be formed by any subset of players in S. Given a component-based utility function u, find a network g^u through the following algorithm. Pick some $h_1 \in g(u, N)$ with a maximal number of links. Next, pick some $h_2 \in g(u, N \setminus N(h_1))$ with a maximal number of links. Iteratively, at stage k pick a new component $h_k \in g(u, N \setminus N(\cup_{i \leq k-1} h_i))$ with a maximal number of links. Once there are only empty networks left stop. The union of the components picked in this way defines a network g^u.

Consider component-balanced transfers such that if i and j are in the same component of g, then $u_i(g) + t_i(g) = u_j(g) + t_j(g)$.

Show that such transfers satisfy equal treatment of equals.

Show that if u is component-based, then g^u is pairwise stable and Pareto efficient (relative to the payoffs including transfers).

Show that if the algorithm above does not have the quantifier "with a maximal number of links", then the resulting g^u can fail to be pairwise stable.

Chapter 7

Diffusion through Networks

Consider the following fundamental scenario where networks play a central role. There is a society of individuals whose relationships are described by a network, indicating who has contact with whom on a regular basis. This might be a network of email, friendships, acquaintances, or even things like sexual relationships or some sort of blood to blood contacts. To keep things simple at this point, let us presume that individuals are either linked or not, so that we abstract away from the fact that some relationships might involve greater or more frequent interaction than others. Now, consider the introduction of a disease. Individuals can catch the virus if they interact with one of their neighbors who is infected with the disease. This happens somewhat randomly, as the chance of interaction might be random and it might also take specific conditions for the disease to be transmitted. Let us also suppose that the chance of a given healthy individual becoming infected increases with the number of neighbors who are infected. Under what conditions will an initial outbreak spread to a nontrivial portion of the population? What percent of the population will eventually become infected? How does this depend on the network of contacts in the society? How does it depend on the contagion probabilities and recovery rates? What if a number of individuals are immune to the disease, or require different frequencies of interaction to be infected? How would immunizing the population affect the spread of the disease?

This is a problem of obvious importance. Beyond the direct application to disease transmission, we can also see that this is closely related to the diffusion through a network of information, opinions, product purchasing, fashions, participation in programs, and various other behaviors.[1] For example, network structure is central to "viral mar-

[1] See Rogers [536] and Strang and Soule [581] for overviews of some of the literature on diffusion and its many applications.

keting" (e.g., see Leskovec, Adamic, and Huberman [408]) as well as "word of mouth marketing" (e.g., see Silverman [559]).[2] Moreover, it is clear that the network structure can be very important in determining the outcome. If there are relatively few contacts between individuals, then the disease might never spread. If some pockets of the society are isolated from others, they might remain relatively uninfected (or uninformed, depending on the application). It can also be that networks where there are some very highly connected individuals end up with different patterns of infection than networks where all individuals have roughly the same degree.

In this chapter I discuss a number of different models of such diffusion processes. The chapter begins with a basic model of disease transmission, and then moves on to some variations on it. Beyond these issues of diffusion, there are also related questions of navigation on networks. That is, individuals are searching through the network to find specific nodes. How difficult is it for an individual to find a specific web page by following links in on the web? How can we understand the ease (in terms of small number of hops) with which subjects in Milgram's [444] "small-world" experiments were able to send something to someone whom they did not know? Finally, there are issues of how fragile networks are to interruption. If we delete some set of nodes, does diffusion or navigation change dramatically? How does this depend on which nodes are removed? The topics of this chapter dovetail with the learning and games on networks that are discussed in the next two chapters, and we will see related themes and tools emerging.

An outline of the chapter is as follows. First, I discuss the Bass model, which is a parsimonious and widely used model of diffusion that incorporates some ideas of imitation but without explicit network structure. Next, I turn to models of diffusion that explicitly incorporate social structure, and discuss results on component size in random networks, and how that relates to the potential size of a diffusion in a society. Next, the chapter turns to standard models from the epidemiology literature, where

[2] In word of mouth marketing, referrals, and direct conversations, and recommendations between consumers are used to spread information about a product (e.g., providing initial access to select individuals and then allowing them to communicate with others, as in the way that the email service "Gmail" was marketed). Part of this builds on the idea of the high weight that people might place on a friend's recommendation for a product. Viral marketing is a more general concept that includes word of mouth as a special case, but also includes other uses of interactions between consumers. For example, the email service "hotmail" was initially marketed by including information about its availability in outgoing emails of hotmail users. This was not voluntary word of mouth of the users, but still took advantage of the social structure for the spreading of information.

contagion across nodes is random and the probability of becoming infected depends on the number of neighbors that a node has and the state of those neighbors. The analysis depends on the extent to which nodes can "recover" from an infection and whether they can become infected again, and the ease with which the disease or information is transmitted from one neighbor to another. The chapter then turns to a related but distinct question of navigation of a network, or following paths in a network to find specific nodes; it examines how this depends on the structure of the network and how much knowledge about the network and the node are used in navigation. The chapter also includes a look at how robust diffusion and navigation results are to the removal of nodes.

7.1 Background: The Bass Model

An early model of diffusions (that is still a workhorse) is the Bass [**?**] model. The model is lean and tractable and incorporates social aspects into its structure. Although it does not have any explicit social network structure, it still incorporates imitation. The model is built on two key parameters: one captures the rate at which agents innovate or spontaneously adopt, and the other captures the rate at which they imitate other agents or adopt because others have.[3] One can also interpret the innovation as a response to outside stimuli, like media or advertising, while the imitation aspect captures social and peer effects.

Consider discrete time periods t and let $F(t)$ be the fraction of agents in a society who have adopted a new product or behavior by time t. The Bass model is then described by a difference equation which takes the form

$$F(t) = F(t-1) + p\,(1 - F(t-1)) + q\,(1 - F(t-1))\,F(t-1),$$

where p is a rate of innovation and q is a rate of imitation. The expression $p\,(1 - F(t-1))$ is the rate of innovation times the fraction of people who have not yet adopted. The expression $q\,(1 - F(t-1))\,F(t-1)$ captures the imitation process where the rate of imitation is multiplied by two factors. The first factor, $(m - F(t-1))$, is again the fraction of people who have not yet adopted, and the second expression $F(t-1)$ is the fraction of agents who have adopted and can therefore be imitated. A continuous time

[3] The version here omits a third parameter m which simply represents the portion of the population which could potentially be adopters. Here it is as if $m = 1$.

Figure 7.1. An S-Shaped Diffusion/Adoption Curve.

version of this is described by

$$\frac{dF(t)}{dt} = (p + qF(t))\,(1 - F(t))\,. \tag{7.1}$$

Solving this when $p > 0$ and with a condition that $F(0) = 0$, leads to an expression of

$$F(t) = \frac{1 - e^{-(p+q)t}}{1 + \frac{q}{p}e^{-(p+q)t}}. \tag{7.2}$$

As the parameters p and q are varied, the Bass model can fit a wide variety of diffusion curves, and as such has been used in both forecasting diffusion and in empirical analyses of diffusion, where one can estimate q and p from fitting the model to data. There are also a number of extensions of the model to include things such as pricing and advertising.[4] Note that the levels of p and q simply multiply time, and the ratio of q to p is the critical parameter that determines the overall shape of the curve. Thus, up to rescalings of time, the curves can be thought of as generated by a single parameter which captures the relative ratio of imitators to innovators.

Part of the insight that emerges from the Bass model is the process behind some widely observed patterns in diffusion studies. Since one of the first studies of diffusion by Tarde [584], who emphasized the importance of imitation in diffusion, many studies have found diffusion curves that are S-shaped. Perhaps the best known such studies where those of Ryan and Gross [544] and Griliches [295], which documented S-shaped diffusion curves in the adoption of hybrid corn seeds among Iowa farmers. Figure 7.1 provides an example of an S-shaped adoption curve, where diffusion begins slowly, then accelerates, and then eventually slows down and asymptotes.

To see how the Bass model works, and why it can exhibit the S-shape, note that initially there no agents in the population to imitate. Thus, the first adopters are almost entirely those who adopt from their own spontaneous "innovation." In equation (7.1), when $F(t)$ is close to zero the equation is approximated by p. As the process progresses, there are more agents around to be imitated and this leads to an increase in the rate of diffusion since now agents adopt through imitation as well as innovation. There is a balance that occurs as the process progresses, since there are more agents around

[4] Examples of recent models of diffusion, which push in various directions beyond that Bass model, are Leskovec, Adamic, and Huberman [408] and Young [632].

to imitate, but fewer around to do the imitating. Eventually, the process has to slow down simply because there are no longer agents left around who might innovate or imitate.

There are many features which are stationary in the original Bass model which can be enriched. For example, when it comes to spontaneous innovation it is not clear that the rate p should be constant over time. As Rogers [**?**] describes, the earliest adopters can often be very different in their characteristics from others who later adopt (even without imitation). One can enrich the model to incorporate things like heterogeneous costs of adoption among the population, as well as different sorts of imitation principles. For example, is it raw numbers of neighbors who have adopted that influence an agent to adopt or fractions of neighbors? I will discuss some such variations of models in what follows and also in Chapter **??**. For now, let us move to examining settings where social structure is modeled more explicitly.

7.2 Spread of Information and Disease

The component structure of a network naturally partitions a society into separate groups who do not interact or communicate with each other. While different components might be subjected to the same outside stimuli, it will take some such external consideration to foster diffusion across components of a network. As such, in many instances, the component structure serves as a natural first limit on the extent of diffusion or contagion when we examine diffusion through a social network. The component structure is also important to understand with respect to navigation, as if one can only follow paths in the network, then components are again natural barriers.

7.2.1 Percolation, Component Size, Immunity, and Diffusion

The general problems of contagion, spreading of information, and navigation through a society all involve determining when there exist paths that connect different nodes of a network, and properties of those paths, including the components that they generate. The variations on the problem incorporate nodes that might be immune to infection or averse to listening to or passing information along, and situations where different links only transmit or function probabilistically. This might reflect the fact that individuals only interact sporadically, or that special conditions need to be met in order for transmission to take place. For many applications, models that provide insight into

diffusion and navigation have to be rich enough to capture such variations.

This also leads to a point of overlap with what is known in the physics and math literatures as "percolation theory."[5] A canonical scenario from percolation theory is one where there is some substance, which is porous, and a central question is whether a liquid on one side of the substance will make it through to the other side. One might think of the substance as having holes or pores in it, and these possibly being connected to each other. The holes or pores can naturally be modeled as nodes with links between each other, and thus as a network or in many cases even as a lattice. The question of percolation is then equivalent to whether there exists a path from one side of the network to the other. The analysis of diffusion and navigation on networks has thus drawn on tools and insights from percolation theory, and in turn enriched that theory.

To begin, let us revisit the scenario studied in Section 4.3, which examined component size when some members of the population are completely immune. This also corresponds to percolation through a network when some nodes are removed. To recall the setting, there is a society of n individuals. One of them is initially infected with a disease. Members of the society are immune with a probability π. The question of whether the disease can spread to a nontrivial fraction of the population amounts to whether or not the initially infected individual lies in a component containing a nontrivial fraction of the population once the immune individuals are removed from the network. In Section 4.3 we considered Poisson random networks, but the analysis generalizes easily to other degree distributions (within the configuration model).

We can do this as follows. Recall from (4.8) that the threshold for the emergence of a giant component in the configuration model is where[6]

$$\left\langle d^2 \right\rangle_\pi = 2 \left\langle d \right\rangle_\pi . \tag{7.3}$$

Here the subscript π indicates that we are operating on a network where a proportion π of the nodes are removed from the network uniformly at random, and the expectations are then taken with respect to the resulting degree distribution. So, we have an answer for the threshold of percolation in this system, or the point at which a single infected individual has a probability of infecting a number of others that becomes infinite as n grows.

Before analyzing this expression with regards to different values of π and degree distributions, let me point out a different argument for why the threshold is such that

[5] See Stauffer and Aharony [582] or Grimmett [297] for background.

[6] The analysis here works within the assumptions and structure behind (4.8).

$\langle d^2 \rangle_\pi = 2\langle d \rangle_\pi$, as in (7.3). We originally found this threshold via a calculation of neighborhood sizes and examining when the expected extended neighborhood sizes became infinite when n grows, but this can also be explained by a simple (heuristic) argument, due to Cohen et al [151]. Consider starting at a given node and then randomly picking one of its neighbors. For the neighborhoods to keep expanding, it should be that the expected degree of this neighbor is at least two (the connection to the original node, plus a continuation to some other nodes). The expected degree of a neighboring node under the configuration model is simply $E_{\widetilde{P}_\pi}[d]$, where recall that $\widetilde{P}_\pi(d) = P_\pi(d)d/\langle d \rangle_\pi$ is the conditional distribution of a neighbor's links, adjusting for the fact that the neighbor was found via a link in the network. This expectation is then

$$E_{\widetilde{P}_\pi}[d] = \sum_d \frac{P_\pi(d)d^2}{\langle d \rangle_\pi} = \frac{\langle d^2 \rangle_\pi}{\langle d \rangle_\pi}.$$

So, the neighborhoods are expected to expand when $\langle d^2 \rangle_\pi / \langle d \rangle_\pi \geq 2$, and not otherwise.

Thus, if we have appropriate expressions for the distribution P_π and some of its moments, then we can find the threshold where the giant component emerges and determine when there is diffusion despite having some fraction of immune nodes. We can calculate $P_\pi(d)$ as follows. Consider the starting network under P and some node that starts with degree d'. If it turns out not to be immune, then it might lose some of its neighbors when we delete the immune nodes from the network. In particular, the probability that a node starting with degree d' ends up with degree $d \leq d'$ follows a binomial distribution. To see this, note that the probability that some specific set of d of the neighbors turned out not to be immune is $(1-\pi)^d$, the probability that the rest are immune is $\pi^{d'-d}$, and there are $\binom{d'}{d}$ different subsets of d neighbors that we can have be not immune, which leads to a probability of

$$\binom{d'}{d}(1-\pi)^d \pi^{d'-d}.$$

Therefore, the degree distribution after eliminating immune nodes can be written as

$$P_\pi(d) = \sum_{d' \geq d} P(d') \binom{d'}{d} (1-\pi)^d \pi^{d'-d}. \tag{7.4}$$

From this, it follows that[7]

$$\langle d \rangle_\pi = \langle d \rangle (1-\pi) \tag{7.5}$$

[7] To see this note that (7.4) implies that $E_\pi[d^t] = \sum_d \sum_{d' \geq d} d^t P(d') \binom{d'}{d} (1-\pi)^d \pi^{d'-d}$, which is

and

$$\langle d^2 \rangle_\pi = \langle d^2 \rangle (1-\pi)^2 + \langle d \rangle \pi (1-\pi). \tag{7.6}$$

Then, the threshold for a giant component of susceptible nodes to emerge is found by rewriting (7.3) using (7.5) and (7.6) as

$$\langle d^2 \rangle (1-\pi) = \langle d \rangle (2-\pi) \tag{7.7}$$

or

$$\pi = \frac{\langle d^2 \rangle - 2\langle d \rangle}{\langle d^2 \rangle - \langle d \rangle}. \tag{7.8}$$

For example, if we examine a regular network of degree $\overline{d}$, then (7.8) provides a threshold where $\pi = (\overline{d}-2)/(\overline{d}-1)$. Thus, if $\overline{d} = 2$, then the threshold is right where $\pi = 0$. Once the degree is 3, then we find $\pi = 1/2$, so that a giant component will emerge if less than half the population is immune.

If we consider a Poisson random network, then since $\langle d^2 \rangle = \langle d \rangle^2 + \langle d \rangle$, and $\langle d \rangle = (n-1)p$, it follows that the threshold in (7.8) corresponds to the threshold where $\pi = 1 - \frac{1}{(n-1)p}$ or $p(n-1)(1-\pi) = 1$ (as found in Section **??**).

If we move to a case of a scale-free network, then we find very different effects. The interesting aspect is that the threshold for contagion is 0 (for $\gamma < 3$), which was first shown by Cohen et al [151]. To see this, simply note that $\langle d^2 \rangle$ is diverging in n whenever we have a degree distribution where $P(d)$ is proportional to $d^{-\gamma}$ for $\gamma < 3$.[8] Thus, for such scale-free degree distributions, (7.8) leads to a limit of $\pi = 1$, and so effectively all the nodes need to be immune before the giant component of susceptible nodes will disappear. Under such degree distributions there are enough very high degree nodes so that many nodes are connected to high degree nodes and the network ends up with a giant component, even when many nodes are eliminated uniformly at random.

It is important to remember that the analysis here is a limiting one, and so the thresholds are at the limit. When we examine a large but finite network, then there will be a maximal degree in the network, and so then $\langle d^2 \rangle$ is finite even for a scale-free

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equal to

$$\sum_{d'} P(d') \sum_{d \le d'} d^t \binom{d'}{d} (1-\pi)^d \pi^{d'-d}.$$

or $\sum_{d'} P(d') M_\pi(d^t : d')$ where $M_\pi(d^t : d')$ is the expectation of d^t from a binomial distribution with parameter $(1-\pi)$ and upper limit d' draws. The claims follow noting that $M_\pi(d : d') = d'(1-\pi)$ and $M_\pi(d^2 : d') = (d')^2(1-\pi)^2 + (d')\pi(1-\pi)$.

[8] For $\gamma < 1$, the mean is also diverging, but the ratio of $\langle d^2 \rangle$ to $\langle d \rangle$ still diverges, so the condition is still satisfied.

Figure 7.2.1. The Threshold Fraction of Nodes that Need to be Immune in a Scale-Free Network in order to Stop Diffusion among Susceptible Nodes as a function of the Maximal Degree among Nodes in the Network.

distribution, and so the threshold in (7.8) is less than one. We can approximate the threshold via (7.8) and see that it converges to 1, but might differ substantially with small caps on the maximal degree, as pictured in Figure 7.2.1 for three levels of γ.

Beyond a calculation of the threshold for the emergence of a giant component, we can also make use of the equation that characterizes the size of the giant component (above the threshold where it emerges and below the threshold where the network becomes connected) in the configuration model. Recalling (4.9), the fraction of nodes in the giant component q is characterized by

$$1 - q = \sum_d (1-q)^d P_\pi(d), \tag{7.9}$$

where here again $P_\pi(d)$ is the appropriate degree distribution associated with the network where we have deleted the fraction π of immune nodes.

The values of q that solve (7.9) as a function of $1 - \pi$ (recalling the expression for this in (4.13)) are plotted for Poisson random networks for mean degrees of 1.5, 2, 5, 10, and 100, in Figure 7.2.1.

Figure 7.2.1. The Fraction in the Largest Component of the Susceptible Population as a Function of the fraction $1 - \pi$ of the Population that is Susceptible, in a Poisson Network.

What we see from this analysis is that the determination of whether or not a network ends up diffusing an infection (or something else), when there are some immune nodes, depends on the size of the variance in degree relative to the mean degree. Relatively higher variation makes a network more conducive to infection, as it provides enough higher degree nodes to lead to the formation of giant components. In general, even with Poisson random networks, thresholds are fairly low in terms of expected degree (compared to the degree that we typically see in varieties of human interaction), and so diffusion can occur even with high fractions of immune nodes. Of course, the extent of the diffusion will depend on the proportion of immune nodes, and the size of the giant component. As we shall see, the extent to which diffusion occurs will also be tempered by other potential impediments.

7.2.2 Breakdown, Attack and Failure of Networks, and Immunization

Another interpretation of the "immune" nodes that we have been discussing is that these are nodes that have failed and been removed from the system. This is particularly relevant in computer applications, but is also relevant in social settings, including, for example, criminal organizations. If the attacks occur uniformly at random, then the analysis is as discussed above, but there are also many other variations that are of interest, depending on the application. For example, it could be that specific nodes or links are targeted (say high degree nodes, or links that are important bridges or lie on many paths), or that links overload due to excess use; or there is spatial correlation in connection and nodes are targeted geographically.[9]

A flip side to this same viewpoint is one of immunization. Suppose that we begin with a network that has a giant component. In such a setting, an initially infected individual can lead to a widespread infection. How many individuals need to be immunized in order to avoid an epidemic spread? How does this depend on whether individuals in the population are immunized at random, or whether "high-risk" (e.g., high degree) nodes are immunized.

To see how the issue of targeting can change the analysis, let us consider a situation where some percentage of the nodes are removed, except that instead of removing nodes

[9] See Broder et al [101], Albert et al [9], Callaway et al [113], Cohen et al [152], Watts [621], Rozenfeld et al [543], Warren et al [**?**], Moren et al [460], Holme and Kim [317], and Motter and Lai [468].

uniformly at random as in our previous analysis, it is the highest degree nodes that are removed, as in, for instance, Broder et al [101], Albert, Jeong, and Barabási [9], Callaway et al [113] and Cohen et al [152].

We can work from the methods above, but now using the truncated distributions. So, we start with a distribution P. We first truncate the distribution removing a percentage π of the highest degree nodes. The resulting distribution of the degrees of the remaining nodes is denoted $P_{\pi,H}$, where H reminds us that the highest degree nodes were eliminated. To develop an expression for the resulting degree distribution $P_{\pi,H}$, it helps to break things into two parts. First, eliminating the highest degree nodes truncates the original distribution P. Second, it also eliminates some of the neighbors of the remaining nodes, thus lowering their degrees. We have to be careful in this second calculation, since the number of links eliminated here is not simply proportional to π (as it was with uniformly random elimination of nodes), but now is much higher as we are eliminating the nodes with the most links.

Consider a case where π is chosen to cut the distribution nicely right at some degree $\overline{d}$, so that all nodes with degree higher than $\overline{d}$ are removed, and nodes with initial degree of $\overline{d}$ and lower remain. So, $\overline{d}(\pi)$ is such that

$$\sum_{d=1}^{\overline{d}(\pi)} P(d) = 1 - \pi.$$

Thus, we end up with a new degree distribution of the remaining nodes, not yet accounting for lost neighbors, which is simply $\frac{P(d)}{1-\pi}$ for degrees up to $\overline{d}(\pi)$ and 0 above that. Next, although we have only removed a fraction π of the nodes, we have removed a much larger fraction of the links, namely

$$f(\pi) = \frac{\sum_{d=\overline{d}(\pi)+1}^{\infty} P(d)d}{\langle d \rangle}.$$

Under the configuration model, a degree d' node then loses each neighbor approximately independently with probability $f(\pi)$. So, we are left with a new degree distribution of the form:

$$P_{\pi,H}(d) = \sum_{d'=d}^{\overline{d}(\pi)} \frac{P(d')}{1-\pi} \binom{d'}{d} (1 - f(\pi))^d f(\pi)^{d'-d}. \tag{7.10}$$

Then, by the same reasoning that established (7.8), it follows that the threshold for there to exist a giant component of the remaining nodes is such that

$$\langle d^2 | d \leq \overline{d}(\pi) \rangle (1 - f(\pi)) = \langle d | d \leq \overline{d}(\pi) \rangle (2 - f(\pi)), \tag{7.11}$$

where $\langle \cdot | d \leq \overline{d}(\pi) \rangle$ indicates that expectations are with respect to the orignial distribution but truncated at $\overline{d}(\pi)$.

To see the effect of this most starkly, let us examine the case of a scale-free distribution where $P(d)$ is proportional to $d^{-\gamma}$ for $d \geq 1$. When $\gamma < 3$, then if the maximal degree is high enough we are past the threshold for a giant component in the case where some fraction of nodes $1 > \pi > 0$ are removed uniformly at random, as we saw in Section **??**. To see how things work when it is the highest degree nodes that are removed, let us work with a continuous approximation of P with density $(\gamma - 1)d^{-\gamma}$, which makes the calculations easy. Straightforward calculations[10] imply a threshold equation of

$$(\gamma - 2)\left(1 - \pi^{(\gamma-3)/(\gamma-1)}\right) = (\gamma - 3)\left(2 - \pi^{(\gamma-2)/(\gamma-1)}\right). \tag{7.12}$$

For example, if we set $\gamma = 2.5$ then (7.12) reduces to $\pi^{1/3} + \pi^{-1/3} = 3$, which is satisfied when $\pi = .056$.[11] This quite a dramatic difference, as then such a scale-free network has diffusion that is robust to elimination of a very large fraction of nodes if they are deleted uniformly at random, but not robust to deletion of even a small fraction of nodes if the highest degree nodes are targeted. To get some better feeling for this, note that eliminating only five percent of the nodes when $\gamma = 2.5$ eliminates all the nodes with degree four or higher! Moreover, this eliminates roughly a third of the links in the network. Thus the remaining nodes that only have initial degree 3 or less, end up losing a nontrivial portion of their links, and so the network that remains can fail to have a giant component. In fact, most of the nodes end up with degree 1 or 0.

Note that this feature of networks has powerful implications for immunization programs. Programs that are aimed at immunizing individuals with the highest connectivity can be much more effective at avoiding an epidemic than a program that immunizes the same number of individuals uniformly at random in a population.

7.2.3 The SIR and SIS Models of Diffusion

One of the canonical models of the spread of disease through a network is what is now known as the "SIS" model, which stands for "susceptible, infected, susceptible"[12] The

[10] Note that $\int_1^x (\gamma - 1)d^{-\gamma} \mathrm{d}d = 1 - x^{-\gamma+1}$. It follows that $\overline{d}(\pi) = \pi^{1/(1-\gamma)}$, $f(\pi) = \pi^{(\gamma-2)/(\gamma-1)}$, $\langle d^2 | d \leq \overline{d}(\pi) \rangle = \frac{(\gamma-1)(1-\overline{d}(\pi)^{-\gamma+3})}{(\gamma-3)(1-\pi)}$, and $\langle d | d \leq \overline{d}(\pi) \rangle = \frac{(\gamma-1)(1-\overline{d}(\pi)^{-\gamma+2})}{(\gamma-2)(1-\pi)}$.

[11] The approximation by a continuous distribution distorts things a bit since it underweights lowest degree nodes, but gives the right order of magnitude. With a discrete distribution, the calculations come out even lower at three percent of the nodes.

[12] See Bailey [25].

idea is that a node can be in either one of two states: either it is infected infected, or else it is not infected but is susceptible to becoming infected. This is a variation on the seminal model in the literature, the "SIR" ("susceptible, infected, removed") model, which dates to Kermack and McKendrick [**?**]. In that model, once infected, a node does not recover, but eventually either dies or becomes completely immune to further infection or transmission (as with the chicken pox). In contrast, in the SIS model a node can recover from being infected, but can then become infected again at a later time (as with certain variations of the common cold).

These models were originally studied within the context of large populations where any individual could randomly meet any other, with equal probability. It was clear from an early date that the structure of interactions could make a big difference, and this was discussed by Rapoport [**?**, **?**]. The modeling has evolved and models that provided for richer interaction structures were studied by Anderson and May [15] and Sattenspiel and Simon [548], and network structure was more explicitly brought into play by Kretschmar and Morris [395] and Pastor-Satorras and Vespignani [504],[505], [506].[13]

7.2.4 The SIR Model

In the SIR model, the diffusion takes place between infected nodes and susceptible nodes. Once a node reaches the "removed" state, it has either recovered and is no longer susceptible or contagious, or it has died. The question of when a small initial infection will end up reaching a nontrivial fraction of nodes is similar to the analysis of diffusion with immune nodes in Section 7.2.1. To see the precise connections, let us examine this in more detail.

Consider the following scenario. Individuals are connected through a network that is generated under the configuration model and is described by the degree distribution $P(d)$. Suppose that the infection process is such that the probability that an infected node will infect a susceptible neighbor before the infected node is removed can be described by a probability of transmission, t. Let the infection operate in an independent fashion across links between susceptible and infected nodes. This maps into what is known as "bond percolation" in percolation theory, where bonds are the equivalent of social links. The independence assumption is clearly violated in many applications. To see the difficulty with independence, consider the following scenario in line with the

[13] See Morris [463] for a survey of the early literature on the subject.

SIR interpretation. An infected node infects a neighbor with a random (say Poisson arrival) time with some intensity ν. The infected node reaches the "R" state also at a random time with some other intensity γ. The probability t that the node infects a given neighbor before recovering is then $t = 1 - e^{-\beta/\gamma}$.[14] This probability is the same for each neighbor. However, it is not independent across neighbors. For example, suppose that the network is a star and the center is initially infected. If it takes a long time for the center to reach the "recover/removed" state, then it might infect many neighbors. If it happens to recover quickly, then it might not infect many neighbors. This introduces correlation in the outcomes of the center's neighbors. Conditional on one neighbor being infected, it is more likely that the others will also be infected, as conditional on a neighbor being infected it is more likely that the center was around for a longer time than what we expect unconditionally. Despite the difficulty with the independence assumption, it still seems to match up well with what happens under simulations of the actual process with random recovery and infection as reported by Newman [479] (see his Figure 1), at least for large numbers of nodes.

One way to view this process is to start with some network, and then pick some node uniformly at random to be our initially infected node. To see the reach of the infection, we can then (in an independent and identical manner) remove links along paths emanating from that node with a probability $1-t$. We then examine the resulting component size. Now, the analysis becomes analogous to that we have already examined. In particular, we generate a degree distribution which represents the remaining network after the links are removed, as follows:

$$P_t(d) = \sum_{d' \geq d} P(d') \binom{d'}{d} t^d (1-t)^{d'-d}. \tag{7.13}$$

This is exactly analogous to (7.4) except with t in place of $(1 - \pi)$.

We then end up with analogous conclusions concerning the treshold for diffusion of the infection to a nontrivial segment of the population, for the expected size of the component of infected (and eventually removed) nodes, and so forth.

[14] As Newman [479] points out, this can be extended to much richer ways of generating t, where β and or γ could also be random variables, as long as the ex-ante expectation of t is the same across links.

7.2.5 The SIS Model

In the SIS model, nodes can become infected and then recover in such a way that they become susceptible again, rather than "removed". This applies to certain diseases, but also is useful as a first approximation of models of behavior where individuals are more likely to undertake a given action as more of their neighbors undertake it, but then can also randomly stop taking the action, with the possibility of taking it up again. This applies to different settings than the SIR model, and so is analyzed a bit differently.

Let us start with the following variation on a matching model, which is really a hybrid between a random matching model and a network. Rather than having every member of the population meet any other with an equal probability in a period, individuals are described by their degree. An individual of degree d_i will have d_i interactions with other individuals from the population in a given period, where probabilities of interaction are governed by the relative probabilities, which are described as. Let P be the degree distribution in the population. The probability that a given meeting of individual i is with an individual who has degree d is (similarly to what we saw in (4.2)) governed by

$$\frac{P(d)d}{\langle d \rangle}. \tag{7.14}$$

Again, this means that an agent is more likely to meet someone who has more meetings - so the probability of meeting someone is proportional to how many meetings she or he has. This is not the same as a fixed network. Individuals interact randomly, but there are differences across individuals in terms of how many meetings they have. This is often thought of as an "approximation" to a large network, but that interpretation is a bit of a stretch. It really is a degree-based random meeting model, and the extent to which a large network would have similar properties is not fully understood. This is also a limiting expression, as if we fix some finite set of agents, then the degrees are no longer independently distributed. So, to be careful, let us consider an infinite number of agents in the matching process, and let $P(d)$ be the measure of agents who have degree d.[15]

[15] This can be done with either a countable set of agents, or agents indexed by a continuum. The latter makes it easier to describe the matching process (here described for a single matching, but this can be extended to multiple matchings and, in the limit, continuous time). If we take the interval $[0, 1]$ to be the interval of agents' labels, and then have subintervals of length $P(d)$ be those with each degree d. We just need to keep track of which subsets of agents in each subinterval are infected at each point, and then who is matched with whom in a given period, so that each agent faces the same distribution of types in each meeting. This can be done in many ways, but one does have to

Keeping track of individuals' degrees is important because individuals with different degrees will tend to have different infection rates. In many cases, individuals who have higher degrees will have more interaction and thus be more prone to infection. How infection rates vary across degrees depends on the details of how transmission works. Suppose that the fraction of individuals of degree d who are infected is currently $\rho(d)$. The chance that a given interaction is with an infected individual, denoted θ, can be calculated using (7.14) as

$$\theta = \frac{\sum P(d)\rho(d)d}{\langle d \rangle}. \tag{7.15}$$

Thus, θ is the probability that a given meeting will be with an infected individual. Note that this is different from the average infection rate in the population, μ, which is simply

$$\rho = \sum P(d)\rho(d). \tag{7.16}$$

The difference is that θ is weighted by degrees and represents the chance that a given meeting will be with an infected individual, which is important in calculating how infection spreads, while ρ keeps track of the population average, which is important in welfare and policy analyses.

Generally, how likely it is that a susceptible individual becomes infected as a function of θ and the individual's degree can take many different forms. For instance, it might be that she or he becomes infected for sure if she or he meets an infected individual. It might also be that it happens by chance. It might also be that there is some threshold, so that it takes a number of repeated meetings with infected individuals before infection occurs.[16]

Let us consider a simple linear form, which is common in studies of the SIS system (e.g., see Pastor-Satorras and Vespignani [504]), such that the chance that a given susceptible individual who has degree d becomes infected in a given period when faced with a probability θ that any given meeting is with an infected individual is

$$\nu\theta d, \tag{7.17}$$

where $\nu \in (0,1)$ is a parameter describing a rate of transmission of infection in a given period. Taking $\nu d \leq 1$ for the maximal degree ensures that this is a well defined

be careful to do this in a measurable manner so that we can still talk about laws of large numbers in a meaningful way. This takes us beyond the scope of this text, but it is not difficult to do. For details on justifying random matching models with infinite sets of agents, see Aliprantis, Camera and Puzzello [11], as well as the appendix of Currarini, Jackson and Pin [171].

[16] See Lopez-Pintado [416] for discussion of the SIS model with various contagion mechanisms.

probability. Exercise 7.3 shows that this is a good approximation of a case where the probability of becoming infected in any given meeting with an infected individual is ν, and ν is relatively small.

In the SIS model, infected individuals can recover and become susceptible again. Again, there are various ways one can imagine this happening. The standard one is such that any infected individual recovers in a given period with a probability $\delta \in (0, 1)$. Here the recovery is random, is the same across all infected individuals, and does not depend on how long an individual has been infected. This is a tractable first approximation, but clearly many diseases involve non-Markovian windows of time where individuals spread infection. Thus, individuals are either susceptible or infected and alternate between these states depending on the infection rate in the population.

Thresholds and Steady-State Infection Rates

We can now ask a series of questions. First, how high does the infection rate ν have to be relative to the recovery rate δ in order to have the infection reach some nonzero steady state in the population? Second, can we estimate the long-run steady-state proportion of infected nodes? Third, can we relate the answers to these questions to the network structure, or in this case the degree distribution?

Maintaining a nonzero steady state infection rate does depend on working with an infinite set of agents. For a finite set of agents, sooner or later, regardless of the details of the parameters, all individuals will happen to be healthy and then the infection will die out. Thus in a finite system, the only steady state is one where all nodes are healthy, unless one introduces some random external infection probabilities, such as the birth of new strains of flu (see Exercise 7.5).

To estimate steady state let us work with a "mean-field" sort of approximation where $\rho(d)$ is a constant over time. The expected change in $\rho(d)$ over time amounts to the measure of susceptible agents who become infected minus the measure of infected agents who recover to become susceptible again, and thus a mean-field approximation to steady state requires that these balance so that

$$0 = (1 - \rho(d))\nu\theta d - \rho(d)\delta. \tag{7.18}$$

The expression $(1 - \rho(d))\nu\theta d$ represents the faction of nodes of degree d that were susceptible and become infected, and $\rho(d)\delta$ represents the fraction of infected nodes that recover to become susceptible again. Letting $\lambda = \nu/\delta$, it follows that

$$\rho(d) = \frac{\lambda\theta d}{\lambda\theta d + 1}. \tag{7.19}$$

Equations (7.15) and (7.19) can then be combined to obtain the following steady-state characterization:

$$\theta = \sum_d \frac{P(d)\lambda\theta d^2}{\langle d\rangle\,(\lambda\theta d + 1)}. \tag{7.20}$$

This will often have more than one solution. There is always a solution of $\theta = 0$. That is, if nobody is infected, then the system stays that way. Note that the system does not have a solution where $\theta = 1$, unless we let λ become infinite (see Exercise 7.6). This reflects the fact that $\delta > 0$ means that individuals are recovering over time, so there are always at least some susceptible individuals in the population. So, when is it that the steady state has a solution where $\theta > 0$? And, how stable is the solution at 0? That is, if we started at a steady state of 0, and infected a small amount of the population would it tend to return to 0 or spread and reach a higher steady state?

Let us first solve this in the simplest case where the degree distribution is regular so that all individual have degree $\langle d\rangle$. In that case, (7.20) becomes

$$\theta = \frac{\langle d\rangle\lambda\theta}{\langle d\rangle\lambda\theta + 1}.$$

In addition to the solution of $\theta = 0$, there is another solution of

$$\theta = 1 - \frac{1}{\lambda\langle d\rangle}, \tag{7.21}$$

which is greater than 0 only if $\langle d\rangle > \frac{1}{\lambda} = \frac{\delta}{\nu}$. This is an intuitive relationship: If the number of meetings is large enough relative to the relative recovery/infection rate, then the infection can be sustained. Otherwise, any infection will die out. Thus, we see a threshold above which a society can maintain an infection and below which it does not.

There is an interesting difference between such a regular network and other networks. For example, if the degree distribution is scale-free, so that a power-law holds, then infection can always be sustained, as shown by Pastor-Satorras and Vespignani [504]. For example, if $P(d) = 2d^{-3}$, [17] then the steady-state equation (7.20) becomes

$$\theta = \sum_{d=1}^{\infty} \frac{2\lambda\theta}{\langle d\rangle\,(d^2\lambda\theta + d)}.$$

Approximating the right hand side by an integral leads and finding a solution where $\theta \neq 0$ leads to

$$1 = \frac{2\lambda}{\langle d\rangle}\log\left(1 + \frac{1}{\lambda\theta}\right),$$

[17] Note that $\sum_{d=1}^{\infty}\frac{2}{d^3}$ is twice Apéry's constant (where Apéry's constant is defined to be $\sum_{d=1}^{\infty}\frac{1}{d^3}$, as discussed in Section **??**). However, below, I use a continuous approximation, and so then $\int_1^{\infty}\frac{2}{d^3}dd = 1$, ensuring that the continuous version is a probability. In this case, $\langle d\rangle = 2$.

Figure 7.2.5. Infection Rate of Randomly Met Indvidual as a Function of the Infection/Recovery Rate

or (noting that $\langle d \rangle = 2$)

$$\theta = \frac{1}{\lambda\left(e^{\frac{1}{\lambda}} - 1\right)}.$$

This expression is always positive, regardless of λ and so there is always a positive steady-state infection rate. It is pictured in Figure 7.2.5.

Non-Zero Steady State Infection Rates

While it is clear from the above, that it will be difficult to solve for the steady-state infection rates without some structure on the degree distribution, there is still much that one can deduce across network structures without explicit functional forms.

For example, let us examine the following approach taken by Lopez-Pintado [416]. We can ask how the system will evolve if we start it with a rate of infection among randomly met individuals at some level θ. The function $H(\theta)$ keeps track of how many people would become infected starting from θ, where

$$H(\theta) = \sum \frac{P(d)d}{\langle d \rangle}\left(\frac{\lambda d\theta}{\lambda d\theta + 1}\right). \tag{7.22}$$

Figure 7.2.5. The Existence of a Positive Steady-State Infection Rate Depends on the Derivative of $H(\theta)$ at 0.

When $H(\theta) > \theta$ then the new infection rate will be higher than the starting infection rate, while if $H(\theta) < \theta$ then the new infection rate will be lower than the starting infection rate. Fixed points of H correspond to steady-state infection levels. Since $H(0) = 0$, 0 is always a fixed point and thus a steady-state, as we noted before. An important observation is that H is increasing and strictly concave in θ. Thus, in order for H to have another fixed point (steady-state) above $\theta = 0$, it must be that the slope of H at $\theta = 0$ is above 1, or else whenever we put in some θ we end up with a lower $H(\theta)$, and thus the infection rate simply declines back to 0. Thus, for another steady-state to exist, it must be that $H'(0) > 1$.[18] This is pictured in Figure 7.2.5.

When $H'(0) > 1$, then the steady state of 0 is unstable. That is, if we start with any tiny infection rate $\varepsilon > 0$, then $H(\varepsilon) > \varepsilon$ and so we end up with a growing infection. Indeed, it will continue to grow until it hits the unique positive point where $H(\theta) = \theta$. Here, the uniqueness comes from the strict concavity of H. So, in situations where $H'(0) > 1$, then there will exist a unique positive steady-state infection rate and the 0

[18]Noting that H is continuous and increasing in θ, $H(0) = 0$, and $H(1) < 1$ (from equation (7.22) as this is the expectation of an expression that is always less than 1), it follows that there will be a fixed point above 0 if and only if $H'(0) > 1$.

steady-state will be unstable, while otherwise 0 will be the only steady-state infection rate.

So, examining $H'(0)$ indicates whether an infection can be sustained in steady-state. Note that

$$H'(\theta) = \sum \frac{P(d)d}{\langle d \rangle} \left(\frac{\lambda d}{(\lambda \theta d + 1)^2} \right),$$

and thus

$$H'(0) = \lambda \frac{\langle d^2 \rangle}{\langle d \rangle}. \tag{7.23}$$

So, in order to have a (unique) positive steady-state infection rate $\theta > 0$ (and a corresponding positive average infection rate $\rho > 0$ across the society), it must be that

$$\lambda > \frac{\langle d \rangle}{\langle d^2 \rangle}. \tag{7.24}$$

For a regular network where $\langle d^2 \rangle = \langle d \rangle^2$, the inequality (7.24) corresponds to the threshold $\lambda = 1/\langle d \rangle$ that we found in (**??**). Under a scale-free distribution, $\langle d^2 \rangle$ is divergent (letting maximal degree grow with the size of the population), and so (7.24) is satisfied for any positive λ. A Poisson degree distribution has $\langle d^2 \rangle = \langle d \rangle^2 + \langle d \rangle$ and so a positive infection requires that

$$\lambda > \frac{1}{\langle d \rangle + 1},$$

which falls between the extremes of the regular distribution and the power distribution.

The intuition behind this is that individuals with high degree serve as conduits for infection. Even very low infection rates can lead them to become infected as they have many meetings. Furthermore, they can infect large numbers of others. In a regular network, every individual has the same degree. If that degree is high enough, then infection will occur. A Poisson distribution with the same average has more of a spread in the distribution and some higher degree individuals are present. This leads to a lower threshold at which infection can be sustained, as the higher degree individuals can begin to serve as the conduits discussed above. As the variation in degree is increased further when we move to a scale-free distribution, then there are arbitrarily high degree individuals who are frequently infected, and infections can be sustained at arbitrarily low net rates of contagion.[19]

[19] Just as with the previous models of diffusion, this is a limiting threshold analysis and so for finite societies there will be thresholds which can be examined through simulations.

Comparisons of Infections Across Network Structure

Let us now examine how infection changes as we vary the network structure. There are two different things that we can consider. One is how the threshold for infection varies as we vary the interaction structure. The other is how the extent of infection depends on the interaction structure.

(7.24) says that whether a positive infection rate can be sustained depends on whether or not $\lambda > \frac{\langle d \rangle}{\langle d^2 \rangle}$. From this, it is clear that if the mean $\langle d \rangle$ is held constant and the variance is increased, so that $\langle d^2 \rangle$ increases, then the threshold for infection decreases. This has an intuitive explanation. Again, higher degree nodes serve as conduits for infection. They have many neighbors and so are easily infected, and they also spread infection to many others. As we take such a mean preserving spread, we shift some weight to higher degree nodes and some weight to lower degree nodes. At infection rates near zero, the higher degree nodes are important to getting an infection started, and so such a shift helps lower the threshold for infection.

What happens if we increase the mean of the distribution, while keeping the variance constant? For instance, what happens if we simply shift the distribution by some amount? If we shift the distribution up by some amount a, then we end up with a new threshold of $\frac{\langle d+a \rangle}{\langle (d+a)^2 \rangle}$ which is decreasing in a in cases where $\langle d^2 \rangle \leq 2\langle d \rangle$, but increasing in a (for small a), otherwise. Thus, this always results in a decrease in threshold if a is large enough.

So far, we have examined how the possibility of an infection taking root depends on the interaction structure. Beyond this, it can also be very important to know what the extent of an infection is and how this varies with the interaction structure. Recall from (7.20) that

$$\theta = \sum_d \frac{P(d)\lambda\theta d^2}{\langle d \rangle (\lambda\theta d + 1)}.$$

We saw that this can be solved in some special cases, such as when the network is regular; more generally we will need to resort to some sort of numerical estimation to how infection rates behave. Nonetheless, there is still much that we can deduce about how infection varies when we change the network structure. Jackson and Rogers [336] show that the resulting steady-state infection rates can be ordered whenever the degree distributions that we are comparing are ordered by stochastic dominance. The basic idea behind this is that the right hand side of the above equation is an increasing and convex function of d, and it can be ordered when we compare different degree distributions in the sense of stochastic dominance.

The interesting conclusion regarding steady-state infection rates is that they depend on network structure in ways that are very different at low levels of the infection rate λ compared to high levels. For instance, as we have seen at several points already, scale-free degree distributions lead to positive infection levels for wide varieties of parameters (at least in the limit when the variance of the distribution becomes large), and in this sense might be more easily infected than networks with regular degrees or links that are formed uniformly at random. While this holds with regards to initial thresholds or small infections, the opposite ordering holds when we examine higher rates of infection. Let us examine this in more detail.

Consider two networks with degree distributions P and P', respectively. The following proposition shows that if the distributions are ordered in the sense of strict first order stochastic dominance or mean preserving spreads (and hence second order stochastic dominance, recalling the definitions from Section 4.5.5), then we can order the resulting highest steady-state infection levels.

PROPOSITION **7.2.1** *[Jackson and Rogers [336]] Consider two distributions P' and P, with corresponding highest steady-state average neighbor infection rates $\overline{\theta}'$ and $\overline{\theta}$, and largest steady-state overall average infection rates $\overline{\rho}'$ and $\overline{\rho}$; and suppose that $\overline{\theta} > 0$.*

(I) If P' and $\widetilde{P}'$ strictly first order stochastic dominate P and $\widetilde{P}$, respectively, then the infection rates are higher under P' than P (so $\overline{\theta}' > \overline{\theta}$ and $\overline{\rho}' > \overline{\rho}$).

(II) If P' is a strict mean-preserving spread of P, then the average neighbor infection rate increases $\overline{\theta}' > \overline{\theta}$. Moreover, there exist bounds on the relative infection to recovery rate, $\underline{\lambda} \leq \overline{\lambda}$, such that

- *If the infection to recovery rate is below the lower bound, so that $\frac{\nu}{\delta} < \underline{\lambda}$, then the steady-state average infection rate is higher under P', so $\overline{\rho}' > \overline{\rho}$.*
- *If the infection to recovery rate is above the upper bound, so that $\frac{\nu}{\delta} > \overline{\lambda}$, then the steady-state average infection rate is higher under P', so $\overline{\rho}' < \overline{\rho}$.*

Before providing a proof of Proposition 7.2.1, let us examine the ideas behind it and some of the comparisons needed.

First, to get an impression of stochastic dominance relations, Figure 7.2.5 shows a first order stochastic dominance relation between two networks, a network of co-authorships in economics and a network of romantic relationships in a U.S. high school. The degree distributions pictured in Figure 7.2.5 are the distributions of neighbors'

Figure 7.2.5. The Distributions of a Neighbor's Degree ($\widetilde{P}(d)$) for the Coauthor Network of Goyal, Moraga-Gonzalez and van der Lief [**?**] in Red and the Adolescent Health Romance Network analyzed by Bearman, Moody and Stovel [47] in Green. The Red Distribution First Order Stochastic Dominates the Green Distribution.

Figure 7.2.5. The Average Highest Steady-State Infection in the SIS Model as a Function of the Log of the Infection/Recovery Rate λ for Three Network Structures with Mean Degree 4, from Jackson and Rogers [336].

degrees (of the form $P(d)d/\langle d\rangle$), but the same relationships hold for the degree distributions themselves.[20]

The result that infections increase with first order stochastic dominance spreads is not surprising, as increasing the density of links in a network increases the possibilities for contagion. The more subtle result is in (II), which concerns mean-preserving spreads and is illustrated in Figure 7.2.5, which pictures infection rates for three varieties of networks (holding average degree constant). Here, how the rate of infection depends on network structure depends on how infectious the disease is. An intuition behind this is as follows. The change in infection rate comes from countervailing sources, as a mean-preserving spread leads to relatively more very high degree nodes and very low

[20]It is possible to find examples of pairs of degree distributions that are ordered by stochastic dominance, but where the distributions of neighbors' degrees do not obey the same orderings, or vice versa; but many standard degree distributions display no such reversals. For example, if we consider regular networks, or Poisson random networks, or scale-free networks, and we shift the mean of the distribution we end up with the same relative orderings for both the degree distribution and the distribution of neighbors' degrees.

degree nodes. As discussed above, very high degree nodes have high infection rates and serve as conduits for infection, thus their presence puts upward pressure on average infection. Very low degree nodes have fewer neighbors to become infected by and thus tend to have lower infection rates than other nodes. Thus, the impact of a mean-preserving spread depends on the balance between these effects. When infection rates are already high, infection rates tend to increase less than linearly in the degree of a node (if simply due to the fact that they cannot increase above one), and this limits the impact of high degree nodes and the impact of having low degree nodes around can decrease infection, and so the overall effect of a mean-preserving spread can actually be a decrease in the infection rate. If instead, infection rates are low, then the upward effect dominates as the increase of some nodes' degrees has a snowball effect and leads to further infection.

Proof of Proposition 7.2.1: Let $H_{P'}$ denote the function defined in 7.22 with respect to the degree distribution P'. It follows directly that

$$H_{P'}(1) = \sum \frac{P'(d)\lambda(d^2+x)}{\langle d\rangle_{P'}(1+\lambda(d+x))} < \sum \frac{P'(d)(d^2+x)}{\langle d\rangle_{P'}(d+x)} \leq \sum \frac{P(d)d^2}{\langle d\rangle_{P'}d} = 1.$$

Thus, since $\overline{\theta}'$ is the largest θ such that $\theta = H_{P'}(\theta)$, and $1 > H_{P'}(1)$ from above, it follows that $\theta > H_{P'}(\theta)$ for all $\theta \in (\overline{\theta}', 1]$.

Let us then show that under either (I) or (II), $\overline{\theta}' > \overline{\theta}$. Suppose to the contrary that $\overline{\theta}' \leq \overline{\theta}$. Then it follows from the above that

$$\overline{\theta} > H_{P'}(\overline{\theta}). \tag{7.25}$$

Then, using the expression for $H(\theta)$ from (7.22), and noting that $\lambda d\theta/(1+\lambda d\theta)$ is strictly increasing when $\theta > 0$, it follows from strict first order stochastic dominance of $\widetilde{P}'$ over $\widetilde{P}$ that $H_{P'}(\theta) > H_P(\theta)$ for any $\theta > 0$. A similar argument works for a mean-preserving spread, noting that $\lambda d^2\theta/(1+\lambda d\theta)$ is strictly convex when $\theta > 0$. Thus, since $\overline{\theta} > 0$, it follows from (7.25) that

$$\overline{\theta} \geq H_{P'}(\overline{\theta}) > H_P(\overline{\theta}),$$

contradicting the fact that $\overline{\theta} = H_P(\overline{\theta})$. We conclude that $\overline{\theta}' > \overline{\theta}$ under the conditions of either (I) or (II).

Next, we must show that in case (I) $\overline{\rho}' > \overline{\rho}$. Since $\rho(d) = \frac{\lambda\theta d}{1+\lambda\theta d}$ is a strictly increasing function of θ for any positive d, it follows that $\overline{\rho}'(d) > \overline{\rho}(d)$ for any $d > 0$. This implies that

$$\overline{\rho}' = \sum_d \overline{\rho}'(d)P'(d) > \sum_d \overline{\rho}(d)P'(d). \tag{7.26}$$

Strict first order stochastic dominance and the fact that $\rho(d) = \frac{\lambda\theta d}{1+\lambda\theta d}$ is strictly increasing in d implies that

$$\sum_d \overline{\rho}(d)P'(d) > \sum_d \overline{\rho}(d)P(d) = \overline{\rho}. \tag{7.27}$$

The result follows from (7.26) and (7.27).

Let us now conclude the second part of (II). The expression for the steady-state $\rho(d)$ in (7.19) can be rewritten as

$$\rho(d)\left(\lambda\theta d + 1\right) = \lambda\theta d. \tag{7.28}$$

Taking expectations with respect to $P(d)$ on each side (and noting that $\sum_d P(d)\rho(d)\lambda\theta d = \lambda\theta^2\langle d\rangle$ by (7.15)) leads to

$$\lambda\theta^2\langle d\rangle + \rho = \lambda\theta\langle d\rangle$$

or

$$\rho = \lambda\theta\langle d\rangle(1-\theta). \tag{7.29}$$

Note that (7.29) implies that ρ is increasing in θ when θ is below 1/2; but decreasing when it is above 1/2. As we showed earlier, if P' is a strict mean-preserving spread of P, then $\overline{\theta}' > \overline{\theta}$. In cases where these are both below 1/2 then this implies that the corresponding ρ's are similarly ordered, but in cases where these are both above 1/2 then this implies that the order is reversed. So, to complete the proof we need only to find bounds on λ that ensure both $\overline{\theta}'$ and $\overline{\theta}$ are below, or above, 1/2. Note that for low enough λ, $H(1/2) = \frac{\langle d^2\rangle\lambda/2}{\langle d\rangle(1+\lambda/2)}$ is less than 1/2 and so the highest steady state must be below 1/2, for high enough λ this is reversed. We can thus find bounds on λ below which both $\overline{\theta}$ and $\overline{\theta}'$ are below 1/2, and a corresponding bound on λ above which both $\overline{\theta}$ and $\overline{\theta}'$ are above 1/2. ∎

7.2.6 Remarks on Models of Diffusion

The models of diffusion that we have discussed provide some basic insights about diffusion: mean-preserving spreads in degree distributions (e.g., scale-free networks compared to Poission of the same degree, etc.) lead to lower thresholds for infection in terms of a variety of factors such as infectiousness, the fraction of susceptible nodes, and the probability of transmission along any given link. The full extent of infection can depend on network structure in more complicated ways depending on how infectious a disease is. Similarly, increases in degree density, as in first order stochastic dominance

shifts, also lower thresholds and unambiguously increase overall infection rates. We also see that networks with large or diverging variances can sustain infections at very low thresholds, and so scale-free networks can be more infected "easily" than some other random networks.

While various models of diffusion offer a number of insights, the models that are solved are still relatively particular in terms of the structures that are assumed and the results. There are two obvious shortcomings: first that analyses are for situations where degrees of neighbors are independent or at least approximately so, and second that the analyses generally examine tree-like networks, where there are few small cycles or loops in the network. These are both incompatible with many observed networks. Clearly, the features omitted in these models can have an impact on diffusion. Correlation in degree can change the basic connectivity patterns which can increase or decrease the size of components depending on how it is introduced. Clustering, leads to some redundancy which can change the reach of new paths in a network, and also change infection patterns. In terms of introducing correlations in degrees, the basic approach is not so difficult a variation on what we have already considered. The main difference is in the calculation of a neighbor's degree, which has been calculated using $\widetilde{P}$. In a model with degree correlation, this function would depend also on the degree of the node whose neighbor we are examining. This changes the equations into systems of equations. While this makes simple closed-forms harder to obtain, one can still obtain approximations via simulations. This has been investigated by Newman [479], Moreno, Pastor-Satorras and Vespignani [459], Boguna et al [**?**], and Vázquez and Weigt [**?**]. The role of clustering has been examined by Serrano and Boguna [558] and Newman [481].[21]

Perhaps the most important aspect that is neglected in the analyses above is that the networks often actively react to the process going on. For example, in the case of a serious disease outbreak some individuals react by seeking immunizations and/or avoiding contact with infected individuals. If the diffusion is of valuable information, then individuals might be creating links, or searching through the network, deliberately to find the information. Such adjustments to the network can either speed up or slow down the diffusion, depending on the application. Some of this is hinted at in the next section on navigating networks, but the main issue of how agents and the network adjust to diffusion is still largely open.

[21] See Dorogovstev and Goltsev [192] for more discussion and references, as well as discussion about component calculations in directed networks and growing random networks.

7.3 Search and Navigation on Networks

Diffusion concerns how a disease, information, or behavior moves through a network following the network structure. A related, but quite distinct, issue comes up when we consider someone or something actively navigating through a network. For instance, consider the problem of finding a node that has a certain attribute. In the classic Milgram [444] experiment, subjects were faced with the task of getting a letter to a particular person. More generally, this might be a challenge of trying to find a webpage with particular information on it, or trying to find someone who knows how to perform a given task, or trying to find a file-sharer that has a given file. This can involve following network structure, but here with a specific goal in mind and perhaps taking advantage of some knowledge about the network and/or attributes of the target. There are various approaches that one might try. One could just randomly navigate the network until one bumps into the target node. One could also take advantage of the structure of the network to better search. For instance, going to nodes that have more neighbors might save time if such nodes can also tell you something about their neighbors. Beyond that, one might use information about the nodes themselves to help in cases where nodes tend to be connected to other nodes with similar attributes. How do different search methods perform? How does search depend on the network structure?

Here, we will examine two different approaches to navigating a network. One makes use of the network structure, for instance gravitating towards nodes of higher degree, but focusing on attributes of nodes that are purely network based (degree, centrality, etc.). The other approach makes use of other information about the nodes, such as profession, age, etc., which is not directly relevant in the network structure. However, when there is homophily in the network, then navigation that takes such traits into account can dramatically speed up navigation, as we shall see. This suggests that homophily can provide some social benefits, at least in terms of navigation speed.

7.3.1 Navigating Random Networks

As a benchmark, let us start with the following problem. There is a single target node in a network of n nodes that we need to find. We cannot know whether we have found the desired node until we examine it.

We can derive an upper bound on the expected number of nodes that we need to visit in order to find a given node. That can be found without taking advantage of

the network structure at all. We can simply exhaustively visit the nodes one by one, picking the order uniformly at random. Here we do not use the network in any way, and there is an equal chance that the desired node will be the first node we visit, or the second, ... or the last. The *expected* number of nodes we would have to visit under this method is the expectation of a uniform distribution, where the probability of it taking k nodes is simply $1/n$ and so summing across k we get the expectation of

$$\frac{1}{n} + \frac{2}{n} + \ldots + \frac{n}{n} = \frac{n+1}{2},$$

or roughly half of the nodes. With large numbers of nodes, this could be very time consuming and inefficient.

Next, let us suppose that we use some aspects of the network structure as follows. We begin by randomly picking a node. If it is not the right node, then we randomly pick one of its neighbors, and so forth. This is similar to the process above.[22] However, let us add a feature to the setting that makes search easier. When visiting a node, in addition to being able to discern whether it is the target node, we can also tell whether any of its neighbors are the target node. For instance, if we are looking for a person, we can just ask the person we are visiting whether they know the person we are looking for. Or, if we are crawling the world-wide-web, when we visit a given page its links could be labeled in such a way that we can tell whether any of those links point to our target page. In this case, when none of the neighbors of the node we are currently visiting is our target node, select the next node to be visited uniformly at random from the list of neighbors that we have not yet visited.[23] To get a feel for the improvement, consider a regular network where each node has degree d. On the first step we would find d nodes. On the second step, we would find an additional $d-1$, presuming that the new nodes found do not overlap with previously visited nodes. If overlap were never an issue, it would take us effectively $\frac{n}{d-1}$ steps to visit the whole network, not counting back-tracking if we hit a dead end. The expected number of steps it would

[22] This could even be less efficient. Suppose that we measure time in terms of the number of links that are crossed to date and at some point we end up at a node whose neighbors have all been visited before, and we cannot simply leap back to an earlier point. For instance, if the network is a tree and we start at a root node, and end up going down a branch that does not have the desired node, we could end up spending substantial time back-tracking.

[23] If we have visited all neighbors, then start over by picking an unvisited node from the overall network, with an equal probability on any unvisited node.

take us if there were no overlap is approximated as

$$\sum_{k=1}^{n} \frac{1}{n}\left(\frac{k}{d-1}\right) = \frac{n+1}{2(d-1)}. \tag{7.30}$$

This just represents the $\frac{1}{n}$ chance that our target is the k-th node found, and the fact that it takes approximately $\frac{k}{d-1}$ steps to find k nodes if there is no overlap. To get some feeling for how overlap slows things down, suppose that for the first half of the nodes searched the rate is only $(d-1)/2$ new nodes found at each step, so that half of the nodes are ones already visited. Then for the next quarter of the nodes visited, the rate is $(d-1)/4$ and so forth. So, if the node happens to be in the first half of the nodes searched, then the expected time to find the node is

$$\frac{\frac{n}{2}+1}{2\frac{(d-1)}{2}},$$

or approximately, $\frac{n}{2d-1}$. If the node happens to be in the next quarter of nodes visited, then the expected time is

$$\frac{\frac{n}{2}}{\frac{(d-1)}{2}} + \frac{\frac{n}{4}+1}{2\frac{(d-1)}{4}}$$

or approximately

$$\frac{n}{(d-1)} + \frac{n}{2(d-1)}$$

If we continue in this manner, the expected time conditional on the node being in the next eighth is

$$\frac{2n}{(d-1)} + \frac{n}{2(d-1)},$$

and so forth. The overall expected time to finding the node is then approximately

$$\sum_{k=1}^{\infty} \frac{1}{2^k}\left(\frac{(k-1)n}{(d-1)} + \frac{n}{2(d-1)}\right) = \frac{n}{2(d-1)}\sum_{k=1}^{\infty}\frac{k-\frac{1}{2}}{2^k} = \frac{3n}{2(d-1)}$$

This has tripled the expected time to finding the node. This is not a precise calculation, since it presumes that the fraction of new nodes found at a given step is roughly proportional to the proportion of unmet nodes in network, which might be an over- or under-estimate depending on the architecture of the network. But at least it gives us the idea that while this slows down the process, it changes it by a factor rather than by a power.

Let us then explore how things change if we examine other network structures. If we examine a network with degree distribution P, then as we randomly pick new nodes

the degree of the new node has a distribution described by $\widetilde{P}(d) = \frac{d\ P(d)}{\langle d \rangle}$ (presuming that the degrees of neighboring nodes are independent, as discussed in Section 4.2.1). Then, ignoring overlap, each new node visited through this search process informs us about an expected number of additional nodes given by

$$\sum_d (d-1)\frac{P(d)d}{\langle d \rangle} = \frac{\langle d^2 \rangle}{\langle d \rangle} - 1.$$

Using this expression in place of the $(d-1)$ from the analysis with a regular network, we have that the expected number of steps until we find our target is roughly a factor times

$$\frac{n\langle d \rangle}{\langle d^2 \rangle}. \tag{7.31}$$

For a Poisson random network it follows that

$$\frac{n\langle d \rangle}{\langle d^2 \rangle} = \frac{n}{\langle d \rangle} = \frac{n}{(n-1)p},$$

which is approximately $\frac{1}{p}$, where p is the probability of a link. Thus, a searching through a Poisson network is quite similar to searching through a regular network. Ignoring overlap is a good approximation for many random networks below a threshold where fixed-sized loops become prevalent, but could lead to under-estimation above such thresholds. Providing fully accurate estimates for rich models of networks admitting nontrivial clustering is a difficult problem, and there is little work on that subject.

Next, let us consider a network that has a degree distribution approximated by a power distribution, so that $P(d)$ is $cd^{-\gamma}$ for some scalar c and $3 > \gamma$, but such that the nodes' degrees are independent (so, for example, generated by the configuration model rather than preferential attachment). To calculate $\langle d^2 \rangle$ for such a random network, we have to know the maximal degree in the distribution, denoted $M < n$. Then

$$\langle d^2 \rangle = \sum_{d=1}^{M} cd^2(d^{-\gamma})$$

which is approximately

$$\langle d^2 \rangle = \int_{d=1}^{M} cd^{2-\gamma} dd = \frac{c}{3-\gamma}\left(M^{3-\gamma} - 1\right).$$

A similar calculation leads to

$$\langle d \rangle = \frac{c}{2-\gamma}\left(M^{2-\gamma} - 1\right).$$

Thus, from (7.31) we know that the expected time to finding the desired node in a power distribution truncated at a maximum degree of M is proportional to

$$\frac{n(3-\gamma)}{2-\gamma}\frac{(M^{2-\gamma}-1)}{(M^{3-\gamma}-1)}. \tag{7.32}$$

For large M and $2 < \gamma < 3$ this is proportional to

$$\frac{n}{M^{3-\gamma}}. \tag{7.33}$$

Since a change in the truncation or maximum degree M, can lead to dramatic changes in the calculation of $\langle d^2 \rangle$ and other moments, we find that it can lead to a significant change in the expected time to finding the desired node. There is no right or wrong way to do things here, as each truncation leads to a valid degree distribution that approaches a continuous power-distribution as the number of nodes expands. But many finite distributions that approach continuous power-distributions in the limit have different features. There are a variety of different specifications that have been explored for the maximum degree (see Newman [480] for some discussion). Cohen et al [151] suggest the setting the maximum on a discrete finite approximate power-law distribution to be $M = n^{\frac{1}{\gamma-1}}$. This is the cutoff that ensures that the expected number of nodes that would have degree larger than M (under the continuous approximation) on a draw of n nodes does not exceed one.[24] That leads the expected number of steps to finding the desired node for (7.33) to be proportional to

$$\frac{n}{n^{\frac{3-\gamma}{\gamma-1}}} = n^{\frac{2(\gamma-2)}{\gamma-1}}. \tag{7.34}$$

For instance, if $\gamma = 2.5$, then the expected time is $n^{2/3}$, which is much more efficient than the linear-in-n-time that we saw for the Poisson and regular networks.

Variations on Navigation Techniques

There are many variations on the navigation procedure that have been examined. For example Adamic et al [5] and Adamic, Lukose, and Huberman [4] analyze situations where instead of just getting information about direct neighbors, a node can also report on second neighbors. Then at each step we learn about a new number of nodes which is proportional to the size of the second neighborhood of a node found by following a random link. Without any overlap, and with independence in neighboring nodes

[24] That is, $n \int_M^\infty d^{-\gamma} dd$ is proportional to 1, up to a rescaling to ensure this is a proper density.

degrees, the size of the second neighborhood of a node found through such search is simply

$$\frac{\langle d^2 \rangle}{\langle d \rangle} - 1 + \left(\frac{\langle d^2 \rangle}{\langle d \rangle} - 1 \right)^2 = \frac{\langle d^2 \rangle}{\langle d \rangle} \left(\frac{\langle d^2 \rangle}{\langle d \rangle} - 1 \right).$$

This is the direct neighborhood size, plus the expected number of distance two neighbors brought in by the new nodes. This roughly squares the number of nodes found at each step. So, for the Poisson and regular networks the expected times become proportional to $\frac{n}{\langle d \rangle^2}$, while for the power distribution it becomes proportional to

$$\frac{n}{n^{2\frac{3-\gamma}{\gamma-1}}} = n^{\frac{3\gamma-7}{\gamma-1}}.$$

Networks that have larger tails in distribution lead to much more effective search. The intuition for this is clear. Since we are more likely to find larger degree nodes through following randomly chosen links, as the degree distribution places more weight on higher degree nodes we end up discovering more of the network by searching fewer nodes.

Adamic et al [5] and Adamic, Lukose, and Huberman [4] also consider another variation on search which takes even greater advantage of the presence of high-degree nodes. When a given node is not the desired node, and neither are its neighbors, then instead of picking an unvisited neighbor uniformly at random to move to next, one chooses the unvisited neighbor with the highest degree. As higher degree nodes have more neighbors, this not only leads to observing more nodes on a given step, but also then leads to improved opportunities (through more draws) of finding even higher degree nodes. Following this process quite quickly proceeds to situations where most of the nodes being searched are at the high end of the distribution. So, for instance, in the power network after a few steps most of the nodes examined have degree near M, and so a rough approximation for the expected time of search is then n/M, which for $M = n^{\frac{1}{\gamma-1}}$ becomes $n^{\frac{\gamma-2}{\gamma-1}}$. This is significantly quicker than simply following links chosen uniformly at random at each stage, which was the process that led to (7.34). As Adamic et al [5] point out, the relative size of improvement depends on γ. If γ is close to 2, then one naturally finds the very largest degree nodes simply by following random links as higher degree nodes have more weight in the distribution, whereas when γ is closer to 3, then there is more of an improvement from explicitly following a degree-based search algorithm as higher degree nodes are a bit rarer.

7.3.2 Navigating Structured Networks: Taking Advantage of Homophily

The analysis above suggests that navigating a network should take a time that is proportional to n in a regular or Poisson network, and some lower power of n if the network's degree distribution follows a power law; provided there is no additional structure of the network that we are able to take advantage of. This seems inconsistent with the Milgram [444] "small-world" experiments described in Section 3.2.1. There, people were able to get a letter to a target in a median number of 5 steps, of those that were successful. This was in a population on the order of hundreds of millions of people, so that even the square root of n is on the order of 10,000. Thus, it must be that the individuals in Milgram's experiment were taking advantage of additional structure of the network in order to choose to whom to forward the letter, as even sending the letter to very highly connected individuals is not enough to hit the median number of 5. It is clear that individuals would not just randomly choose a neighbor to send the letter to, but would instead try to send the letter to someone who has something in common with the target, or else to someone who they think might be closer to someone who has something in common with the target. Indeed, Killworth and Bernard [373] show that people in small-world letter experiments are primarily guided by occupation and/or geography in their choices of whom to forward the letter to. To see how this might help substantially, let us examine navigation in a more structured setting.

The main distinction to be drawn here is that the previous search algorithms that were based entirely on network primitives without reference to any other characteristics of the nodes. In situations where the formation of links is actually governed by some sort of underlying social structure, there can be much more efficient methods of navigation that use such social information. To see this quite plainly, consider a society of individuals who form a network that is described by a hierarchy in the form of a binary tree as follows. Each individual has a label. The first group are of type 0. This group forms the "root" of the tree. Next there are two groups, of types 00 and 01, which form the second level of the tree. Next there are four groups, of types 000, 001, 010 and 011, which form the third level, etc. A given individual is linked to all other individuals who are of the same type, as well as all of those who are of a type that that differs from the individual's own type by the addition or deletion of one terminal digit. So, someone of a type 0101 is connected to those with labels 010, 0101, 01010 and 01011. Thus, they are connected to the individuals of the same type, as well as

Figure 7.3.2. A Network Organized by Types, with 3 Agents of Each Type and a Tree Structure Among Types.

the type immediately preceding them in the tree, and the two types that follow them in the tree (unless they are at the last level of the tree). An example is pictured in Figure 7.3.2.

The "tree" has K levels, so the vectors of types have length at most K.

We can think of types as specifying individuals by a list of attributes, which we can think of as including all sorts of information such as their ethnicity, gender, profession, education, physical attributes, hobbies, geographic location, favorite music, etc.; which we code as vectors of 0 and 1's.[25]

If there are m individuals of each type, then the society consists of

$$n = m \sum_{k=0}^{K} 2^k = m \left(2^{K+1} - 1\right). \tag{7.35}$$

individuals in total.

[25] While this may sound restrictive, it is also clear that we can arbitrarily closely approximate any continuous variables by including a larger number of entries for a given attribute. It is important to keep in mind how K will vary as we code individuals.

Now, let us measure the distance between any two individuals in this network. It takes at most $2(K-1)$ links to get from one individual to another. We can also keep track of how this relates to the overall population size. (7.35) implies that

$$K = \frac{\log(n+m) - \log(m)}{\log(2)} - 1.$$

Therefore, the maximum distance of $2(K-1)$ is

$$2\frac{\log(n+m) - \log(m)}{\log(2)} - 3.$$

Thus, the maximum distance is growing proportionally to $\log(n)$ for a fixed m.

Now we find that if the society has hundreds of millions of people, then the maximum distance will be on the order of 10, and the median distance even less. This is much more in line with data from the Milgram [444] experiments, in which observed distances had a median of 5 and maximum of 12 steps. To see how an individual might navigate the network, suppose that we pick an individual at random and give him or her a letter and then ask him or her to get the letter to some other target agent in the society with a known type. An individual can simply follow the "greedy algorithm" of sending the letter to the neighbor who is closest to the other target, as Milgram [444] discusses in the context of his experiments. This is clearly an optimal algorithm and follows a shortest path. This takes the following form for an individual with a type ℓ of length k:

- If the target is a neighbor then send it directly.
- If the target is not a neighbor, but has a type equal to ℓ plus some additional entries (so lies further "down" the tree), then send it to any acquaintance whose type has a $k+1$-st entry that matches that of the target.
- If the target is not a neighbor and has a type that does not match ℓ in the first k entries, then send it to a neighbor who is "higher" in the tree.

It is worth remarking that implementing the algorithm only requires an individual to have an idea of which neighbor lies closer to the target, rather than having a full appreciation of the network structure. It is also critical, however, that the algorithm make use of the types of the individuals and the underlying social structure that indicates where different individuals appear in the tree. Moreover, it is clear that the

hierarchichal nature of the tree is used in the algorithm, although it could be adapted to some other sorts of structures.

While the setting described here is quite stylized, it provides some insight into how the structure of a network can help speed up navigation. The idea of using some sort of hierarchical structure to navigate a network is analyzed in various settings by Kleinberg [382] as well as Watts, Dodds and Newman [624], where they consider random graphs rather than the fully structured trees described above.[26]

To get a feeling for how things change in a random network with less structure than the 'tree' above, let us examine the model of Watts, Dodds and Newman [624]. Again, let individuals be described by vectors of 0's and 1's, but such that each type is exactly K entries long. This is equivalent to only considering the individuals whose types lie at the leaves of the tree in Figure 7.3.2. Let us keep track of the "social" distance between two individuals i and j, and denote it by x_{ij}, defined as follows. If two individuals are of the same type let their distance be 1. Two individuals who differ only in their last entry are at a distance of 2. Individuals whose first point of difference is their second to last entry or later are at a distance of 4, and whose first point of difference is the third to last entry are at a distance of 6, and so forth. This keeps track of how many links one would have to travel in the tree in Figure 7.3.2 to get from one type at the bottom row to some other type at a bottom row. These distances are just "social" distances, which are some measures of similarity, but do not yet correspond to actual distances in the network. The random network is then formed as follows. Uniformly at random pick a node i. Next pick a distance of $x \in \{1, 2, 4, 6, \ldots, 2(K-1)\}$, where K is the depth of the social tree, with probabilities $ce^{-\alpha x}$, where c normalizes the probabilities to sum to one and α is a parameter that adjusts how sensitive the link formation process is to similarity. Once x is chosen, then uniformly at random select a node j at that distance x from i and connect those nodes (provided there is not already a connection). Repeat this process until some average number of links per node, d, has been reached. When α is high, then nodes will form most of their links to other nodes that are more similar to themselves, whereas when α is low, then the links are formed more uniformly at random.

Since this is now a random network, it is possible that there will not exist a path between two nodes. Nevertheless, individuals can still follow a greedy algorithm of forwarding the letter to the neighbor who has a minimal social distance x_{ij} to the target, although that might no longer be a fully optimal algorithm given that the

[26] For a precursor to these models, see Killworth and Bernard [374].

network structure is now randomly determined. Watts, Dodds and Newman [624] construct such random networks through simulation, and then examine the results of following the above described algorithm for randomly selected pairs of nodes. They set population size $n = 10^8$, average degree $d = 300$, the "homophily parameter" $\alpha = 1$, work with a tree with ten branches at each level, and 100 individuals in each group at the leaf of a hierarchy.[27] They then posit a probability of .25 that a message is lost during any step, so that it is possible that some messages never reach their targets. Based on this, they measure the average distance of messages that eventually reach their targets and find it to be about 6.7, which is quite close to the 6.5 from the Milgram experiments.

7.3.3 Social Structure and Navigation Speed*

The Watts, Dodds and Newman [624] random network based on social types is similar to one analyzed by Kleinberg [382]. Kleinberg proves that there exist parameter values for which as n grows, two nodes picked uniformly at random will be connected at a distance of at most $O(\log(n))$ with a probability of at least $1 - \varepsilon(n)$ for some function $\varepsilon(n) \to 0$.[28] Interestingly, Kleinberg also shows that it is critical for α to be *exactly* 1 in order for such a result to hold. As a rough intuition, if α becomes too small, then the network begins to resemble a uniformly random network, which has a longer navigation time, as we argued previously. If α is too large, then the network connections are only formed to nearby nodes. Let us explore this in more detail to sharpen the insights.

Consider a set of n nodes. The primitive distances between nodes are described by a hierarchical structure of a tree. The tree T has $b \geq 2$ branches at each level, and has n leaves, which correspond to the nodes that we will form a random directed network over. Thus, we can write n as b^K where K is the depth of the tree T. The distance between two nodes i and j, denoted by x_{ij}, is half of the distance in the tree between two nodes i and j. Thus, x_{ij} corresponds to the depth of the smallest subtree that contains both i and j. This is not the distance in the random network that will be formed based on the tree, but just an auxiliary distance which might be thought of as

[27] They also work with two different hierarchies at once. Individuals are assigned to groups in each of the hierarchies uniformly at random, and then the social distance x_{ij} between two individuals i and j is taken to be the minimum distance over the different hierarchies.

[28] $O(\log(n))$ is standard "big O" notation, which denotes that something is of an order no larger than $\log(n)$. More generally, $f(n) = O(g(n))$ indicates that $\limsup \frac{|f(n)|}{|g(n)|} < \infty$, or in other words that there exists γ and n' such that $f(n) \leq \gamma g(n)$ for all $n \geq n'$.

some primitive measure of how dissimilar two nodes are.

For each node i, form d directed links, where the node at the other end of a given link is formed is chosen independently at random where the probability of choosing node j is proportional to $b^{-\alpha x_{ij}}$.[29]

Kleinberg then proves the following theorem.

An algorithm for searching to find a directed path from node i to node j is *decentralized* if it only uses information about the identities of the neighbors of i and their location as leaves in the tree, and the location of node j as a leaf in the tree.

Let us say that the search time is *polylogarithmic* if there exists γ for which a starting node and target node picked uniformly at random are connected by a directed path of length at most $O\left([\log(n)]^{\gamma}\right)$ with a probability of at least $1-\varepsilon(n)$ for some function $\varepsilon(n) \to 0$. Thus, search time is polylogarithmic if two randomly selected nodes are likely to be within a distance which is a power of $\log(n)$.

Let us say that the outdegree d of a sequence of random networks indexed by n is *polylogarithmic* if there exists γ such that the degree is proportional to $(\log(n))^{\gamma}$.

THEOREM **7.3.1** *[Kleinberg [382]] Consider a sequence, indexed by n, of random networks formed on n nodes based on a group structure as described above.*

(a) If $\alpha = 1$ and $d \geq c\left(\log_b(n)\right)^2$ for some $c > 0$, then there exists a decentralized algorithm for which search time is polylogarithmic (with exponent 1).

(b) If $\alpha \neq 1$ then there is no polylogarithmic degree for which there exists a decentralized algorithm with a search time that is polylogarithmic.

I sketch a proof of this theorem, as it helps one to understand the criticality of $\alpha = 1$, and it is not too long so the insight can be seen fairly directly.

Proof of Theorem 7.3.1: Recall the procedure that we used to assign neighbors in the construction of the random network, with neighbors at different distances being assigned with different probabilities. The normalizing constant of the distribution of

[29] Kleinberg is not explicit about how to handle the possibility of duplicate links. Let us proceeds as follows. Form the links in an independent and identically distributed manner, and then delete any duplicate links. For any given n there is be a probability that fewer than d links per node are formed, but that will vanish as n becomes large if d does not grow too fast as a function of n. In any case, this can be dealt with in the proof of Kleinberg's main result, as worked out below.

distances over nodes linked to by node i is denoted $Z(n)$ and described by

$$Z(n) = \sum_{j \neq i} b^{-x_{ij}} = \sum_{k=1}^{\log_b(n)} (b-1)b^{k-1}b^{-k} = \frac{b-1}{b}\log_b(n) \leq \log_b(n).$$

Let us prove (a). Uniformly at random select a starting node i and a target node j. Let them be a "social" (not network) distance x_{ij} apart, which is the depth of the smallest subtree T' of the tree T that contains them both. Consider the subtree T'' of depth $x_{ij} - 1$ that contains j. Since i is at a distance of x_{ij} from each leaf in T'', and there are $b^{x_{ij}-1}$ leaves in T'' the probability that i is not directedly linked to any leaf in T'' is

$$\left(1 - b^{x_{ij}-1}\frac{b^{-x_{ij}}}{Z(n)}\right)^d \leq \left(1 - \frac{1}{\log_b(n)}\right)^{c(\log_b(n))^2} \to e^{-c\log_b(n)} = n^{-c/\log(b)}.$$

Thus, we can guarantee that the probability that i fails to have a directed link to some node in T'' is at most $n^{-c/\log(b)}$. If we find a directed link to some node in T'' take one to a node in the smallest subtree possible that contains j, and call this node i'. This new tree has depth no more than $x_{ij} - 1$. Now repeat the argument starting from i', noting that we establish the same upper bound bound on the probability of failure to find a new directed link to a further subtree, and so forth. Given the maximal depth of the tree T, it takes at most $x_{ij} \leq \log_b(n)$ steps in this manner to reach the target j from the starting node i and thus the search time is polyalgorithmic with exponent 1. Moreover, the probability of a failure at any step is at most $n^{-c/\log(b)}$. So the overall probability of failing to find a directed path is at most $\log_b(n)n^{-c/\log(b)}$, which converges to 0 as n grows, establishing (a).

To see (b), consider two separate cases. When $\alpha < 1$, then the normalizing constant $Z(n)$ is such that for large n

$$Z(n) = \sum_{j \neq i} b^{-\alpha x_{ij}} = \sum_{k=1}^{\log_b(n)} (b-1)b^{k-1}b^{-\alpha k} \geq \frac{n^{1-\alpha}}{b}.$$

Consider a sub-tree T' containing a target node j and having between n^γ and bn^γ leaves, where $0 < \gamma < 1 - \alpha$. For any node i' not in T', the probability that i' has any link into T' is at most

$$\frac{dbn^\gamma}{n^{1-\alpha}/b} = dbn^{\gamma+\alpha-1}.$$

For any polylogarithmic d the expression $n^{-1+\gamma+\alpha}$ still dominates the expression, and so with a high probability it will still take more than a polylogarithmic number of

draws of nodes before finding any one with a link into T'. It follows easily that in any decentralized algorithm with high probability it will take more than a polylogarithmic number of steps from a starting node i outside of T' before any link into T' is found. The claim then follows.

If $\alpha > 1$, then $Z(n)$ is larger than some constant Z. Then consider a node i such that the distance of i to the target j is $\log_b(n)$, so that the smallest subtree containing i and j is T. Note that such a starting node and target will be selected with a nonvanishing probability (in fact of just more than $\frac{b-1}{b}$). Let T' be the tree of depth $\log_b(n) - 1$ that contains j. Each of i's directed out-links go to any given node in T' with a probability of no more than $b^{-\alpha \log_b(n)}/Z = n^{-\alpha}/Z$. Thus, the probability that any of i's directed links goes to a node in T' is at most $dn^{1-\alpha}/Z$. Again, it follows easily that in any decentralized algorithm with high probability it will take more than a polylogarithmic number of steps from a starting node i outside of T' before any link into T' is found; and so (b) is established. ∎

The remarkable thing about Kleinberg's result is that the distribution over links in the random network needs to be very specific in order to obtain the small-world conclusions that were observed in Milgram's letter experiments and that have emerged in many follow-ups.[30] To better understand this, note that the critical aspect of the proof of (a) is that we have a similar probability of a link going into any subtree. The size of the subtree in terms of nodes is balanced by the probability that a link goes to that subtree. That is, there are few nodes close-by in terms of social distance, but they have a proportionally higher probability of being linked to; and there are more nodes that are further away in terms of social distance and they have a proportionally lower probability of being linked to. When $\alpha = 1$ the balance is just right so that we end up with a sort of uniformity in the distribution over the "social distances" that different links span. When α differs from one then this proportionality is upset and one ends up with either a limiting probability that almost all links span socially dissimilar nodes, which makes it difficult to eventually approach a node; or else almost all links span socially similar nodes, which makes it difficult to reach between distant nodes.

This line of argument is not particular to the hierarchical tree structure. In fact, Kleinberg [382] shows that the results extend to the following more general random

[30] Polylogarithmic distance may not be very short, depending on the exponent. Nevertheless, in a large society it will generally be orders of magnitude shorter than distances which are not polylogarithmic. This, it still offers substantial insight into shorter versus longer distances, and what is needed to obtain shorter distances.

network process that is governed by a social structure.[31] Consider a set of n nodes. The primitive distances between nodes are described by what Kleinberg refers to as a "group structure." There are subsets of the n nodes, denoted by a generic element R. The collection of groups $\mathcal{R}$ satisfies the following criteria for some $\lambda < 1$ and $\beta > 1$:

- The set $\{1, \ldots n\}$ is a group.
- If $R \in \mathcal{R}$ is a group with at least two members and $i \in R$, then there exists another group R' which is a strict subset of R that includes i and has size at least $\min(\lambda|R|, |R| - 1)$.
- If i is in each of groups $R_1, \ldots R_k$, and each of these groups has fewer than q members, then the union of the groups has fewer than βq members.

As Kleinberg points out, the last condition is a sort of bounded growth condition so that as teh network grows an individual does not belong to an increasing number of disparate categories.

Let the distance between i and j, again denoted by x_{ij}, be defined to be the size of the smallest group that contains both i and j, or $x_{ij} = \min_{R:\{i,j\}\subset R} |R|$. Given a group structure, form a random network as follows. For each node i, form d links, where each link is formed to a node which is chosen independently at random where the probability of choosing node j is proportional to $x_{ij}^{-\alpha}$.

As Kleinberg [382] shows, conclusions (a), and (b) for the case of $\alpha < 1$, of Theorem 7.3.1 extend to such network structures. The case of $\alpha > 1$ requires some additional structure requiring that nodes are not too close in underlying the group structure.

We are left with the following conundrum. Theorem 7.3.1 seems to suggest that a very special balance in network formation based on social distance is necessary in order to have the network turn out to be easily navigable. Yet, we see such quick navigation in quite large societies. It is unlikely that societies just happen to hit the right balance. It is more likely that something is missing from the models, and it is clear that the network formation process underlying many social networks is much more complex than these models. Nevertheless, the models do provide us with a basic insight: it is necessary to have some balance of enough long-distance links as well as short distance links in order to make a network easily navigable. Such a balance can

[31] Kleinberg [382] also shows that the results extend to situations where nodes have a large enough, but constant out-degree as a function of n.

arise for a variety of reasons; and moreover it can be seen not only in terms of some random link formation process, but also in terms of the incentives that individuals have to form such links. Generally, we expect links at shorter social distances to be easier or less costly to maintain. This follows since individuals who are quite similar have more in common and may find it easier to communicate, trust each other, and so forth. While individuals who are at greater distance might find it more costly to maintain a relationship, such relationships that span greater social distance can be very valuable because they provide more access to other distant individuals, as well as information, ideas, and insights that are less likely to duplicate that already obtained from those who are more similar in type. The most important point is that such longer distance relationships become more valuable to the extent that there are fewer of them. Thus, the balance can naturally arise *precisely because* people wish to navigate the network, or are interested in obtaining varied information, etc. This idea behind small worlds is discussed in Section 6.5.1, but the analysis above also provides a navigation basis for understanding the conclusions there.

7.4 Exercises

EXERCISE **7.1** *Immunity Thresholds and Mean-Preserving Spreads.*

Consider diffusion in the presence of immune nodes as discussed in Section 7.2.1. Consider a degree distribution for which the threshold π for the emergence of a giant component of susceptible nodes is between 0 and 1. Describe how the threshold in (7.8) changes as we introduce a mean-preserving spread of the degree distribution.

EXERCISE **7.2** *Immunity in the SIR Model.*

Consider the SIR model in a situation where a proportion π of the nodes (selected uniformly at random) are immune from the outset. Develop an estimate of the threshold for infection analogous to (7.8) relating π and the probability of transmission t to statistics from the degree distribution. Plot combinations of π and t at the threshold for several values of average degree in the Poisson random network model.

EXERCISE **7.3** *Linear Infection Approximations in the SIS Model*

Consider a case where the probability of becoming infected in any given meeting with an infected individual is ν, while one cannot become infected from a susceptible (non-infected) individual. Then the probability of becoming infected in d random meetings with individuals who are (independently) infected with a probability θ is

$$\sum_{x=1}^{d} \left(1-(1-\nu)^x\right) \binom{d}{x} \theta^x (1-\theta)^{d-x}.$$

Here the sum is over the number of infected neighbors, x, that an individual with d meetings is likely to have, where $\binom{d}{x}\theta^x(1-\theta)^{d-x}$ is the probability of having x infected meetings. The expression $(1-(1-\nu)^x)$ is then the probability of becoming infected in at least one of the meetings, which is just 1 minus the probability of not becoming infected in any of the meetings with infected individuals.

Show that ν is small relative to d, (so that $(1-\nu)^x$ is approximately $1-\nu x$ for any $x \leq d$), then this expression approaches (7.17).

EXERCISE **7.4** *Average Neighbor Behavior in the SIS Model*

Consider a variation on the SIS model where instead of having a probability of $\nu\theta d$ of becoming infected when being of degree d and having a neighbor infection rate of θ, the probability is $\nu\theta$. This would be the case if, for instance, infection transmission depends on the fraction of neighbors being infected rather than the absolute number.

Show that in this case, $\rho(d)$ is independent of d and that $\rho = \theta = \frac{\lambda-1}{\lambda}$ if $\lambda > 1$ and is 0 otherwise.

EXERCISE **7.5** *Mutation in the SIS Model.*

Consider the SIS model where the infection rate (7.17) is modified to be

$$\nu\rho d + \varepsilon,$$

where $\varepsilon > 0$ is a rate at which a node "mutates" to become infected, regardless of contact with infected nodes. Develop an expression for the steady-state θ as a function the degree distribution, and provide a solution for regular degree distributions.

EXERCISE **7.6** *Less than Full Infection in the SIS Model*

Show that a solution θ to (7.20) is less than 1 whenever the support of P and λ are finite.

EXERCISE **7.7** *Navigating a Structured Network on a Hypercube.*

As in Section 7.3.2, code individuals in a binary manner as vectors of 0 and 1's, but now have each individual have a vector of length K. An individual with a given vector of attributes is linked to all other individuals with exactly the same attributes, and also to people who have vectors of attributes that differ by one entry. Thus, the network can be thought of as a hypercube or a regular lattice. So, for instance if $K = 4$, then an individual with attributes $(0, 1, 0, 0)$ is connected to individuals of the same type as well as individuals of types $(0, 0, 0, 0)$, $(1, 1, 0, 0)$, $(0, 1, 1, 0)$, and $(0, 1, 0, 1)$. Again, there are m individuals with each label.

Calculate the average distance in path length between two nodes picked uniformly at random (allowing for the second node to be identical to the first). How does this vary with the number of individuals in the society n? How is average degree growing in this network?

EXERCISE **7.8** *Navigating Random Networks Based on Groups**

Consider the extension of Theorem 7.3.1 to the situation where the random network is governed by group structures, as described in Section 7.3.3.

Show that (a) of Theorem 7.3.1 extends to this setting. Show that (b) holds when $\alpha < 1$.

Chapter 8

Learning and Networks

Social networks play a central role in the sharing of information and the formation of opinions. This is true in the context of advising friends on which movies to see, relaying information about the abilities and fit of a potential new employee in a firm, debating the relative merits of politicians, or even simply providing information about scientific research and results. Given the role of social networks in the formation of opinions and beliefs, and the subsequent shaping of behaviors, it is critical that we have a thorough understanding of this how the structure of social networks affects learning and the diffusion of information. Some fundamental questions that arise concern how social networks influence

- whether individuals in a society come to hold a common belief or remain divided in opinions,
- which individuals have the most influence over the beliefs in a society,
- how quickly individuals learn, and
- whether initially diverse information scattered throughout the society can be aggregated in an accurate manner.

Various answers have been given to these questions, and in this chapter we shall explore some of the basic models. I start with some background on a few of the classic sociological studies that sparked theories of opinion leaders, and provide basic evidence of the role of social networks in the formation of beliefs and opinons. This provides some of the first answers to the second question above, as some of the studies focussed on questions of which individuals tend to become opinon leaders. From there, I discuss

two different types of models. The first is a Bayesian learning model, where individuals observe actions and results experienced by their neighbors and the information in a sophisticated manner. While Bayesian updating has firm normative foundations, it is a bit cumbersome to use in such complex settings. Nevertheless, the model does provide some insight into the first question above, as it provides conditions under which individuals come to act similarly over time. The second model is based on a much more naive, but still natural form of updating, where individuals exchange information with their neighbors over time and then update by taking some weighted average of what they hear. This class of models turns out to be quite tractable, and allows us to incorporate rich network structures and to provide explicit answers to each of the above questions.

8.1 Early Theory and Opinion Leaders

Early theory on information transmission in social networks includes the seminal work on the role of "opinion leaders" of Lazarsfeld, Berelson and Gaudet [403][1] and the subsequent fuller development by Katz and Lazarsfeld [360]. These studies examined the formation of opinions in voting and various other household decisions. The study by Lazarsfeld, Berelson and Gaudet [403] provides a basis for the identification of opinion leaders through observations of how individuals reached voting decisions in an Ohio town in the 1940 U.S. presidential campaign. Lazarsfeld et al define "opinion leaders" to be individuals throughout society who become informed through various media and other interactions who then form opinions and convey information to and influence other individuals who are less directly informed. This theory of opinion leaders was developed in more detail and structure by Katz and Lazarsfeld [360]. They also conducted a very influential and extensive study of opinion formation, this time in Decatur, Illinois in the early 1950's. They conducted two sets of interviews with women over the age of sixteen, and asked the subjects about things beyond political opinions. In particular, Katz and Lazarsfeld asked the women about their opinions regarding household goods, fashion, movies, and local public affairs (including politics). The study was cleverly designed to interview the same women multiple times, a couple of months apart, so that changes in opinions could be identified. When finding a change in opinion, Katz and Lazarsfeld then asked questions that helped them

[1] There are earlier studies that provide roots for theories on opinion leaders, such as Merton [**?**]. See the background chapter in Katz and Lazarsfeld [360] for more details on the birth of the theory.

trace the sources that influenced the change in opinion. They did this by asking the women whose opinion changed, who had influenced their decisions, as well as by asking subjects if they had influenced others' decisions. This allowed Katz and Lazarsfeld to identify individuals who played a role in multiple changes of opinion, and they dubbed these individuals the "opinion leaders." Katz and Lazarsfeld found evidence that while sometimes opinion leaders held higher social status, there were many cases where opinion leaders were at the same social status as those whom they influenced, especially when it came to various household decisions. Opinion leaders were often distinguished by their gregariousness and the size of their families (which is then correlated with their age and experience).[2]

Beyond the applications mentioned above, which provide just a glimpse of some of the early research on opinion leaders, there are important shapings of opinions that occur through families, education, religion, and various organizations. The role that opinion leaders play in the dissemination of information and the influence of opinions and decisions has been of primary importance to those interested in marketing, social programs, education, and campaigning, and more general diffusion properties (e.g., see Rogers [**?**]). I do not wish to survey the large empirical literature on belief and opinion formation; but it is important to mention the work above because it was critical in showing how social connections play a role in learning and the formation of opinions, and that different agents in a society have different influences. To more fully understand how this might work, we need to examine models that explicitly account for social network structure in the patterns of information dissemination. Some of these models will allow us to operationalize social influence and opinion leadership in the context of explicit social networks.

8.2 Bayesian and Observational Learning

I take the models out of historical sequence, starting first with later models on observational learning, and then returning to the more classic models of social influence, consensus formation, and opinion formation. This allows us first to digest a fairly basic insight on consensus, at least in terms of actions, and then turn to the richer modeling

[2] There is also some evidence from Coleman, Katz, and Menzel [154], in another influential study about the adoption of a drug (see Section **??**), that early adopters tend to be more highly connected, and that adoption then later spreads to less socially connected individuals, which often correlates with age and experience.

of social influence.

A central conclusion in the observational learning setting is that if agents can observe each other's actions and outcomes over time, and all agents have the same preferences and face the same form of uncertainty, then they end up with similar payoffs over time. The idea is that an agent who is doing significantly worse than a neighbor must come to realize this over time, and will eventually change actions and come to do as well as the neighbor. This then implies that all connected agents must end up with the same limiting payoffs. This does not imply that they all learn to take the best possible action - it could be that they all end up with suboptimal payoffs. However, if in addition, agents start with sufficient diversity in opinions so that they have incentives to experiment with different actions, then they will have a high probability of converging to the right action. Of course, this relies on a great amount of stationarity in the environment, and similarity in preferences and situations across agents; but it provides a benchmark.

The following learning environment is a variation on that studied by Bala and Goyal [26]. There are n agents who are connected in an undirected social network. In each period $t \in \{1, 2, \ldots\}$, the agents simultaneously choose among a finite set of actions. The payoffs to the actions are random and their distribution depends on an unknown state of nature. The agents are all faced with the same set of possible actions and the same unknown state of nature. They all have identical tastes and face the same uncertainty about the actions. At each date, in addition to observing his or her own outcome, an agent also observes his or her neighbors' choices and outcomes.

The main results and ideas can be most easily seen in a a situation with two choices of action, A or B, and easily generalized to any finite number of actions. For the purpose of exposition, suppose that A results in a payoff of 1 per period for certain, while B pays 2 with probability p and 0 with probability $1 - p$. An agent would like to maximize the expected sum of discounted payoffs,

$$E\left[\sum_t \delta^t \pi_{it}\right],$$

where $\delta \in (0, 1)$ is a discount parameter, and π_{it} is the payoff that i receives at time t. If $p > 1/2$ then every agent would prefer to choose B, while if $p < 1/2$ then every agent would prefer to choose action A. However, p is unknown to the agents, and can take on a finite set of values $p \in \{p_1, \ldots, p_K\}$ with each $p_k \neq 1/2$.[3] Let agent i begin with

[3]The finiteness of values is not critical to the result. However, the conclusion that all agents end

a prior μ_i over this set, such that $\mu_i(p_k) > 0$ is the probability that i initially assigns to state p_k being the probability that action B pays 2. This is a standard multi-armed bandit problem, except that an individual can observe the actions and outcomes chosen by his or her neighbors.

The learning in such an environment can be quite complicated. For instance, seeing that a neighbor chooses an action B might indicate that the individual's neighbors have had good outcomes from B in the past. Thus, beyond simply seeing actions and outcomes, an individual can make inferences about outcomes of indirect neighbors by observing the action choices of neighbors. Such full Bayesian learning is explored in the context of three link networks by Gale and Kariv [248] (see also Choi, Gale and Kariv [141] and Celen, Kariv, and Schotter [**?**]), but quickly becomes intractable in larger networks. Instead, Bala and Goyal examine a limited form of Bayesian updating, where agents only process the information from actions and outcomes and ignore any indirect information that might be gleaned from the action sequences of neighbors.

In this version of the model, observing a 0 or 2 must obviously indicate the an agent took action B and a payoff of 1 indicates that the agent took action A. Thus we can keep track of an agent i's beliefs at time t simply by knowing the initial beliefs μ_i and then the history of the payoffs of i and each of i's neighbors through time t, denoted by h_{it}. So, let $\mu_i(h_{it})$ denote i's belief of the probability that action B will result in a payoff of 2, updated according to Bayes' rule conditional on observing history h_{it}.

The following proposition is a slight strengthening of the main conclusion from Bala and Goyal [26], in terms of claiming that players play the same strategy after some time rather than getting the same limiting payoff, due to having different payoffs to different actions.

PROPOSITION **8.2.1** *[Bala and Goyal [26]] With probability one, there exists a time such that all agents in a component settle down to play the same action from that time onwards.*

The proof is straightforward, and the main points are as follows. It suffices to consider a given component, so let the n agents be in a single component. If action B is not played infinitely often, then all agents must play A after some time and the conclusion follows. So, consider a case where action B is played infinitely often. Then

up taking the same action depends on the two actions providing different average payoffs. If the two actions lead to the same average payoff, then there is still a conclusion that agents end up with the same long-run utility.

some agent, say i, plays B infinitely often. By the strong law of large numbers (see Theorem 4.5.2), with probability one, $\mu_i(h_{it})$ will converge to the true p_k.[4] Thus, in order for agent i to play B infinitely often it must be that $p_k > 1/2$. Then, since $\mu_i(h_{it})$ converges to p_k almost surely, there is a (random) time after which i will play B exclusively. Each neighbor sees i's play and, again with probability one, will have the same limiting beliefs. Thus each neighbor must have limiting beliefs that B offers a higher payoff, and so each of i's neighbors will play B exlusively after some random time. Iterating on this logic leads to the claim.

The basic reasoning behind this result extends to other sorts of behavioral assumptions. For example, a similar conclusion holds if each agent chooses the action chosen last period by the agent who has the highest payoff to date in his or her neighborhood (including themselves); although the proof for that case is different. The critical thing is that players observe the streams of payoffs of their neighbors and can see if there is an action that would do better than the one they are currently choosing.

The fact that all agents end up choosing the same action does not imply that they end up with the same limiting beliefs, nor does it imply that they end up choosing the "right" action. For instance, they might end up choosing A while $p > 1/2$ and B would end up with a higher payoff, and this could happen because they each start with low μ_i's. Moreover, and the beliefs can then remain different from each other. In terms of picking the right action, it is impossible (that is, it happens with probability 0) that agents end up choosing B infinitely often when A is the right action, as they will learn the payoff to B almost surely. So, in this version of the model, for them to fail to pick the right action it must be that they end up picking action A, while B would have been better. If there is enough optimism about the payoff of B by at least one agent in the society, then that agent will play B for a long time regardless of the observed history, and so the society will have a high probability of learning the higher payoff action. This is the content of the following claim, which is a variation on a proposition in Bala and Goyal [26].[5]

CLAIM **8.2.1** *For any ε, there exists a $\mu < 1$ such that if there exists at least on i who*

[4] Here, one does not need to invoke the Martingale Convergence Theorem, as the convergence of μ_i is easily established directly from the Strong Law of Large Numbers and Bayes Rule. A detail to worry about is that i is also seeing some finite set of neighbors' actions and payoffs. However, that can only lead to more observations of B and the beliefs will still converge almost surely to knowing the true probability of B.

[5] The proposition of Bala and Goyal (Proposition 4.1) has an additional condition bounding the number of neighbors that an agent has. That is not needed here, since I consider a finite society.

has an initial belief that action B will pay 2 with probability greater than μ, then the probability that all agents in i's component eventually converge to choosing the "correct" action (with the higher true expected payoff) is at least $1-\varepsilon$.

The idea here is that if there is enough optimism by at least one agent then, regardless of the initial string of outcomes, that agent will play B a large enough number of times so that there is a probability of at least $1-\varepsilon$ that the component will end up learning whether B has a payoff above or below that of A. Bala and Goyal [26] also investigate some other conditions ensuring convergence to the correct action, which are conditions on having enough agents with independent neighborhoods, so that some agents will be trying the better action enough to learn it.

It is easy to see that the above results extend easily to situations where A's payoff is also uncertain, and to situations where there are more than two actions. Variations on such a result can also be established in a fully Bayesian rational setting, as by Gale and Kariv [248]. Convergence to a consensus action does depend on various aspects of the formulation, and the limits of such results with respect to variations on who observes what and when, and other aspects of the formulation, is explored by Rosenberg, Solan and Vieille [539].

While the above results show the potential for the reaching of an eventual consensus, at least in terms of beliefs over which is the best action, they do not give us much impression of what happens in the shorter run, which might often be quite relevant, especially if the world is not stationary. More importantly, the network structure does not enter the above analysis in a substantial way, as connectedness and optimisim (or some large numbers of agents with independent neighborhoods) that are doing the work in the results. Let me now turn to a set of models that bring network structure explicitly into the analysis.

8.3 Imitation and Social Influence Models: The DeGroot Model

The seminal network interaction model of information transmission, opinion formation, and consensus formation is due to DeGroot [180]. It is a very simple and quite natural starting point for a theory that will allow us to more fully understand how the structure of a network influences the spread of information and opinion formation.

Individuals in a society start with initial opinions on a subject. Let these be represented by an n-dimensional vector of probabilities, $p(0) = (p_1(0), \ldots, p_n(0))$. Each $p_i(0)$ lies in the interval [0,1], and might be thought of as the probability that a given statement is true, or the quality of a given product, or the likelihood that the individual might engage in a given activity, etc. The interaction patterns are captured through a possibly weighted and directed $n \times n$ nonnegative matrix T. In particular, let T be a (row) stochastic matrix, so that its entries across each row sum to one. The interpretation of T_{ij} is that it represents the weight or trust that agent i places on the current belief of agent j in forming his or her belief for the next period. Beliefs are updated over time so that

$$p(t) = Tp(t-1) = T^t p(0). \tag{8.1}$$

This process is illustrated in the following example.

EXAMPLE **8.3.1** *Updating in the DeGroot Model*

There are three individuals and an updating matrix described by

$$T = \begin{pmatrix} 1/3 & 1/3 & 1/3 \\ 1/2 & 1/2 & 0 \\ 0 & 1/4 & 3/4 \end{pmatrix}.$$

This updating process is pictured in Figure 8.3.

Agent 1 weights all beliefs equally, while agent 2 weights agents 1 and 2 equally but ignores 3, and agent 3 weights 2 and 3 but ignores 1; and agent 3 places more weight on his or her own belief. Suppose that we begin with a vector of beliefs given by

$$p(0) = \begin{pmatrix} 1 \\ 0 \\ 0 \end{pmatrix}.$$

So, agent 1 starts with a belief of 1 (of the probability of some event), while agents 2 and 3 start with a belief of 0. Here,

$$p(1) = Tp(0) = \begin{pmatrix} 1/3 & 1/3 & 1/3 \\ 1/2 & 1/2 & 0 \\ 0 & 1/4 & 3/4 \end{pmatrix} \begin{pmatrix} 1 \\ 0 \\ 0 \end{pmatrix} = \begin{pmatrix} 1/3 \\ 1/2 \\ 0 \end{pmatrix}.$$

Figure 8.3. An Updating Process

Then, as agents update again, beliefs become

$$p(2) = Tp(1) = \begin{pmatrix} 1/3 & 1/3 & 1/3 \\ 1/2 & 1/2 & 0 \\ 0 & 1/4 & 3/4 \end{pmatrix} \begin{pmatrix} 1/3 \\ 1/2 \\ 0 \end{pmatrix} = \begin{pmatrix} 5/18 \\ 5/12 \\ 1/8 \end{pmatrix}.$$

Iterating this process leads to beliefs that converge:

$$p(t) = Tp(t-1) = T^t p(0) \to \begin{pmatrix} 3/11 \\ 3/11 \\ 3/11 \end{pmatrix}.$$

The way in which we can calculate the limit belief is discussed in detail below.

This process has the following motivation, discussed by DeMarzo, Vayanos and Zwiebel [183]. Agents are connected by a (possibly directed) network indicating whose information they get to observe over time. At time $t = 0$, each agent sees a noisy signal $p_i(0) = \mu + e_i$ where $e_i \in I\!R$ is a noise term. An agent i then hears the opinions his or her neighbors, and assigns precision π_{ij} to the signal of agent j. If agents are Bayesian and the noise terms are normally distributed with zero mean, then agent i

would update according to (8.1), setting $T_{ij} = \pi_{ij}/\sum_k \pi_{ik}$, where $\pi_{ik} = 0$ if i does not have a directed link to k.[6] Now, at time $t = 2$, agents would realize that their neighbors now have new information (collected by the neighbors at time $t = 1$), and so it is worthwhile listening to their neighbors again to collect this indirect information. The fully "optimal" processing of the neighbors' new beliefs with in this second stage is a bit more complicated, as now one has to account for how much new information is in the signal, and what the precision is at that stage. With each iteration, the inference problem becomes even more complicated. The DeGroot model can be thought of as a boundedly rational version of this process, where the agents do not adjust their weightings over time. Nevertheless, iterating on the updating process allows agents to incorporate more distant information and possibly to reach a consensus. Moreover, as we shall see, there are situations where updating according to this very simple process will still lead agents to converge to a fully accurate belief in the limit.

8.3.1 Incorporating Media and Opinion Leaders

In view of the discussion of media and opinion leaders in Section 8.1, it will also be of interest to understand how external sources of information can influence a society, and how opinion leaders might shape the opinions of others. This model easily incorporates various forms of external information providers, who are not influenced by the opinions of the members of the society, but who are listened to. Such fixed sources of information can simply be viewed as i's with $T_{ii} = 1$ and $T_{ij} = 0$ for all $j \neq i$, but for whom $T_{ji} > 0$ for some j's. Thus, an external source of information is modeled as an agent i whose opinion stays fixed at $p_i(0)$, but whom other nodes pay attention to.

Opinion leaders will arise naturally in the model, as individuals who are listened to by others and who have non-negligible influence on the opinions of at least some other agents. That is, the influence of an agent j over the final beliefs in the society will depend on how much weight other individuals place on the agent, as captured through T_{kj}'s. This is explored more explicitly below.

8.3.2 Convergence

A first question that arises is: under what conditions will the updating process in (8.1) converge to a well-defined limit? A second question is then what limit does it converge to. Let us examine these questions in sequence.

[6] Also, see DeGroot and Schervish [?] (Section 6.3) for background on such updating.

Figure 8.3.2. A Society with a Convergent Updating Process

A social influence matrix T is *convergent* if $\lim_t T^t p$ exists for all initial vectors of beliefs p.

This is illustrated in the following example.

EXAMPLE **8.3.2** *Convergence*

There are three individuals and an updating matrix described by

$$T = \begin{pmatrix} 0 & 1/2 & 1/2 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \end{pmatrix}.$$

This updating process is pictured in Figure 8.3.2.

Here, one can check that

$$T^2 = \begin{pmatrix} 1/2 & 1/2 & 0 \\ 0 & 1/2 & 1/2 \\ 1 & 0 & 0 \end{pmatrix}, T^3 = \begin{pmatrix} 1/2 & 1/4 & 1/4 \\ 1/2 & 1/2 & 0 \\ 0 & 1/2 & 1/2 \end{pmatrix}, T^4 = \begin{pmatrix} 1/4 & 1/2 & 1/4 \\ 1/2 & 1/4 & 1/4 \\ 1/2 & 1/2 & 0 \end{pmatrix}, \ldots.$$

and

$$T^t \to \begin{pmatrix} 2/5 & 2/5 & 1/5 \\ 2/5 & 2/5 & 1/5 \\ 2/5 & 2/5 & 1/5 \end{pmatrix}.$$

Thus, no matter what beliefs $p(0)$ the agents start with, they all end up with limiting beliefs corresponding to the entries of $p(\infty) = \lim_t T^t p(0)$ where

$$p_1(\infty) = p_2(\infty) = p_3(\infty) = \frac{2}{5}p_1(0) + \frac{2}{5}p_2(0) + \frac{1}{5}p_3(0).$$

Example 8.3.2 not only shows that beliefs converge over time, but it also illustrates that the agents reach a consensus, and that agents 1 and 2 have twice as much influence over the limiting beliefs as agent 3 does. This sort of result is obtained under very natural conditions, and we shall see how to characterize the limiting influence below.

It is also possible for an updating process to fail to converge. This is illustrated in the following example.

EXAMPLE **8.3.3** *Non-Convergence*

This is a slight variation on Example 8.3.2, where we change only the third person's weights so that she places all of her weight on agent 1.

$$T = \begin{pmatrix} 0 & 1/2 & 1/2 \\ 1 & 0 & 0 \\ 1 & 0 & 0 \end{pmatrix}.$$

This updating process is pictured in Figure 8.3.2.

Here,

$$T^2 = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1/2 & 1/2 \\ 0 & 1/2 & 1/2 \end{pmatrix}, \; T^3 = \begin{pmatrix} 1/2 & 1/2 & 0 \\ 1 & 0 & 0 \\ 1 & 0 & 0 \end{pmatrix}, \; T^4 = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1/2 & 1/2 \\ 0 & 1/2 & 1/2 \end{pmatrix} \ldots.$$

and so the matrix simply oscilates and there is no convergence. For example, if we start with an initial set of beliefs with $p_1(0) = 1$ and $p_2(0) = p_3(0) = 0$, then since 1 updates based on 2 and 3's beliefs, and 2 and 3 update based on 1's belief, the agents simply end up swapping their beliefs over time.

The key to the failure of convergence in Example 8.3.3 is that there is a directed cycle in the network pictured in Figure 8.3.2 and that *all* the cycles are of lengths that are multiples of 2. The updating/interaction matrix T is said to be *periodic*, and this allows the process to cycle without converging.

Figure 8.3.2. A Society with a Non-Convergent Updating Process

To be more specific, let us say that T is *aperiodic* if the greatest common divisor of all the directed cycle lengths is one; where the directed cycles are defined relative to a directed network where a directed link exists from i to j if and only if $T_{ij} > 0$.

This condition is satisfied in Example 8.3.2 where there are directed cycles of length 2 and of length 3 so that the greatest common divisor of the directed cycle lengths is 1, while it fails in Example 8.3.3 where there all directed cycles are of lengths that are multiples of 2.

Standard results in Markov chain theory[7] are easily adapted to this model to conclude that if T is strongly connected (so that there is a directed path from any node to any other node, also referred to as being irreducible), and aperiodic, then it is convergent. As such, much of the literature simply presumes that T is strongly connected and that $T_{ii} > 0$ for some or all i, which implies then implies that the matrix is aperiodic (since it has a at least one cycle of length 1), and therefore convergent. However, it is not necessary to have $T_{ii} > 0$ for even a single i in order to ensure convergence, as we see from Example 8.3.2. The full necessary and sufficient condition for convergence is

[7]See Meyer [442], for example. Section 4.5.8 provides some basic definitions concerning Markov chains.

as follows, as pointed out in Golub and Jackson [278].[8]

Before stating the convergence result, the following definition is needed.

A *closed* set of agents is a $C \subset \{1, \ldots, n\}$ such that there is no directed link from an agent in C to an agent outside of C (that is, there is no pair $i \in C$ and $j \notin C$ such that $T_{ij} > 0$).

EXAMPLE **8.3.4** *Closed Sets of Nodes*

Consider a society of $n = 6$ agents with an updating process

$$T = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 1/4 & 1/4 & 0 & 0 & 1/4 & 1/4 \\ 0 & 0 & 1/2 & 1/2 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 1/4 & 0 & 3/4 & 0 \\ 0 & 0 & 0 & 1/3 & 0 & 2/3 \end{pmatrix}.$$

This is pictured in Figure 8.3.2

Here there are many closed sets of nodes: for instance $\{1, 2, 3, 4, 5, 6\}$ is closed. Also, $\{1\}$ is closed, as are $\{3, 4, 5\}$, $\{1, 3, 4, 5\}$, $\{3, 4, 5, 6\}$, and $\{1, 3, 4, 5, 6\}$.

The only strongly connected and closed sets of nodes are $\{1\}$ and $\{3, 4, 5\}$, as pictured in Figure 8.3.2

Convergence for the overall society holds if and only if each closed and strongly connected set of nodes converges, which happens if and only if each such set is aperiodic (as in 8.3.2).

THEOREM **8.3.1** *T is convergent if and only if every set of nodes that is strongly connected and closed is aperiodic.*

Again, the sufficiency of aperiodicity for convergence follows fairly easily by adapting theorems on steady-state distributions of Markov chains. The necessity is shown by providing an algorithm for constructing a nonconvergent $p(0)$ whenever there is a strongly connected and closed group such that all of the directed cycles have a common divisor greater than one. The proof is provided in Golub and Jackson [278].

[8] There are also other necessary and sufficient conditions. For instance, it is necessary and sufficient that the submatrix of T restricted to any strongly connected and closed group of nodes be a primitive matrix (e.g., see Theorem 1 in the appendix of Hegselmann and Krause [307]). This can be shown to be implied by the aperiodicity of T on these nodes.

Figure 8.3.2. Closed Sets of Nodes

Figure 8.3.2. The Only Closed and Strongly Connected Sets of Nodes

8.3.3 Consensus in Beliefs

Beyond knowing whether or not beliefs converge, we are also interested in characterizing what beliefs converge to when they converge, which agents have substantial influence in the society, and when it is that a concensus is reached. These correspond to several of the questions that we began the chapter with.

Let us begin with a couple of simple observations. First, it is straightforward to see that if beliefs converge, then a strongly connected and closed group of agents will reach a concensus.

Let us say that a group of agents $C \subset \{1, \ldots, n\}$ *reaches a consensus* under T for an initial vector of beliefs $p(0)$ if $\lim_t p_i(t) = \lim_t p_j(t)$ for each i and j in C.

PROPOSITION **8.3.1** *Under T, any strongly connected and closed group of individuals reaches a consensus for every initial vector of beliefs if and only if it is aperiodic.*

Proof of Proposition 8.3.1: First, we know from above that such a group will have convergent beliefs if and only if it is aperiodic. Since a consensus cannot be reached if beliefs do not converge, to conclude the claim it suffices to show that aperiodicity of a strongly connected and closed group implies consensus. So, suppose to the contrary that for some $p(0)$ the belief of the agents in C converge, but to some p' such that $p'_i \neq p'_j$ for some i and j in C. Without loss of generality, we may ignore agents outside of C, so consider C to be the full set of agents $\{1, \ldots, n\}$ and relabel the agents so that $p'_1 \geq p'_2 \geq \cdots \geq p'_n$. Find the minimal i such that $p'_i > p'_{i+1}$. Given that agents are strongly connected, it must be that some agent $k \leq i$ has $T_{kh} > 0$ for some $h \geq i+1$. Convergence then implies that for any ε, we can find a large enough t' such that for all $t > t'$:

$$p_k(t) = \sum_j T_{kj} p_j(t-1) \leq \sum_j T_{kj} p'_j + \varepsilon \leq (1 - T_{kh}) p'_1 + T_{kh} p'_h + \varepsilon.$$

But since the right hand expression is less than p'_k for a small enough ε, we reach a contradiction. ∎

Thus, we have a complete characterization of consensus for strongly connected and closed groups, which is that they reach a consensus whenever they converge. The logic is evident from the proof, which is basically that a given individual cannot reach a higher limit than each of his or her neighbors, since his or her belief involves a weighted average of those beliefs.

So let us partition the society into strongly connected and closed groups of individuals, and then the remaining individuals. If there is more than one strongly connected and closed group, then clearly the society will not always reach a consensus except in the rare cases where the initial beliefs are such that separate closed and strongly connected groups happen to reach the same limit. For instance, if one closed group starts with common beliefs at 1 and a separate closed group starts with common beliefs at 0, they will forever stay apart. So, in order to reach consensus when the initial beliefs are not chosen exceptionally, it must be that there is exactly one closed and strongly connected group in the society. Note that it is easy to see that there always exists at least one such group (see Exercise 8.7), and that a society can be partitioned into some number of strongly connected and closed groups and then a remaining set of agents who each have at least one directed path to an agent in a strongly and connected group.

COROLLARY **8.3.1** *A consensus is reached in the DeGroot model if and only if there is exactly one strongly connected and closed group of agents and T is aperiodic on that group.*

This also leads to another characterization of consensus due to Berger [51].

COROLLARY **8.3.2 (Berger [51])** *A consensus is reached in the DeGroot model if and only if there exists t such that some column of T^t has all positive entries.*

We can think of an entry $[T^t]_{ij}$ as keeping track of the indirect weight that an agent i places on agent j, through paths of length t. Thus, if some column of T^t has all positive entries, then every agent is putting some indirect weight on the agent corresponding to that column. This implies that all agents must have an indirect path to some agent, and so there must be exactly one strongly connected and closed group of agents. Once a column is all positive, it stays that way, which guarantees aperiodicity (a not too difficult proof, but one that takes some thought).

8.3.4 Consensus and Non-Constant Updating Rules

The consensus result does not rely on T being a stationary matrix. It holds in a variety of models where T varies with time or with the beliefs themselves.

The following are some generalizations of the DeGroot model such that the updating can vary with time and circumstances.

EXAMPLE **8.3.5** *Time-varying weight on own beliefs.*

DeMarzo, Vayanos and Zwiebel [183] examine a variation on the DeGroot model (related to a variation on DeGroot's model due to Chatterjee and Seneta [138]) where the updating rule is:

$$p(t) = \left[(1-\lambda_t)I + \lambda_t \widehat{T}\right] p(t-1)$$

where I is the identity matrix, $\lambda_t \in (0,1]$ is an adjustment factor, and $\widehat{T}$ is a stochastic matrix. If λ_t is constant over time, then this corresponds to the DeGroot model, while otherwise it allows updating to vary over time, so that an agent might place more (or less) weight on his or her own belief over time.

EXAMPLE **8.3.6** *Only Weighting those with Similar Beliefs.*

The following model of Krause [**?**] (see also Hegselmann and Krause [307]) allows an agent to only pay attention to other agents whose beliefs are not far from his or her own. Thus, the agent has a sort of distrust for information that is too different from his or her own. Here,

$$T(p(t),t)_{ij} = \begin{cases} \frac{1}{n_i(p(t))} & \text{if } |p_i(t) - p_j(t)| < d, \text{ and } n_i(p(t)) = \#\{k : |p_i(t) - p_k(t)| < d\} \\ 0 & \text{otherwise.} \end{cases}$$

Thus, an agent places equal weight on all opinions that are within some distance d of his or her own current opinion. This substantially complicates the process, as the updating depends on the specifics of the opinions rather than just on time. This is also closely related to the model of Deffuant et al [179] and Weisbuch et al [**?**], where at each time two agents are randomly matched and then update their beliefs only if the beliefs are close enough to each other.

The reaching of a consensus in the above generalizations of the DeGroot model are covered under the following result of Lorenz [419].

THEOREM **8.3.2** *Suppose that $T(p(t),t)$ satisfies the following conditions:*

- *There exists $\delta > 0$ such that $T(p(t),t)_{ij} > 0$ if and only if $T(p(t),t)_{ij} > \delta$, for all t, i, j and $p(t)$.*
- *$T(p(t),t)_{ii} > 0$ for all i, t, and $p(t)$.*
- *$T(p(t),t)_{ij} > 0$ if and only if $T(p(t),t)_{ji} > 0$ for all t, i, j and $p(t)$.*

Then, the society can be partitioned into sets of agents such that each group of agents reaches a consensus, and any two agents who place weight on each other infinitely often are in the same group.

The proof works by bounding below the weights that agents must place on anyone with whom they communicate other over time, and then tying these back to the initial beliefs and establishing convergence. Effectively, with weights bounded below, a belief cannot stay too much above or below its neighbors' beliefs over time, and so convergence to a consensus is still guaranteed. The reader is referred to Lorenz [419] for the details. The assumptions of each agent updating based on his or her own beliefs at every time, agents paying mutual attention to each other, and having a lower bound on attention (which then also puts an upper bound on how many agents an agent can pay attention to) are stronger than necessary, but simplify the analysis, and allow the theorem to capture quite non-stationary updating processes in a class that significantly generalizes the basic DeGroot model in some directions. The requirement of symmetric attention paid implies that any path connected agents are strongly connected, which is a way of guaranteeing that beliefs reach an overall consensus. If for instance, this condition is violated, and there are two separate strongly connected groups and an agent who pays attention to both of these groups, then the two groups might reach different consensuses, and the agent paying attention to both might have an intermediate limiting belief. The assumption that $T_{ii} > 0$ is not really essential to the result, but is an easy way to guarantee that the setting is aperiodic no matter how T varies with time and circumstances so that things converge nicely. The bounding below of positive weights by some $\delta > 0$ is not a necessary condition, but some sort of bound is needed. To see this, simply consider an example where two agents pay attention to each other, but the weight each one places on the other's belief goes to 0 at a sufficiently high rate as the others beliefs get closer, and then their beliefs never converge (see Exercise 8.9).

It is clear that Theorem 8.3.2 must allow for various sets of agents to have different limiting beliefs, as in the Krause [**?**] model, no updating occurs at all between agents whose beliefs start out at a distance of more than d. For example, if $d < 1/2$ it is easy to find examples in that model where there will be multiple limiting sets of beliefs.

The Krause model has a discontinuity in it, as an agent will pay attention to one belief at a certain distance, but not another one which a disance of more than ε away. That discontinuity turns out to be important in determining whether or not beliefs differ across different subgroups. For instance, consider the following continuous variation of that model.

EXAMPLE **8.3.7** *Continuous updating with "close" beliefs.*

Consider the following model where agents place positive weight on all others, but

place higher weight on opinions closer to their own:

$$T_{ij}(p(t),t) = \frac{e^{-\gamma_{ij}|p_i(t)-p_j(t)|}}{\sum_k e^{-\gamma_{ik}|p_i(t)-p_k(t)|}},$$

where $\gamma_{ij} > 0$ for all ij. Here, there is lower bound on weights and all are positive, so a consensus reached among all agents from any starting belief.

The following generalization of the DeGroot model shows that it is possible that a consensus is never reached, even when all agents are strongly connected, if agents keep looking back to their initial beliefs in updating.

EXAMPLE **8.3.8** *Time varying weight on own beliefs.*

Friedkin and Johnsen [241] examine a model in which updating always mixes in some weight on an individual's initial beliefs. Let D be an $n \times n$ matrix where entries are only positive along the diagonal, and $D_{ii} \in (0,1)$ indicates the extent to which agent i pays attention to others' attitudes. The evolution is described by

$$p(t) = D\widehat{T}p(t-1) + (I-D)p(0)$$

Here, it is easy to see that consensus may never be reached. For example, simply set $n = 2$, $D_{ii} = 1/2$ and $\widehat{T}_{12} = 1 = \widehat{T}_{21}$. Then an agent is always averaging his original belief with the latest belief of the other agent as follows:

$$p(t) = \begin{pmatrix} 1/2 & 0 \\ 0 & 1/2 \end{pmatrix} \begin{pmatrix} p_1(t-1) \\ p_2(t-1) \end{pmatrix} + \begin{pmatrix} 1/2 & 0 \\ 0 & 1/2 \end{pmatrix} \begin{pmatrix} p_1(0) \\ p_2(0) \end{pmatrix},$$

so that

$$p_i(t) = \frac{p_j(t-1)}{2} + \frac{p_1(0)}{2}.$$

Starting agent 1 with belief 1 and agent 2 with belief 0, it is straightforward to check that beliefs converge to 2/3 for agent 1 and 1/3 for agent 2.

From what we have seen here, there is a wide set of circumstances where a consensus is eventually reached, provided that agents do not (discontinuously) select whom they pay attention to based on agreement with their current beliefs, and as long as they do not cling too directly to the past. This still leaves important questions open, as we still are interested in knowing what beliefs converge to when they converge, and also how quickly beliefs change. If convergence takes many iterations, and updating is infrequent, then eventual convergence may not be so relevant. These are the issues that I discuss next.

8.3.5 Social Influence

In order to ascertain how each agent in the social network influences the limiting belief, let us return to the DeGroot model.

To start with, consider a closed and strongly connected group of agents, and for now let them be $\{1, \ldots, n\}$. Suppose also that T is aperiodic so that by Proposition 8.3.1 all beliefs converge and a consensus is reached. Let $p(0)$ be an arbitrary starting belief vector and $p(\infty) = (p^\infty, \ldots, p^\infty)$ be the vector of limiting consensus beliefs. To keep track of the limiting influence that each agent has, let us look for a vector $s \in [0,1]^n$, such that $\sum_i s_i = 1$ and

$$p^\infty = s \cdot p(0) = \sum_i s_i p_i(0).$$

If such an s exists, then limiting beliefs would be weighted averages of the initial beliefs, and the relative weights would be the influences that the various agents have on the final consensus beliefs.

To get a feeling about where such weights would come from, suppose that such an influence vector exists that keeps track of the influence of each agent regardless of the initial beliefs. Then since starting with $p(0)$ or starting with $p(1) = Tp(0)$ yields the same limit, it must be that $s \cdot p(1) = s \cdot p(0)$. Therefore,

$$s \cdot (Tp(0)) = s \cdot p(0).$$

Since this has to hold for every $p(0)$, it follows that

$$sT = s. \tag{8.2}$$

Thus, s is a left-hand unit eigenvector of T.[9] In the case where T is strongly connected, aperiodic, and row stochastic, there is a unique such unit eigenvector (eigenvector with eigenvalue 1) that has nonnegative values, and in fact it has all positive values.[10]

Indeed, there is also an easy way to calculate this eigenvector, as it must be that $s \cdot p(0)$ leads to the same belief as any entry of $p(\infty) = (p^\infty, \ldots, p^\infty) = T^\infty p(0)$. Thus, it must be that each row of T^∞ converges to s. We already saw this in Example 8.3.2.

EXAMPLE **8.3.9** *Social Influence in Example 8.3.2*

[9] See Section 2.4 for definitions and discussion of eigenvectors and eigenvalues.

[10] This follows from variations on the Perron-Frobenius Theorem and results in Markov chain theory. For details, see Lemma 5 in Golub and Jackson [278].

Recall the updating matrix described by

$$T = \begin{pmatrix} 0 & 1/2 & 1/2 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \end{pmatrix}.$$

where

$$T^t \to \begin{pmatrix} 2/5 & 2/5 & 1/5 \\ 2/5 & 2/5 & 1/5 \\ 2/5 & 2/5 & 1/5 \end{pmatrix}.$$

Note that $s = (2/5, 2/5, 1/5)$ is a unit eigenvector of T, that is:

$$sT = (2/5, 2/5, 1/5) \begin{pmatrix} 0 & 1/2 & 1/2 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \end{pmatrix} = (2/5, 2/5, 1/5) = s.$$

In general, an easy way to calculate or at least approximite the left-hand unit eigenvector of a stochastic matrix T is simply to iterate on T^t and find its limits. One can also solve $sT = s$ directly in cases where n is not too large.

It is worth noting the relationship between this measure of social influence and the eigenvector-based centrality measures discussed in Section 2.2.4. Indeed, this model can be thought of as providing an explicit basis for some of eigenvector-based measures of centrality and influence.

If there is only one closed strongly connected group, then the above reasoning tells us what its beliefs converge to, and the relative social influences that each of its members has. The remaining agents must then each have directed paths leading to the strongly connected group, and must reach the same consensus belief (Proposition 8.3.1). Thus, these other agents end up without any social influence on the limiting belief, and their initial beliefs are completely irrelevant in determining the limiting belief.

In the case where there are several closed strongly connected groups, each will reach its own consensus, with its own social inluence weights, and then the remaining agents who are path-connected to the strongly connected groups will end up with some weighted average of the limit beliefs of the strongly connected groups. This is shown by DeMarzo, Vayanos and Zwiebel [183], and stated as follows.

Given T, let $\mathcal{M}$ be the collection of closed and strongly connected sets of agents, and let $M = \bigcup_{B \in \mathcal{M}} B$.

THEOREM **8.3.3** *[DeMarzo, Vayanos, and Zwiebel [183][11]] Given T, partition the set of agents into closed and strongly connected groups $B_1, \ldots, B_K$ and let R denote the remaining agents who are not in any closed and strongly connected group. A stochastic matrix T is convergent if and only if there is a nonnegative row vector $s \in I\!R^n$ such that*

- $\sum_{i \in B_k} s_i = 1$ *for any closed and strongly connected group of agents B_k,*
- $s_i > 0$ *if i is in a closed and strongly connected group and $s_i = 0$ otherwise,*
- s_{B_k} *is the left-hand nonnegative unit eigenvector of T restricted to B_k,*
- *for any vector p and B_k, $\left(\lim_{t\to\infty} T^t_{B_k} p\right)_{B_k} = s_{B_k} p_{B_k}$,*

and for each agent $j \in R$ who is not in any closed strongly connected group there exists a $w^j_{B_k} \geq 0$ for each B_k such that $\sum_k w^j_{B_k} = 1$ such that

- $(\lim_{t\to\infty} T^t p)_j = \sum_k w^j_{B_k} s_{B_k} p_{B_k}$.

Theorem 8.3.3 states that (provided a society converges) each closed and strongly connected set of nodes converges to a consensus belief that is determined by the social influence vector for that group times the group's initial beliefs. Agents outside of the closed and strongly connected sets then converge to some weighted average of the closed and strongly connected groups limiting beliefs. This is illustrated in the context of Example 8.3.4

EXAMPLE **8.3.10** *Social Influence in Example 8.3.4.*

Given the updating in the six person society from Example 8.3.4 we can determine the social influence weights, and other weights as follows. First, it is clear that agent 1 will just stick with his or her initial beliefs, and so $s_1 = 1$. Next, the only other closed and strongly connected set of agents is $\{3, 4, 5\}$. These agents only pay attention to each other in updating and will reach a consensus as if they were an isolated society. If we examine the left-hand unit eigenvector of T restricted to these three agents, the restricted T is

$$T_{\{3,4,5\}} = \begin{pmatrix} 1/2 & 1/2 & 0 \\ 0 & 0 & 1 \\ 1/4 & 0 & 3/4 \end{pmatrix},$$

[11] Their result assumes that $T_{ii} > 0$ for each i, which is not necessary. Theorem 8.3.3 is a version stated and proven in Golub and Jackson [278].

and it has a unit eigenvector of $(2/7, 1/7, 4/7)$, and so these are the corresponding entries of s. Thus, these three agents will converge to a belief of $\frac{2}{7}p_3(0)+\frac{1}{7}p_4(0)+\frac{4}{7}p_5(0)$, and the overall influence vector is

$$s = (1, 0, 2/7, 1/7, 4/7, 0).$$

Note that this vector sums to 2, the number of closed strongly connected groups, and each group converges to its own consensus. As for the remaining agents, 6 only pays attention to 6 and 4. Given that 4 eventually converges, 6's belief will converge to 4's belief regardless of 6's initial belief. Therefore, 6 has a weight of 1 on $\{3, 4, 5\}$, and so $w^6_{\{1\}} = 0$ while $w^6_{\{3,4,5\}} = 1$. Next let us consider agent 2's limiting belief. Agent 2 is paying equal attention to 1, 2, 5, and 6. As 1, 5 and 6's beliefs converge to various limits, 2's initial belief will not matter. Given that 6 will converge to the same belief as 5, then effectively 2 has twice as much weight on the limiting belief of 5 (2/4) compared to that of 1 (1/4). We can also see this by simply noting that 2's limiting beliefs have to satisfy the following:

$$p_2(\infty) = \frac{1}{4}p_1(\infty) + \frac{1}{4}p_2(\infty) + \frac{1}{4}p_5(\infty) + \frac{1}{4}p_6(\infty),$$

and so given that $p_6(\infty) = p_5(\infty)$ we have that

$$\frac{3}{4}p_2(\infty) = \frac{1}{4}p_1(\infty) + \frac{1}{2}p_5(\infty),$$

or

$$p_2(\infty) = \frac{1}{3}p_1(\infty) + \frac{2}{3}p_5(\infty).$$

Thus $w^2_{\{1\}} = 1/3$ and $w^2_{\{3,4,5\}} = 2/3$, and so 2's limiting beliefs are obtained by giving weight 1/3 to 1's belief and 2/3 to the consensus limit of 3,4,and 5.

These last calculations provide us with a general approach to solving for the w's. We know that for any i who is not in a closed and strongly connected group, the limiting beliefs of i will have to satisfy the following equation in order to have converged:

$$p_i(\infty) = T_{ii}p_i(\infty) + \sum T_{iB_k}p_{B_k}(\infty) + \sum_{j\in R, j\neq i} T_{ij} \sum_k w^j_k p_{B_k}(\infty),$$

for any limiting beliefs $p_{B_k}(\infty)$ of the closed strongly connected groups B_k, where $T_{iB_k} = \sum_{\ell\in B_k} T_{i\ell}$. This implies that

$$w^i_{B_k} = \frac{T_{iB_k} + \sum_{j\in R, j\neq i} T_{ij}w^j_k}{1 - T_{ii}}.$$

This is generally an easily solved set of equations.[12]

In terms of influence, we can deduce some general insights. Note that since s corresponds to a (left-hand unit) eigenvector of T, it follows that

$$s_j = \sum_i T_{ij} s_i \tag{8.3}$$

for all j. This implies that an agent derives influence by being listened to by people who are influential themselves.

From this observation we can derive some easy conclusions about social influence. If one agent, say j, receives systematically more weight than another, say k, so that $T_{ij} \geq T_{ik}$ for all i, then j will have more influence than k. This gives us an obvious and natural notion of opinion leaders - they are simply individuals that dominate others in the weights assigned to them in the communication and updating process. It is also easy to see that if two individuals receive similar weights, then the one who receives weight from agents who in turn have higher social influence will have more influence. There are also some benchmark cases that we can consider: If the society is reciprocal, so that $T_{ij} = T_{ji}$ for all i and j, then all agents will have equal weight, regardless of actual distribution of weights. This follows from the result that if $\sum_i T_{ij} = 1$ for all j, then each agent has the same influence (see Exercise 8.10).

To get a feel for how the social influence vector's depend on the social structure, let us examine a particular application.

EXAMPLE **8.3.11** *An Application: Influence in Krackhardt's Advice Network*

Krackhardt [389] collected data regarding a small manufacturing firm on the west coast of the United States. The firm had about 100 employees and 21 managers. Krackhardt collected information from the managers about who sought advice from whom. The resulting directed network is pictured in Figure 8.3.5.[13]

[12] The equations always have a unique solution, by the following argument pointed out to me by Ben Golub. The equations can be written as $(I - T_R)w_k = c$ for $k \in \{1, \ldots, K\}$, where T_R is the restriction of T to R, I is the $|R| \times |R|$-identity matrix, w_k is an $|R| \times 1$ vector that has j-th entry $w^j_{B_k}$, and c is a vector that does not involve w_k. There is a unique solution if $I - T_R$ is invertible. That follows from observing that $T_R^t \to 0$ since the weights in T_R sum to less than 1 for at least one row, which then implies that T_R does not have a unit eigenvalue.

[13] Krackhardt asked each manager to fill out a questionnaire indicating the full advice network. The data used here has a directed relation from i to j if both i and j responded that i seeks advice from j (these are the data in the "LAS" matrix from page 129 of Krackhardt [389]).

Figure 8.3.5. Krackhardt's Network of Advice among Managers

Based on these data, we can develop a T matrix by normalizing each row of the advice matrix to sum to one, so that it gives an idea of how a given agent weights others' opinions in forming his or her own. So, if i seeks advice from seven different agents including agent j, then $T_{ij} = 1/7$. This might not correspond to the actual weights that different agents place on each other, but the data do not contain any weighted information. This also does not contain any self-weighting. This could be added, but again the data do not provide any direct insight into how much agents self-weight.

Given this matrix T we can then calculate the s vector directly as the left-hand unit eigenvector.[14] The resulting influence weights s are reported in Table 8.1.

[14]This was done using the program Matlab, which reports all 21 eigenvecors and eigenvalues for the 21×21 T matrix.

Table 8.1: Influence in Krackhardt's Network of Advice among Managers

label	s	level	dept.	age	tenure
1	0.048	3	4	33	9.3
2	0.132	2	4	42	19.6
3	0.039	3	2	40	12.8
4	0.052	3	4	33	7.5
5	0.002	3	2	32	3.3
6	0.000	3	1	59	28
7	0.143	1	0	55	30
8	0.007	3	1	34	11.3
9	0.015	3	2	62	5.4
10	0.024	3	3	37	9.3
11	0.053	3	3	46	27
12	0.051	3	1	34	8.9
13	0.000	3	2	48	0.3
14	0.071	2	2	43	10.4
15	0.015	3	2	40	8.4
16	0.000	3	4	27	4.7
17	0.000	3	1	30	12.4
18	0.106	2	3	33	9.1
19	0.002	3	2	32	4.8
20	0.041	3	2	38	11.7
21	0.201	2	1	36	12.5

There are some interesting patterns that help provide us with insight regarding the influence weights s. First, there are four agents (6, 13, 16, 17) whom no other agents seek advice from. Each of these agents is then outside of the single closed strongly connected group here, which contains all of the other agents. Next, we see that the influence can be much different from indegree. For example, agent 21 has the highest influence, even though he or she is the advisor of eight other agents, while agent 18 advises twelve other agents. This happens for at least two reasons. First, influence is higher when an agent is paid attention to by other agents who are in turn paid attention to more; and second, one gets more influence when advising agents who seek

advice from relatively fewer agents. For instance, agent 7 (the head of the firm) has substantial influence even though he or she only advised six other managers. What is crucial to this, is that agent 7 advises 2, 18, and 21, who all have substantial influence themselves (and are at the second level of the hierarchy in the firm).

As mentioned above, social influence as defined in the context of the DeGroot model provides a foundation for eigenvector based centrality measures. It also provides a basis for understanding other related systems. In particular, the structure of Google's "PageRank" system[15] is analagous to the influence vectors here, where the T matrix is derived by normalizing the directed matrix of links between web pages (so that $T_{ij} = 1/d_i$ if page i has a link to page j, and d_i is the number of directed (out) links that page i has to other pages).

8.3.6 Segregation and Time to a Consensus*

While eventual convergence of beliefs and the reaching of a consensus is important, it is also important to know how quickly beliefs will reach their limit. In many applications there might only be a few rounds of updating, or we might expect there to be new information entering the system over time, or updating might happen over long time horizons. If the convergence is slow, then it could be that we would observe very heterogeneous beliefs in a society even though it might tend towards a consensus. So, let us examine how quickly beliefs will reach a consensus, and whether we can generally quantify this.

Two Agents

In order to develop the basic intuitions and begin to quantifying the speed of convergence, it is useful to start with the case of two individuals, as that is particularly transparent and actually provides the basis for a general analysis.

Before developing the formal analysis, it is useful to discuss the basic ideas. If the two individuals have very similar weightings, so that the weight that 1 places on 1, T_{11}, is similar to the weight that 2 places on 1, T_{21}, (which happens if and only if T_{12} is close to T_{22}), then they will clearly quickly have beliefs that are close, and in fact the end social influence of 1 will be close to T_{11} and the influence of 2 will be close to T_{22}.

[15] Some other citation and ranking measures are also based on eigenvectors, as for instance the measure of Palacios-Huerta and Volij [495].

Thus, similar weightings, in terms of similar rows of T, produce "fast" convergence. Conversely, if the weightings of the two agents are very different, then their beliefs can differ substantially for longer periods and convergence will be relatively slower. For instance, if each agent weights his or her own opinion very heavily and pays little attention to the other agent, then the beliefs will be slow to converge and slow to reach a consensus.[16] So, heuristically, we should expect that the rate of convergence should be related to some measure of how much T_{11} differs from T_{21}.

In what follows, let us focus in on the only nontrivial case which is that of strongly connected aperiodic setting (so the off-diagonals of T are positive) and where the agents do not place identical weights on each other. Thus things will converge and each agent has some limiting influence, and convergence is not instantaneous.

To develop this more formally, we need to have an idea of how beliefs at time t, $p(t) = T^t p(0)$, differ from the initial beliefs $p(\infty)$. One way to keep track of this difference is to keep the difference between T^t and its limit T^∞ (which, recall from above, has as its rows the influence vector s which is the left-hand unit eigenvector). Now, in order to see how T^t behaves as we increase t, it is useful to rewrite T using what is known as its "diagonal decomposition." In particular, let u be the matrix of left hand eigenvectors of T. Then u has the following form

$$u = \begin{pmatrix} s_1 & s_2 \\ 1 & -1 \end{pmatrix}, \tag{8.4}$$

where (s_1, s_2) is the unit eigenvector corresponding to the social influence weights, and (1,-1) is the other eigenvector. It is easy to check that here $s_1 = \frac{T_{21}}{1+T_{21}-T_{11}}$ and $s_2 = \frac{1-T_{11}}{1+T_{21}-T_{11}}$. Also, in the case of a row stochastic T with $n = 2$, (1,-1) is always the second eigenvector, since

$$(1,-1)T = (T_{11} - T_{21}, T_{12} - T_{22}) = (T_{11} - T_{21}, -(T_{11} - T_{21})) = (T_{11} - T_{21})(1,-1).$$

Moreover, not only is (1,-1) the second eigenvector, but its associated eigenvalue is $T_{11} - T_{21}$.

Since u is the matrix with rows being the eigenvectors, we know that

$$uT = \Lambda u, \tag{8.5}$$

[16] Note that this also happens when each agent weights the other agent heavily and himself or herself only a small amount, in which case beliefs can oscilate over time, but still can be slower to converge.

where Λ is the matrix with the first and second eigenvalues λ_1 and λ_2 (ranked in terms of absolute values) on its diagonal:

$$\Lambda = \begin{pmatrix} \lambda_1 & 0 \\ 0 & \lambda_2 \end{pmatrix} = \begin{pmatrix} 1 & 0 \\ 0 & T_{11} - T_{21} \end{pmatrix}.$$

From (8.4) and given that $s_1 > 0$ and $s_2 > 0$ we know that u has an inverse, u^{-1} which is easily seen to be

$$u^{-1} = \begin{pmatrix} 1 & s_2 \\ 1 & -s_1 \end{pmatrix}. \tag{8.6}$$

From (8.5) it follows that

$$T = u^{-1}\Lambda u, \tag{8.7}$$

This is the *diagonal decomposition* of T.[17] From (8.7) it follows that

$$T^2 = u^{-1}\Lambda u u^{-1}\Lambda u = u^{-1}\Lambda^2 u,$$

and more generally that

$$T^t = u^{-1}\Lambda^t u. \tag{8.8}$$

So, the convergence of T^t is directly related to the convergence of Λ^t,

$$\Lambda^t = \begin{pmatrix} \lambda_1^t & 0 \\ 0 & \lambda_2^t \end{pmatrix} = \begin{pmatrix} 1 & 0 \\ 0 & (T_{11} - T_{21})^t \end{pmatrix}.$$

Given that $\lambda_2 = (T_{11} - T_{21}) < 1$, it follows that λ_2^t converges to 0, and so the distance of T^t from T^∞ is simply a factor times the second eigenvalue raised to the t-th power, or $(T_{11} - T_{21})^t$. Thus, we confirm the heuristic relationship that we started with: the convergence of T is tied to the level of differences in the weights of the agents.

To get the full expression for T^t note that by (8.8) it follows that

$$T^t = \begin{pmatrix} 1 & s_2 \\ 1 & -s_1 \end{pmatrix} \begin{pmatrix} \lambda_1^t & 0 \\ 0 & \lambda_2^t \end{pmatrix} \begin{pmatrix} s_1 & s_2 \\ 1 & -1 \end{pmatrix} = \begin{pmatrix} s_1 + \lambda_2^t s_2 & s_2 - \lambda_2^t s_2 \\ s_1 - \lambda_2^t s_1 & s_2 + \lambda_2^t s_1 \end{pmatrix}. \tag{8.9}$$

[17] It is sometimes useful to note that u^{-1} is the matrix of right-hand eigenvectors of T, and that they have the same matrix of eigenvalues as u. To see this, note that from (8.5) it follows that $uTu^{-1} = \Lambda u u^{-1} = \Lambda$, Thus $u^{-1}uTu^{-1} = u^{-1}\Lambda$ and so $Tu^{-1} = u^{-1}\Lambda$, and u^{-1} is the vector of right hand eigenvectors. The left-hand and right-hand eigenvectors also go by the names of the row and column eigenvectors, respectively. The diagonal decomposition can then be stated in terms of u and its inverse, or equivalently in terms of the two matrices of column and row eigenvectors.

Therefore,

$$p_1(t) = \left(s_1 + \lambda_2^t s_2\right) p_1(0) + \left(s_2 - \lambda_2^t s_2\right) p_2(0) = p_1(\infty) + \left(T_{11} - T_{21}\right)^t s_2 \left(p_1(0) - p_2(0)\right). \tag{8.10}$$

or

$$|p_1(t) - p_1(\infty)| = |T_{11} - T_{21}|^t s_2 |p_1(0) - p_2(0)|. \tag{8.11}$$

or

$$|p_1(t) - p_1(\infty)| = \frac{|T_{11} - T_{21}|^t (1 - T_{11})}{1 - T_{11} + T_{21}} |p_1(0) - p_2(0)|.$$

Thus, the difference between the beliefs of agent 1 at time t and the limit varies linearly with the difference in the agents' starting beliefs and with the influence of the other agent, and declines exponentially quickly in time: proportionally to the t-th power of the difference in weights that the agents have.

Convergence that is exponential in t is generally considered to be "fast", although that depends on the application in terms of how frequently updating occurs and how different the weight are. If agents are only updating a few times, and they have very different weights, then they can maintain quite different beliefs. Having a direct expression for T^t allows one to see how close beliefs are to their limit (and also to consensus) at any date.

Many Agents

The place at which we relied on $n = 2$ in the above derivation was for the precise expression of the second eigenvalue and eigenvectors. The facts that T has a diagonal decomposition as $T = u^{-1}\Lambda u$ and that

$$T^t = u^{-1}\Lambda^t u, \tag{8.12}$$

extend readily to $n > 2$, where Λ is the diagonal matrix with entries that are the eigenvalues of T and u is the matrix of corresponding left-hand (row) eigenvectors.[18] So, here the convergence of T^t to the limit T^∞ depends on how quickly λ_k^t goes to 0 for each k, where λ_k is the k-th largest eigenvalue of T. This will generally be governed by the second largest eigenvalue as the others will converge more quickly.[19] By (8.12)

[18] This holds when u is invertible, and thus when u is nonsingular, so for generic T. When $n > 2$, some eigenvalues can be complex-valued but the decomposition is still valid.

[19] The Perron-Frobenius Theorem (e.g., see Meyer [**?**]) tells us that if T is stochastic, strongly connected, and aperiodic, then the second eigenvalue is less than one. The Perron-Frobenius Theorem

(noting that u^{-1} has a first column that is all ones[20]) it follows that

$$\left[T^t\right]_{ij} = s_j + \sum_{k\geq 2} \lambda_k^t u_{ik}^{-1} u_{kj}.$$

Thus, the exact expression for the difference between the beliefs of agent i at time t and the limiting beliefs is given by

$$p_i(t) - p_i(\infty) = \sum_j p_j(0) \sum_{k\geq 2} \lambda_k^t u_{ik}^{-1} u_{kj}. \tag{8.13}$$

The expression (8.13) provides the basis for the following theorem. Many such convergence results exist in the theory of Markov chains, as well as in the specific context of social influence models (e.g., see Seneta [556] or DeMarzo, Vayanos and Zweibel [**?**]).

THEOREM **8.3.4** *Let T be strongly connected and aperiodic and let λ_2 be the second-largest eigenvalue of T. Moreover, suppose that the matrix of left-hand eigenvectors u is nonsingular and thus invertible, so that T is diagonalizable.*[21] *Then $|\lambda_2(T)| < 1$ and there exists $C > 0$ such that for each $i \in \{1, \ldots, n\}$:*

$$|p_i(\infty) - p_i(t)| \leq C \left|\lambda_2^t\right|. \tag{8.14}$$

Moreover, if T is nonsingular, then there exists some i and $p(0)$ and $c > 0$ such that for all large enough t

$$|p_i(\infty) - p_i(t)| \geq c \left|\lambda_2^t\right|. \tag{8.15}$$

The inequality in (8.14) follows direcly from (8.13) noting that $|\lambda_2^t|$ is larger than any other $|\lambda_k^t|$ for any k, and that the other parts of the expression are independent of t. The inequality in (8.15) also follows from (8.13), although a full proof requires showing that the weighting term on the second eigenvalue (plus any further eigenvalues that take on the same value as the second) on the right hand side of (8.13) (i.e., $u_{i2}^{-1} u_{2j}$) must be nonzero for some i and j. Then setting $p_j(0) = 1$ and $p_k(0) = 0$ $k \neq j$. For a full proof of the second claim, see Karlin and Taylor [**?**].

applies to primitive matrices (those with all positive entries), but T^t has all positive entries for large enough t, which can be shown by variations on the Perron-Frobenius Theorem, or more directly given the strong connection and aperiodicity.

[20] It is easy to check that the unit column eigenvector is a vector of all 1's.

[21] The case of non-diagonalizable T is non-generic, but that does not mean that such matrices might not pop up in practice, especially if T is derived from normalizing some adjacency matrix that has 0-1 entries. The case of non-diagonalizable T have a similar result with an adjustment to the expression in (8.14); see Seneta [556].

EXAMPLE **8.3.12** *Convergence Speed in Krackhardt's Advice Network*

The second largest eigenvalue in magnitude corresponding to Krackhardt's advice network discussed in Example **??** is .4825.[22] From (8.13) we can get a very rough upper bound on the C in (8.14), simply by noting that the sum is less than $\lambda_2^t 20$, given that $n = 21$. Thus, a crude upper bound on the distance from a consensus at time t is $20 \times (.5)^t$.

While Theorem 8.3.4 offers detailed information about the rate of convergence of beliefs, the second largest eigenvalue is not directly intuitive. In the case of two agents we were able to relate the second eigenvalue to the difference in one of the agent's self weight and the incoming weight from the other agent, and so it had a natural interpretation. In the case of more than two agents, however, it does not have quite as direct an interpretation. Nonetheless, the second eigenvalue still has a relationship to the level of difference in the weights that different agents place on each other. A result developed by Hartfiel and Meyer [305] relates the second eigenvalue of a stochastic matrix to another measure which has a more intuitive feel and is related to the difference of weights that we find in the two agent case.

Given some $A \subset N$, let

$$T_{A,A^c} = \sum_{i \in A, j \notin A} T_{ij}.$$

Thus, this is the total weight that all agents in A place on agents outside of A.

Let the *coupling of* T, denoted $\sigma(T)$, be defined by

$$\sigma(T) = \min_{B \neq \emptyset, C \neq \emptyset : B \cap C = \emptyset} \left(T_{B,B^c} + T_{C,C^c} \right). \tag{8.16}$$

This examines how strongly interconnected all the different subgroups of a society are. If the coupling measure is low, then there are two disjoint groups who pay little attention to anyone outside of their respective groups. In such a situation, those two groups can maintain different beliefs for a longer time, and then convergence will be relatively slow and it will take a long time to approach a consensus. To understand why the uncoupling measure looks at two groups and not just one, note that if there is just one group that is introspective, then the rest of the society must be paying some attention to that group so that convergence can still be fast. For instance, if everyone is paying substantial attention to a single agent, say i, then convergence can still be

[22] Again, this was calculated using the program Matlab from the stochastic matrix described in Example **??**.

fast. Thus the coupling measure needs to ensure are two disjoint groups with little communication in order to have slow convergence.

THEOREM **8.3.5** *[Hartfiel and Meyer [305]] For any $\varepsilon > 0$, there exists a $\delta > 0$ such that if T is a strongly connected stochastic matrix and $\sigma(T) < \delta$, then $|\lambda_2(T)| > 1 - \varepsilon$. Conversely, for any $\delta > 0$ there exists a $\varepsilon > 0$ such that if T is a strongly connected stochastic matrix and and $|\lambda_2(T)| > 1 - \varepsilon$, then $\sigma(T) < \delta$.*

Putting this together with Theorem 8.3.4 we can conclude that for any $\varepsilon > 0$, there exists a $\delta > 0$ such that such that if T is strongly connected and aperiodic with coupling less than δ, then we can find initial beliefs $p(0) \in I\!R^n$, an agent $i \in A$, and a $C > 0$ such that for all large enough t

$$|p_i(\infty) - p_i(t)| \geq C(1 - \varepsilon)^t. \tag{8.17}$$

Conditions that ensure that the second eigenvalue is close to 0, and so convergence is fast, are not as readily available. The above analysis suggests that the coupling measure is closely related to the second eigenvalue so that if coupling is close to one then the second eigenvalue is close to 0. When $n = 2$ this is true, and in fact the coupling measure is precisely 1 minus the the absolute value of the second eigenvalue (see Exercise **??**). When $n > 2$ such a relationship does not hold in general, although there there are some special cases where such results can be found.

Consider special class of T's known as *expander graphs* (e.g., see Hoory, Linial, and Widgerson [**?**]). These are T's which are d-regular and symmetric, so that there exists a degree $d \geq 1$ such that each i has $T_{ij} = \frac{1}{d}$ for d agents $j \neq i$, and where $T_{ij} = T_{ji}$. So, this can be thought of as a situation where communication is mutual and where agents split their time evenly between a set number of neighbors. Here, it is clear that the influences of the agents are equal (and are $s_i = \frac{1}{n}$ for each i as in Exercise 8.10), so the limit belief is the average of initial beliefs. Even though the influences are equal, the rate of convergence can still vary depending on how the agents are arranged.

There are various studies that examine how quickly neighborhoods grow in expansion graphs. If the expansion is slow, then some neighborhoods of agents are talking mainly amongst themselves and not so much to the remaining agents and we would expect slow convergence. Situations where the expansion is high, so that all neighborhoods of agents are placing high weight on outsiders, then the expansion is faster and so should be the convergence. A measure of this expansion rate is the *expansion ratio*

of a symmetric and d-regular T defined by

$$h(T) = \min_{B:|B|\leq n/2} \frac{T_{B,B^C}}{|B|} \tag{8.18}$$

Given the normalization by the size of B, it is clear that h lies between 0 and 1. So, this is keeping track of the percentage of the weight that the most inward-weighting group B places on outside groups. This has a similar structure to the coupling measure, except that it only looks at one B rather than two disjoint groups. Here, given the symmetry of the network, if B places low weight on the outside world, then the outside world must also place low weight on B, and similarly for high weight. Thus, it is sufficient to look across single groups.

A number of results on expander graphs relate the second eigenvalue to the expansion ratio. For example, it is known that $\lambda_2(T) \leq 1 - \frac{(h(T))^2}{2}$ (such results date to Cheeger [139], e.g., see Theorem 2.4 in Hoory, Linial, and Widgerson [320]). Combining this with Theorem 8.3.4 leads to the following proposition, as noted by Golub and Jackson [278]:

PROPOSITION **8.3.2** *If T is strongly connected, d-regular, and symmetric, then there exists $C > 0$ such that for each i:*

$$|p_i(\infty) - p_i(t)| \leq C \left(1 - \frac{(h(T))^2}{2}\right)^t.$$

With some feeling as to speed of convergence, let us now turn to the questoin of when it is that a society that reaches a consensus will reach an accurate one.

8.3.7 When a Consensus is Correct: Wise Crowds

While we have seen that strongly connected and closed groups agents following variations of repeated updating rules will reach consensus beliefs, provided that the updating rules they follow are convergent, this does not tell us whether the consensus beliefs are "correct". That is, it might be that the information that individuals are sharing concerns some objectively measurable event. For instance, they might be estimating the reliability of a product, or the probability that something will occur. In such cases, as they update their beliefs and those beliefs converge, we can ask whether or not those beliefs converge to the right probability (or expectation, etc.).

This question was analyzed in the context of the DeGroot model by Golub and Jackson [278], as follows. They consider a sequence of societies, indexed by n, where

n grows. Each society is strongly connected and convergent,[23] and described by the updating matrix T^n. There is a true state of nature described by μ, and each agent i in network n observes a signal so that the initial belief of i in society n is a random variable $p_i^n(0)$ that is distributed with mean μ, a finite variance of at least $\sigma^2 > 0$, and support that is a subset of a compact set $[-M, M]$. The signals are independently but not necessarily identically distributed.

In each social network of the sequence, the belief of each agent i in network n converges to the consensus limit belief $p^n(\infty) = \sum_i s_i^n p_i^n(0)$, where the social influences s_i^n are defined in Theorem 8.3.3. The sequence of networks is *wise* if $p^n(\infty)$ converges in probability to the true state μ as n grows. That is, the sequence $(T_n)_{n=1}^{\infty}$ is *wise* if for every $\varepsilon > 0$

$$\lim_n \Pr\left[|p^n(\infty) - \mu| \geq \varepsilon\right] = 0.$$

We know from the law of large numbers (Theorems 4.5.1 and 4.5.2) that if we simply average the signals, then the limiting average will converge to be accurate with a probability one. This implies that if the agents in the sequence of societies have equal influence, then they will converge to accurate beliefs, and so such a sequence of societies is wise. So, it is sufficient to have, for instance, $\sum_i T_{ij}^n = 1$ for each j; or to have reciprocal weights. But these are clearly not necessary conditions. What is necessary and sufficient is that no agent retain too much influence. This is, the necessary and sufficient condition for have a wise sequence of societies is that $\max_i s_i^n$ goes to zero (see Exercise 8.14). This follows since if some individual retains a non-vanishing weight, then the consensus will involve a nontrivial weight on this single signal and will retain a non-vanishing variance and cannot be wise. So, characterizing wise sequences of societies amounts to understanding when it is that no agent ends up with too much influence as the society grows.

It is clear that if there is some $\delta > 0$ and j such that all agents have weight at least δ on j (so $T_{ij}^n > \delta$ for all i and n), then j will have a weight of at least δ in each society, so that $s_j^n \geq \delta$ for all n (following directly from (8.3)). Thus, too strong an opinion leader will lead the society to a limiting belief that will not become accurate, as it retains too much weight on the single opinion. If that opinion is infinitely more accurate than others, then that could be useful, but in a situation where all agents have some error in their initinal beliefs, this will hinder the consensus's accuracy. Is it then possible to have some opinion leader j, but such that the weights of all agents

[23] Clearly, this is without loss of generality, as this is necessary for the society to reach a concensus.

Figure 8.3.7. Agent 1 retains social influence 1/2.

$i \neq j$ on j go to 0 as n grows? The following example from Golub and Jackson [278] shows that this can still lead to problems.

EXAMPLE **8.3.13** *An Influential Agent with High Relative Weight*

Consider the following updating rule. Each agent places weight δ on himself or herself. Agents other than 1 place weight δ on agent 1, while agent 1 places weight δ on each $j > 1$, as in Figure 8.3.7.

Regardless of the level of δ, even as it goes to 0 much more rapidly than $1/n$, agent 1 maintains social influence 1/2, and the limiting consensus is half agent 1's signal and half an average of all the other agents' signals (see Exercise 8.15). Here agent 1 gets much more weight relative any other agent, even though that could be a small amount of weight.

One might expect that bounding the relative weight that goes in to any agent relative to the weight going out would be enough. However, the following example shows that this is not the case. Indirect weight matters too.

EXAMPLE **8.3.14** *An Influential Agent with High Indirect Weight*

Here each agent places weight δ on the agent with the next lower label and $1 - \delta$ on the agent with the next higher label, except agent 1 who places weight δ on himself or herself, and agent 2 with self-weight $1 - \delta$. This is pictured in Figure 8.3.7.

Figure 8.3.7. A lack of balance in and out - Many agents maintain non-vanishing influence.

Here, one can verify from (8.3) (see Exercise 8.16) that

$$s_i^n = \left(\frac{\delta}{1-\delta}\right)^{i-1} \cdot \frac{1-\left(\frac{\delta}{1-\delta}\right)}{1-\left(\frac{\delta}{1-\delta}\right)^{n+1}}.$$

For instance, if δ is small, then s_1^n becomes large (close to 1) as n grows. This example shows the difficulty in providing conditions to guarantee the wisdom of crowds, as indirect trust is critical in building an agent's social influence.

Golub and Jackson [278] provide the following sufficient conditions for wise crowds.

Let $T_{AB} = \sum_{i \in A, j \in B} T_{ij}$ be the total weight placed by agents in A on agents in B.

The first condition is as follows. A sequence T^n is balanced if for every sequence of sets of agents B_n such that $|B_n| \leq n/2$,

$$\sup_n \frac{T^n_{B_n^C, B_n}}{T^n_{B_n, B_n^C}} < \infty,$$

for each n, where B_n^C is the complement of B_n.

This condition requires that a smaller group cannot be getting infinitely more weight in from a larger group than it gives back. This rules out not only examples like Example 8.3.13, where a single agent gets an unbalanced amount of weight, but also situations where some group of agents gets an unbalanced weight as otherwise some subset of them could retain nonvanishing influence.

The next condition is not a relative condition, but one on absolute weights.

A sequence T^n satisfies *minimal dispersion* if there is a $q \in \{1, 2, \ldots\}$ and $r > 0$ such that for any sequence of B_n and C_n such that $|B_n| \geq q$ and $|C_n| \geq n/2$, we have $T^n_{B_n, C_n} > r$ for all large enough n.

This condition requires groups that have some minimal number of agents in them must give some minimum weight to groups that contain more than half of the agents.

THEOREM **8.3.6** *[Golub and Jackson [278]] If $(T_n)_{n=1}^{\infty}$ is a sequence of convergent stochastic matrices satisfying balance and minimal dispersion, then it is wise.*

The reader is referred to Golub and Jackson [278] for the proof and other sufficient conditions. The basic outline is as follows. If the wise crowds condition fails, then there is some group of agents who retain nontrivial influence as the society grows. The number of agents who can retain influence, and the amount of influence that they can retain is limited by the fact that the influences sum to one in any society. The balance condition implies that the influential group cannot be getting its weight just from the

non-influential agents, as it would need a large amount of weight from them as their influence is going to 0. But then the dispersion condition implies that there is not enough weight coming just from the influential group, as they must be putting some of their weight to the outside.

Interestingly, the conditions for the wisdom of a society are not so closely related to the conditions which affect the speed of convergence. It is possible for a society to be wise and to converge quickly, as for example when every agent weights all agents equally and so convergence occurs in one period and the society is wise, or it could be that the society is wise and yet converges quite slowly, as for example when the agents are connected in a large circle each paying most of his or her attention to himself or herself and a small amount to his or her two closest neighbors. It is also possible for a society to be unwise and converge either quickly or slowly. For instance, if all agents pay substantial attention to a single agent, then convergence can be quite fast but too heavily influenced by the initial beliefs of that agent. Or, if society is split into two groups who pay most of their attention to two different agents, but with some small amount of communication between groups, then those two agents will have substantial influence and convergence can be quite slow.

The DeGroot model and its variants are tractable and powerful as tools for studying a variety of issues associated with the diffusion of information and learning. As the T matrix is something that can be examined empirically, it holds substantial promise as a tool for empirical research. In closing this chapter, let me offer a couple of thoughts on important directions for further development of the theory. In many settings, it is clear that opinions and beliefs do not converge to a consensus, despite the fact that societies are strongly connected, and yet in other contexts we do see a consensus. Persistent differences can be due to a number of factors, including updating that occurs infrequently or only for a few iterations, or having weights that change over time, or agents who care heterogeneously about events and concentrate differently on updating, or nonstationarities in the underlying environment so that new information is constantly coming in. The DeGroot model and some of its variations provide powerful starting points for analyzing the evolution of beliefs, but there is still much for us to learn in terms of seeing in which circumstances these models provide useful predictions and in further development of the theory.

8.4 Exercises

EXERCISE **8.1** *Extension of Proposition 8.2.1*

Show that Proposition 8.2.1 extends to situations where both A and B have uncertain payoffs, provided there are a finite number of possible distributions of payoffs for each and that each distribution over payoffs for A has a different mean expected payoff from each distribution of B. Argue that it then also holds with some finite number of action choices, under the same assumption of distinghuished distributions.

EXERCISE **8.2** *Failure of Action Consensus*

Argue that Proposition 8.2.1 fails to be true if there is some p_k for which $p_k = 1/2$. But argue that even in this case all agents must still have the same limiting payoff.

EXERCISE **8.3** *Failure of Payoff Consensus*

Argue that Proposition 8.2.1 fails to be true if there different agents face different realizations of p.

Argue that Proposition 8.2.1 fails to be true if agents face the same p as their neighbors at each point in time, but there is an (arbitrarily) small probability $\varepsilon > 0$ in each period that nature redraws the p with which it chooses payoffs and the p stays fixed until the next time nature redraws it.

EXERCISE **8.4** *Observational Learning in a Directed Network*

Argue that Proposition 8.2.1 holds if g is strongly connected and possibly directed.

EXERCISE **8.5** *Observational Learning in a Directed Network*

Consider the setting of Proposition 8.2.1, with the following variation. There are two agents. Agent 1 observes agent 2's actions and payoffs over time, but not her own, and agent 2 observes agent 1's actions and payoffs over time, but not his own. Suppose that an agent chooses the action that maximizes his or her expected current period payoff given his or her updated beliefs conditional on his or her information. Show that the two agents will eventually choose the same action, almost surely.

EXERCISE **8.6** *Herding, Cascades, and Observational Learning*

Consider the following variation of the observational learning model, which is due to Banerjee [34] and Bikhchandani, Hirshleifer and Welch [60]. Agents choose an action only once. The action A pays 1, while the action B pays either 0 or 2, with equal probability. Agents choose sequentially and cannot communicate other than to observe each others' actions (but not payoffs). Agents see all of the previous actions before making a choice themselves. So, agent 1 makes a choice and gets a payoff. Then agent 2 sees agent 1's choice (but not payoff) and chooses an action and gets a payoff. Then agent 3, having see the actions of 1 and 2, but not their payoffs, chooses an action and gets a payoff, and so forth. In terms of uncertainty: action B is either "good" and pays 2 for all of the agents who choose it, or "bad" and pays 0 for all of the agents who choose it. Agents know that the chances that B is bad or good are equal. In addition, they each get to observe a private signal about the state of nature ("good" or "bad"). The signal of agent i, denoted s_i takes on a value "good" or "bad". If the true state is "good", then the signal is "good" with a probability p, where $1 > p > 1/2$, and similarly if the state is "bad" then the signal is "bad" with probability p. The signals are independent across the agents, conditional on the state. All of the agents have had a course in basic probability, and choose the action which they think leads to the highest expected payoff conditional on all the information that they have. If they think there is an equal chance of good or bad, then they flip a coin.

So, let us think about how this process will evolve. The first agent has only her own signal. Thus, if she sees "good" then she thinks there is a p probability that the state is "good" and thus chooses action B. If she sees "bad" then she thinks that there is a p probability that the state is "bad", and so chooses action A. Therefore, based on the action of the first agent, all of the subsequent agents can deduce her signal. So, consider the case where the first agent chose B (the other case is analogous). If the second agent sees "good" then he has effectively seen two good signals, and so chooses A. If the second agent sees "bad", then he has effectively seen one good and one bad signal, and so chooses with equal probability. Note that the third agent cannot always be sure of the second agent's signal. If the third agent sees an action sequence B, A, then she can be sure that the signals were "good", "bad". But if the third agent sees B, B she cannot be sure of what the second agent's signal was.

Show that the third agent, conditional on seeing B, B will ignore her own signal and choose B regardless. Show that this will be true for all of the subsequent agents.

EXERCISE **8.7** *Existence of a Strongly Connected Closed Group*

Show that for any row-stochastic T, there always exists at least one closed and strongly connected set of nodes.

Show that the society can be partitioned into some number of strongly connected and closed groups, and then a remaining set of agents who each have at least one directed path to an agent in a strongly and connected group.

EXERCISE **8.8** *Convergence with Asynchronous updating and Periodicity**

Consider the following variation on the DeGroot model. Each period is divided into n sub-periods. In period t agents start with a vector of beliefs $p(t-1)$, and updating proceeds as follows. Agents update one at a time. Set $p(0,t) = p(t-1)$. Agent 1 updates first, and so a vector $p(1,t)$ is reached where only 1 has updated from $p(0,t)$. Next, agent 2 updates from $p(1,t)$ to form $p(2,t)$; and so on so that i updates from $p(i-1,t)$ to form $p(i,t)$, and then $p(t) = p(n,t)$.

Argue that beliefs converge to a consensus in any closed strongly connected component, regardless of whether it is aperiodic or not. (Hint: consider the highest belief and lowest beliefs at any time, and show that they must converge to each other over time.)

EXERCISE **8.9** *Non-convergence with Time/Distance Varying Weights*

Provide an example with $n = 2$ of the model in Example 8.3.5 where $p(0) = (0,1)$, and all entries of $T(p(t),t)$ are positive at all times, and beliefs converge, but such that a consensus is not reached. Why doesn't this contradict Theorem 8.3.2?

EXERCISE **8.10** *Equal Influence in an Updating Network*

Use 8.2 (and the result on the uniqueness of the influence vector) to show that if $T_{ji} = T_{ij}$ for all i in a strongly connected and aperiodic society, then every agent has the same influence. Show this is a consequence of the stronger claim (from Golub and Jackson [278]) that if $\sum_j T_{ji} = 1$ for all i, then every agent has the same influence.

EXERCISE **8.11** *A Stubborn Agent in an Updating Network*.*

Start with a strongly connected T in the DeGroot model. Pick some agent i, and generate $T(\varepsilon)$ as follows. For any $j \neq i$ set $T_{jk}(\varepsilon) = T_{jk}$. For i, set $T_{ik}(\varepsilon) = \varepsilon T_{ik}$ for $k \neq i$ and $T_{ii}(\varepsilon) = 1 - \sum_{k \neq i} T_{ik}(\varepsilon)$. Thus, as ε is becoming small, we are increasing the

weight that i places on himself or herself, and scaling down the weight that i places on other agents; while not changing the weights of any agent other than i at all.

Let $s_i(\varepsilon)$ be i's social influence. Show that as $\varepsilon \to 0$, i's social influence goes to 1. That is, show that $s_i(\varepsilon) \to 1$ and so the consensus beliefs in the society converge to being i's initial belief as ε becomes small.

EXERCISE **8.12** *Convergence Speed with Two Agents*

Consider the DeGroot model with two agents and

$$T = \begin{pmatrix} 1/2 & 1/2 \\ 1/4 & 3/4 \end{pmatrix}. \tag{8.19}$$

Find the social influence vector and the second eigenvalue. Using this and (8.10) find the exact expression for $p_1(t)$ when $p_1(0) = 1$ and $p_2(0) = 0$.

EXERCISE **8.13** *Convergence Speed and Integration with Two Agents*

Show that in the DeGroot model, when $n = 2$ and T is strongly connected, then the coupling measure is exactly 1 minus the absolute value of the second eigenvalue.

EXERCISE **8.14** *Necessary and Sufficient Conditions for Wise Crowds*

Prove the following Lemma from Golub and Jackson [278]:

LEMMA **8.4.1** *If $(T_n)_{n=1}^{\infty}$ is a sequence of strongly connected and aperiodic updating matrices, then*

$$\lim \Pr\left[\left|\sum_i s_i^n p_i^n(0) - \mu\right| \geq \varepsilon\right] = 0$$

for all $\varepsilon > 0$ if and only if $\max_i s_i^n \to 0$.

For the "if" part, build from the proof of Theorem 4.5.1. Argue the "only if" part directly.

EXERCISE **8.15** *Unwise Crowds: High Relative Weight.*

Show that agent 1's social influence is 1/2 in Example 8.3.13 for all n.

EXERCISE **8.16** *Unwise Crowds: Indirect Weight.*

Show that agent 1's social influence is

$$s_i^n = \left(\frac{\delta}{1-\delta}\right)^{i-1} \cdot \frac{1-\left(\frac{\delta}{1-\delta}\right)}{1-\left(\frac{\delta}{1-\delta}\right)^{n+1}}.$$

in Example 8.3.14.

EXERCISE **8.17** *Wise Crowds.*

Consider the updating rules from Examples 8.3.13 and 8.3.14 and show whether each satisfies or violates the balance condition and the dispersion condition.

Chapter 9

Decisions, Behavior, and Games on Networks

Peers exert enormous influence on human behavior. It is easy to cite examples, ranging from which products we buy, whether or not we engage in criminal activities, how much education we pursue, to which profession we choose. There is a vast literature on the subject including research by social psychologists, sociologists, researchers in education, and economists. We have already seen examples of studies that touch on these issues, and there is also a good bit known about statistical issues of identifying peer effects (see Chapter 13). The purpose of this chapter is to provide foundations for understanding how the structure of social networks influences behavior. For example, if we change the network of social interactions, how will behavior change? This issue has a rich history in sociology, and has more recently emerged in economics and computer science. Some aspects of this were touched on in the chapters on diffusion and learning, but there are many situations where social influences involve human decision-making rather than pure contagion or updating. The focus in this chapter complements those earlier chapters by expanding the analysis to explicitly account for how individual decisions and strategies are influenced by those of their neighbors.

The main complication in the analysis of this chapter compared to the study of diffusion and learning is that behavior depends in more complicated ways on what neighbors are doing. For example, if an individual is choosing a piece of software or some other product and wants it to be compatible with a majority of neighbors, then this is a coordination game, and behavior can change abruptly depending on how many neighbors are taking a certain action. It might also be that an individual only wants to buy a product or make an investment when his or her neighbors do not. These

interactive considerations require game theoretic reasoning, adapted and extended to a network setting.

The chapter begins by showing how a variation on the ideas we saw in the learning and diffusion analyses can be used to study behaviors. In particular, I start with a model where people react to their neighbors in a way that can be captured probabilistically, predicting their actions as a function of the distribution of their neighbors' play. After this, I introduce game-theoretic settings, where richer behaviors are studied . Here there are two main types of situations that are considered and which capture many of the applications of interest. One type is where there are strategic complementarities, as in choosing compatible technologies or pursuing education, where players' incentives to take a given action increase as more neighbors take that action. This leads to nice properties of equilibria and we can deduce quite a bit about how players' strategies will vary with their position in a network and how overall behavior in the society responds to network structure changes. The type of strategic interaction considered is one with the opposite incentive structure: that of strategic substitutes. There players can "free ride" on the actions of their neighbors, such as in gathering information or providing certain services, and a player's incentive to take a given action decreases as more neighbors take that action. This leads to quite different conclusions about player behavior and equilibrium structure. I also discuss models that are designed to capture dynamics of behavior.

9.1 Decisions and Social Interaction

Let me begin by discussing an approach to modeling interactive behavior that builds from the tools from the last two chapters on diffusion an learning. To model decisions in the face of social interaction one needs to characterize how a given individual will behave as a function of the actions of his or her neighbors. For instance, will the individual want to buy a new product if some particular subset of his or her neighbors are buying the product? Generally, the answer to such a question depends on a series of characteristics of the individual, the product, the alternative products, as well as the set of neighbors buying the product.[1] As a useful starting point, we can think

[1] The implications of interdependencies in consumer choices have been studied in a variety of contexts including the implications for how firms might price goods (e.g., see Katz and Shapiro [362]) and implications for increasing returns (e.g., see Arthur [19] and Romer [**?**]). For more background on consumers' behavior and network externalities see the survey by Economides [202].

of this as being stochastic, with a probability of the individual taking a given action depending on the actions chosen by the neighbors.

9.1.1 A Markov Chain

In order to fix ideas and provide a benchmark, consider a setting where interaction is symmetric in the sense that any individual can be influenced by any (or every) other, and the particular identities of neighbors are not important, just the relative numbers of agents taking various actions. Each individual chooses one of two actions. This might be a choice of either smoking or not, or choosing between two different technologies, going to one park or another, going to vote or not, voting for one of two candidates, etc.

The two actions are labeled as 0 and 1, and time evolves in discrete periods, $t \in \{1, 2, \ldots\}$. The state of the system is described by the number of individuals who are taking action 1, denoted by s_t, at the end of period t.

In some applications, if the state of the system is $s_t = s$ at time t, then there is a well-defined probability that the system will be in state $s_{t+1} = s'$ at time $t + 1$. That is, if we know how many people are taking action 1 at date t, then there is a well-defined distribution over the number of people taking action 1 at date $t + 1$. This might be deterministic or random, depending on what we assume about how people react to others. For example, it might be that each person looks at the state at the end of time t and then chooses the action which leads to the greatest benefit for that individual presuming that others will act as at time t; for instance if we pick one person at random from the society and ask them to update their choice. It might be that we have all individuals respond, or each one respond probabilistically. What is critical is that are well-defined probabilities of being in each state tomorrow as a function of the state today. Let Π be the $n \times n$ matrix describing these *transition probabilities* with the entry in row s and column s' being

$$\Pr(s_{t+1} = s' \mid s_t = s).$$

This results in a (finite state) Markov chain (recalling definitions from Section 4.5.8). If the Markov chain is irreducible and aperiodic, then it has a steady-state distribution described by the vector $\mu = (\mu_0, ..., \mu_n)$, where μ_s is the probability of state s, or that s players choose action 1. Thus, in situations where behavior can be described by a Markov chain, we have sharp predictions about behavior over the long run. Let us now examine some applications of this reasoning.

9.1.2 Individual by Individual Updating

Consider a setting where at the beginning of a new period, one individual is picked uniformly at random[2] and updates his or her action based on the current number of people in the society taking action 1 or 0.[3] How an individual updates his or her action depends on the state of the system. In particular, let p_s denote the probability that the individual chooses action 1 conditional on s out of the other $n-1$ agents choosing action 1. This form of updating could be a form of best reply behavior, where an individual (myopically) chooses an action which gives a highest payoff given the current actions of the other individuals. So, for instance, the individual decides on whether or not to go to/stay at the beach based on how many others are there. It could also be something similar to the contagion of a disease that we saw before, but now where the transition between infection and susceptible is a richer function of the state of the system.

Given this, the transition probabilities from one state to another are completely determined by the vector $p = (p_0, \ldots, p_{n-1})$. For example the probability of going from s to $s+1$ is the probability that one of the $n-s$ players choosing 0 out of the n players in total is selected to update, and then that player has a probability of p_s of selecting action 1, and so the probability is $fracn - snp_s$. The full list of transition probabilities is

$$\begin{aligned}
\Pr\left(s_{t+1} = s+1 \mid s_t = s\right) &= \frac{n-s}{n} p_s, \text{ for } 0 \leq s \leq n-1 \\
\Pr\left(s_{t+1} = s-1 \mid s_t = s\right) &= \frac{s}{n}\left(1 - p_{s-1}\right), \text{ for } 1 \leq s \leq n \\
\Pr\left(s_{t+1} = s \mid s_t = s\right) &= \frac{n-s}{n}\left(1 - p_s\right) + \frac{s}{n} p_{s-1}, \text{ for } 0 \leq s \leq n \\
\Pr\left(s_{t+1} = s' \mid s_t = s\right) &= 0, \text{ otherwise.}
\end{aligned}$$

This Markov chain has several nice properties. Provided that $1 > p_s > 0$ for each s, any state is eventually reachable from any other state and so the Markov chain is irreducible. Moreover, there is a chance of staying in any state, and so the Markov chain is aperiodic. Thus it has a unique steady-state distribution over states.

[2] This is not important, as one can use any method of picking the individual as long as it is Markovian, and it could weight different individuals differently, and as dependent on the state.

[3] Note that the interpretation of dates here is flexible. Effectively, time simply keeps track of the moments at which some agent makes a decision, and need not correspond to any sort of calendar time. The arrival process of when decisions are made can be quite general, with the main feature here being that only one agent is updating at any given moment.

In the setting here, the Markov chain takes a particularly simple form as only one individual is changing actions at a time. At steady-state, the probability of ending up in a state s is simply the probability of being in an adjacent state $s-1$ or $s+1$ and then getting one more individual or one fewer to choose action 1, or else starting at s and staying there. Thus,

$$\begin{aligned}
\mu_0 &= \mu_0(1-p_0) + \mu_1\left(\frac{1}{n}\right)(1-p_0) \\
\mu_s &= \mu_{s-1}\left(\frac{n-(s-1)}{n}\right)p_{s-1} + \mu_{s+1}\left(\frac{s+1}{n}\right)(1-p_s) + \mu_s\left(\frac{n-s}{n}\right)(1-p_s) + \mu_s\left(\frac{s}{n}\right)p_{s-1} \\
\mu_n &= \mu_{n-1}\left(\frac{1}{n}\right)p_{n-1} + \mu_n p_{n-1}
\end{aligned}$$

Solving this system leads to

$$\frac{\mu_{s+1}}{\mu_s} = \left(\frac{n-s}{s+1}\right)\left(\frac{p_s}{1-p_s}\right) \tag{9.1}$$

for all $0 \leq s \leq n-1$; which, together with $\sum_s \mu_s = 1$, completely determines the solution.

Ants, Investment and Imitation

To see an application of this, consider a model due to Kirman [376] where individuals imitate each other. In particular, Kirman's work was motivated by the observation that ants tend to "herd" on the food sources that they exploit even when faced with equally useful sources. Moreover, ants also switch which source they exploit more intensively. Kirman discusses similar such patterns of behavior in human investment and other forms of imitation. He models this by considering a dynamic where at each time an individual is selected uniformly at random from the population. With a probability ε the individual flips a coin to choose action 0 or 1 and with a probability $1-\varepsilon$ the individual selects another individual uniformly at random and mimics his or her action.

That model is a special case of the framework above, where[4]

$$p_s = \frac{\varepsilon}{2} + (1-\varepsilon)\frac{s}{n-1}.$$

[4]Kirman also allows for a probability that an individual does not change his or her action, but that is equivalent in terms of long run distributions, as it simply slows the system down and can be thought of as just changing the length of a time period.

Then

$$\frac{\mu_{s+1}}{\mu_s} = \frac{n-s}{s+1}\left(\frac{(n-1)\varepsilon + 2s\,(1-\varepsilon)}{2(n-1)-(n-1)\varepsilon - 2s\,(1-\varepsilon)}\right). \tag{9.2}$$

Given the symmetry of this setting, the long run probability (starting from a random draw of actions) of any individual choosing either action is 1/2. If $\varepsilon = 0$, then this is a system of pure imitation, and eventually the system is absorbed into the state 0 or n and then stays there forever. If $\varepsilon = 1$ then this is a system where individuals simply flip coins in choosing actions irrespective of the rest of society. Then $\frac{\mu_{s+1}}{\mu_s} = \frac{n-s}{s+1}$ and the system has a pure binomial distribution with a parameter of 1/2, so that the probability of having exactly s individuals choosing action 1 at a given date in the long run is $\mu_s = \binom{n}{s}\left(\frac{1}{2}\right)^n$. In that case, the extreme states are less likely and the most likely state is that half of the society is choosing action 1 and half choosing action 0.[5]

To get a uniform distribution across social states it must be that $\mu_{s+1} = \mu_s$ for each s. It is easily checked from (9.2) that this holds when $\varepsilon = 2/(n+1)$.[6]

To get the behavior of the ants, with tendencies to herd on action choice, the high and low states need to be more likely than the middle states. This requires that individuals pay more attention to others than in the situation just examined where the distribution across states is uniform. Thus, it must be that the probability that an individual ignores society and flips a coin is $\varepsilon < 2/(n+1)$. Then behavior is sensitive enough to the state of the society so that there is heavier weight on the more extreme states where all individuals follow one action or the other ($s = 0$ and $s = n$). This is pictured in Figure 9.1.2 for several different values of ε.

Thus, to get the "herding", one needs to have a high enough probability of imitating other agents so that the natural tendency towards even mixing is overturned.

Sensitivity to Societal Action and Herding

As I now show, Kirman's result about the relationship between social sensitivity and herding can be formalized and is true for more general processes than the pure imitation process described above. To see this, consider a class of processes that treat actions 0 and 1 symmetrically. That is, suppose that $p_s = 1 - p_{n-1-s}$, so that the chance of choosing action 1 conditional on s out of the other $n-1$ agents choosing action 1 is

[5] Note that each configuration of choices of actions across individuals is equally likely, but there are many more configurations (keeping track of players' labels) where half the society is choosing 1 and half 0 than there are configurations where all are choosing 0.

[6] This is slightly different from Kirman's expression since ε here is the chance that an agent flips a coin, where as it is the chance that an agent changes actions in Kirman's labeling.

Figure 9.1.2. Kirman's [375] Ant-Imitation Model for Three levels of Random Behavior.

the same as the chance of choosing action 0 conditional on s out of the other $n-1$ agents choosing action 0.

Say that a social system $p' = (p'_0, \ldots, p'_n)$ is *more socially sensitive* than another social system $p = (p_0, \ldots, p_n)$ if $p'_s \geq p_s$ when $s > \frac{n-1}{2}$ and $p'_s \leq p_s$ when $s < \frac{n-1}{2}$, with at least one strict inequality. Thus, an individual in a society described by p' is more likely to choose the same action as the majority of the population than an individual in a society described by p. Note that this does not require that an individual want to match the majority of a society. This admits processes where $p'_s < 1/2$ when $s > \frac{n}{2}$ so that an individual is actually choosing against the current of the society. The social sensitivity comparison is a relative comparison between two societies.

PROPOSITION **9.1.1** *If two different societies, described by p and p', each treat actions 0 and 1 symmetrically and the process p' is more socially sensitive than p, then the steady-state distribution over numbers of people taking action 1, $(\mu'_0, \ldots, \mu'_n)$ corresponding to p' is a mean-preserving spread of the steady-state distribution $(\mu_0, \ldots, \mu_n)$ corresponding to p. In fact, there exists $\overline{s} > \frac{n}{2}$ such that $\mu'_s > \mu_s$ if and only if $s > \overline{s}$ or $s < n - \overline{s}$.*

The proof of Proposition 9.1.1 can be deduced from (9.1) and is left as Exercise 9.2.

This result is not surprising, as it states that increasing the extent to which an individual's choice of action matches that of a majority of the society then increases the extent to which the society tends to extremes, in terms of spending more time in states where higher concentrations of individuals choose the same action. Nevertheless, such a result provides insight as to the type of behavior that leads to herding (or lack thereof). This is a different sort of herding than the consensus formation we saw in our discussion of learning in Chapter 8,[7] as the society here will oscillate between the actions over time, but with specific patterns of either herding to one action or the other, or else splitting among the two.[8]

Calvó-Armengol and Jackson [119] use such a model to study social mobility. Action 1 can be interpreted as pursuing higher education and the n individuals as being the families in some community. When a family is randomly chosen to make a new choice,

[7] This is also distinct from the "herding" literature of Banerjee [34], Bikhchandani, Hirshleifer and Welch [60], and others, who examine how situations with uncertainty and private information about the benefits of actions can lead individuals to follow a herd of others in choosing an action (see Exercise [**?**]).

[8] For example, if people wish to avoid congestion, so that they are likely to choose the action chosen by the minority, then the most likely state becomes that of $s = n/2$.

it is interpreted as having a child in the family replacing the parent and making a choice. Social mobility patterns are determined by how likely it is that a child makes the same choice that his or her parent did. Provided p_s is nondecreasing in s, a parent and child's decision will be positively correlated. The idea is that the child is most likely to choose action 1 when there are many others in the community who have chosen action 1, which is relatively more likely to happen in situations where the parent also chose action 1. Here one ends up with correlation between parent and child actions even though there is no direct link between the two, only the fact that the surroundings that influence their decisions overlap. Thus, this presents an explanation of social mobility that is complementary (no pun intended) to that of direct parent-child interaction.

For example, the probability that the parent and child both choose action 1 is $\sum_s \mu_s \frac{s}{n} p_{s-1}$. This comes from summing across states the probability of state s, μ_s, times the probability that the parent is a 1, $\frac{s}{n}$, times the probability that the child will also choose action 1, p_{s-1} (as there are $s-1$ others choosing action 1 given that the parent was choosing 1).

As a quick demonstration that such a model can easily generate outcomes consistent with observed patterns, Calvó-Armengol and Jackson [121] restrict attention to a special case where there are just two parameters that govern the Markov chain. There $p_s = q$ for some $1 > q > 0$ whenever $s \geq \tau$ and $p_s = 1 - q$ whenever $s < \tau$, where $\tau \in \{0, \ldots, n-1\}$ is a threshold. Thus, individuals choose action 1 with probability q if at least τ others have, and with probability $1 - q$ otherwise (see Exercise 9.3).

The following tables show a few representative observations of father-daughter education decisions from the Calvó-Armengol and Jackson [121] fitting exercise. The data are the relative frequencies of observations of father and daughter education choices based on wave 5 of the European Community Household Panel data set. 0 represents that the individual had no more than high school graduation; while 1 represents pursuing some education beyond high school. Here the Countries are AU=Austria, GR=Greece, and UK=the United Kingdom. The row choice of 0 or 1 is the father's choice while the column is the daugher's.

The second column of the table represents the probabilities that come out of the simple threshold model when the community size is 25 families, with the best fit q and τ (from a search on a grid of q to hundredths, and across each τ).

FATHER/DAUGHTER EDUCATION CHOICES.

data			estimation		
AU	0	1		0	1
0	.903	.033	0	.902	.048
1	.054	.008	1	.048	.003
				q=.95,τ=14	
GR	0	1		0	1
0	.646	.192	0	.648	.157
1	.124	.038	1	.157	.038
				q=.81,τ=15	
UK	0	1		0	1
0	.246	.223	0	.230	.250
1	.254	.278	1	.250	.270
				q=.52,τ=25	

The fitted values do not match exactly, and for instance in the fitted matrices the probability of 0,1 is the same as 1,0; which is a function of the simplified threshold model. Allowing for richer choices of the p_s's would provide a better fit. This is simply meant to show that such simple models can lead to patterns that are quite close to observed ones, and that social interaction is a viable part of explaining parent-child correlations, among other things.

9.1.3 An Interaction Model with Network Structure

While the simple Markov model of social interactions discussed above provides insight into broad patterns of social behavior, it does not incorporate the micro-details of who interacts with whom. Such network relations can have a profound effect on the process. To incorporate networked interactions, we need a richer structure. Consider the following process that allows us to incorporate a (possibly weighted and directed) network.

Again, individuals choose between two actions 0 and 1, and now the social state needs to keep track of which agents are taking which actions. The social state is thus an n-dimensional vector $x(t)$, where $x_i(t)$ for $i \in \{1, \ldots, n\}$ is the action that agent i took at period t.

Interaction is described by w, which is an $n \times n$-dimensional matrix, where entry $w_{ij} \in [0, 1]$ is a weight that describes the probability that individual i's choice in period $t + 1$ is the action that j took in period t. This is a row-stochastic matrix.

In addition, let us allow for a probability, denoted $\varepsilon_i(1)$, that i chooses action 1 independently of the state of the system, and a probability, denoted $\varepsilon_i(0)$, that i chooses action 1 independently of the state of the system. Letting $\Pr(x_i(t+1) = 1|x(t))$ denote the probability that $x_i(t+1) = 1$ given the state at time t is described by the vector $x(t)$, it follows that

$$\Pr\left(x_i(t+1) = 1|x(t)\right) = \varepsilon_i(1) + (1 - \varepsilon_i(1) - \varepsilon_i(0)) \sum_j w_{ij} x_j(t)$$

Allowing for $w_{ii} > 0$, we can encode the possibility that the agent does not update his or her action at all.

The Kirman "ants" model that we considered in Section 9.1.2 is the special case where $w_{ij} = \frac{1}{n-1}$ for $j \neq i$ and $j \leq n$, and $\varepsilon_i(1) = \varepsilon_i(0) = \frac{\varepsilon}{2}$.

Much richer models than the ants model can now be encoded. Just to get a feeling for the variables, consider an example where with probability 1/4 individual i sticks with his or her previous action, with probability 1/4 follows the action of agent $i-1$, with a probability follows the action of agent $i+1$, and with probability 1/4 randomizes between 0 and 1. This corresponds to $\varepsilon_i(1) = \varepsilon_i(0) = 1/8$ and then having equal (1/3) weights on i, $i+1$ and $i-1$ (mod n), or

$$w = \begin{pmatrix} 1/3 & 1/3 & 0 & 0 & \dots & 0 & 0 & 1/3 \\ 1/3 & 1/3 & 1/3 & 0 & \dots & 0 & 0 & 0 \\ 0 & 1/3 & 1/3 & 1/3 & \dots & 0 & 0 & 0 \\ & \vdots & & \ddots & & & \vdots & \\ & \vdots & & & \ddots & & \vdots & \\ 0 & 0 & 0 & 0 & \dots & 1/3 & 1/3 & 1/3 \\ 1/3 & 0 & 0 & 0 & \dots & 0 & 1/3 & 1/3 \end{pmatrix}$$

This framework allows an individual's choice of actions to depend on arbitrary neighborhoods of others, placing varying weights on different agents. Correspondingly, the process becomes a bit more cumbersome to deal with as we now need to keep track of each agent's social state in each period, rather than just an aggregate statistic. Nonetheless, this is still a well-defined finite-state Markov chain, which allows us to deduce quite a bit about actions over time. First, in situations where the system is irreducible and aperiodic, there will exist a steady-state distribution (again, see Section 4.5.8). Second, although the steady-state distribution is a potentially quite complex

joint distribution the full vector of agents' actions, it is easy to deduce the steady-state probability that any given agent takes action 1.

We do this by the following "trick" to encode the ε_i-based choices of the individuals. Let us expand the society to include two fictitious extra individuals, labeled $n+1$ and $n+2$. Agent $n+1$ always takes action 0, and agent $n+2$ always takes action 1. Now, we can encode an individual's actions entirely in terms of an $(n+2) \times (n+2)$ matrix, W. This is done by setting $W_{i,n+1} = \varepsilon_i(0)$, $W_{i,n+2} = \varepsilon_i(1)$, and $W_{ij} = (1 - \varepsilon_i(0) - \varepsilon_i(1))w_{ij}$ for $j \leq n$, and weights 1 on themselves for the extra individuals.

Then let $X(t) = (x_1(t), \ldots, x_n(t), 0, 1)$ be the $(n+2) \times 1$ vector representing larger state space including our extra "constant" individuals' actions. This allows us to write

$$\Pr(X_i(t+1) = 1 | X(t)) = [WX(t)]_i .$$

More importantly, for any $t' > t$ it follows that

$$\Pr(X_i(t') = 1 | X(t)) = \left[W^{t'-t} X(t)\right]_i . \tag{9.3}$$

where $W^{t'-t}$ is the matrix W raised to the $t' - t$ power.

In many cases, this vector of probabilities will converge to a steady-state probability from any starting state. For example, if there is a directed path from each i to at least one of $n+1$ and $n+2$, then the limit is unique and well-behaved.

PROPOSITION **9.1.2** *If for each individual i either $\varepsilon_i(0) + \varepsilon_i(1) > 0$ or there is a directed path*[9] *from i to some j for whom $\varepsilon_j(0) + \varepsilon_j(1) > 0$, then there is a unique limiting probability that i chooses action 1 and this limiting probability is independent of the starting state. Moreover, the vector of limit probabilities is the unique (righthand-side) unit-eigenvector of W such that the last two entries ($n+1$ and $n+2$) are 0 and 1.*

Proof of Proposition 9.1.2: The convergence of W^t to a unique limit follows from Theorem 2 in Golub and Jackson [278]. Given that there is a directed path from each i to at least one of $n+1$ and $n+2$, and each of these places weight 1 on itself, the only minimal closed sets (minimal directed components with no directed links out) are the nodes $n+1$ and $n+2$ viewed as separate components. It then follows from Theorem

[9] This refers to a directed path in the directed graph on the original n individuals where a link ij is present if $w_{ij} > 0$.

3 in Golub and Jackson [278] that $\lim_t W^t X(0)$ is of the form $W^\infty X(0)$ where

$$W^\infty = \begin{pmatrix} 0 & 0 & 0\ldots & 0 & \gamma_1 & \pi_1 \\ 0 & 0 & 0\ldots & 0 & \gamma_2 & \pi_2 \\ & \vdots & \ddots & & \vdots & \\ 0 & 0 & 0\ldots & 0 & \gamma_i & \pi_i \\ & \vdots & \ddots & & \vdots & \\ 0 & 0 & 0\ldots & 0 & \gamma_n & \pi_n \\ 0 & 0 & 0\ldots & 0 & 1 & 0 \\ 0 & 0 & 0\ldots & 0 & 0 & 1 \end{pmatrix}. \tag{9.4}$$

It also must be that $WW^\infty = W$, and so $W\pi = \pi$ (where $\pi = (\pi_1, \ldots, \pi_n, 0, 1)$ which implies that π is a right hand side unit eigenvector of w. ▮

To get a feeling for this, let us consider an application of Proposition 9.1.2.

EXAMPLE **9.1.1** *An Application: Probability of Action in Krackhardt's Advice Network*

We revisit Example 8.3.11, which concerned Krackhardt's [389] data an advice network among managers in a small manufacturing firm on the west coast of the United States.

Let us suppose that the action is whether to meet go to a bar after work. This happens repeatedly, and each day the managers find out who went the previous night. Consider the following action matrix based on Krackhardt's data. A manager with outdegree d chooses to go to the bar with probability $1/(d+2)$, not to go with probability $1/(d+2)$, and with the remaining probability of $\frac{d}{d+2}$ uniformly at random picks one of his or her neighbors and then goes to the bar if that neighbor did on the previous day. This is true for all of the managers, except for the top-level managers (labeled 2, 7, 14, 18, and 21) who are biased towards going to the bar. The top-level managers use a similar rule except that they use weights $1/(d+1)$ and do not place any weight on action 0. We can then calculate the frequency with which each manager will go to the bar in the long run.

Table 9.1: Probability of Action in Krackhardt's Network of Advice among Managers

label	Prob of 1	level	dept.	age	tenure
1	0.667	3	4	33	9.3
2	0.842	2	4	42	19.6
3	0.690	3	2	40	12.8
4	0.666	3	4	33	7.5
5	0.690	3	2	32	3.3
6	0.585	3	1	59	28
7	0.771	1	0	55	30
8	0.676	3	1	34	11.3
9	0.681	3	2	62	5.4
10	0.660	3	3	37	9.3
11	0.656	3	3	46	27
12	0.585	3	1	34	8.9
13	0.680	3	2	48	0.3
14	0.821	2	2	43	10.4
15	0.687	3	2	40	8.4
16	0.651	3	4	27	4.7
17	0.671	3	1	30	12.4
18	0.737	2	3	33	9.1
19	0.685	3	2	32	4.8
20	0.685	3	2	38	11.7
21	0.755	2	1	36	12.5

The probabilities were calculated via Matlab as the (righthand-side) unit-eigenvector of W.

It is important to emphasize that this does not give us the joint distribution over people going to the bar. It is easy to see that there will be correlation and long periods of time when very many people go to the bar, and then long periods of time where very few people go to the bar. Moreover, even this very myopic sort of behavior by people can lead them to coordinate. The technique of calculating the marginals, however, only allows us to see the individual probabilities and not the joint distribution. The joint distribution is over 2^{21} (more than 2 million) different states, and so it gets a bit

difficult to keep track of.

Beyond the difficulties in keeping track of the full joint distribution, there are two other limitations to this analysis, which motivates a game-theoretic analysis. The first is that the individuals are backward looking. That is, they look at what their neighbors did yesterday in deciding whether to go to the bar, rather than coordinating with their neighbors on whether they plan to go to the bar today. Second, tagent i weights the actions of the others in a separable way. Alternatively, an individual might prefer to go when a larger group is going (or might, in contrast, want to avoid congestion and stay away on crowded nights). This sort of decision is precluded by the separability in the way that an individual i treats the actions of the others. In particular, it is that aspect of the framework above that allows for us to solve for the probabilities of action . To see this explicitly, consider an example with $n = 3$ people. Suppose that individual 1 has $w_{12} = w_{13} = 1/2$ and $\varepsilon_1(0) = \varepsilon_1(1) = 0$. Now, let us consider how indivudal 1 will play in period 1, as a function of how we choose the starting state. In one case, let us pick the initial choices of individuals 2 and 3 in an independent manner, selecting 1 with probability p. In that case, individual 1 will choose 1 with probability p. Instead, let us pick the initial actions of individuals 2 and 3 to be the same, so with probability p they are both 1, and with probability $1-p$ they are both 0. This does not make any difference in calculating the probability that individual 1 will be choosing action 1 in the first period. It is still p. The joint distribution over all players actions will change, but the probability that any given individual will be choosing action 1 is unaffected.

This special property that leads to such power in calculating steady-state probabilities of actions is not always satisfied. In fact, many applications of interest have a more complex structure to the incentives. For example, suppose that individual 1 would like to choose 1 if both of the others choose action 1, but not otherwise. This would be true if action 1 has a cost with it (slightly higher than the cost of taking action 0), but agent 1 would like to choose an action that is compatible with the most others. Then, if we pick 2 and 3's actions independently, then there is only a p^2 chance that both 2 and 3 will choose action 1, and then that individual 1 will choose action 1 in period 1. If instead, we pick 2 and 3's actions to be the same, then there is a p chance that they will both choose action 1 and that individual 1 will then choose action 1 in period 1.

Although we can still write the system as a Markov chain, it is not quite as powerful a tool now, as the transition probabilities and evolution of behavior are quite a bit more complicated. To get a better handle on such more complicated interaction structures, let us turn to game theoretic reasoning.

9.2 Graphical Games

As mentioned above, individual decisions often depend on the relative proportions of neighbors taking actions, as in deciding on whether to buy a product, change technologies, learn a language, smoke, engage in criminal behavior, and so forth. This can result in multiple "equilibrium" points: for instance, it might be that people are only willing to adopt a new technology if others do, and so it would be possible for nobody to adopt it, or for some nontrivial fraction to adopt it. A way of introducing such reactive or "strategic" behavior into the analysis of social interaction is to model the interaction as a game.

A useful class of such interactions was introduced by Kearns, Littman and Singh [366] as what they called "graphical games".[10]

More formally, there is a set N of players, with cardinality n, who are connected by a network (N, g). Each player $i \in N$ takes an action in $\{0, 1\}$. The payoff of player i when the profile of actions is $x = (x_1, ..., x_n)$ is given by:

$$u_i(x_i, x_{N_i(g)}) \tag{9.5}$$

where $x_{N_i(g)}$ is the profile of actions taken by the neighbors of i in the network g.

There is nothing about this definition that precludes the network from being directed. For instance, it could be that player i cares about how player j acts, but not the reverse. Most of the definitions that follow work equally well for directed and undirected cases. I note points at which the analysis is special in the directed case. Most of the examples will examine the undirected case for ease of exposition.

In a graphical game players' payoffs depend on the actions taken by their neighbors in the network. Nevertheless, a player's behavior is related to that of indirect neighbors since a player's neighbors' behavior is influenced by their neighbors, and so forth, and equilibrium conditions tie overall behaviors in the network together. Note that we can view this formulation as being without loss of generality, because we can define the network to include links to all of the players that a given player cares about. As an

[10] These can also be viewed as a special case of "multi-agent influence diagrams," often referred to as "MAID's", which are discussed by Koller and Milch [**?**]. Earlier discussion of the possibility of using MAID's to model strategic interaction where players only care about other subsets of agents' actions dates to Shachter [555], but the first fuller analysis appears in Koller and Milch [**?**]. Even though the general MAID approach allows for encoding of multiple types of problems, information structures, and complex interaction structures, and hence includes graphical games as a special case, most of the analysis examines special cases that preclude the graphical games structure that is discussed here.

extreme case, where a player cares about everyone's behavior, we have the complete network which is a standard game with n players.

9.2.1 Examples of Graphical Games

To fix ideas, consider a couple of examples.

EXAMPLE **9.2.1** *Threshold Games of Complements*

Many of the applications mentioned so far involve "strategic complements," such that a player has an increasing incentive to take a given action as more neighbors take the action. In particular, consider situations the benefit to a player from taking action 1 compared to action 0 (weakly) increases in the number of neighbors who choose action 1, so that

$$u_i(1, x_{N_i(g)}) \geq u_i(0, x_{N_i(g)}) \text{ if and only if } \sum_{j \in N_i(g)} x_j \geq t_i$$

where t_i is a threshold. In particular, if more than t_i neighbors choose action 1, then it is best for player i to choose 1, and if fewer than t_i neighbors choose action 1 then it is better for player i to choose action 0.

A special case is where action 1 is costly (for instance investing in a new technology or product) but the benefit of that action increases as more neighbors undertake the action, and for instance

$$\begin{aligned} u_i(1, x_{N_i(g)}) &= a_i \left(\textstyle\sum_{j \in N_i(g)} x_j \right) - c_i \\ u_i(0, x_{N_i(g)}) &= 0, \end{aligned}$$

for some $a_i > 0$ and $c_i > 0$. Here, the threshold is such that if at least $t_i = \frac{c_i}{a_i}$ neighbors choose action 1, then it is best for player i to choose 1, and otherwise it is better for player i to choose action 0.

EXAMPLE **9.2.2** *A "Best-Shot" Public Goods Game*

Another case of interest has quite the opposite incentive structure. An example is where if a player or any of the player's neighbors take action 1, then that gives the player a benefit of 1. For instance, the action might be learning how to do something, where that information is easily communicated; or buying a book or other product that

is easily lent from one player to another.[11] Taking the action 1 is costly and a player would prefer that a neighbor take the action than having to do it himself or herself; but, taking the action and paying the cost is better than having nobody take the action. This is what is known as a "best-shot" public goods game (e.g., see Hirshleifer [311]), where

$$\begin{aligned} u_i(1, x_{N_i(g)}) &= 1 - c \\ u_i(0, x_{N_i(g)}) &= 1 \qquad \text{if } x_j = 1 \text{ for some } j \in N_i(g) \\ u_i(0, x_{N_i(g)}) &= 0, \qquad \text{if } x_j = 0 \text{ for all } j \in N_i(g), \end{aligned}$$

where $1 > c > 0$.

9.2.2 Equilibrium

Given the graphical game structure, we can use game theory to make predictions about how players will behave and how that depends on network structure. I strongly recommend that those not familiar with game theory read Section 9.10, which provides a quick and basic tutorial in game theory, before proceeding with the remainder of this chapter.

In a graphical game, a *pure-strategy Nash equilibrium* is a profile of strategies $x = (x_1, \ldots, x_n)$ such that

$$\begin{aligned} u_i(1, x_{N_i(g)}) &\geq u_i(0, x_{N_i(g)}) \qquad \text{if } x_i = 1, \text{ and} \\ u_i(0, x_{N_i(g)}) &\geq u_i(1, x_{N_i(g)}) \qquad \text{if } x_i = 0. \end{aligned}$$

So, the equilibrium condition requires that each player choose an action which offers the highest payoff in response to the actions of his or her neighbors: no player should regret the choice that he or she has made given the actions taken by other players.

Pictured below are some pure strategy equilibria for a threshold game of complements as outlined in Example 9.2.1 for a case where the threshold is 2 for all players and where the network is undirected. That is, a player prefers to buy a product if at least two of his or her neighbors do, but prefers not to otherwise. Note that the case pictured in Figure 9.2.2, such that all players take action 0, is an equilibrium for any game where all players have a threshold of at least 1 for taking action 1.

[11] The distinction between "private" and "public" goods is a standard one in economics. The term "public good" refers to the fact that one player might acquire the good, information, etc., and yet it can be consumed by others and hence is not "private" to that player but is "publicly" available. The term "local" refers to the fact that the benefits of a given player's action are only public to an extent limited by his or her neighborhood.

Figure 9.2.2. An Equilibrium in a Game of Complements with Threshold 2.

There is generally a multiplicity of equilibria in such threshold games. For instance, the configuration pictured in Figure 9.2.2 is also an equilibrium. There is also an equilibrium where there is a maximal possible configuration of players who take action 1. The configuration pictured in Figure 9.2.2 has each player take the maximal action that he or she takes in any equilibrium.

While the above example shows that there can exist multiple equilibria in graphical games, it is also possible for none to exist. This is illustrated in the following example.

EXAMPLE **9.2.3** *A Fashion Game and Non-Existence of Pure Strategy Equilibria.*

Consider a graphical game where there are two types of players. One type consists of "conformists" and the others are "rebels". Conformists wish to take an action that matches the majority of their neighbors, while rebels prefer to take an action that matches the minority of their neighbors. This is a variation on a classic game called "matching pennies" where one player wishes to choose the same action as the other, while the second player wishes to mismatch (see Section **??**). It is easy to check that pairing one conformist and one rebel in a dyad gives an example where there is no pure strategy equilibrium, as that is exactly the game of matching pennies. More generally, there will be many graphical game structures for which there is no pure

Figure 9.2.2. Another Equilibrium in a Game of Complements with Threshold 2.

Figure 9.2.2. The 'Maximal Equilibrium' in a Game of Complements with Threshold 2.

strategy equilibrium, as well as some for which there are. For example, to see a class of networks for which there are pure strategy equilibria, note that if all players have more than half of their neighbors being conformists, then there is a pure-strategy equilibrium where all the conformists take one action, and all the rebels take the other.

In light of Example 9.2.3, it is useful to define mixed-strategy equilibria for a graphical game. Denote a mixed strategy of i by σ_i where $\sigma_i \in [0,1]$ is the probability with which player i chooses $x_i = 1$ and $1 - \sigma_i$ is the probability with which the player chooses $x_i = 0$. Letting σ_{-i} denote a profile of mixed strategies of the players other than i, let $u_i(x_i, \sigma_{N_i(g)})$ denote the expected utility of player i who plays x_i and whose neighbors play $\sigma_{N_i(g)}$. Let $u_i(\sigma_i, \sigma_{N_i(g)})$ be the corresponding expected utility when i plays a mixture σ_i. [12] Then, a mixed-strategy equilibrium is a profile $\sigma = (\sigma_1, \ldots, \sigma_n)$ of mixed strategies such that for every i:

$$u_i(\sigma_i, \sigma_{N_i(g)}) = \max\left[u_i(1, \sigma_{N_i(g)}), u_i(0, \sigma_{N_i(g)})\right].$$

.

As graphical games have a finite set of strategies and players, they always have at least one equilibrium, which may be in mixed strategies (see Section **??**). Many graphical game settings always have pure strategy equilibria, including the examples of best-shot games and threshold games that we saw above. But we have also seen some natural situations that will only have mixed-strategy equilibria, such as the fashion game.

Let us turn to a class of graphical games that will cover many applications of interest and also are nicely behaved, allowing for a tractable analysis of how social structure relates to behavior.

9.3 Semi-Anonymous Graphical Games

There are many situations where a player's choice is influenced mainly by the relative popularity of a given action among his or her neighbors and is not dependent on the

[12] Thus,

$$u_i(x_i, \sigma_{N_i(g)}) = \sum_{x_{N_i(g)} \in \{0,1\}^{d_i(g)}} u_i(x_i, x_{N_i(g)}) \Pr(x_{N_i(g)} | \sigma_{N_i(g)}),$$

and

$$u_i(\sigma_i, \sigma_{N_i(g)}) = \sigma_i u_i(1, \sigma_{N_i(g)}) + (1 - \sigma_i) u_i(0, \sigma_{N_i(g)}).$$

.

specific identities of which neighbors take the action. While this is, of course, an approximation, it can be a very useful one and has many natural applications. A class of such graphical games is examined by Galeotti et al [**?**], and I will refer to these as "semi-anonymous" graphical games.

This is not quite an anonymous game (e.g., see Kalai [**?**]), where a player is affected by the actions of all other players in a symmetric way; since in a graphical game a player cares only about a subset of the other players' actions. But it is anonymous in the way that a player cares about his or her neighbors. That is, the player cares only about how many of his or her neighbors take action 0 versus 1, but not precisely which of the neighbors take action 1 versus action 0. So "semi-anonymity" refers to this anonymity on a neighborly level. In addition, there is another aspect of anonymity that is invoked here: players have similar payoff functions, so that differences between players arise due to the network structure, and not some other innate characteristics. A player's utility function depends on his or her degree, and not on his or her label.

9.3.1 Payoffs and Examples

Formally, *semi-anonymous graphical game* is a graphical game such that the payoff to player i with a degree d_i who chooses action x_i is described by a function $u_{d_i}(x_i, m)$ where m is the number of players in $N_i(g)$ taking action 1.

Thus, the payoff function is dependent on the player's degree, the player's own action, and the number of neighbors who take each action. Note that given that since the function depends on both the degree d_i and the number of neighbors choosing action 1, m, we could equivalently have defined it to be a function of the degree and the number of players taking action 0 (which is simply $d_i - m$) or on the degree and the fraction of players taking action 1 (or 0). Note also that the best-shot game of Example 9.2.2 is a semi-anonymous graphical game, as is the fashion game in Example 9.2.3. The threshold games in Example 9.2.1 are semi-anonymous in cases where each player's threshold only depends on his or her degree. Here are some other examples.

EXAMPLE **9.3.1** *A Local Public Goods Game*

Consider a game where each player's action contributes to some local public good: that is an action by a given player provides some local benefits to all neighbors. This generalizes the best-shot public goods graphical game to allow for situations where having multiple players take action 1 is even better than having just one player take

the action. For example, having each player study a given candidate's record and then share that information with his or her neighbors could lead players to be more informed about how to vote in an election than just having one player study a candidate's record. In this case, a player who has m neighbors take action 1 gets a payoff of

$$u_{d_i}(x_i, m) = f(x_i + \lambda m) - cx_i,$$

where f is a nondecreasing function and $\lambda > 0$ and $c > 0$ are scalars. The case where $\lambda = 1$, $f(k) = 1$ for all $k \geq 1$, and $f(0) = 0$, is the best-shot public good graphical game.

EXAMPLE **9.3.2** *A "Couples" Game*

Imagine learning a skill that is most easily enjoyed when there is at least one friend to practice it with. This might be something like tennis, some video games, or learning to play gin rummy. In this situation, a player prefers to take action 1 if at least one neighbor takes action 1, but prefers to take action 0 otherwise. We can think of this as having a cost of investing in the skill of c, along with a benefit of 1 if there is a partner to participate with. Here

$$\begin{aligned} u_{d_i}(1, m) &= 1 - c \quad \text{if } m \geq 1, \\ u_{d_i}(1, 0) &= -c, \qquad \text{and} \\ u_{d_i}(0, m) &= 0. \end{aligned}$$

This game is a special case of a threshold game of complements where the threshold is 1.

EXAMPLE **9.3.3** *A Coordination Game*

Consider a situation where a player prefers to coordinate his or her action with other players, and his or her payoff is related to the fraction of neighbors who play the same strategy.

$$\begin{aligned} u_{d_i}(1, m) &= a\tfrac{m}{d_i} \\ u_{d_i}(0, m) &= b\tfrac{d_i - m}{d_i}. \end{aligned}$$

This is a special case of a threshold game of complements, where the threshold for a player i who has degree d_i is $t_i = d_i \frac{b}{a+b}$.

9.3.2 Complements and Substitutes

In the examples we have seen, as in many applications, the incentives of a player to take an action either increase as other players take the action or decrease as other players take the action. Distinguishing between these cases is important since they result in quite different behaviors. These two broad-reaching cases are captured by the following definitions.

A semi-anonymous graphical game[13] exhibits *strategic complements* if it satisfies a property called increasing differences; that is, for all d and $m \geq m'$:

$$u_d(1, m) - u_d(0, m) \geq u_d(1, m') - u_d(0, m').$$

A semi-anonymous graphical game exhibits *strategic substitutes* if it satisfies decreasing differences; that is, for all d and $m \geq m'$:

$$u_d(1, m) - u_d(0, m) \leq u_d(1, m') - u_d(0, m').$$

These notions are said to apply strictly if the inequalities above are strict whenever $m > m'$.

The best-shot public goods game is one of strategic substitutes, as is the local public goods game in cases such that f is concave. There, higher levels of actions by neighbors (that is, higher m), lead to an incentive for a given player to take the lower action or to "free-ride". Other examples are items that can be shared, such as products and information, as well as other situations with externalities such as pollution reduction and defense systems (where the network could be one of treaties and players countries).

The couples game is one of strategic complements. Local public goods games in cases such that f is convex, so there are increasing returns to action 1, also exhibit strategic complementarities. Other examples of strategic complementarities include situations where peer effects are important. It is important to emphasize that complementarities can exist for many different reasons. For instance, in decisions of whether or not to pursue higher education, it could be that neighbors serve as role models for a given individual. It could also be that they provide information about the potential benefits of higher education, or serve as future contacts in relaying job information.

[13] These definitions extend readily to settings beyond the semi-anonymous case, by working with set inclusion. That is, complements are such that if the actions of all of a player's neighbors do not decrease and some increase, then the player's gain in payoffs from taking higher actions compared to lower actions increases; and substitutes are the reverse case. See Exercise 9.8.

It could be that an individual has an incentive to conform to patterns of behavior of his or her peers. The critical common feature is that increased levels of activity among a given player's neighbors increase the incentives or pressures for that player to undertake the activity.

9.3.3 Equilibria and Thresholds

The nice aspect of semi-anonymous graphical games is that the behavior of a given individual can be succinctly captured by a threshold. In the case of strategic complements, there is a threshold $t(d)$, which can depend on a player's degree d, such that if more than $t(d)$ neighbors choose action 1 then the player prefers to choose action 1, while if fewer than $t(d)$ neighbors choose 1 then the player prefers to choose 0. It is possible to have situations where an individual is exactly indifferent at the threshold. For the case of strategic substitutes, there is also a threshold, but the best response of the player is reversed, so that he or she prefers to take action 0 if more than $t(d)$ neighbors take action 1, and prefers action 1 if fewer than $t(d)$ neighbors take action 1. The best-shot public goods game and the couples game are games of strategic substitutes and strategic complements, respectively, where the threshold is 1 (irrespective of degree).

As is discussed in more detail in Section **??**, semi-anonymous graphical games with strategic complementarities always have a pure strategy equilibria. In fact, the set of pure strategy equilibria has a nice structure to it, and is what is known as a complete lattice, as outlined in Exercise 9.5. This implies that there exist a maximum equilibrium such that each player's action is at least as high as in every other equilibrium, and similarly a minimum equilibrium where actions take their lowest values out of all equilibria. For the network pictured in Figures 9.2.2 through 9.2.2, the minimum equilibrium is in Figure 9.2.2 and the maximum equilibrium is in Figure 9.2.2. (There is one other pure strategy equilibrium for this network not pictured in Figures 9.2.2 through 9.2.2, which is the topic of Exercise 9.4.)

Semi-anonymous graphical games of strategic substitutes do not always have a pure strategy equilibrium, but always have at least one equilibrium in mixed strategies. There are games of strategic substitutes that have pure strategy equilibria, as we have seen in the case of the best-shot public goods game, and they can have multiple equilibria. Figures 9.3.3 and 9.3.3 exhibit two different pure-strategy equilibria in a best-shot public goods game for the same network as in Figures 9.2.2 through 9.2.2.

There are other equilibria for this network (see Exercise **??**), but the structure of

Figure 9.3.3. An Equilibrium in a Best-Shot Public Goods Graphical Game.

Figure 9.3.3. Another Equilibrium in a Best-Shot Public Goods Graphical Game.

equilibria in best-shot public goods game does not exhibit a lattice structure. Nevertheless, there still always exists at least one pure strategy equilibrium for a best-shot public goods graphical game, for the case where the network is undirected. Exercise 9.6 shows the possibility of nonexistence of equilibrium in directed networks.

9.3.4 Comparing Behavior as the Network is Varied

With some examples and definitions in hand, let us examine a few basic properties of how behavior changes as we vary the structure of a network. Such comparisons show how social structure influences behavior.

First, it is easy to see that in games of complements where the threshold for taking action 1 is nonincreasing in degree, adding links will lead to (weakly) higher actions as players will have higher numbers of neighbors taking action 1.

PROPOSITION **9.3.1** *Consider a semi-anonymous graphical game of strategic complements on a network (N, g) and such that the threshold for taking action 1 is nonincreasing as a function of degree (so that $t(d+1) \leq t(d)$ for each d). If we add links to the network to obtain a network g' (so that $g \subset g'$), then for any pure strategy equilibrium x under g there exists an equilibrium x' under g' such that all players play at least as high an action under x' as under x.*

Proposition 9.3.1 notes that if incentives to take an action go up as one has more neighbors who take an action then denser networks lead to higher numbers of players choosing the action. This result is not dependent on the 0-1 action space we have been considering, but extends to more general actions spaces as outlined in Exercise 9.8. This conclusion requires that players care about absolute amounts of activity by neighbors rather than a proportion.

The more subtle case is that of strategic substitutes, where things are no longer so clear cut. Adding links can change the structure of payoffs in unpredictable ways, as illustrated in the following example of adding a link in a best-shot graphical game, which is drawn from an insight of Bramoullé and Kranton [95]. One might expect, reversing the intuition from the complements case, that adding links leads to new equilibria where all agents take less action than they did before. However this is not quite right, as decreasing actions for some agents can lead to increasing actions for others in the case of strategic substitutes, and so changing network structure leads to more complex changes in behavior, as pictured in Figure 9.3.4.

Figure 9.3.4. Adding a Link Changes the Equilibrium Structure in a Best-Shot Graphical Game

In the top panel of Figure 9.3.4 there is an equilibrium where both players who are the centers of their respective stars provide the public good and other players free-ride. This is the overall cheapest way of providing the public good to all players and so has a strong efficiency property. However, as we add a link between these two center agents, it is no longer an equilibrium for both of them to provide the public good. Thus, adding a link can change the structure of equilibria in complicated ways.

Nevertheless, there is still a well-defined way in which the equilibrium adjusts so that, despite Figure 9.3.4, we can still say that adding links decreases actions when we make a comparison that keeps track of how all of the equilibria change.

PROPOSITION **9.3.2** *[Galeotti et al [256]] Consider a best-shot graphical game on a network (N, g) and any pure strategy equilibrium x of $g + ij$. Either x is also an equilibrium of g, or there exists an equilibrium under g in which a strict superset of players chooses 1.*

Thus, although there are generally multiple equilibria and a particular equilibrium might not be an equilibrium when a link is added, any new equilibrium in the network with a new link have a subset of players take action 1 compared to some equilibrium of

Figure 9.3.4. The Equilibria in Various Three-Player Best-Shot Graphical Games

the old network. Indeed, in Figure 9.3.4 the equilibrium in the bottom half of the figure is also an equilibrium without the link being present. It is just that the equilibrium in the top panel no longer survives. Thus, there is a sense in which adding links implies fewer players providing the public good. The proof of the proposition follows easily from the structure of maximal independent sets (e.g., see Observation [**?**]).

The proposition is illustrated by examining all of the pure-strategy equilibria on the networks of three individuals, as pictured in Figure 9.3.4.

In Figure 9.3.4, we see how the equilibria vary as links are added or deleted, and although a particular equilibrium might not be an equilibrium when links are deleted, it can be compared to some other equilibrium.

Considering changes beyond the addition of links, for instance, "moving links" or changing the degree distribution but keeping the mean degree constant, can change the landscape of equilibria in more complicated ways. The sensitivity of behavior to network changes leaves the graphical games model without sharp comparisons of behavior resulting from changes in network structure. However, there is a variation on graphical games where behavior varies in predictable ways in response to general changes in network structure. This is not to say that one or the other is a better model, as they fit different situations, and the difference in the sharpness of their predictions

is reflective of the differences across those settings.

9.4 Randomly Chosen Neighbors and Network Games

While graphical games nicely model a number of networked-interactions where players have a good idea of their neighbors' actions when choosing their own, or where they can adjust their behavior, there are also many situations where players have to choose actions in at least partial ignorance of what their neighbors will do, or even in ignorance of who their neighbors will be. This applies when players are learning a skill or making some investment and they are not sure of their future interaction. For example, they might be choosing majors in college, which will eventually be very important in interaction with their employers, their colleagues, and so forth. In choosing what major to undertake, they might know something about the number of other people choosing that action and what the job market for different majors looks like, without knowing with whom they will be interacting in the future.[14] These ideas are formalized in a setting from Galeotti et al [256], Jackson and Yariv [**?**], and Sundararajan [583]. For expositional purposes, I stick to a setting with just two actions, but the analysis extends to richer settings.

A player knows his or her own degree as well as the distribution over the likely degrees of his or her neighbors, but nothing more about the network structure, when choosing an action. Degree can be thought of as the number of interactions that a player is likely to have in the future.

Define a strategy to indicate which action is chosen as a function of a player's degree. In particular, let $\sigma(d) \in [0, 1]$ be the probability with which a player of degree d chooses action 1. For most degrees this will turn out to be either a 0 or a 1, but in some cases might involve some mixing.

This definition implicitly builds in a symmetry where players of the same degree follow the same strategy.[15] In many cases, this is without loss of generality, as players with the same degree face the same payoffs as a function of their actions and will often have a unique best response.

[14] See Pasini, Pin, and Weidenholzer [503] for some discussions of another application (to buyer-seller markets) where this network games formulation is appropriate.

[15] The equilibrium definition below allows any player to deviate in any way, and so this symmetry in behavior is an equilibrium phenomenon and is payoff maximizing for the players and not a constraint on behavior.

The degrees of a player's neighbor are drawn from a degree distribution $\widetilde{P}$. Recall that $\widetilde{P}(d) = \frac{P(d)d}{\langle d \rangle}$, approximates the distribution over a neighbor's degree from the configuration model with respect to a degree sequence represented by P. Under $\widetilde{P}$ there is a well-defined probability that a neighbor takes action 1, which is

$$p_\sigma = \sum_d \sigma(d)\widetilde{P}(d).$$

Thus, the probability that exactly m out of the d_i neighbors of player i choose action 1 is given by the binomial formula $\binom{d_i}{m} p_\sigma^m (1-p_\sigma)^{d_i - m}$. Therefore, the expected utility of a player of degree d_i who takes action x_i is

$$U_{d_i}(x_i, p_\sigma) = \sum_{m=0}^{d_i} u_{d_i}(x_i, m) \binom{d_i}{m} p_\sigma^m (1-p_\sigma)^{d_i - m}, \tag{9.6}$$

where $u_{d_i}(x_i, m)$ is the payoff corresponding to an underlying graphical game. One can then think of this as a sort of graphical game, where players choose their strategies knowing how many links they will have but not knowing which network will be realized. However, the above formulation does not require a specification of the precise set of players or even how many players there will be. Players just need to know their own degrees and have beliefs over their neighbors' behavior, and they do not need to have a fully specified model of the world.

The formulation above presumes independence of neighbors' degrees. However, the results extend to allow for correlation among neighbors' degrees. This is important since, as we have seen, many networks exhibit correlation in degrees. Here I stick to the independent case since it makes the exposition much more transparent, and I refer the interested reader to Section **??** and to Galeotti et al [256] for details on the appropriate definitions for extensions of these results.[16]

A specification of a utility function u_d for each d and a distribution of neighbors' degrees $\widetilde{P}$ is referred to as a *network game*.

It is now easy to define a (Nash) equilibrium of a network game.[17] An equilibrium

[16] Effectively, the generalization allows each degree to have a different anticipated distribution over vectors of neighbors' degrees. What is required in the case of strategic complements is that higher degree players have a distribution over neighbors' degrees that lead them to expect (weakly) higher degrees among their neighbors than a lower degree player would. This is reversed for substitutes. Comparing joint distributions over different sized vectors is based on the concept of association discussed in Section **??**.

[17] Such an equilibrium where players' strategies depend on a "type" (here their degree) and where players are not sure of the other players' types when they choose their action is also known as a "Bayesian equilibrium."

in a network game is a strategy σ such that for each d:

- if $\sigma(d) > 0$ then $U_d(1, p_\sigma) \geq U_d(0, p_\sigma)$, and
- if $\sigma(d) < 1$ then $U_d(1, p_\sigma) \leq U_d(0, p_\sigma)$.

9.4.1 Degree and Behavior

Players' strategies can be ordered as a function of their degrees. The idea behind this is that players with higher degree have more neighbors, and hence an expectation of having more neighbors choosing 1. In games of strategic complements, if having more total activity among one's neighbors leads one to prefer the higher action, then this leads higher degree players to prefer a higher action compared to a lower degree player. This reverses itself for substitutes.

The conclusion that players with higher degree will have more of an incentive to take higher actions is not guaranteed simply by having strategic complementarities since that condition examines a given player's incentives as his or her neighbors' behavior is changed. It does not make comparisons of how incentives vary with degree. To make comparisons across degrees, let us focus on a case where payoffs depend on absolute numbers of neighbors taking action 1 so that

$$u_d(x_i, m) = u_{d+1}(x_i, m), \tag{9.7}$$

for each $m \leq d$ and x_i. (9.7) is not necessary for the results that follow, which hold for much more general payoff settings, including those where players care about the percentage of neighbors taking a given action rather than absolute number of neighbors. This is the subject of Exercise 9.9. However, this simplifies the exposition and conveys the basic ideas. What is needed for the following results is a payoff structure such that if a higher degree individual is faced with the same typical behavior by any given neighbor, then he or she prefers to choose action 1 over 0 whenever a lower degree player would prefer to choose action 1 over 0.

Under such conditions, it is straightforward to deduce the existence of an equilibrium where higher types take higher actions, and similarly for substitutes and lower actions, which leads to the following proposition. This is quite useful in deducing how behavior varies with network structure.

PROPOSITION **9.4.1** *[Galeotti et al [256]] Consider a network game where payoff functions satisfy (9.7). If it is a game of strategic complements then there exists an equilibrium that is nondecreasing in degree,*[18] *and if is a game of strategic substitutes then there exists an equilibrium that is nonincreasing in degree. If the game is one of strict strategic complements, then all equilibria are nondecreasing in degree, and analogously if it is of strict strategic substitutes then all equilibria are nonincreasing in degree.*

The proof of Proposition 9.4.1 follows the logic of a variety of game theoretic analyses in the presence of strategic complementarities (e.g., see Topkis [596], Vives [**?**], and Milgrom and Roberts [445]), here adapted to the network setting. The idea is that if we begin with some σ that is nondecreasing in degree, then under 9.7 there is a best response for the players that is nondecreasing in degree. An equilibrium is a fixed point of the best response correspondence. The set of nondecreasing strategies is convex and compact, and so then a fixed point exists by any of a variety of theorems on fixed points; and the same holds for substitutes. Let me sketch a more direct and intuititive proof. Let σ^t be such that $\sigma^t(d) = 1$ if $d \geq t$ and $\sigma^t(d) = 0$ for $d < t$ (allowing for $t = \infty$ to allow all players to play 0). First, let us consider the case of strategic complements. Note that if 1 is a best response to some strategy σ for a player of degree d then action 1 is a best response for all higher degree players, and similarly if 0 is a best response to some σ for a player of degree d then it is a best response for all lower degree players. Begin with σ^1. If this is an equilibrium, then stop. Otherwise, it must be that a degree 1 player prefers to play action 0 in response to σ^1. So, consider σ^2. It must now be that action 0 is still a best response for the degree 1 players, as there is less aggregate action by other players. So, if this is not an equilibrium, it must be that degree 2 players prefer to play 0 to 1. Iterating on this logic, either the process eventually stops at some σ^t where the degree t players do not wish to change from action 1 to 0, or else this continues for all degrees in which case all players playing 0 (σ^∞) is an equilibrium.

Note that this shows that for the case of complements, there is actually an equilibrium in pure strategies. The case of strategic substitutes is slightly more complicated, as lowering the action of a given type might actually reverse their incentives. For instance, consider a situation where all players have degree d and a best-shot public goods game. In that case, the equilibrium will involve mixing, also since if players were to choose 1 then any given player would prefer to play 0, and vice versa.[19]. Nevertheless,

[18] Nondecreasing refers to $\sigma(d)$ being a nondecreasing function of d.

[19] Recall that strategies are specified as a function of degree, and so in a regular setting all players

there is still nice structure to incentives across degrees, so that if 1 is a best response to some strategy σ for a player of degree d then action 1 is a best response for all *lower* degree players, and similarly if 0 is a best response to some σ for a player of degree d then it is a best response for all higher degree players. One can then follow a similar algorithm as above, but starting at σ^∞. As a first step examine whether or not degree 1 players would prefer to change to action 1. If they do, then raise their action but this time raise the action continuously from $\sigma(1) = 0$ to $\sigma(1) = 1$. Given the continuity of preferences, the difference in utility for such players between action 0 and 1 will change continuously. Either at some point degree 1 players are indifferent between the two actions in response to this mixture and action 0 by other degree players, or else action 1 is a strict best response for them to a situation where they play action 1 and all others play action 0. Continue in this manner.

The claim that *all* equilibria are nondecreasing when the strategic complements or substitutes are strict follows from noting that players with higher degrees expect to have more neighbors choosing action 1 (in terms of first order stochastic dominance) and is the subject of Exercise 9.11.

The fact that players' incentives vary monotonically with their degree does not necessarily guarantee that their payoffs vary monotonically with their degree. That depends on how the actions of others affect a given player. To get an impression of this, note that just because incentives of a player to choose action 1 go up when more neighbors choose action 1, that does not mean that the players are better off in this situation. For example, consider a game that involves athletes' choices of whether or not to engage in "doping," as in a case where they take illegal drugs or undergo blood transfusions to give them an advantage in competition. A player's neighbors are other athletes that the player competes against. The strategy in the game is either to dope or not to dope. Doping improves an athlete's performance, but also has ethical costs, health costs, and potential costs of detection and punishment. Regardless of exactly how these different factors weigh on a given player's payoffs, as more neighbors are doping, a player is faced with tougher competition and has greater incentives to dope himself or herself just to stay in competition. This will generally be a game of (strict) strategic complements. Nevertheless, all players would be better off in a situation where nobody doped compared to one where everyone doped. So, conditions on incentives, such as strategic complementarities, do not necessarily imply things about overall payoffs without more structure to the game. If the game is such that

must take the same action.

Figure 9.4.1. Behavior as a Function of Degree with Complementarities

increased choices of action 1 by neighbors lead to higher payoffs, then indeed, higher degree players will get higher payoffs (see Exercise 9.10); but things could also be reversed, as in the doping example above, so that increased choices of action 1 by neighbors decrease payoffs.

While Proposition 9.4.1 is relatively straightforward to prove, and quite intuitive, it provides a conclusion that more connected members of a society will take higher action in situations with complementarities and lower action in situations in situations with substitutes. This is consistent, for instance, with the data of Coleman, Katz, and Menzel [154] that we saw in Section **??**. In the case of strict strategic complements, it also means that the equilibrium can be characterized in terms of a threshold degree, such that all players with degree above the threshold degree take action 1 and players with degree below the threshold degree take action 0; with the reverse for substitutes. It could be that players right at the threshold degree randomize. Figure 9.4.1 illustrates this for a particular degree distribution.

Figure 9.4.1 shows a possible frequency distribution of neighbors' degrees, $\widetilde{P}$, as a function of degree, and then has the threshold degree such that players with higher degree take action 1 and players with lower degree take action 0. Thus, in Figure 9.4.1 the probability of a neighbor taking action 1 is just the sum of the distribution

Figure 9.4.2. A Shift in the Degree Distribution Leads to More Action

of neighbors' degrees under $\widetilde{P}$ to the right of the threshold degree (adjusting for any mixing by the players exactly at the threshold).

9.4.2 Changes in Networks and Changes in Behavior

This analysis also leads to predictions of how behavior will change as we change the distribution of neighbors' degrees. Suppose that we compare the equilibrium behavior under the distribution pictured in Figure 9.4.1 with that under a different distribution, such as the dashed distribution in Figure 9.4.2.

As we see in Figure 9.4.2, the new dashed degree distribution places higher weight above the original threshold degree. If the equilibrium strategy did not change, then that would lead to a higher probability that any given one of a player's neighbors plays action 1 and to a higher expected number of neighbors taking action 1. This means that players of any given degree now have a weakly higher incentive to play action 1 versus 0 than they did before. This implies that the threshold should move down. As it moves down, even more players have an incentive to play action 1, and so we move to a new equilibrium where even more neighbors play action 1.

This intuition is formalized in the following proposition. It is stated for the case

of strategic complements, but also holds for the case of strategic substitutes, with an appropriate reversal of the direction of the shifts of thresholds and probabilities of action.

PROPOSITION **9.4.2 (Galeotti et al [256])** *Consider a network game of strict strategic complements that satisfies (9.7) and has a distribution of neighbors' degrees given by $\widetilde{P}$ and an equilibrium with threshold t. If the distribution of neighbors' degrees is changed to $\widetilde{P}'$ such that $\sum_{d\leq t}\widetilde{P}'(d) \leq \sum_{d\leq t-1}\widetilde{P}(d)$ then there is an equilibrium threshold under $\widetilde{P}'$ that is at least as low as t, and the probability that any given neighbor chooses action 1 (weakly) rises. If instead, $\sum_{d\geq t}\widetilde{P}'(d) \geq \sum_{d\leq t+1}\widetilde{P}(d)$ then there is an equilibrium threshold under $\widetilde{P}'$ that is at least as high as t, and the probability that any given neighbor chooses action 1 (weakly) falls.*

Note that Proposition 9.4.2 effectively allows us to compare any two degree distributions. The only complication is where the two distributions are very close and only differ right at the thresdhold.[20]

Proof of Proposition 9.4.2: Let σ denote the equilibrium under $\widetilde{P}$, and consider the case where $\sum_{d\leq t}\widetilde{P}'(d) \leq \sum_{d\leq t-1}\widetilde{P}(d)$, as the other case is analogous. If σ is played under $\widetilde{P}'$, then there is a new probability $p'_\sigma \geq p_\sigma$ that any given neighbor will choose action 1. It is then easily verified that for any given degree d, this leads to a first order stochastic dominance shift in the distribution of m, the number of neighbors who choose action 1. Given strict strategic complements, $u_d(1,m)-u_d(0,m)$ is an increasing function of m, and so given the first order stochastic dominance shift, $U_d(1,p_\sigma) - U_d(0,p_\sigma)$ is at least as large as it was before for any d under the new distribution of neighbors' degrees. Thus, $\sigma(d)$ is still a best response to σ for all $d > t$. If action 1 is a best response for degree t players, then set their strategy to action 1. So, following the notation of the discussion after Proposition 9.4.1, we have strategy σ^t. Note also that if 1 is a best response to some strategy for a player of degree d then action 1 is a best response for all higher degree players, and similarly if 0 is a best response for a player of degree d then it is a best response for all lower degree players. Then consider the best response of degree $t-1$ players to σ^t under $\widetilde{P}'$. If it is action 0, then σ^t is an equilibrium and the conclusions of the proposition hold. Otherwise move to strategy σ^{t-1}, and then consider the best responses of degree $t-2$ players.

[20] If the starting equilibrium involves no mixing by the threshold degree players, then the conclusion also holds under the weaker conditions that $\sum_{d\leq t-1}\widetilde{P}' \leq \sum_{d\leq t-1}\widetilde{P}$, or $\sum_{d\geq t}\widetilde{P}' \leq \sum_{d\geq t}\widetilde{P}$, which then handles all possible comparisons.

Continue in this manner either stopping at some $\sigma^{t'}$ with $t' < t$, or hitting σ^1 in which case all players choosing action 1 is an equilibrium. In either case, the conclusions of the proposition hold. ∎

Proposition 9.4.2 concludes that the probability of a neighbor choosing action 1 goes up when we shift the distribution of neighbors' degrees to place more weight above the threshold, but does not claim that the probability that the overall fraction of players choosing action 1 goes up at the new equilibrium. There is an important distinction between fractions of neighbors and fractions of players, which goes back to the distinction between neighbors' degrees and players' degrees. Neighbors are more likely to be higher degree players. The conclusion that the overall fraction of players choosing action 1 goes up, holds if it is also true that the weight that P' places below t is less than the weight that P places below $t-1$, where P' and P are the degree distributions corresponding to $\widetilde{P}'$and $\widetilde{P}$, respectively. In many instances this is the case, but one can find examples where it does not hold (e.g., see Galeotti et al [256]).

To get an impression of the potential usefulness of Proposition 9.4.2 consider Figure 9.4.2. This pictures two degree distributions from empirical studies. Here we see that that the red distribution first order stochastically dominates the green distribution, and thus has higher weight above any threshold degree. While these are distributions from different applications, this still shows that examining empirically generated degree distributions can allow for comparisons of the type treated in Proposition 9.4.2.

9.5 Richer Action Spaces

The analysis up to this point has focused on situations with two actions. While this captures many applications and offers broad insights, there are settings where the intensity of activity plays a substantial role. I present two such models. The first is a public goods model where we see interesting implications for specializing in activities, and the second is a model with complementarities that exhibits an interesting relationship between levels of activity and network centrality. For this section I return to the graphical games formulation.

9.5.1 A Local Public Goods Model

The following model analyzed by Bramoullé and Kranton [95] is a variation on a local public goods graphical game, like the one in Example 9.3.1, but where the action space

Figure 9.4.2. Green: Distribution of Neighbors' Degrees under the Romance Network of Bearman, Moody and Stovel [47]; Red: Distribution of Neighbors' Degrees under the Co-authorship Network of Goyal, van der Leij, and Moraga-Gonzalez [286].

for each player is $X_i = [0, \infty)$. Players benefit from their own action plus the actions of their neighbors and payoffs as described by

$$u_i(x_i, x_{N_i(g)}) = f(x_i + \sum_{j \in N_i(g)} x_j) - cx_i,$$

where f is a continuously differentiable, strictly concave function and $c > 0$ is a cost parameter.

The interesting case is one where $f'(0) > c > f'(x)$ for some large enough x, as otherwise optimal action levels are 0 or ∞. In this case, in every equilibrium each player's neighborhood will have some production of the public good (at least with positive probability). Letting x^* be such that $f'(x^*) = c$, it is easy to see that any pure strategy equilibrium must have at least x^* produced in each player's neighborhood (so that $x_i + \sum_{j \in N_i(g)} x_j \geq x^*$ for each i) , or else a player could increase his or her payoff by increasing his or her action. In fact, a strategy profile $(x_1, \ldots, x_n)$ is an equilibrium if and only if the following holds for each i

- if $x_i > 0$ then $x_i + \sum_{j \in N_i(g)} x_j = x^*$, and
- if $x_i = 0$ then $\sum_{j \in N_i(g)} x_j \geq x^*$

So, a pure strategy equilibrium is any profile of actions such that every player's neighborhood has at least x^* produced, a player only chooses a positive activity level if his or her neighbors produce less than x^* in aggregate, and in that case the player produces just enough to bring his or her aggregate neighborhood activity level to x^*.

Figure 9.5.1 pictures some pure strategy equilibria for some three-person networks for a setting where $x^* = 1$.

There is a class of equilibria, which Bramoullé and Kranton [95] refer to as "specialized equilibria," where players either choose an action level of x^* or 0. Thus, there are players who specialize in providing the information or public good (like the "opinion leaders" of Katz and Lazarsfeld discussed in Section **??**), and then others who free-ride on their neighbors' behavior. Even though the action spaces are richer here, the specialized equilibria turn out to have the same structure as those of the pure strategy equilibria in the best-shot public goods graphical games. That is, the specialized equilibria are precisely those where the players who specialize in providing the local public good at the level x^* form a maximal independent set and the remaining players choose an action of 0.

Figure 9.5.1. Examples of Equilibrium Local Public Good Provision equilibrium neighborhood production levels of $x^* = 1$

There is a sense in which the specialized equilibria are more robust than other equilibria. As Bramoullé and Kranton [95] point out, only specialized equilibria (and in fact only a subset of them) satisfy the following notion of stability.[21]

- Start with a pure-strategy equilibrium profile $(x_1, \ldots, x_n)$.
- Perturb it slightly by adding some small perturbation ε_i to each x_i, with a requirement that $x_i + \varepsilon_i \geq 0$. Denote this by $x^1 = (x_1 + \varepsilon_1, \ldots, x_n + \varepsilon_n)$.
- Consider the best-responses to x^1. That is, for each i find a level of action that maximizes u_i presuming that x^1_{-i} will be played by the other players. Let this profile of best-responses be denoted $x^2 = (x^2_1, \ldots, x^2_n)$ where x^2_i is the best response to x^1_{-i}.
- Iterate on the best responses, at each step examining the best responses x^k of the players to the previous step's strategies x^{k-1}.

[21] This is a classic notion of stability that has been used in a variety of settings. See Chapter 1 in Fudenberg and Tirole [245] for more discussion and references.

If there is some $\overline{\varepsilon} > 0$ such that this process always converges back to $(x_1, \ldots, x_n)$ starting from any admissible perturbations such that $|\varepsilon_i| < \overline{\varepsilon}$ for all i, then the original equilibrium is said to be "stable."

In this setting, the best responses to some x_{-i} take a simple form: if $\sum_{j \in N_i(g)} x_j \geq x^*$ then the best response is an action of 0, while otherwise a best response is the action that raises the neighborhood production to x^*, so it is $x^* - \sum_{j \in N_i(g)} x_j$. From this, it follows fairly directly that the only stable equilibria, if they exist, are specialized equilibria such that each non-specialist player has at least two specialists in his or her neighborhood, and each specialist has no neighbors providing. With at least two specialists in every non-specialist's neighborhood, even a slight perturbation leads to a best response dynamic where the non-specialist to returns to an action of 0, and then the specialists return to an action of x^*. So, such equilibria are stable. If there are fewer than two specialists in some non-specialists neighborhood, then the equilibria are unstable. This takes a bit more argument, but to see the basic idea, consider a dyad where there is no equilibrium with two specialists. It is easy to see that there are no stable equilibria: consider any pure-strategy equilibrium, which must be such that $x_1 + x_2 = x^*$. At least one of the two strategies is larger than 0, so suppose that $x_2 > 0$. Then perturb the strategies to $x_1 + \varepsilon, x_2 - \varepsilon$. This is also an equilibrium for any $\varepsilon \leq x^2$, and so the best responses do not converge back to the original point and so no equilibrium is stable. In Figure 9.5.1, only the upper right hand equilibrium is a stable one, and there are no stable equilibria for the complete network.

It is also worth noting that all equilibria in this public good game are inefficient, in the sense that they stop short of maximizing total utility. Each player is maximizing his or her own payoff, and yet his or her action also benefits other agents. For example in a dyad, the total production is x^* which maximizes $f(x) - cx$, while overall societal utility is $2f(x) - cx$ which will generally have a higher maximizer if f is smooth and strictly concave. This is endemic to public goods provision and players generally under-provide public goods because they do not fully account for the benefits that their actions bestow on others. In this setting, there are also some differences across equilibria in terms of the total utility that they generate. For example, if we consider the two different equilibria in the top two networks in Figure 9.5.1, they result in different aggregate payoffs. The one with one specialist on the left results in a payoff of $3f(1) - c$, while the one with two specialists on the right results in a payoff of $f(2) + 2f(1) - 2c$. Here we can rank these two equilibria, as the one on the left generates more total utility. We see this by noting that the difference between the one on the left and the one on the right

is $c - f(2) + f(1)$. Since $x^* = 1$ and f is strictly concave, it follows that $c > f(2) - f(1)$ (as otherwise, a player would prefer to increase the production to 2 even by himself or herself) and so this difference is positive. For more general networks, the comparisons across equilibria will depends on the specific configurations and payoffs, but we can conclude that equilibria are generally inefficient and that the stable equilibria are not always the most efficient equilibria.

This analysis of local public goods, although stylized, provides us with some basic insights into the emergence of individuals who provide local public goods such as information and who might act as opinion leaders, while other individuals "free-ride" and benefit from this activity, while not providing any themselves. An important aspect of this is to note that the only stable equilibria are actually asymmetric ones, even in very symmetric networks, and so this heterogeneity among individuals emerges because of the network interactions, even when there is no other a priori difference among individuals. While there can exist multiple equilibria, so this analysis does not always offer pointed predictions as to precisely who will become the providers or opinion leaders, if one introduces heterogeneity into costs and benefits across individuals, that can help in cutting down on the multiplicity.

Network Formation and Implications for Behavior: What is Really "Stable"?

Before moving on, let me comment on an aspect of the predictions of specialization and equilibria in graphical games more generally. To get a feeling for this, consider a simple example where there are four players and $x^* = 1$, and the individuals are connected in a "circle" network, as in Figure 9.5.1.

In this case, there are only three pure strategy equilibria, as pictured in Figure 9.5.1. According to the stability notion above, the two specialist equilibria are the only stable ones. However, if there is any cost to maintaining a link, neither of those networks would be pairwise stable in the sense of Section **??**, as a player would not maintain a link to a neighbor who provides no public good. In contrast, there are situations where the middle network in Figure 9.5.1 is pairwise stable (in particular, in situations where the cost of a link is less than $f(1) - f(2/3)$ and greater than $f(4/3) - f(1)$).

The implication of this is that the graphical games analyses that we have been conducting are affected by considering the network to be endogenous. Indeed, people form relationships with people who provide local public goods, and they are expected to

Figure 9.5.1. Examples of Equilibrium Public Good Provision Choices

reciprocate in some fashion.[22] This is not to say that the insights behind specialization drawn from the analysis above are flawed, but that they need to be explored in a larger context. For example, if players were involved in two separate local public goods problems at the same time, with some players specializing in becoming informed about political campaigns and others about good local restaurants, then it could be possible to support specialized equilibria in conjunction with each other and an endogenous network. Some of the interplay between network formation and behavior on networks is examined in Section **??**, but is still a largely under-explored subject.

9.5.2 Quadratic Payoffs and Strategic Complementarities

The public goods model above is one where activities are strategic substitutes. Let us now examine a different model, where actions are again continuously adjustable, but where there are strategic complementarities between players' actions. The following is a variation of the model of Ballester, Calvó-Armengol and Zenou [31], which admits strategic complementarities.

[22] One can also consider explicit transfers as a means for sustaining specialist equilibria. For more on transfers and stability, see Section **??**.

Each player chooses an intensity with which he or she undertakes an activity. Let $x_i \in I\!R_+$ indicate that intensity, so that higher x_i corresponds to higher action. A player i's payoff is described by

$$u_i(x_i, x_{-i}) = a_i x_i - \frac{b_i}{2} x_i^2 + \sum_{j \neq i} w_{ij} x_i x_j, \tag{9.8}$$

where $a_i \geq 0$ and $b_i > 0$ are scalars, and the w_{ij}'s are weights that the player places on j's action. If $w_{ij} > 0$, then i and j's activities are strategic complements so that more activity by j leads to increased incentives for activity by i, while if $w_{ij} < 0$ then i and j's activities are strategic substitutes and increased activity by j lowers i's activity. The expression $\frac{b_i}{2} x_i^2$ leads to some diminishing returns from activity for player i, so that player i sees some trade-off to taking the action ensuring a well-defined optimal strategy.

The payoff-maximizing action for player i is found by setting the derivative of the payoff $u_i(x_i, x_{-i})$ with respect to the action level x_i equal to 0, which leads to a solution of

$$x_i = \frac{a_i}{b_i} + \sum_{j \neq i} \frac{w_{ij}}{b_i} x_j. \tag{9.9}$$

The interdependence between the players' actions is quite evident.

Let $g_{ij} = \frac{w_{ij}}{b_i}$ (and set $g_{ii} = 0$). We can think of g as a weighted and directed network.[23] This captures the relative dependence of i's action choice on j's action choice. The vector of actions that satisfy (9.9) is described by[24]

$$x = \alpha + gx, \tag{9.10}$$

where x is the $n \times 1$ vector of x_i's and α is the $n \times 1$ vector of $\frac{a_i}{b_i}$'s. If $a_i = 0$ for each i, then (9.10) becomes $x = gx$ and so then x is a unit right-hand eigenvector of g. Otherwise,

$$x = (I\!I - g)^{-1} \alpha, \tag{9.11}$$

where $I\!I$ is the identity matrix, provided $I\!I - g$ is invertible and the solution ends up being nonnegative. The matrix $I\!I - g$ is invertible and the solution is nonnegative if the

[23] It could even allow for some negative weights depending on the w_{ij}'s.

[24] Finding solutions to this problem is related to what is known as the "linear complementarity problem". See Ballester and Calvó [30] for some discussion of the relation and more general formulations of such games.

b_i's are large enough so that the entries of g are small.[25] From (9.10), by substituting for x repeatedly on the right hand side, we also see that

$$x = \sum_{k=0}^{\infty} g^k \alpha. \tag{9.12}$$

(9.11) and (9.12) have nice interpretations. They are variations on the centrality indices that we saw in Section [**?**]. The intuition is similar. Being linked to players who are more active (having higher levels of x_i) leads a player to want to increase his or her level of activity, presuming g nonnegative. Correspondingly, the more active a player's neighbors' neighbors are, the more active the player's neighbors are, and so forth. Thus, we end up with a system where activity levels depend on activity levels. The fact that the payoffs are quadratic in the Ballester, Calvó-Armengol and Zenou [31] model leads to a precise relationship to centrality measures, but even more generally, we would expect similar effects to be present.

To develop this a bit further, Ballester, Calvó-Armengol and Zenou [31] also examine a case where $a_i = a$ and $b_i = b$ for all i, so that the only heterogeneity in the society comes through the weights in the network of interactions, the w_{ij}'s. In that case, the equilibrium levels of actions in (9.11) can be written as

$$x = (I - \frac{1}{b}w)^{-1}\frac{a}{b}\mathbb{1}. \tag{9.13}$$

This looks very close to the equations for Katz Prestige-2 (2.9) and Bonacich centrality (2.10). In fact, we can write[26]

$$x = \frac{a}{b}\left(\mathbb{1} + P^{K2}(w, \frac{1}{b})\right), \tag{9.14}$$

where $P^{K2}(w, \frac{1}{b})$ is the Katz Prestige-2 we saw in (2.9) (which is the same as the Bonacich centrality $Ce^B(w, \frac{1}{b}, \frac{1}{b})$ from (2.10)). To ensure that x is well defined, the term $\frac{1}{b}$ has to be small enough so that the Katz Prestige-2 measure is well-defined and nonnegative. There are various sufficient conditions, but ensuring that the rows (or columns) of $\frac{1}{b}w$ each sum to less than 1 (presuming they are all nonnegative) is enough to ensure convergence.

[25] A sufficient condition for this is that the sum of the entries of each row of g be less than 1 and the sum of entries in each column of g be less than 1, in a case where they are nonnegative.

[26] To see this note that (9.12) implies that $x = \left(1 + (\frac{1}{b})w + (\frac{1}{b})^2 w^2 \ldots\right)\frac{a}{b}\mathbb{1}$ whereas the corresponding Katz Prestige-2 from (2.7) is $P^{K2}(w, \frac{1}{b}) = \left(\frac{1}{b}w + (\frac{1}{b})^2 w^2 \ldots\right)\mathbb{1}$.

We can see some clear comparative statics. If we decrease b or increase a then the solution x increases, and the action of every player increases. There is a direct effect of making higher levels of x_i more attractive fixing the level of the other players' actions, and then this feeds back to increase other neighbors' actions, which then further increases incentives to increase player i's action, and so forth. Next, presuming that w is nonnegative, increasing an entry of w, say w_{ij}, increases the equilibrium actions of all players who have directed paths to i in w. This takes a bit of proof, and can be shown via different methods. A direct technique is to start at an equilibrium x, increase w, and then consider each players' best response to x at the new w. Player i's best response will be higher, as he or she has an increased benefit from neighbors' actions. Then iterating on the best responses, any player ℓ such that $w_{\ell i} > 0$ will increase his or her action in response to i's higher actions, and those having links to ℓ will increase their actions, and so forth. Actions will only move upwards, and so convergence is monotone upwards to a new equilibrium, provided that an equilibrium is still well-defined.[27]

This model provides a tractable formulation that allows us to see how actions relate to network position in a very intuitive manner. Its tractability also allows one to examine the equilibrium in more detail, given its closed form. For example, one interpretation of the above model that Ballester, Calvó-Armengol and Zenou [31] pursue is that players are choosing levels of criminal activity. A player sees direct benefits ($a_i x_i$) and costs ($-b_i x_i^2$) to crime, and also has interactive effects where there are complementarities with one's neighbors ($\sum_{j \neq i} w_{ij} x_i x_j$) so that more criminal activity by player's neighbors leads to greater benefits from crime to that player. This can be due to coordination on crime where cooperation allows for higher impact criminal activity, or this might reflect things such as learning from neighbors. In the context of criminal activity, a natural question that arises is then which player would one want to remove in order to have the maximal impact on actions. For instance, if some police authority wants to lower criminal activity and can remove a single player, which player should it target? In the case where the a_i and b_i terms coincide, then the interactive effects boil down to the centrality measure and the structure of w. The question is then how players' activity levels are when all players are present compare to equilibrium activity levels when we remove a player. By (9.14), this amounts to asking how does

[27] Another way to see the increase in the equilibrium action levels is to examine (9.12) noting that the entries of g^k go up in some row j for some large enough k if and only if there is a directed path from j to i in g; and note that no entries decrease.

removing one player impacts the Katz Prestige-2 measures. Ballester, Calvó-Armengol and Zenou [31] show that the largest reduction in the total activity comes from of removing the player with the highest value of a variation on the Katz measure, which adjusts for the extent to which a player's prestige comes from paths back to himself or herself. Removing the player with the highest (adjusted) centrality measure results in the maximal reduction in overall action.

9.6 Dynamic Behavior and Contagion

The analyses of behavior up to this point are "static" in that they examine equilibrium behavior. In many situations, we are interested in the extent to which a new behavior diffuses throughout a society. For instance, if a new movie opens or a new product becomes available how many people will take advantage of it? If there are complementarities in the product, so that a person is more likely to want to purchase it if another does then the system may well have multiple equilibria, but simply examining them does not give us a full picture of which behavior is likely to emerge.

A powerful way of answering such questions is by examining the best-response behavior of a society over time. We have already seen some uses of iterating on best-responses in checking for stability and identifying equilibria, but it has been a prominent dynamic for more general analyses. That is, we can think of starting out by having some small portion of the population adopt a new action, say action 1. Then in a situation with complementarities, we can see how their neighbors respond. How many of them will buy the product in response? This then leads to further waves of adoption or diffusion. This has been examined in variations on network settings by Ellison [206] and Blume [76] among others. An analysis that ties directly to the graphical games setting is one by Morris [464], that helps illustrate some interesting ideas.

Morris [464] considers a semi-anonymous graphical game where there are strategic complements. He examines a case where each player cares about the *fraction* of neighbors playing action 1 versus 0. There is a threshold fraction q such that action 1 is a best response for a given player if and only if at least a fraction q of the player's neighbors choose 1. This fraction is the same for all players independent of their degrees.[28] In the nontrivial case where q lies strictly between 0 and 1, this is effectively a coordination game and there are at least two equilibria, one where all players choose

[28] This is a special case of complements games where the threshold in terms of numbers of neighbors of degree d is simply qd.

action 0 and the other where all players choose action 1.

What else can we deduce about equilibrium structure? For example, when is it possible to have both actions co-existing in a society, so that there is an equilibrium where some nonempty strict subset of the society plays action 1 and the rest plays action 0?

Let S be the subset of the society that plays action 1. This requires that each player in S have at least a fraction q of his or her neighbors in the set S. It must also be that every player outside of S has a fraction of no more than q of his neighbors in S, or equivalently has a fraction of at least $1-q$ of his neighbors outside of S.

To capture this, given $1 \geq r \geq 0$, Morris [464] defines the set of nodes S to be *r-cohesive* with respect to a network g if each node in S has at least a fraction r of its neighbors in S. That is, S is r-cohesive relative to g if

$$\min_{i \in S} \frac{|N_i(g) \cap S|}{d_i(g)} \geq r, \tag{9.15}$$

where $0/0$ is set to 1.

Figure 9.6 illustrates this definition with disjoint sets of nodes that are each 2/3-cohesive.

If a set is such that each player has at least some fraction r of his or her neighbors within the set, then it is easy to see that each player must have at least a fraction r' of his or her neighbors within that set when $r' < r$. Thus, let us define the *cohesiveness* of a given set S relative to a network (N, g) to be the maximum r such that S is r-cohesive.

So, we have the following proposition, for which the proof is direct.

PROPOSITION **9.6.1 (Morris [464])** *Consider a network (N, g) and a coordination game such that action 1 is a best response for any player if and only if at least a fraction of at least q of his or her neighbors play action 1. Both actions are played by different subsets of the society in some pure strategy equilibrium if and only if there exists some nonempty and strict subset of players S which is q-cohesive and such that its complement $N \setminus S$ is $(1-q)$-cohesive.*

A sufficient condition for this is to have at least two separate components, as then different actions can be played on each component. The cohesiveness of a component is 1, and thus it is also q- and $(1-q)$-cohesive for any q.

Beyond components, cohesiveness provides enough of a "separation" in a network for different equilibria to exist adjacent to each other. For example in Figure 9.6, the

Figure 9.6. The Set of Red Nodes and the Set of Green Nodes are each 2/3-Cohesive.

red and green sets of nodes are connected to each other, but are both inward-looking enough so that they can each sustain different equilibria in any game where q is between 1/3 and 2/3.

Morris [464] also asks the following question.[29] Consider a given network (N, g) and start with all nodes playing action 0. Next, "infect" some number m of the nodes by switching them to play action 1 (and they can never switch back). Next, let players (other than the initially infected) best respond to the current action of their neighbors, switching players to action 1 if their payoffs are at least as good with action 1 as with action 0 against the actions of the other players. Repeat this process starting from the new actions, and stop at a stage where no new players change to action 1. If there is some set of m nodes whose initial infection leads to all players taking action 1 under the best response dynamic, then we say that there is *contagion from m nodes*.

Let us say that a set S is *uniformly no more than* r-cohesive if there is no nonempty subset of S that is more than r-cohesive. We then have the following proposition.

[29] Morris [464] works with infinite networks. I have adapted his formulation and results to a finite setting to match with graphical games.

PROPOSITION **9.6.2** *Consider a network (N, g) and a coordination game such that action 1 is a best response for any player if and only if at least a fraction of at least q of his or her neighbors play action 1. Contagion from m nodes occurs if and only if there exists a set of m nodes such that its complement is uniformly no more than $(1-q)$-cohesive.*

Proof of Proposition 9.6.2: Consider a set S of m nodes. If its complement has some subset A that is more than $1-q$-cohesive, then that set A of nodes will all play 0 under the process above, at every step. Thus, it is necessary for the complement to be uniformly no more than $1-q$-cohesive in order to have contagion to all nodes. Next, let us show that this is sufficient. Since the complement is uniformly no more than $1-q$-cohesive, then the complement is no more than $1-q$-cohesive. This means that there must be at least one player in the complement who has at least a fraction of q of his or her neighbors in S. So, at the first step, at least one player changes strategies. Subsequently, at each step, the set of players who have not yet changed strategies is no more than $1-q$ cohesive, and so some player must have at least q neighbors who are playing 1 and will change. Thus, as long as some players have not yet changed, the process will have new players changing, and so every player must eventually change. ∎

A set is uniformly no more than $(1-q)$-cohesive if every subset of at least one node has more than q of its neighbors outside of that subset. Thus, it is a situation where the network is quite dispersed in terms of how it is connected and does not have any highly segregated groups.

COROLLARY **9.6.1** *Consider a network (N, g) and a coordination game such that action 1 is a best response for any player if and only if at least a fraction of at least q of his or her neighbors play action 1. If a set S of nodes is uniformly no more than r-cohesive, then there will be contagion starting from the complement of that set, provided $q \leq 1-r$.*

While cohesion is an easy concept to state and provides for compact and intuitive characterizations of contagion, it is not always an easy condition to verify. Part of this simply owes to the fact that there are 2^n different subsets of players in any given network of n players, and so checking the cohesion of each subset becomes impractical even with relatively few players. Thus, verifying whether a given network is r-cohesive needs to take advantage of some structural characteristics of the network. To get some feeling for the cohesion of different network structures, let us check the cohesion of a

few types of networks, beginning with the simplest case of the complete network. A subset of players S of a complete network is $\frac{|S|-1}{n-1}$-cohesive, since each player in S has $|S|-1$ neighbors in S and the remaining $n-1$ neighbors outside of S. So, as the size of a set S grows, so does its cohesion. As the number of players becomes large and the S becomes large relative to N, we end up with a cohesion approaching 1, which makes contagion nearly impossible. Clearly, this type of network is extraordinary on at least two dimensions: first the degree of each player is large and second every subset of agents forms a clique and the network is very highly clustered. So, let us examine the opposite extreme of a tree networks where all agents have degree of no more than some d. To keep things simple, let us consider a tree where all agents have degree either d or 1. Here it is easy to hit the upper bound of a strict subset being $\frac{d-1}{d}$ cohesive. To see this, simply pick a subtree as in Figure 9.6, so that there is only one link from one player to the rest of the network. That player has $\frac{d-1}{d}$ of his or her neighbors in the subtree and the other players in the subtree have all of their neighbors in the subtree. As we know that many random networks will have some some subsets of nodes that will be nearly tree-like in their structure when n is large (e.g., see Exercise 1.2), there are many networks where the cohesion of some subsets will be quite high, and so contagion will require quite a low threshold.[30]

When we see bridge links in a network (so that deleting that link would lead to a new component structure), then it is clear that the two sets of nodes that are bridged will each have relatively high cohesion, in fact being $\frac{d_i-1}{d_i}$ where i is the bridging node. This makes contagion difficult, and the support of different actions in equilibrium relatively easier.

Contagion is demanding in that it requires that all nodes be reached. This means that a network that has even a few players who are very cohesive amongst themselves will fail to allow for contagion under the definition above, even though play of action 1 might spread to almost the entire network. The ideas behind cohesion still provide partial characterizations, as it then must be that there is some large set that has low cohesion. A precise characterization of partial contagion is the subject of Exercise 9.17. To get a better feeling for multiplicities of equilibria and partial diffusion of actions, let us return to the network games setting.

[30] Morris [464] examines only connected networks on an infinite set of nodes and for those he shows that an upper bound on the contagion threshold is 1/2 (by showing that every co-finite set contains and infinite subset that is 1/2 cohesive). That turns out not to be a good approximation for (even very) large finite networks, as we see from the high cohesiveness of various finite networks.

Figure 9.6. A Subtree which is 2/3-Cohesive.

9.7 Multiple Equilibria and Diffusion in Network Games*

The various models we have explored have often had multiple equilibria, and some of the analyses of stability and contagion consider things like movement from one equilibrium to another. Indeed, the multiplicity of equilibria is important in many applications and there are many case studies (e.g., see Rogers [536]) where in some cases a product of behavior diffuses broadly while in other cases it does not. The analysis of contagion above gives us some feeling for this, but is extreme in requiring that one end up with an action being adopted by the entire population. As we have seen in the network games setting, and many case studies, there will often be some heterogeneity in a population with some people sticking with one behavior and others adopting a different behavior. Introducing some heterogeneity among players, beyond their degrees, can actually help in producing a more tractable analysis of the structure and stability of multiple equilibria, and the diffusion of behavior.

9.7.1 Best Response Dynamics and Equilibria

An analysis of such diffusion is performed by Jackson and Yariv [345] (see also [344]), in the following context. The setting is similar to the network game setting with a couple of modifications.

Players all begin by taking action 0, which can be thought of as a status quo; for instance, not having bought a product, not having learned a language, not having become educated, and so forth. Players are described by their degrees, which indicate the number of future interactions they might undertake. Players preferences are as in network games, described by (9.6), with one variation. The players also can have some idiosyncratic cost of taking action 1, which is described by c_i. This captures the idea that some players might have some personal bias towards buying a given product, or some proclivity or aversion to learning a language, or becoming educated, etc. If the c_i's are all 0, these are the network games that we considered before. But in the more general model, the payoff to a player is

$$U_{d_i}(0, p)$$

if the player sticks with action 0, where p is the probability that any given neighbor will be choosing action 1 and U is the network game payoff as described in (9.6), and

$$U_{d_i}(1, p) - c_i$$

if the player switches to adopt action 1.

Without loss of generality, normalize the payoff to staying at action 0 to be 0, so that $U_{d_i}(1, p) - c_i$ captures the change in payoffs from switching to action 1 for a given player of degree d_i with idiosyncratic cost c_i and faced with a probability of neighbors' adoptions of p. Thus, player i prefers to switch to choose action 1 when

$$U_{d_i}(1, p) \geq c_i.$$

Let us focus on the case of strategic complements so that player's payoff from switching to action 1, $U_d(1, p)$, is increasing in the probability p of neighbors taking action 1. The case of strategic substitutes is examined in Exercise 9.18.

Let F describe the distribution function of costs, so that $F(c)$ is the probability that any given player's cost c_i will be less than or equal to c. Then, the probability that a player of degree d prefers action 1 is the probability that his or her cost is below the benefit from adopting action 1 of $U_d(1, p)$ and so that probability is

$$F(U_d(1, p)).$$

Now let us consider the following dynamic.[31] Start with some beginning probability that a player's neighbors will choose action 1, say p^0. If players best-respond to p^0, this results in a new fraction of players who wish to adopt action 1, p^1, and so forth. Under strategic complements, this will be a monontone process, so that players will never wish to switch back as the adoption increases over time. In particular, given a probability that a neighbor wishes to choose action 1, p^t, the new probability that a neighbors wishes to choose action 1 is

$$p^{t+1} = \phi(p^t) \equiv \sum_d \widetilde{P}(d) F(U_d(1, p^t)). \tag{9.16}$$

An equilibrium corresponds to a probability p of neighbors' choosing action 1 such that $p = \phi(p)$. Figure 9.7.1 pictures a hypothetical function $\phi(p)$ indicating the best-response levels of action 1 as a function of the starting level of action 1.[32]

In Figure 9.7.1 we see three different equilibria. There are also situations, as in Figure 9.7.1, where there is a unique equilibrium. There, $\phi(0) > 0$, so that there are some players who would choose action 1 regardless of whether or not any other players do.

9.7.2 Stability

As we discussed above, there are various notions of stability of equilibria. Here, with dynamics described by best responses and the function ϕ, we can define stability similarly to the way we did in Section **??**. That is, we can start at some equilibrium $p = \phi(p)$, and then perturb p to $p + \varepsilon$ or $p - \varepsilon$ for some small ε, with the constraint that the perturbed probability lie in [0,1]. If iterating on ϕ from this point always converges back to p for small enough ε, then the equilibrium is stable, while if it does not always converge back for arbitrarily small ε then it is unstable. A stable equilibrium is pictured in Figure 9.7.2.

Generally, when ϕ cuts the 45 degree line from above, then the equilibrium will be stable, while if it cuts the 45 degree line from below, then it will be unstable.[33] Figure

[31] This "dynamic" has various interpretations. It can explicitly be a dynamic, or it might also simply be a tool for us to define stability of equilibria and to study the properties of various equilibria.

[32] This sort of analysis of the multiplicity of, dynamics leading to, and stability of equilibria draws from quite standard techniques for analyzing the equilibria of a system. For example, see Fisher [232] for a survey of the analysis of the equilibria of economic systems and Granovetter [291] for an application of such techniques to a social setting.

[33] It is possible to have ϕ be tangent to the 45 degree line as well, in which case the equilibrium will be unstable.

Figure 9.7.1. The Resulting Fraction of Neighbors Who Choose Action 1 ($\phi(p)$) as a Best Response to a Fraction of Neighbors Who Choose Action 1 (p).

Figure 9.7.1. A Unique Equilibrium.

Figure 9.7.2. A Stable Equilibrium.

9.7.2 shows a multiplicity of equilibria, where some are stable and some are not.

Figure 9.7.2 shows some interesting aspects of equilibria. Here, 0 is stable, and then the next higher equilibrium is unstable. That equilibrium serves as a sort of "tipping point" such that if p is pushed above that level, then the best response dynamics carry things upward to the higher stable equilibrium. Thus, if some initial adoption pushes things above the tipping point, then behavior diffuses up to the higher stable equilibrium. If instead, the initial adoption never reaches the tipping point, then the dynamics lead back down to the 0 equilibrium, so that action 1 does not survive in the population.

9.7.3 Equilibrium Behavior and Changes in the Environment

A change in the environment, such as a change in the cost of adopting action 1, or a change in the relative attractiveness of the two actions, or a change in the network structure, will lead to a change in the best response function ϕ.

In cases where the shift is systematic, so that we get a shift of $\phi(p)$ upwards (or downwards) for every p, then we can deduce how equilibria change. For instance, in Figure 9.7.3 the best response to any p is higher under the dashed curve. As we see

Figure 9.7.2. Multiple Equilibria: Some Stable, Some Not.

Figure 9.7.3. The Change in Equilibria Due to a Shift in Best Responses.

in Figure 9.7.3, as ϕ shifts upwards, the unstable equilibria move down to lower levels and the stable equilibria move up to higher levels. This makes it easier to reach tipping points, leads dynamics to reach higher equilibria, and so makes diffusion of behavior more prevalent in a well-defined way. Thus, any changes in the setting that lead to systematic shifts in ϕ lead to conclusions about how equilibrium behavior will respond, even in the presence of multiple equilibria.

To be careful, these conclusions about changes in equilibria due to an upward shift in ϕ hold for small enough shifts in ϕ and presume that ϕ is a continuous function, which is satisfied if F and U are continuous. Given continuity of ϕ, any stable equilibrium is locally unique; however, unstable equilibria may not be unique and may even be such that ϕ is tangent to the 45 degree line at some point. If ϕ is continuous, then the precise statements that we can make are that if we shift $\phi(p)$ upwards at every point, then for every stable equilibrium there is a new equilibrium which is higher than the old one, and for every unstable equilibrium p it is possible that is no longer any equilibrium at or below it.[34] So, in what follows the conclusions based on shifts in the best response function ϕ should be interpreted with these consequences in mind.

From (9.16) the best response to a given p is described by

$$\phi(p) = \sum_d \widetilde{P}(d) F(U_d(1,p)). \tag{9.17}$$

As Jackson and Yariv [345] point out, this makes clear some types of changes that will systematically shift ϕ upwards. Let us examine some such changes.

Lowering the Cost of Changing Actions

Changing F, so that costs of adopting action 1 are lower (for instance having $F(c)$ increase for each c), leads to a shift upwards in ϕ and so to lower tipping points and higher stable equilibrium choices of action 1.[35] Lowering the costs of taking action 1 correspond to increasing the probability that the cost of choosing action 1 is below its benefit $U_d(1,p)$, so this corresponds to increasing $F(U_d(1,p))$ for any given d and p. This leads to an increase on the right-hand side of (9.17) and so indeed ϕ shifts upwards at every point.

[34] In situations where $p = 1$ was an equilibrium to begin with, then it is impossible to have $\phi(1)$ increase, but any shift upwards of ϕ at other points, would still leave 1 as an equilibrium. Note also the new equilibrium above a given stable equilibrium might no longer be stable, as it could now be that the new ϕ is tangent to the 45 degree line at the higher equilibrium.

[35] This presumes that ϕ is continuous after the change.

Changes in Network Structure

Beyond lowering costs, other changes can lead to the same sorts of systematic changes observed above. For example, suppose that we consider a first order stochastic dominance shift from $\widetilde{P}$ to some new distribution of neighbors' degrees $\widetilde{P}'$. If the payoff to choosing action 1, $U_d(1,p)$, is increasing in degree d for any positive proportion $p > 0$ of neighbors taking action 1 and the distribution of costs F is increasing (which is true whenever it corresponds to a continuous density function on the relevant range), then again this would lead to an increase on the right-hand side of (9.17) at every positive p and an upward shift of ϕ at every positive p. This would then lead to an increase in stable equilibria and a lowering (or disappearance) of the unstable equilibria or tipping points, and so similarly to the lowering of costs we should expect higher overall diffusion in the sense that there are lower thresholds for diffusion and higher eventual rest point equilibria.

Note that we can compare this to Proposition 9.4.2, which did not distinguish between stable and unstable equilibria, but also covered shifts. Here, by accounting for all equilibria and seeing how ϕ adjusts we have a more complete picture of how equilibria change with changes in the environment. The changes detailed in Proposition 9.4.2 only concluded that for any equilibrium under the old distribution, there is at least one that has moved up under the new distribution - so the highest equilibrium is (weakly) higher than it was before.

As Jackson and Yariv [344] point out, we can also examine changes in terms of mean-preserving spreads of the degree distribution, recalling how such spreads affect the expectation of a convex function (see Section 4.5.5). The impact of such a change depends on the convexity of $F(U_d(1,p))$ as a function of d. If this turns out to be convex and increasing in d, then the change in equilibria can be well ordered as $\phi(p)$ will increase for every p. That is, a mean preserving spread in the degree distribution, such as a change from a Poisson degree distribution to a Scale-Free degree distribution, will lead to more diffusion of action 1 (in the sense of shifting stable equilibria to be higher and unstable equilibria to be lower). This might apply in the case of strategic-complements, provided there are sufficient complementarities. In contrast, if this compound function $F(U_d(1,p))$ is concave and decreasing in d, then the shift is exactly reversed. Thus, if $F(U_d(1,p))$ is increasing and convex in d, then power, Poisson, and regular degree distributions with identical means generate corresponding best response functions $\phi^{power}, \phi^{Poisson}$, and $\phi^{regular}$ such that $\phi^{power}(p) \geq \phi^{Poisson}(p) \geq \phi^{regular}(p)$ for all p.

The various graphical game and network game models we have examined have provided us with some basis for understanding how equilibria behave as a function of payoffs, player degree or position in the network, and network characteristics. The multiplicity of equilibria make systematic conclusions a challenge, and we also see some sensitivity of the conclusions to fine details of the setting. Nonetheless, things like strategic complementarities provide powerful tools that allow us to draw some fairly pointed conclusions about equilibrium properties and how they vary with network structure.

9.8 Computing Equilibria*

Beyond the analysis of graphical games and network games, is also important to know something about how to compute an equilibrium, and how difficult it is to find an equilibrium. This is not only important to us as researchers or scientists exploring how a society behaves, but is also important in determining whether the society will reach an equilibrium. There are a variety of ways that we might posit that players adjust their behavior, including deductively reasoning, communicating with others, updating strategies over time in response to what actions have been played in the past, or it might be that evolutionary or other selective pressures influence strategies over time. Regardless of which of these is responsible for leading a society towards an equilibrium point, the process itself involves either real steps or at least steps in thought. If computing an equilibrium as a researcher with the full description of the game at our disposal is so complicated that we could not expect to be able to do it in finite time, it is hard to expect any system to lead to equilibrium (as otherwise we could mimic that system to compute our equilibria). Finally, knowing something about the multiplicity of equilibria is also important, for at least two reasons. Having many equilibria lowers predictive power, as more profiles of behavior are consistent with the model. And, beyond that, having many equilibria can make it difficult for players to coordinate or reach equilibrium, even if they can communicate with each other.

Obviously, these issues have not escaped game theorists' attention, and a good deal of attention has been devoted understanding multiplicities of equilibria, computing equilibria, modeling how societies might learn or evolve to play equilibria, refining equilibrium predictions, and also studying focalness, social norms, and other methods of coordination. I will not try to distill such a breadth of material here; and instead refer the reader to standard game theory texts, such as Binmore [65], Fudenberg and

Tirole [245], Myerson [474], and Osborne and Rubinstein [489] for starting points to learn more about these issues. It is important, however, for us to see how these issues manifest themselves in graphical games. So let us begin by computing equilibria.

Computing equilibria for the threshold games described in Example 9.2.1 is quite easy, and takes advantage of the strategic complementarities of the game, as we have already seen in some special cases. Here is a method that takes at most $(n+1)n/2$ steps for any threshold game (and can take that many steps in some cases).

Set all of the players' actions to 1. Now consider player 1. If player 1 would improve by changing to action 0, then do so and otherwise leave the profile of actions as it is. Next, do the same for player 2, given the new profile of actions. Continue iterating in this manner. After passing through all of the players, repeat the procedure. Stop when a round has been reached where all of the players have been considered and no actions have changed.

This algorithm takes advantage of the fact that players' actions only change from 1 to 0, and that given the strategic structure of the game this can only lead other players' to want to change from 1 to 0, but never to move back up. Actually, this algorithm finds the maximum equilibrium in the sense that there is no other equilibrium where any player ever takes a higher action (see Exercise 9.22). Moreover, this technique also finds the maximum equilibrium in a wider class of games where strategies are ordered and there are such complementarities between strategies.[36]

Next, consider the best-shot public goods game in the case of an undirected network.[37] As we have noted, the pure strategy equilibria are the situations where the players who take action 1 form a maximal independent set. Maximal independent sets are easy to find.

For instance, some of the maximal independent sets on a tree can be found as follows. The follwoing set A is a maximal independent set:

$$A = \bigcup_{m\,:\,m \text{ is even}} D_i^m(g),$$

where $D_i^m(g)$ are the nodes that are at a distance of m from some i in g (with $D_i^0(g) = \{i\}$ being one of the sets where m is even).

[36] For more background on games with strategic complementarities, see Topkis [596], Vives [**?**] and Milgrom and Roberts [445].

[37] In the case of a directed network in the best-shot public good game the analysis is a bit different, as outlined in Exercise 9.6.

Even when the network is not a tree, there still exist obvious (and fast) methods of finding maximal independent sets. Here is an algorithm that finds an equilibrium for a connected network (N, g). By applying this to each component this provides an algorithm for any network. At a given step k, the algorithm constructs sets A_k and B_k, with the interpretation that the eventual maximal independent set will be final A_k. In terms of finding an equilibrium to the best-shot game, the final A_k is the list of players who take action 1, and he final B_k is the set of players who take action 0.

Step 1: Pick some node i and let A_i be i and B_1 be i's neighbors ($A_1 = \{i\}$ and $B_1 = D_i^1(g)$).

Step 2: Next, pick some node j at distance two from i ($j \in D_i^2(g)$) and let $A_2 = \{i, j\}$ and $B_2 = B_1 \cup D_j^1(g)$.

Step k: Iterate on by picking one of the players j' who has a minimal distance to i out of those players not yet assigned to a set A_{k-1} or B_{k-1}. Let $A_k = A_{k-1} \cup \{j'\}$ and $B_k = B_{k-1} \cup D_{j'}^1$.[38]

End: Stop when $A_k \cup B_k = N$.

Although varying the starting player i and the order in which new players are chosen in each step k finds a number of different equilibria, there can be many more which are not found by this algorithm (see Exercise 9.23).

Once we move to the general class of graphical games, computing equilibria becomes more challenging. For example, consider a game where players have thresholds for choosing action 1, but also have some congestion concerns, so that they do not want to take action 1 if too many neighbors choose action 1. In particular, a player has a lower threshold and an upper threshold, so that the player prefers action 1 if and only if the number of neighbors playing 1 lies between the two thresholds. Moreover, allow the lower and upper thresholds to differ across players. In such a setting, which might not admit any pure strategy equilibria, it could be quite hard to find even one equilibrium pure or mixed. Each time we adjust one player's strategy, we may have to adjust the strategies of previously considered players in response, as these can feedback on each other. In the best-shot and threshold examples, changing a player's strategy in

[38] Note that this is well-defined, since no neighbors of j' can be in A_{k-1} as otherwise j' would have been in B_{k-1}.

one direction had clear implications for how others would be set in response, but more generally, as in the example just mentioned with multiple thresholds, the feedback and interaction can be quite complex. The details of how to define what is meant by saying an equilibrium is "hard to find," take us a bit beyond the scope of this text, but let me sketch the basic ideas.

To any algorithm that computes equilibria, there are some inputs that describe the game. In the case of a graphical game, the inputs are the number of players, the network that connects them, and each player's payoff function. The number of players is simply n, and the information about the network can be coded in an $n \times n$ matrix, so involves n^2 bits of information to convey (although this can be lowered in some classes of games). If each player has a degree of at most some d, then each player's payoff matrix has 2^{d+1} entries, indicating the payoff as a function of each vector of choices of 0 or 1 for each neighbor and the player. Thus, the full description of the game involves something on the order of n^2 plus n times a constant (related to the maximum d) bits of information. Now, given this information, we start to construct an algorithm for finding an equilibrium. This involves a description of a series of steps that use the information we have about the game and do some calculations, and then eventually spit out a list of strategies for each player. The question is how many steps will it take to terminate and tell us what an equilibrium is. The method of counting steps that is generally followed is to look at the upper bound, or worst possible performance. So, the performance measure is to find a game and payoff structure that would lead to the most steps before the given algorithm would find an equilibrium, and to keep track of this as a function of n. Algorithms which are considered to be relatively quick are those for which the upper bound on the number of steps needed to find an equilibrium is at most some polynomial function of n. Algorithms which are considered slow are those such that there exist games for which finding an equilibrium takes a number of steps beyond polynomial in n as, for example, in a setting where worst case scenarios require that any algorithm use a number of steps that grows exponentially in n. It is difficult to show that a problem is such that all algorithms sometimes require more than a polynomial number of steps, and there is a very deep and long-standing open question on which hinges the answer for a number of problems including equilibrium computation in a class of graphical games.[39]

There are a number of side issues which accompany such a discussion. For instance, is it reasonable to measure the performance of an algorithm for computing equilibria

[39] For more background on algorithms and complexity see Papadimitriou [498].

based on worst cases? Is an exponential number of steps really that much more than a high order polynomial when we examine some given number n, or how large does n have to be before there is a serious distinction for the problem in question? Is this the right accounting for "complexity" given that we are not keeping track of how complicated the calculation at each step might be? Are there large classes of graphical games for which things will be much easier, and are the graphical games for which computing an equilibrium is difficult very interesting? What happens when we look for approximate equilibria (so that players nearly maximize their payoff) instead of exact equilibria? Are there other definitions of equilibria for which computation is easy? These are all questions that have received attention, and do not have easy answers. There are also some more difficulties that we face with graphical games. For instance, if players do not have some maximal degree, but the maximal degree grows with n, then even describing payoffs could take up to 2^n bits of information. Part of the reason that the threshold and best shot games were easy to handle as that the payoffs were quite simple to describe.[40]

Let me briefly summarize what is known about finding equilibria of graphical games. In the case where the network is a tree, then there are algorithms which involve a number of steps which is polynomial in n and find an equilibrium of *any* graphical game on a tree, as shown by Littman, Kearns and Singh [**?**]. Once we venture beyond trees, however, the strong conjecture is that there is no such algorithm with a number of steps that is always polynomial in n (see Daskalakis, Goldberg, Papadimitriou [174]).[41] Although this is somewhat pessimistic with regards to being able to make predictions of behavior in the broad class of graphical games, there is often much more structure to the games that we are insterested in compared to the worst case scenarios that might tend to lead to high computation time. As we have seen, strategic complementarities make finding equilibria easy and very fast.[42]

[40] For more about the complexity of describing payoffs and representing such games see Daskalakis and Papadimitriou [175].

[41] The "strong conjecture" is based on the fact that the problem of computing Nash equilibria in a graphical game has been shown to be equivalent to a problem (lying in a class called "PPAD-complete") that is conjectured to have no polynomial time algorithm for finding a solution. That conjecture is among a class of long-standing open problems regarding the complexity of algorithms, which have received a great deal of attention.

[42] It is also worth remarking, that while computing Nash equilibria in general graphical (and other large) games can be hard, there are polynomial-time algorithms for finding correlated equilibria (which are a generalization of Nash equilibria that admit correlation in the players' strategies) in certain graphical games that have nice representations. See Kakade et al [355] and Papadimitriou and

9.9 Exercises

EXERCISE **9.1** . *Fashionable Ants.*

Consider the model described in Section 9.1.1. Suppose that a player has a probability $\varepsilon > 0$ of flipping a coin to choose an (binary) action, and a probability of $1-\varepsilon$ of matching the action being taken by the majority of other individuals. Taking n to be even, so that the number of other individuals is always odd, describe the p_k's. Next, pick a value of n and for several values of ε plot the steady-state probability of there being k individuals taking action 1 as a function of k (similar to Figure 9.1.2).

EXERCISE **9.2** . *Proof of Proposition 9.1.1.*

Prove Proposition 9.1.1.

EXERCISE **9.3** . *Steady-State Probabilities of Action.*

Consider the following variation model of social interaction of Section 9.1.2 from Calvó-Armengol and Jackson [121]. Let $p_s = q$ for some $1 > q > 0$ whenever $s \geq \tau$ and $p_s = 1 - q$ whenever $s < \tau$, where $\tau \in \{0, \ldots, n-1\}$ is a threshold. Thus, individuals choose action 1 with probability q if at least τ others have, and with probability $1-q$ otherwise. Solve for the steady-state probability μ_s as a function of μ_0.

EXERCISE **9.4** . *Another Pure Strategy Equilibrium for the Game in Figures 9.2.2 through 9.2.2.*

Find a pure strategy equilibrium of the game in Figures 9.2.2 through 9.2.2 that is not pictured there.

EXERCISE **9.5** *The Lattice Structure of Equilibria in Semi-Anonymous Games of Complementaries*

Show that if $x = (x_1, \ldots, x_n)$ and $x' = (x'_1, \ldots, x'_n)$ are pure strategy equilibria of a semi-anonymous graphical game with strategic complementarities, then there exists a pure strategy equilibrium $\overline{x}$ such that

$$\overline{x}_i \geq \max(x_i, x'_i)$$

Roughgarden [499].

for all i; as well as a pure strategy equilibrium such that

$$\overline{x}_i \leq \min(x_i, x_i')$$

for all i. This property means that the set of equilibria form a lattice. (In fact, the lattice is complete, so that for any set of pure strategy equilibria we can find a pure strategy equilibrium which is greater than or equal to each one and another pure strategy equilibrium that is less than or equal to each one.)

EXERCISE **9.6** *Possible Non-existence of Pure Strategy Equilibria in Best-Shot Graphical Games on a Directed Network*

Provide an example of a directed network with three players for which the only equilibria to a best shot game played on that network are in mixed strategies. Identify a mixed-strategy equilibrium.

EXERCISE **9.7** *Existence of Pure Strategy Equilibria Semi-Anonymous Graphical Games of Strategic Complements with Infinite Action Spaces.**

Consider a graphical game on a network (N, g) where player i has a compact action space $X_i \subset [0, M]$. Let $u_i(x_i, x_{N_i(g)})$ be continuous for each i.

A graphical game exhibits *strategic complements* if

$$u_i(x_i', x'_{N_i(g)}) - u_i(x_i, x'_{N_i(g)}) \geq u_i(x_i', x_{N_i(g)}) - u_i(x_i, x_{N_i(g)}) \tag{9.18}$$

for every i, $x_i' > x_i$ and $x'_{N_i(g)} \geq x_{N_i(g)}$.[43]

Show that there exists a pure-strategy equilibrium in such a game. Show that the set of pure strategy equilibria form a complete lattice (see Exercise 9.5). Show that there are examples where each of these conclusions fails if we set $X_i = \mathbb{R}_+$.

EXERCISE **9.8** *Graphical Games of Complements**

Consider a graphical game as in Exercise 9.7 but that is also semi-anonymous so that all agents have the same action space and payoffs depend only on the vector $x'_{N_i(g)}$ up to a relabeling of the agents.[44]

[43] This indicates that each coordinate of $x'_{N_i(g)}$ is at least as large as the corresponding coordinate of $x_{N_i(g)}$.

[44] That is, if there exists a bijection π from $N_i(g)$ to $N_i(g)$ such that j-th coordinate of $x'_{N_i(g)}$ is equal to the $\pi(j)$-th coordinate of $x_{N_i(g)}$ for each j, then $u_i(\cdot, x_{N_i(g)}) = u_i(\cdot, x'_{N_i(g)})$.

Suppose also that for any z that is in $[0, M]^{d_i}$

$$u_{d_i}(x_i, z) = u_{d_i+1}(x_i, (z, 0)). \tag{9.19}$$

Thus, if we add a link from one player to a second player who is choosing action 0 then the payoff is as if the second player was not there.

Show that if $g \subset g'$ then for every pure strategy equilibrium x under g there exists an equilibrium $x' \geq x$ under g'.

Next, consider a case where the inequality in (9.18) is strict whenever $x'_{N_i(g)} \neq x_{N_i(g)}$, and where X_i is connected for each i. Show that if an equilibrium x relative to g is such that $x_i < M$ for each i, then there exists an equilibrium x' under $g + ij$ in which all players in the component of i and j play strictly higher actions.

Show that these conclusions can fail if (9.19) is violated.

EXERCISE **9.9** *Payoffs Increase with Degree**

Galeotti et al [256] say that a network game exhibits *degree complementarity* if

$$U_d(1, \sigma) - U_d(0, \sigma) \geq U_{d'}(1, \sigma) - U_{d'}(0, \sigma) \tag{9.20}$$

whenever $d > d'$. This states that facing the same behavior by other players, a player with a higher degree has at least as big an incentive to take action 1 as compared to a player with a lower degree.[45]

Show that if (9.7) holds and the network game is one of strategic complements, then degree complementarity holds. Show that degree complementarity also holds in the case of strategic complements when a player cares about the fraction of neighbors taking action 1, so that $u_d(1, m) = \frac{m}{d} - c$ and $u_d(0, m) = b\frac{m}{d} - a$.

Show that a network game that satisfies this condition has an equilibrium that is non-decreasing in degree.

EXERCISE **9.10** *Payoffs Increase with Degree*

Consider the setting of Proposition 9.4.1. Suppose that there are *positive externalities* , so that for each d and x_i, $u_d(x_i, m)$ is nondecreasing in m.[46] Show that in *every*

[45] Analogously, payoffs exhibit *degree substitution* if the inequality above is reversed, and the following statements hold as well.

[46] This is different from a network formation setting, where externalities were defined relative to network structure. Here the actions considered are those in the graphical game.

equilibrium in a game with either strategic complements or substitutes, the payoff to a player with degree d', where $d' > d$, is at least as high as the payoff to a player with degree d.

EXERCISE **9.11** *All Equilibria of a Network Game are Monotone**

Consider the setting of Proposition Proposition 9.4.1. Show the last claim that if the game is one of strict strategic complements then all equilibria are nondecreasing in degree.

EXERCISE **9.12** *A Local Public Goods Graphical Game Where Players have Heterogeneous Costs*

Bramoullé and Kranton [95] also consider a variation on the model of Section 9.5.1 in which players can have different costs of providing the public good. That is, payoffs are given by

$$u_i(x_i, x_{N_i(g)}) = f(x_i + \sum_{j \in N_i(g)} x_j) - c_i x_i,$$

where c_i can differ across players. Let the function f be increasing and strictly concave, x_i^* denote the maximizer of $f(x) - c_i x$, and suppose that x_i^* is well-defined and non-zero for every player.

Provide an algorithm that finds an equilibrium in a setting where $c_1 < c_2 < \cdots < c_n$. Provide an example where there is more than one stable equilibrium.

EXERCISE **9.13** *Convex Costs in a Local Public Goods Graphical Game*

Consider the following variation on the local public goods graphical game of Bramoullé and Kranton [95] from Section 9.5.1. Payoffs are given by

$$u_i(x_i, x_{N_i(g)}) = f(x_i + \sum_{j \in N_i(g)} x_j) - c(x_i), \tag{9.21}$$

where f is strictly concave and c is strictly convex, and there exists $x^* > 0$ such that $f'(x^*) = c'(x^*)$, which is the action level that an individual chooses if he or she is the only provider.

Find a pure strategy equilibrium on a complete network and show that it is the unique pure strategy equilibrium and that all players choose positive actions.

Next, consider a circle network with an even number of players, and suppose that $f'(2x^*) < c'(0)$. Describe a specialized equilibrium where only some players choose positive actions.

EXERCISE **9.14** *Cohesiveness.*

Find a partition of the set of nodes in Figure 9.6 into two sets such that one set is 2/3-cohesive and its complement is 3/4-cohesive.

EXERCISE **9.15** *Labelings of Nodes and Cohesion.*

Consider a network (N, g) and a coordination game such that action 1 is a best response for any player if and only if at least a fraction of at least q of his or her neighbors play action 1. Show the following result from Morris [464]. Let a labeling of nodes be a bijection (one-to-one and onto function) ℓ from N to N. Let $\alpha_\ell(i)$ be the fraction of $\ell(i)$'s neighbors who have labels less than $\ell(i)$. Show that there is a contagion from m nodes if and only if there exists a labeling ℓ such that $\alpha_\ell(i) \geq q$ for all $i \geq m + 1$.

From this show that there exists a set S that is uniformly no more than r-cohesive if and only if there is a labeling ℓ such that $\alpha_\ell(i) \geq 1 - r$ for all $i \geq m + 1$ where m is the cardinality of the complement of S.

EXERCISE **9.16** *A Sufficient Condition for the Failure of Contagion*

Consider a network (N, g) and a coordination game such that action 1 is a best response for any player if and only if at least a fraction of at least q of his or her neighbors play action 1. Show that sufficient condition for never having contagion from any group of m nodes is to have at least $m + 1$ separate groups that are each more than $1 - q$ cohesive.

EXERCISE **9.17** *Contagion to a Subset of Nodes.*

Consider a network (N, g) and a coordination game such that action 1 is a best response for any player if and only if at least a fraction of at least q of his or her neighbors play action 1. Show that $B \cup A$ is the eventual set of nodes playing 1 under the contagion system described in Section **??** if and only if the complement of $B \cup A$, denoted C, is more than q-cohesive and for every nonempty subset D of B, $D \cup C$ has a cohesiveness of no more than q.

EXERCISE **9.18** *Diffusion of Behavior in Network Games of Strategic Substitutes.*

Consider the network games setting from Section **??** and suppose that $U_d(1,p)$ is decreasing and continuous in p for each d and suppose that F is increasing and continuous on the entire range of U_d for each d. Show that there is a unique equilibrium p and that it is a stable equilibrium.

EXERCISE **9.19** *Adoption Patterns by Degree: Diffusion of Behavior in Network Games.*

Consider the network games setting from Section **??** in a case such that $U_d(1,p) = pd$ and F is uniform on $[0,5]$, so that $F(U_d(1,p)) = min\,[pd,5]\,/5$.

Suppose that the network game is regular so that all players have degree d.

What is the unique equilibrium p for $d < 5$?

What are the two equilibria p when $d > 5$?

What are the equilibrium p's when $d = 5$?

Consider a degree distribution which has equal weights on degrees $\{1,2,\ldots,10\}$ (so you need to use the corresponding $\widetilde{P}$ which will be biased towards higher degrees with weight $d/55$ on degree d to get the distribution of neighbors' degrees). Using a simple spreadsheet, or program of your choosing, start with an initial $p^0 = .1$ and trace the evolution of the proportion of degree d types that have chosen action 1 at a sequence of dates $t = 1,2,...$ until you have some sense of convergence. Plot the resulting adoption curves for $d = 1$, $d = 5$, $d = 10$ over time.

EXERCISE **9.20** *S-Shaped Adoption Curves: Diffusion of Behavior in Network Games.*

"S-shaped" adoption curves have been found in a variety of studies of diffusion, so that adoption starts slowly, then increases its rate of diffusion, and then eventually slows down again.[47] In terms of diffusion in the network games setting from Section **??**, as a proxy for rates of diffusion, we can keep track of $p^{t+1} - p^t = \phi(p^t) - p^t$ to proxy for the rate of diffusion.

Let $H(d,p) = F(U_d(1,p))$, which lies between 0 and 1 for every d and p since F is a distribution function. Suppose that $H(d,0) > 0$ for some d such that $\widetilde{P}(d) > 0$, and that H is twice continuously differentiable and increasing in both variables and strictly concave in p.

Show that ϕ will be "S-shaped". That is, show that there exists $p^* \in [0,1]$ such that $\phi(p) - p$ is increasing when $p < p^*$ and then decreasing when $p > p^*$ (whenever $\phi(p) < 1$).

[47] See Bass [**?**] for some discussion of this, Rogers [536] for more detailed references, and Young [633] for alternative learning-based models of this.

EXERCISE **9.21** *The Expected Number of Equilibria in a Generic Graphical Game.*[48]

Consider an arbitrary network (N, g) as the basis for a graphical game. Suppose that we then define the payoffs for players as a function of their actions as follows. For each player i and configuration of strategies $(x_i, x_{N_i(g)}) \in \{0,1\}^{d_i(g)+1}$, assign the payoff $u_i(x_i, x_{N_i(g)})$ according to an atomless distribution F on $\mathbb{R}$. Do this independently for each player and profile of strategies. So, once we have specified all of the u_i's, we have a well-defined graphical game. It might turn out to have one pure strategy Nash equilibria, it might have several, or it might turn out not to have any, depending on the values of the u_i's. Show that the the expected number of pure strategy Nash equilibria is 1.

Hint: What is the probability that $x_i = 1$ will be a best reply to some $x_{N_i(g)}) \in \{0,1\}^{d_i(g)}$? Then what is the probability that some profile of actions $(x_1, \ldots, x_n)$ will turn out to be an equilibrium?

EXERCISE **9.22** *Finding Equilibria in Graphical Games of Strategic Complements*

Show that the algorithm for threshold games described in Section 9.8 finds the maximal equilibrium x, in the sense that $x_i \geq x'_i$ for all other equilibrium x' and all i.

Describe an algorithm for finding the minimal equilibrium x such that $x_i \leq x'_i$ for all other equilibrium x' and all i.

Argue that the claims above are true even when considering mixed strategy equilibria; so that x_i is at least as large (small, respectively) as the max of the support of the strategy of player i in any alternative equilibrium.

Show that the algorithm also works for any graphical game of strategic complements with an action space of $\{0,1\}$.

EXERCISE **9.23** *Finding all Equilibria in Best-Shot Graphical Games*

Provide an example of an equilibrium of a best-shot public goods graphical game that would not be found via the algorithm for best-shot games described in Section 9.8.[49]

[48] This is based on a result by Daskalakis, Dimakis, and Mossel [173].

[49] To see an algorithm for finding all maximal independent sets see Johnson, Papadimitriou, and Yannakakis [350].

9.10 Appendix: A Primer on Non-cooperative Game Theory

This appendix treats what is known as "non-cooperative" game theory, where agents are acting in self-interested ways to maximize their own payoffs and equilibrium notions are applied to predict outcomes. "Cooperative" game theory examines coalitions and how payoffs might be allocated within coalitions. It is examined in Section **??**.

The basic elements of performing a (non-cooperative) game theoretic analysis are (i) framing the situation in terms of the actions available to players and their payoffs as a function of actions, and then (ii) using various equilibrium notions to make either descriptive or prescriptive predictions. In framing the analysis, a number of questions become important. First, who are the players? They may be people, firms, organizations, governments, ethnic groups, etc. Second, what actions are available to them? This should include a complete list of all the actions that they might take which could have some impact on the payoffs to anyone involved in the game. Third, what is the timing of the interaction? One part of this is whether actions are chosen simultaneously or sequentially. Another part of this is whether the interaction is repeated. The order of play will be important in determining who knows what. Moving after another player may give you an advantage of knowing what the other player has done, it may also put you at a disadvantage as you may have lost time and possibly an ability to commit to some action. Embodied in this aspect of the game is also a question of what information different players have when they take actions. Fourth, what are the payoffs to the various players as a result of the interaction? Ascertaining this will involve estimating the costs and benefits of each potential set of choices by all players. In many situations it may be easier to estimate payoffs for some players (such as yourself) than others, and it may be unclear whether other players are also thinking strategically. This suggests that careful attention be paid to a sensitivity analysis.

Once we have framed the situation, we can begin to look from different players' perspectives to analyze which actions are optimal for them. There are various criteria we can use.

9.10.1 Games in Normal Form

Let us begin with a standard representation of a game, which is known as a *normal form* game, and sometimes also called a game in *strategic form*.

The set of players is $N = \{1, \ldots, n\}$.

Player i has a set of actions, X_i, available. These are generally referred to as *pure strategies*. This might be a finite set, or it might be infinite.

Let $X = X_1 \times \cdots \times X_n$ be the set of all profiles of pure strategies or actions, with a generic element denoted by $x = (x_1, \ldots, x_n)$.

Player i's payoff as a function of the vector of actions taken is described by a function $u_i : X \to I\!R$, with the interpretation that $u_i(x)$ is i's payoff if the x is the profile of actions chosen in the society.

Normal form games are often represented via a table. Perhaps the most famous such game is the *prisoners' dilemma*, which is represented as follows.

		Player 2	
		C	D
Player 1	C	-1, -1	-3, 0
	D	0, -3	-2, -2

Here there are two players who each have two pure strategies, where $X_i = \{C, D\}$, with the interpretation that C stands for "cooperate" and D stands for "defect". The first entry indicates the payoff to the "row player" or player 1 as a function of the pair of actions, while the second entry is the payoff to the column player or player 2.

The usual story behind the payoffs in the prisoners' dilemma is as follows. The two players have committed a crime and are now in separate rooms in a police station. The prosecutor has come to each of them and told them each the following. If you confess and agree to testify against the other player, and the other player does not confess, then I will let you go. If you both confess, then I will send you both to prison for 2 years. If you do not confess and the other player does, then you will be convicted and I will seek the maximal possible prison sentence of 3 years. If nobody confesses, then I will charge you with a lighter crime for which we have enough evidence to convict you without any confession or testimony and you will each go to prison for 1 year. So, the payoffs in the matrix represent the lost time in terms of years in prison. The term "cooperate" refers to cooperating with the other player. The term "defect" refers to confessing and agreeing to testify, so breaking the (implicit) agreement with the other player.

Note that we could also multiply each payoff by a scalar and add a constant, and end up with an equivalent representation (as long as we rescale all of a given player's payoffs in the same way). For instance, here I have doubled each entry and added 6.

		Player 2	
		C	D
Player 1	C	4, 4	0, 6
	D	6, 0	2, 2

This transformation leaves the strategic aspect of the game unchanged.

There are many games that might have different descriptions behind them, but end up with a similar normal form in terms of the strategic aspects of the game. Another example where we end up with the same game as above is what is known as a "Cournot duopoly." The story is as follows. Two firms produce identical goods. They each have two production levels, high production or low production. If they produce at high production, they will have a lot of the good to sell, while at low production they will have less of the good to sell. If they "cooperate" then they agree to each produce at low production. In this case, the product is rare and fetches a very high price on the market and they each make a profit of 4. "Defect" refers to producing at high production. If they each produce at high production, then they will depress the price and even though they sell more of the goods, the price will drop enough so as to lower their overall profits to 2 each. If one defects and the other cooperates, then the price is in a middle range. The firm with the higher production sells more goods and earns a higher profit of 6, while the firm with the lower production ends up just covering its costs and earning a profit of 0.

9.10.2 Dominant Strategies

Given a game in normal form, we then can make predictions about which actions will be chosen. Predictions are particularly easy in a case where there are dominant strategies. A dominant strategy for a player is a one which produces the highest payoff of any strategy available *for every possible action of the other players.*

That is, a strategy $x_i \in X_i$ is a *dominant* (or weakly dominant) strategy for player i if

$$u_i(x_i, x_{-i}) \geq u_i(x_i', x_{-i})$$

for all x_i' and all $x_{-i} \in X_{-i}$.

A strategy is a *strictly dominant strategy* if the above inequality holds strictly for all $x_i' \neq x_i$ and all $x_{-i} \in X_{-i}$.

Dominant strategies are powerful both from an analytical point of view, and from a player's perspective. An individual does not have to make any predictions about what

other players might do, and still has a well-defined best strategy.

In the prisoners' dilemma, it is easy to check that each player has a strictly dominant strategy to defect - that is to confess to the police and to agree to testify. So, if we use dominant strategies to predict play, then the unique prediction is that each player will defect and both players fair worse than at the alternative strategies where neither defects. A basic lesson from the prisoners' dilemma is that individual incentives and overall welfare need not coincide. The players both end up going to jail for 2 years, even though they would have only gone to jail for 1 year if they could have managed not to defect. The problem is that they cannot trust each other to cooperate: no matter what the other player does, a player is best off defecting.

An important comment is that this analysis presumes that all of the relevant payoff information is included in the payoff function. If, for instance, a player fears retribution for confessing and testifying, then that should be included in the payoffs and can change the incentives in the game. If the player cares about how many years the other player spends in jail, then that can be written into the payoff function as well.

When dominant strategies exist, they make the game theoretic analysis relatively easy. However, such strategies do not always exist, and then we can turn to equilibrium notions.

9.10.3 Nash Equilibrium

A pure strategy Nash equilibrium[50] is a profile of strategies such that each player's strategy is a best response (results in the highest available payoff) against the equilibrium strategies of the other players.

A strategy x_i is a *best reply*, also known as a *best response*, of player i to a profile of strategies $x_{-i} \in X_{-i}$ for the other players if

$$u_i(x_i, x_{-i}) \geq u_i(x_i', x_{-i}) \tag{9.22}$$

for all x_i'.

A best response of player i to a profile of strategies of the other players is said to be a *strict best response* to if it is the unique best response.

[50] On occasion referred to as Cournot–Nash equilibrium, with reference to Cournot [**?**] who first developed such an equilibrium concept in the analysis of oligopoly (a set of firms in competition with each other).

A profile of strategies $x \in X$ is a *pure strategy Nash equilibrium* if x_i is a best reply to x_{-i} for each i. That is, x is a Nash equilibrium if

$$u_i(x_i, x_{-i}) \geq u_i(x_i', x_{-i}) \tag{9.23}$$

for all i and x_i'.

This definition might seem somewhat similar to that of dominant strategy, but there is a critical difference. This only requires that the action taken by each agent be best against the actions taken by the other players, and not necessarily against all possible strategies of the other players.

A Nash equilibrium has the nice property that it is stable: if each player expects x to be the profile of strategies played, then no player has any incentive to change his or her action. Another way to put this, is that no player would regret having played the strategy that he or she played in a Nash equilibrium.

In some cases, the best response of a player to the strategies of the other players is unique. A Nash equilibrium such that all players are playing strategies that are unique best responses is called a *strict* Nash equilibrium.

A profile of dominant strategies is a Nash equilibrium, but not vice versa.

To see a Nash equilibrium in action, consider the following game between two firms who are choosing whether or not to advertise. Total available profits are 28 to be split between the two firms. Advertising costs a firm 8. Firm 1 currently has a larger market share than firm 2, so it is seeing 16 in profits while firm 2 is seeing 12 in profits. If they both advertise, then they will split the market evenly 14 each, but bear the cost of advertising so they will see profits of 6 each. If one advertises, while the other does not, then the advertiser gets three quarters of the market (but also pays for advertising) and the non–advertiser sees one quarter of the market. (There are some obvious simplifications here: just considering two levels of advertising and assuming that advertising only affects the split and not the total profitability.) The net payoffs are given in the following table.

		Firm 2	
		Not	Adv
Firm 1	Not	16, 12	7, 13
	Adv	13, 7	6, 6

To find the equilibrium, we have to look for a pair of actions such that neither firm would want to change its action given what the other firm has chosen. This is made a bit easier in this case since firm 1 has a strictly dominant strategy of not advertising.

Firm 2 does not have a dominant strategy; which strategy is optimal for it depends on what firm 1 does. But given the prediction that firm 1 will not advertise, firm 2 is best off advertising. This forms a Nash equilibrium since neither firm wishes to change strategies. You can easily check that no other pairs of strategies form an equilibrium.

While each of the previous games provides us with a unique prediction, there are games where there are multiple equilibria.

Here are three examples.

The first is an example of a coordination game.

		Player 2	
		A	B
Player 1	A	5, 5	0, 3
	B	3, 0	4, 4

This might be thought of as picking between two technologies, or else coordinating on a location to go to. Players earn higher payoffs when they choose the same action than when they choose different actions. But here there are two (pure strategy) Nash equilibria: (A,A) and (B,B).

This is also a variation on Rousseau's "stag hunt" game.[51] The story is that two hunters are out and they can either hunt for a stag (strategy A) or look for hares (strategy B). Succeeding in getting a stag takes the effort of both hunters, and the hunters are separated in the forest and cannot be sure of each other's behavior. If both hunters are convinced that the other will hunt for stag, then hunting stag is a strict or unique best-reply for each player. However, if one turns out to be mistaken and the other hunter hunts for hare, then one will go hungry. Both hunting for hare is also an equilibrium and hunting for hare is a strict best-reply if the other player is hunting for hare. Here we can begin to see the subtleties of making predictions in games with multiple equilibria. On the one hand, (A, A) (hunting stag by both) is a more attractive equilibrium and results in high payoffs for both players. Indeed, if the players can communicate and be sure that the other player will follow through with an action, then playing (A, A) is stable and a reasonable prediction. However, (B,B) (hunting for hare) has properties which make it a useful prediction as well. It does not offer quite as high a payoff, but it has less "risk" associated with it in the sense that if the other player does not act as expected, then this action offers a safer option. Here playing B guarantees a minimum payoff of 3, while the minimum payoff to A

[51] To be completely consistent with Rousseau's story, B,B should result in payoffs of 3,3; as the payoff to hunting for hare is independent of the actions of the other player in Rousseau's story.

is 0. There is an extensive literature on this subject, and more generally on how to make predictions when there are multiple equilibria (see, e.g., texts by Binmore [65], Fudenberg and Tirole [245], Myerson [474], or Osborne and Rubinstein [489]).

The next example is another form of coordination game, but with some asymmetries in it. This is often referred to as a "battle of the sexes" game.

		Player 2	
		A	B
Player 1	A	3, 1	0, 0
	B	0, 0	1, 3

The players have an incentive to choose the same action, but they each have a different "favorite" action. There are again two (pure strategy) Nash equilibria: (A,A) and (B,B). Here, however, player 1 would prefer that they play equilibrium (A,A) and player 2 would prefer that the go to (B,B). The "battle of the sexes" title refers to a couple trying to coordinate on where to meet for a night out. They prefer to be together, but also have different preferred outings.

There are also what are known as "anti-coordination" games, with the prototypical version being what is known as the "hawk-dove" game or the "chicken" game, with payoffs as follows.

		Player 2	
		Hawk	Dove
Player 1	Hawk	0, 0	3, 1
	Dove	1, 3	2, 2

Here there are two pure strategy equilibria, (Hawk, Dove) and (Dove, Hawk). The interpretation is that players are in a potential conflict and can either be aggressive like a hawk or timid like a dove. If they both act like hawks, then the outcome is destructive and costly for both players and payoffs are 0 for both. If they each act like doves, then the outcome is peaceful and each gets a payoff of 2. However, if the other player acts like a dove, then a player would prefer to act like a hawk and take advantage of the other player, receiving a payoff of 3. If the other player is playing a hawk strategy, then here it is best to play a dove strategy and at least survive rather than to be hawkish and lead to mutual destruction.

9.10.4 Randomization and Mixed Strategies

In each of the above games, there was at least one pure strategy Nash equilibrium. There are also simple games where there does not exist any pure strategy equilibrium. To see this, consider the following simple variation on a penalty kick in a soccer match. There are two players: the player kicking the ball and the goalie. Suppose, to simplify the exposition, that we restrict the actions to just two for each player (there are still no pure strategy equilibria in the larger game, but this makes the exposition easier). The kicking player can either kick to the left side of the goal or the right side of the goal. The goalie can either move to the left side of the goal or the right side of the goal, and has to choose before seeing the kick as otherwise he or she has too little time to react. To keep things very simple, let us assume that if the player kicks to one side, then she scores for sure if the goalie goes to the other side, while the goalie saves it for sure if the goalie goes to the same side. The basic payoff structure is as follows:

		Goalie	
		L	R
Kicker	L	-1, 1	1, -1
	R	1, -1	-1, 1

This is also a game which is known as "matching pennies". The goalie would like to choose a strategy which matches that of the kicker, and the kicker would like to choose a strategy which mismatches the goalie's strategy.[52]

It is easy to check that there is no pair of pure strategies which form an equilibrium. What is the solution here? It is just what you see in practice: the kicker randomly picks left versus right, in this particular case with equal probability, and the goalie does the same.

To formalize this we need to define randomized strategies, or what are called mixed strategies. For ease of exposition let us suppose that X_i is finite, and the definition extends to infinite strategy spaces with proper definitions of probability measures over pure actions.

A *mixed strategy* for a player i is a distribution μ_i on X_i, with the interpretation that $\mu_i(x_i)$ is the probability that x_i is chosen. A profile of mixed strategies $(\mu_1, \ldots, \mu_n)$

[52] For an interesting empirical test of whether or not goalies and kickers on professional soccer teams randomize properly see Chiappori, Levitt and Groseclose [140]; and see Walker and Wooders [611] for an analysis of randomization in the location of tennis serves in professional tennis matches.

forms a mixed-strategy Nash equilibrium if

$$\sum_{x} \left(\prod_{j} \mu_j(x_j) \right) u_i(x) \geq \sum_{x_{-i}} \left(\prod_{j \neq i} \mu_j(x_j) \right) u_i(x_i', x_{-i}) \tag{9.24}$$

for all i and x_i'.

So, a profile of mixed strategies is an equilibrium if no player has some strategy that would offer a better payoff than his or her mixed strategy in reply to the mixed strategies of the other players. Note that this implies that a player must be indifferent between each strategy that he or she chooses with a positive probability under his or her mixed strategy. Also, players' randomizations are independent.[53] A special case of a mixed strategy is a pure strategy, where probability 1 is placed on some action.

It is easy to check that each mixing with probability 1/2 on L and R is the unique mixed strategy of the matching pennies game above. If a player, say the goalie, places weight of more than 1/2 on L for instance, then the kicker would have a best response to choose R with probability 1, but then that could not be an equilibrium as the goalie would want to change his or her action, and so forth.

There is a deep and long-standing debate about how to interpret mixed strategies, and the extent to which people really randomize. Let me point out that in the goalie and kicker game, what is important is that each player not know what the other player will do. For instance, it could be that the kicker decided before the game that if there was a penalty kick then she would kick to the left. What is important is that the kicker not be known to always kick to the left.[54]

We can begin to see how the equilibrium changes as we change the payoff structure. For example, suppose that the kicker is more skilled at kicking to the right side than the left. In particular, let us keep the payoffs the same as before, but now suppose that the kicker has an even chance of scoring when kicking right when the goalie goes right. This leads to the following payoffs:

[53] An alternative definition of correlated equilibrium allows players to use correlated strategies, but requires some correlating device that only reveals to each player their prescribed strategy and that these be best responses given the conditional distribution over other players' strategies.

[54] The contest between pitchers and batters in baseball is quite similar. Pitchers make choices about the location, velocity and type of pitch (whether various types of spin are put on the ball, etc.). If a batter knows what pitch to expect in a given circumstance, that can be a significant advantage. Teams scout each other's players and try to note any tendencies or biases that they might have and then try to respond accordingly.

		Goalie	
		L	R
Kicker	L	-1, 1	1, -1
	R	1, -1	0, 0

What does the equilibrium look like? To calculate the equilibrium, it is enough to find a strategy for the goalie that makes the kicker indifferent, and a strategy for the kicker that makes the goalie indifferent.[55]

Let μ_1 be the kicker's strategy and μ_2 be the goalie's strategy. It must be that the kicker is indifferent, and the kicker's payoff from L is $-\mu_2(L) + \mu_2(R)$ and the payoff from R is $\mu_2(L)$, so it must be that

$$-\mu_2(L) + \mu_2(R) = \mu_2(L),$$

or $\mu_2(L) = \frac{1}{3}$ and $\mu_2(R) = \frac{2}{3}$. For the goalie to be indifferent, it must be that

$$\mu_1(L) - \mu_1(R) = -\mu_1(L) + \mu_1(R),$$

and so the kicker must choose $\mu_1(L) = \frac{1}{2} = \mu_2(R)$.

Note that as the kicker gets more skilled at kicking to the right, it is the *goalie's* strategy that adjusts to moving to the right more often! The kicker still mixes evenly. It is a common misconception to presume that it should be that the kicker who should adjust to using his or her better strategy with more frequency.[56]

While not all games have pure strategy Nash equilibrium, every game with a finite set of actions has at least one mixed strategy Nash equilibrium (with a special case of a mixed strategy equilibrium being a pure strategy equilibrium). This was a shown in an important paper by Nash [475].

[55] This is a bit subtle, as we are not directly choosing actions which maximize the goalies payoff and maximize the kicker's payoff, but instead looking for a mixture by one player which makes the other indifferent. This is a feature of mixed strategies which it takes a while to grasp, but which experienced players seem to understand well (e.g., see Chiappori, Levitt and Groseclose [140]; and see Walker and Wooders [611]).

[56] Interestingly, there is evidence that professional soccer players are better at playing games that have mixed strategy equilibria than people with less experience in such games, which is consistent with this observation (see Palacios-Huerta and Volij [496]).

9.10.5 Sequentiality, Extensive-Form Games and Backward Induction

Let us now turn to the question of timing. In the above discussion it was implicit that each player was selecting a strategy with beliefs about the other players strategies, but without knowing exactly what they were.

If we wish to be more explicit about timing, then we can consider what are known as games in "extensive-form" which is a complete description of who moves in what order, and what they have observed when the move etc.[57] There are advantages to working with extensive form games as they allow for more explicit treatments of timing, and for equilibrium concepts that require credibility of strategies in response to the strategies of others.

Definitions for a general class of extensive form games is notationally intensive. In this book, we mainly look at a special class of extensive form games, finite games of perfect information, which allows for a treatment that avoids much of the notation. These are games where players move sequentially in some pre-specified order (sometimes contingently on which actions have been chosen), and each player moves at most a finite number of times, and each player is completely aware of all the moves that have been made previously. These games are particularly well-behaved, and can be represented by simple trees, where a node is associated with the move of a specified player, and then an edge corresponds to different actions the player might take. I will not provide formal definitions, but simply refer directly to games representable by such finite game-trees.

Each node has a player's label attached to it. There is an identified *root node*, which corresponds to the first player to move, player 1 in Figure 9.10.5, and then subsequent nodes which correspond subsequent players who make choices. In Figure 9.10.5, player 1 has a choice of moving either left or right. The branches in the tree correspond to the different actions available to the player at a given node. In this game, if player 1 moves left then it is player 2 who moves next, while if player 1 moves right then it is player 3 who moves next. It is also possible to have trees where player 1 chooses twice in a row, or where no matter what choice a given player makes it is a certain player who follows, and so forth. The payoffs are given at the end nodes, and are listed for

[57] One can collapse certain types of extensive form games into the normal form, by simply defining an action to be a complete specification of how an agent would act in all possible contingencies, and then having agents choose these actions simultaneously at the beginning of the game, but then the normal form becomes a more complicated thing that the two-by-two games we saw above.

Figure 9.10.5. A Game Tree with 3 Players and Two Actions Each.

the three respective players. The top payoff is for player 1, the second for player 2, and the bottom for player 3. So the payoffs depend on the set of actions taken, which then determines a path through the tree. An equilibrium provides a prediction about how each player will move in each possible contingency and thus makes a prediction about which path will be taken, and we refer to that as the *equilibrium path*.

We can apply Nash equilibrium to such games, which here is a specification of what each player would do at each node with the requirement that each player's strategy be a best response to the other players' strategies. Nash equilibrium does not always make sensible predictions when applied in the extensive form. To illustrate this, let us reconsider the advertising example discussed above. Suppose that firm 1 makes its decision prior to firm 2, and that firm 2 knows firm 1's choice before it chooses. This is represented below.

If we work with Nash equilibrium for this extensive form game, then we must specify what each player does at each node. There are two Nash equilibria of this game in pure strategies. The first is where firm 1 advertises, and firm 2 does not (and firm 2's strategy conditional on firm 1 not advertising is to advertise). The other equilibrium corresponds to the one we identified in the normal form. It is that firm 1 does not advertise, and firm 2 advertises regardless of what firm 1 does. This is an equilibrium,

Figure 9.10.5. Advertising Choices of Two Competitors

since neither wants to change its behavior given the other's strategy. However, this is not really credible in the following sense: it involves firm 2 advertising even after it has seen that firm 1 has advertised, and even though this is not in firm 2's interest in that contingency.

In order to capture the idea that each player's strategy has to be credible, we can solve the game backwards. That is, we can look at each decision node that has no successors, and start by making predictions at those nodes. Then, given those decisions, we can roll the game backwards and decide how player's will act at next-to-last decision nodes, anticipating the actions at the last decision nodes, and then iterate. This is called *backward induction*. Consider the choice of firm 2, given that firm 1 has decided not to advertise. In such a case, firm 2 will choose to advertise since 13 is larger than 12. Next, consider the choice of Firm 2, given that firm 1 has decided to advertise. In such a case, firm 2 will choose not to advertise since 7 is larger than 6. Now we can collapse the tree. Firm 1 will predict that if it does not advertise, then firm 2 will advertise, while if firm 1 advertises then firm 2 will not. Thus when making its choice, firm 1 anticipates a payoff of 7 if it chooses not to advertise, and 13 if it chooses to advertise. Its optimal choice is to advertise. The backwards induction prediction about the actions that will be taken is for firm 1 to advertise and firm 2 not

to.

Note that this offers a different prediction from that in the simultaneous move game we analyzed before. Firm 1 has gained a first mover advantage in the sequential version. Not advertising is no longer a dominant strategy for firm 1, since firm 2's decision depends on what firm 1 does. By committing to advertise, Firm 1 forces firm 2 to choose not to advertise. Firm 1 is better off being able to commit to advertise in advance.

A solution concept which formalizes the backward induction solution that we found in this game, and applies to more general classes of games, it what is known as *subgame perfect equilibrium* (due to Harsanyi [**?**]). A subgame in terms of a finite game tree is simply the subtree that one obtains starting from some given node. Subgame perfection requires that the stated strategies constitute a Nash equilibrium in every subgame (including those where there is just one move left). So, it requires that if we start at any node, then the strategy taken at that node must be optimal in response to the remaining the specification of strategies. In the game between the two firms, it requires that firm 2 choose an optimal response in the subgame following a choice by firm 1 to advertise, and so it coincides with the backward induction solution for such a game.

Let me close this appendix by noting that moving first is not always advantageous. Sometimes it allows one to commit to strategies which would otherwise be untenable, which can be advantageous; but in other cases it may be that the information that the second mover gains from knowing which strategy the first mover has chosen is a more important consideration. For example, playing the matching pennies game sequentially is not clearly not good for the first player to move.

9.10.6 Exercises on Games

EXERCISE **9.24** *Product Choices.*

Two electronics firms are making product development decisions. Each firm is choosing between the development of two alternative computer chips. One system has higher efficiency, but will require a larger investment and will be more costly to produce. Based on estimates of development costs, production costs, and demand, the following present value calculations represent the value of the alternatives (high efficiency chips or low efficiency chips) to the firms.

		Firm 2	
		High	Low
Firm 1	High	1, 2	4, 5
	Low	2, 7	5, 3

The first entry in each box is the present value to firm 1 and the second entry is the present value to firm 2. The payoffs in the above table are not symmetric. Firm 2 has a cost advantage in producing the higher efficiency chip, while firm 1 has a cost advantage in producing the lower efficiency chip. Overall profits are largest when the firms choose different chips and do not compete head to head.

(a) Firm 1 has a dominant strategy. What is it?

(b) Given your answer to part a), what should firm 2 expect firm 1's choice to be? What is firm 2's optimal choice given what it anticipates firm 1 to do?

(c) Do firm 1's strategy (answer to (a)) and firm 2's strategy (answer to (b)) form an equilibrium? Explain.

(d) Compared to (c), firm 1 would make larger profits if the choices were reversed. Why don't those strategies form an equilibrium?

(e) Suppose that firm 1 can commit to a product before firm 2. Draw the corresponding game tree and describe the backward induction/subgame perfect equilibrium.

EXERCISE **9.25** *Hotelling's Hotels.*

Two hotels are considering a location along a newly constructed highway through the desert. The highway is 500 miles long with an exit every 50 miles (including both ends). The hotels may choose to to locate at any exit. These will be the only hotels for any traveler using the highway. Each traveler has their own most preferred location along the highway (at some exit) for a hotel, and will choose to go the hotel closest to that location. Travelers most preferred locations are distributed evenly, so that each exit has the same number of travelers who prefer that exit. If both hotels are the same distance from a traveler's most preferred location, then that traveler flips a coin to determine which hotel to stay at. A hotel would each like to maximize the number of travelers who stay at it.

If Hotel 1 locates at the 100 mile exit, where should Hotel 2 locate?

Given Hotel 2's location that you just found, where would Hotel 1 prefer to locate?

Which pairs of locations form Nash equilibria?

EXERCISE **9.26** *Backward Induction.*

Find the backward induction solution to Figure 9.10.5 and argue that there is a unique subgame perfect equilibrium. Provide a Nash equilibrium of that game that is not subgame perfect.

EXERCISE **9.27** *The Colonel Blotto Game.*

Two armies are fighting a war. There are three battlefields. Each army consists of 6 units. The armies must each decide how many units to place on each battlefield. They do this without knowing how many units the other army has committed to a given battlefield. The army who has the most units on a given battlefield, wins that battle, and the army that wins the most battles wins the war. If the armies each have the same number of units on a given battlefield then there is an equal chance that either army wins that battle. A pure strategy for an army is a list (u_1, u_2, u_3) of the number of units it places on battlefields 1, 2, and 3 respectively, where each u_k is in $\{0, 1, \ldots, 6\}$ and the sum of the u_k's is 6. For example, if army A allocates its units (3,2,1), and army B allocates its units (0,3,3), then army A wins the first battle, and army B wins the second and third battles and army B wins the war.

Argue that there is no pure strategy Nash equilibrium to this game.

Show that mixing uniformly at random over all possible configurations of units is not a mixed strategy Nash equilibrium (hint - placing all units on one battlefield is not a good idea).

Show that each army mixing with equal probability between (0,3,3), (3,0,3) and (3,3,0) is not an equilibrium.[58]

EXERCISE **9.28** *Divide and Choose.*

Two children must split a pie. They are gluttons and each prefers to eat as much of the pie as they can. The parent tells one child to cut the pie into two pieces and then allows the other child to choose which piece to eat. The first child can divide the pie into any multiple of a tenth (for example, 1/10 and 9/10, 2/10 and 8/10, etc.). Show that there is a unique backward induction solution.

EXERCISE **9.29** *Take it or Leave it Bargaining.*

[58] Finding equilibria to Colonel Blotto games is notoriously difficult. One exists for this particular version, but finding it will take you some time.

Two players are bargaining over a pie. The first player can suggest a division x_1, x_2 such that $x_1 + x_2 = 1$ and each share is nonnegative. Thus, this is an extensive form game with an infinite number of strategies for the first player. The second player can then say either "yes" or "no". If the second player says "yes", then they each get their proposed share. If the second player says "no," then they each get nothing. Player's payoffs are their share of the pie.

Argue that there is a *unique* subgame perfect equilibrium to this game.

EXERCISE **9.30** *Information and Equilibrium.*

Each of two players receives an envelope containing money. The amount of money has been randomly selected to be between 1 and 1000 dollars (inclusive), with each dollar amount equally likely. The random amounts in the two envelopes are drawn independently. After looking in their own envelope, the players have a chance to trade envelopes. That is, they are simultaneously asked if they would like to trade. If they both say "yes," then the envelopes are swapped and they each go home with the new envelope. If either player says "no," then they each go home with their original envelope. What is the highest amount for which either player says "yes" in a Nash equilibrium.

(Hint: Should a player say "yes" with 1000 dollars in their envelope?)

Chapter 10

Networked Markets

Classic theories of supply and demand, and the competitive models that underly them, are built on the trade of precisely defined and known commodities. This allows for markets that are largely anonymous and unmodeled. The idea that modern societies can produce regular goods and deliver them across large and effectively anonymous markets was championed by by Adam Smith [**?**] and has become a cornerstone of modern economic analysis. Indeed, there are many goods and services are such that the quality and reliability are predictable and delivery is easy and contractable, and where transactions can occur between parties who need not know each other outside of a single instance. This is true of many final goods, such as various consumer products. However, even in the most modern societies there are many goods and services that are not so uniform across large numbers of buyers and sellers, and might involve specific features tailored to a particular situation or involve smaller numbers of buyers and sellers. Labor markets are an example. Because of this, many markets operate through decentralized networks or at least partly throughnetworked interactions. This is true of many intermediate goods and services, where parts or inputs are supplied from one firm to another, or one individual to another. The importance of social networks in the market is evident to anyone who has ever searched for employment, and the extent and importance of the embeddedness of economic activity in social networks in developed markets is cogently argued by Granovetter [292].[1]

This chapter explores the role of social networks in various markets. A series of questions arise. To what extent are social and economic networks used in the exchange of goods and services? Which markets tend to be 'networked' and why? Does the use

[1] For an early discussion of the social embeddedness of economic activity see Polanyi [517].

of networked markets affect the terms of trade, prices and efficiency of a market? How do social networks impact wages and employment patterns? How does position in a network affect the trade and welfare of an individual or firm? Which networks are likely to emerge in the context of networked markets? This chapter addresses these questions and also provides groundwork for further research on this important subject.

10.1 The Social Embeddedness of Markets and Exchange

Social networks have been the primary fabric of many economic interactions for centuries, if not millenia (e.g., recall the discussion of fifteenth century Florence in Section **??**), and there has been detailed research on the embeddedness of various markets in social networks for over six decades. To begin this chapter, I provide an overview of some of the empirical work on this subject, and some discussion of which markets we should expect to be networked and why.

10.1.1 The Use of Job-Contacts in Labor Markets

The importance of social contacts in obtaining information about jobs and in the referral process is so prevalent, that it comes to embody part what we understand by the term "networking". In fact, a definition of "networking" in the Merriam-Webster dictionary (online, 2007) is "the cultivation of productive relationships for employment or business." Indeed, a substantial portion of jobs are filled through referrals from social contacts of current employees of a firm. This observation is not only important as an example of the role of social networks, but also because it has implications for employment, wages, and the efficiency of labor markets. It shows how understanding social networks can help us to gain new and deeper insights into the workings of a market.

To get an impression of the extent to which social networks play a role in labor markets, let us consider statistics from some studies.[2] An early study by Myers and Shultz [472] of textile workers found that 62 percent of interviewed workers found out about their job openings through a social contact, while only 23 percent found the job by a direct application, and 15 percent through an employment agency, advertisement, or some other means. This sort of pattern is not unique to the textile industry, it is

[2] See Montgomery [455] and Ioannides and Loury [**?**] for more references and discussion.

also found across other professions. For instance, Rees and Shultz [531] interviewed workers in a Chicago neighborhood and kept track of what percentage of them found out about their current jobs through friends or relatives. They considered twelve different occupations and found rates of jobs obtained through social contacts ranging from a low of 23.5 percent (for accountants) to a high of 73.8 percent (for material handlers). The array of occupations they considered was broad, including typists (37.3 percent from social contact), janitors (65.5 percent), electricians (57.4 percent), and truck drivers (56.8 percent), to take a few examples. While these are mostly manual labor jobs, similar patterns are exhibited across different types of work. Granovetter's [289], [290] interviews of residents of Amherst Massachusetts found similar patterns across various types of occupations. He found that 44 percent of technical workers found their jobs through a social contact, as did 56 percent of professional workers, and 65 percent of managerial workers. Corcoran, Datcher, and Duncan [**?**] examine the Panel Study in Income Dynamics data set (the "PSID") and compare across race and gender. They found the following percentages for finding jobs by social contact: Black Males 58.5 percent, Black Females 43 percent, White Males 52 percent, and White Females 47.1 percent.

These numbers provide an impression of the extent to which social networks play a role in labor markets. There are also a variety of studies that examine how the role of social networks in labor markets varies across different groups and professions (see Ioannides and Loury [**?**] for more of an overview). As an example, Pellizzari [510] examines data from European countries and finds a range of differences of how prevalent social contacts are in the labor market, as well as whether jobs obtained through social means lead to higher or lower wages. While going into the details of those differences is beyond the scope of this text, it is clear that it is very important to develop models that help us to understand why and when employers will use referrals as a means of filling job vacancies, and how social network structure plays into this. While there are some models that shed light on these issues, this area is still under-developed.

10.1.2 The Features of some Networked Markets

To provide further background, it is helpful to discuss a couple of examples of studies of networked markets and some of the features that those markets exhibit.[**?**, **?**,]

An influential study is Uzzi's [598] investigation of the importance of social relationships in the apparel industry in New York. First, Uzzi interviewed the executive officers of 43 "better dress" firms in New York City with annual sales between five

hundred thousand dollars and one billion dollars. The firms are basically divided into two groups: manufacturers and contractors. For instance, a contractor might have a design for a particular garment and want a given number of them produced and delivered. A manufacturer would then take the garment design and produce and deliver the garments. The firms were selected via a stratified random sample. Uzzi's focus was on the type of relationships that firms had with each other. One type of relationship he categorized as "market" or "arm's length" relationships which included many one-time transactions, and the other he categorized as "special" or "close" relationships which included many relationships with repeated interaction and ones that involved idiosyncracies in products or special investments. Based on the interviews, Uzzi identified three main ingredients that are associated with close ties but not with arm's length ties: trust, fine-grained information transfer, and joint problem solving. This view is derived from interpretations of the interviews and associated anecdotes. Uzzi quotes an example where trust is associated with dealing with an unforeseen problem, such as a fabric not producing the sort of garments that a contractor desires, and then reaching some agreement on how to deal with this problem rather than leaving the manufacturer at a loss. The fine-grained information transfer refers to passing along useful information, for instance about a new design, fabric, or technique, to someone with whom one is in a repeated relationship. Firms involved in close relationships have more of an incentive to pass along such information, and can also do so in a credible manner. The joint problem solving refers to being able to quickly deal with problems that arise, which often hinges on knowing what the capabilities and situations of both firms in a relationship are.

Using these insights of how close relationships might help firms, Uzzi builds a hypothesis that firms that have more embedded relationships will have a higher probability of survival. To test this hypothesis, he examines 1991 data from the International Ladies Garment Workers' Union, which keeps detailed records of inter-firm transactions in the industry. Over 80 percent of the firms are unionized, and these data cover most of the active firms in New York that year. Based on these data, Uzzi examines the contractors who failed versus those who did not. Out of the 479 contractors with complete records in the data set, 125 failed during this year.[3] Uzzi measures how embedded a contractor i is by examining $\sum_j P_{ij}^2$ where P_{ij} is the percentage of all of contractor i's output contracted with manufacturer j. If a contractor deals with only

[3] Only 8 of 89 manufacturers in the data set failed, and so Uzzi does not report the relationship between survival and embeddedness for manufacturers.

one manufacturer then this will be 1, whereas if the contractor spreads its business out among many manufacturers then this will tend towards 0. 15 percent of the contractors send 100 percent of their business to one manufacturer, and 45 percent send at least 50 percent of their business to one manufacturer, while almost 20 percent send less than 25 percent to any one manufacturer. Thus, there is some variation in the data, but also substantial embeddedness according to this measure. Uzzi then regresses the survival variable on this embeddedness measure, as well as a series of other background variables (geographic location, age of the firm, size of the firm, some network centrality measures, and other neighborhood variables). He finds a positive and significant relationship (at the 95 percent confidence level) between survival and embeddedness. Based on the fitted regression line, a typical firm (setting other controls to average levels) that has an embeddedness score of 0 will fail to exist at the end of the year with a probability of .27, while a firm with an embeddedness score of 1 will fail to exist at the end of the year with a probability of .14.

As with any cross-sectional statistical analysis, it is difficult to draw causal conclusions from an observed correlation. It could be that embeddedness helps firms to survive, or it could be that firms that are near failure have a harder time establishing close relationships. Uzzi argues that it is the former. There could also be many other factors that are not observed and that contribute to the type of arrangements that firms have. For example, it might be that more complicated garments require specialized relationships and also are in a less competitive part of the business. Regardless of what the precise explanation for the observed correlations, or which direction the causation goes, Uzzi's [598] study provides evidence that many firms in this industry do a substantial portion of their business with just a few, and in many cases just one, partner; and also provides some insight into the potential differences between a network of close relationships versus a more distant market-style relationships.

Another example of a partly-networked market is that of the Marseille fish market as analyzed by Kirman [378] and Weisbuch, Kirman, and Herreiner [626]. The fish market has several critical features. First, the fish are perishable. This means that the ability for buyers and sellers to smooth inventory is quite limited, as the "fresh" fish need to be consumed soon after they are caught.[4] Second, the supply of fish is variable

[4] This is changing over time, as methods of freezing and transporting fish are advancing. "Fresh" is in quotes, as in fact some types of fish that are considered fresh are frozen on board the boats on which they are caught. Nevertheless, there is a demand for local fish in the Marseille market (e.g., as ingredients in Marseille's famous bouillabaisse).

as the catch is random and affected by various conditions including weather, water conditions, and fish populations. Third, the buyers of the fish differ in their demand elasticities for the fish; that is, they differ in the importance of fish for them and how their willingness to pay varies with quantity. A famous restaurant that has built a reputation on serving Marseille's finest bouillabaisse has to be able to consistently buy fish of a reliable quantity. Another local restaurant that does not specialize in bouillabaisse can adjust its menu and ingredients as availability changes.

Weisbuch, Kirman, and Herreiner [626] examine the market between 1988 and 1991 considering buyers and sellers in the market for more than 8 months. There are 45 sellers and over 1400 buyers, and a wide range of fish. The buyers are restaurants and retailers and there are no posted prices so that each price transaction is decided bilaterally between the buyer and seller. In terms of a network structure, they find that a sizeable fraction of buyers are loyal to a single seller, while other buyers buy from many sellers. For example, with regards to cod, almost half (48 percent) of the buyers purchase more than 95 percent of their cod from just one seller. With regards to whiting and sole, more than half of the buyers buy more than 80 percent of their fish from just one seller. They break this down by the patterns of buyers and note that buyers purchasing large quantities are significantly more likely to be loyal than other buyers. For example, dividing buyers into those who bought more than two tons per month and those who bought less, the ones who bought more transact on average 85 percent of the time with their most visited seller while this drops to 56 percent of the time for those who buy less. This suggests that one sees some established relationships, as well as some shopping around. Weisbuch, Kirman, and Herreiner [626] examine a simple model of this, where the driving force is predictability of available fish and of demand for fish. The model builds on what one might think of as a complicated version of musical chairs: buyers must choose to go to just one seller each day and the seller is either able to meet the buyer's demand. Buyers follow an adaptive updating rule, with a higher tendency to visit sellers who have met their demands in the past. This is a sort of metaphor that captures the idea that as a buyer shops around during the day, time is lost and fewer fish are available. On a day where there is a relatively large catch this might result in a better price, but on a day where there is a relatively small catch this might result in a relatively high price or being closed out of the market. Thus, there are some frictions in this type of market so that it does not simply clear as a classic supply and demand model all at once, but requires some search by buyers, and price-setting by individual and only partly-informed sellers. Buyers face some coordination issues

and also learn about the available supply of different sellers over time. Having a larger demand, among other things, tilts a buyer towards settling down with just one (large) seller, partly due to the predictability of the supply.

10.1.3 Which Markets Should be Networked?

These examples point to some of the issues that underly why specific relationships might emerge in the trade of goods and services. The garment industry analysis highlights "trust" as a central part of the importance of repeated relationships. The fish market analysis highlights predictability as a central part of the importance of repeated relationships. There are a variety of situations that lead to some advantages of a repeated or close relationship, basically having to do with difficulties in contracting. This is related to some of the theory developed by Williamson [629] explaining the organization of firms. Williamson examines a variety of different frictions that can make it difficult for two parties to completely contract upon the exchange of goods or services. Williamson then argues that if a single organization or firm is on both sides of the transaction, then it can internalize the difficulty and overcome the obstacle to contracting. Granovetter [292] critiques Williamson's argument pointing out that it is not so clear that placing things within a firm provides a solution that could not be handled through some sort of other relationship. For example, reputations and repeated interactions can help discipline transactions and this could take place within the fabric of a network instead of being internal to a firm. Also, contracting parties being within the same firm does not imply that their incentives are aligned.

Drawing from the above examples and studies of incomplete contracting, let us examine some of the features of given transactions that might favor placing them within the context of a network of transactions where reputations and/or repeated relationships are relied upon to help circumvent difficulties inherent in a given transaction.

In many situations, there are unforeseen contingencies that arise between two parties involved in a contractual relationship. It may be that some specific input is not available, or a new regulation appears that requires the redesign of a product and some delay, and so forth. One can try to write a contract that completely covers all possible contingencies, but complex transactions (for instance, the construction of a building) this might not be possible. If the relationships between the parties are repeated, so that they deal with each other on an ongoing basis then these problems are not viewed as a one-time expense on one of the two parties' side, but instead can be evened out over time. This can make the bargaining over such unforseen issues smoother, as suggested

by some of Uzzi's [598] interviews.

Contractual incompleteness can arise not only because of unforeseen contingencies, but also because of specific investments that might need to be made for particular transactions and require long-term use to realize their full value. Contractual incompleteness can also arise because of asymmetries in information. Asymmetries in information manifest themselves in the form of moral hazard problems, where one party to a contract cannot fully observe the actions of the other, and adverse selection problems where one party does not fully observe some attributes of the good being traded. Once again, long-term relationships can help resolve these issues. For example, in terms of moral hazard problems, having a repeated interaction allows one party to examine long run performance of the other. If a customer takes a car to a local mechanic on a regular basis, and the mechanic frequently claims that the car requires extensive and expensive repairs, the customer can look for a new mechanic. The fact that current performance can influence future business helps temper the moral hazard problem. In contrast, if a car needs a repair far from home, and it is a one time interaction, the incentives for the mechanic to suggest a more expensive repair than is necessary can be substantially larger. Similar reasoning favors long term relationships in the face of adverse selection. If a firm buys parts whose reliability or longevity cannot be observed except with the passage of time, then having repeated transactions can help provide incentives for the supplier to deliver a specified quality of parts.

There are tradeoffs to maintaining such closed relationships, as it limits one's ability to shop around for alternative prices. It might be that a given firm wants to work with two or three suppliers of the same parts over time. One can also rely on the transmission of information through a network to help temper asymmetric information problems. Maintaining a "reputation" for providing high-quality parts or service can help provide incentives that overcome some of the difficulties arising from asymmetries in information, if word of mouth can spread information about outcomes to other potential future business partners. Thus, we might see more complex network relationships for various reasons.

Beyond these asymmetric information considerations, we also saw the issues of predictability and more basic uncertainty as potential explanations for the relationships in the Marseille fish market.[5] As an incentive for a continued relationship, a regular customer might be given access to better produce or a higher chance at getting a desired

[5] See also the study by Podolny [514] of investment banking showing an increased concentration of transaction relationships when market uncertainty increases.

quantity of produce. In situations where the uncertainties of the crop or production totals are not fully insurable, risk-aversion can then favor the formation of repeated interactions.

There are other aspects of networks that can be valuable in the trade of goods and services beyond those which arise between the parties directly involved in the transaction. Networks also serve as an integral part of many markets in terms of putting different buyers and sellers in touch with each other. Labor markets serve as an excellent example. A firm wanting to hire a new employee might ask its existing employees for referrals. This could happen for a variety of reasons.[6] A very basic reason is simply that it wants to hire people similar to the employees that it already has. Given the homophily in many social networks, a firm can take advantage of its existing workforce in order to find other people with similar characteristics. For example, if a fast-food restaurant wants to hire someone willing to work part-time on weeknights and for minimum wage with low benefits, it might ask its employees if they know of anyone else who would be available in similar circumstances. This can save the time and cost of advertising and then sifting through applications. Beyond this, using current employees might reach potential hires that might not be reached via the advertising. It can also be that current employees are good at communicating with potential employees regarding whether a potential job is a good match. In addition to the benefits of locating potential hires who fit well with the firm, current employees might be credible sources of information about the quality of a potential hire. A recommendation coming from a current employee or a friend or other sort of acquaintance could carry more weight than that of a stranger.

This discussion has sketched potential benefits and reasoning behind networked relationships. Let us now examine some models of such interactions in order to get a fuller understanding of some of the potential implications of network structure for economic transactions and welfare, and also for incentives to form such networks.

[6] See Fernandez, Castilla, and Moore [228] for discussion of some factors favoring the use of referrals and evidence from a study of hiring practices in a phone bank that there can be economic benefits to firms who hire through referrals. In addition to some of the benefits from better matching, they also examine the extent to which hiring friends of current employees affects turnover in the firm, which might be related to the social environment of the firm.

10.2 Networks in Labor Markets

The pervasiveness of networks in labor markets makes them a leading example of networked markets and a source of a variety of insights. So, let us begin by analyzing different aspects of networked labor markets.

10.2.1 Strong and Weak Ties

As discussed in Section 3.2.7, the role of social networks in finding jobs was central to Granovetter's [289], [290] influential research that distinguished between "strong" and 'weak" social ties. To recall those data, Granovetter measured the strength of a tie by the number of times that individuals had interacted in a past year (strong = at least twice a week, medium = less than twice a week but more than once a year, and weak = once a year or less). Of the 54 people whom he interviewed who had found their most recent job through a social contact, he found that 16.7 percent had found their jobs through a strong tie, 55.7 percent through a medium tie, and 27.6 percent through a weak tie.[7]

Building on a distinction between strong and weak ties, Boorman [85] modeled individuals' decisions of how to allocate their time between maintaining these two different forms of ties in one of the first "economic" models of social networks. Boorman's model is based on the following structure. An individual has to divide his or her time between maintaining strong and weak ties. Strong ties take more time, and so the individual is faced with a tradeoff having more ties, but weak ones, or fewer ties, but strong ones. Boorman represents this by requiring that an individual have T units of time spent maintaining relationships. If W is the number of weak ties that an individual has, and S is the number of strong ties, then they must satisfy:

$$W + \lambda S = T \tag{10.1}$$

where $\lambda > 1$ is a factor indicating how much more time must be spent to maintain a strong tie.

Boorman's ties also lead to different benefits. Strong ties have priority in obtaining job information from social contacts. This operates as follows. Time ticks by in discrete periods. In any period, with probability μ an individual has need of a job. This is

[7] There is also a series of studies that have examined how strong and weak ties affect labor outcomes, and some debate about the relative effectiveness of weak ties. For example, see Lin, Ensel and Vaughn [412] and Bridges and Villemez [98] and the literature that follows.

the same across individuals and independent of history and the state of the system in the previous period. Effectively, the system restarts in each period. If an individual needs a job then he or she can find a job in two ways. First, the individual can hear about a job directly, which again happens at some exogenous rate δ, independent of the state of the system. In that case, the individual takes the job. Second, the individual might not hear directly, but instead might have a friend who is employed who happens to randomly hear about a job. In that case, the employed friend looks around at his or her strong ties and weak ties. If some of the strong ties are unemployed, then the employed friend passes the job to one of them uniformly at random. If all of the strong ties are employed, then the employed friend passes the job on to one of the weak ties uniformly at random. Thus, strong ties have a priority in hearing about a job. Boorman examines networks that are trees with infinite numbers of nodes so that one does not have to worry about the issue of two neighbors being neighbors of each other. He also considers situations where all individuals choose the same allocation of ties, so that the network is regular in a strong sense. Let $q_s \leq q_w$ be the probability that one does *not* hear about a job through a given strong tie and weak tie respectively, when in need. The chance of getting a job when in need can then be written as

$$\delta + (1-\delta)\left(1 - q_s^S q_w^W\right).$$

A given agent thus trades off the higher probability that strong ties lead to job information against being able to maintain fewer of them. One can derive the expressions for q_s and q_w as a function of the parameters of the model. For instance, q_s will depend on the probability that a given strong friend will be employed and how many other strong ties might be competing for job information at a given time. With expressions for q_s and q_w in hand, one can then look for an equilibrium of the system where individuals are optimally choosing S, W given the anticipated q_s and q_w, and the anticipated q_s and q_w correspond to the ones generated by the choices that individuals have made concerning S, W. This is hard to solve for directly, and can involve multiple equilibria, but one can at least work out simulations for some parameter values, as Boorman does.

There are several intuitive effects that Boorman reports from simulations. First, as λ increases, the relative cost of strong versus weak ties goes up and so the equilibrium involves fewer strong and more weak ties. Second, as μ decreases, so that one is less likely to need a job, the relative value of weak ties goes up. One only gets job information via a weak tie when all of the weak acquaintance's strong neighbors are employed, which is more likely when μ is low.

The Boorman model makes important strides in terms of considering strong and weak ties to be choice variables, and in terms of deriving tradeoffs between different forms of ties. However, the model lacks a number of things that we might be interested in. As a model of strong and weak ties, it is missing one of the critical ingredients that was the basis for Granovetter's theory: the idea that weak ties were more likely to bridge to parts of a network that are not accessed more directly whereas strong ties are more likely to link to nodes that are already at a short path distance. Such aspects of network architecture are missing from Boorman's model. Also, the model is missing the correlation in employment and time series implications that we might be interested in from the perspective of explaining how labor markets work. The fact that the state of the network is history independent simplifies the model (with the need for jobs being independent of history and the previous state of the network), but then we miss interesting dynamics and patterns of employment as a function of social structure.

10.2.2 A Networked Model of Employment

Calvó-Armengol and Jackson [119], [120] examine a model that is similar to Boorman's in having job information arrive directly and through neighbors, but that brings network structure to the forefront to see how network structure can impact employment and wage dynamics and distribution across a society.[8] Before getting into the model in detail, let me start with a brief overview of it. In the simplest version of the model, workers are connected by an undirected network. Randomly, an employed worker can lose his or her job. If that happens, then the worker looks for work. Information about new job openings arrives randomly to the workers in the network. A worker can hear about a job directly. If the worker is unemployed, then he or she takes the job. Similarly to the Boorman model, if the worker is employed, then the worker randomly picks an unemployed neighbor to receive the information; but in this case treating all unemployed neighbors with equal weight. The system operates over time, so that the starting state at the beginning of one period is state the system ended in the last period, and so dynamic patterns can be studied. The network becomes important in several ways. Having more neighbors gives a worker potential access to more job information

[8] Such information arrival processes are also in Diamond [188], without networks. Calvó-Armengol [115] developed a networked variation of Diamond's and Boorman's models of information passing to study incentives for network formation. Calvó-Armengol and Jackson [119], [120]developed a richer model in bringing in wages and variations on job information passing and used it to study employment and wage patterns and dynamics.

and so a higher average employment rate and higher average wages (in the version of the model with wages). This also leads to correlation in neighbors' employment status. An unemployed worker who has an employed neighbor is more likely to hear about a job opening than a similar worker with an unemployed neighbor, leading to a higher probability that a worker becomes employed in any given period as a function of how many of his or her neighbors are employed. This leads to a positive correlation in employment.

Beyond this basic structure, there are a number of things that can be analyzed. The model described above leads to a Markov chain, so that one can keep track of what tomorrow's employment pattern is likely to look like given today's employment pattern. From this, one can deduce long run steady-state distributions of employment and how these vary with network structure. In addition to things like the correlation structure, one can also examine the time series of employment. For instance, a prevalent observation in the labor economics literature is what is known as duration dependence. That refers to the fact that workers who have been unemployed for more periods are less likely to find work in a given period than workers who are just recently unemployed. There are various partial explanations for this, but the network model exhibits this quite naturally. Conditional on a worker being unemployed for a longer time, it is likely that many of the worker's neighbors are also unemployed, and hence have not been passing information along. This means that it is less likely that such a worker will be hearing about a job in the next period, compared to a worker whose neighborhood has a higher employment level. One can also enrich the model to allow for different types of jobs, different wage levels, and decisions such as whether or not to pursue education.

The Model Description

I present the simplest version of the model. For variations with heterogeneous jobs and multiple wage levels, see Calvó-Armengol and Jackson [120]. In the version presented here, all jobs are identical and there is just one wage level, which simplifies the analysis.

There are n workers or agents who are connected by an undirected network, represented by the $n \times n$ symmetric matrix g, which has entries in $\{0, 1\}$. Time evolves in discrete periods indexed by $t \in \{1, 2, \ldots\}$.

The n-dimensional vector s_t describes the employment status of the agents at time t. If agent i is employed at the end of period t, then $s_{it} = 1$ and if i is unemployed then $s_{it} = 0$.

Period t begins with some agents employed and others unemployed, as described by the state s_{t-1}. The first thing that happens in a period is that information about new job openings arrives. Each agent directly hears about a job opening with a probability $a \in [0,1]$. This job arrival process is independent across agents. If an agent i is unemployed ($s_{i,t-1} = 0$) and hears about a job then he or she takes that job and becomes employed. If an agent i is employed ($s_{i,t-1} = 1$) and hears about a job then he or she picks an unemployed neighbor ($j \in N_i(g)$ such that $s_{j,t-1} = 0$) and passes the job information to that neighbor. If agent i has several unemployed neighbors, then the agent picks one uniformly at random. If agent i's neighbors are all employed, then the job information is lost.

The probability of the joint event that agent i learns about a job and this job ends up in agent j's hands is described by $p_{ij}(s_{t-1})$, where

$$p_{ij}(s_{t-1}) = \begin{cases} a & \text{if } s_{i,t-1} = 0 \text{ and } i = j; \\ \frac{a}{\sum_{k:s_{k,t-1}=0} g_{ik}} & \text{if } s_{i,t-1} = 1, s_{j,t-1} = 0, \text{ and } g_{ij} = 1; \text{ and} \\ 0 & \text{otherwise.} \end{cases} \tag{10.2}$$

At the end of a period some employed agents lose their jobs. This happens randomly according to an exogenous breakup probability, $b \in [0,1]$, independently across agents.

Some Simple Examples

It is useful to start with some simple examples to see how things evolve.

EXAMPLE **10.2.1** *An Isolated Agent*

First, let us consider an isolated agent as a benchmark. Let μ be the long-run steady-state probability that the agent is employed.[9] This must satisfy

$$\mu = (1-b)\left(\mu + a(1-\mu)\right). \tag{10.3}$$

This keeps track of the two different ways the agent could be employed. First, it could be that at the end of last period the agent was employed, which has a probability μ, and then the agent did not lose his or her job at the end of this period, which happens

[9] This is a probability that may be thought of in two ways. First, regardless of what the agent's initial state is, this is the limit of the probability that the agent will be employed in a distant period in the future. Second, if one starts by randomly setting the agent's initial state with this probability, then it is the probability that the agent will be employed tomorrow, and at any date in the future.

with probability $1-b$. Second, it could be that the agent was unemployed at then end of last period and then heard about a job in the beginning of this period, which has a probability $a(1-\mu)$, and then the agent did not lose his or her job at the end of this period, which happens with probability $1-b$. Solving (10.3) for μ leads to

$$\mu = \frac{(1-b)a}{b+(1-b)a} = \frac{1}{1+\frac{b}{(1-b)a}}. \tag{10.4}$$

As one would expect, the steady-state employment probability is increasing in the probability of hearing about a job, a; and decreasing in the probability of losing a job, b; is no more than the probability of retaining a job $(1-b)$; but approaches $(1-b)$ as a approaches 1. Moreover, it is not the absolute values of a and b that matter, but their relative values. In particular, it is how $\frac{b}{1-b}$ compares to a that is critical.

EXAMPLE **10.2.2** *A Dyad*

Next, let us consider a dyad. Here $n=2$ and $g_{12}=g_{21}=1$. Given the symmetry of this setting, the steady-state distribution can simply be kept track of through the probability that no agents are employed, μ_0, one agent is employed, μ_1, and both agents are employed, μ_2.

We can then keep track of the transitions as follows. The situation with two employed workers can happen in three ways. It could be that they were both employed at the end of last period and neither lost a job, which happens with probability $\mu_2(1-b)^2$, or it could be that only one was employed at the end of the last period and at least one heard about a job and neither lost a job, which happens with probability $\mu_1(1-(1-a)^2)(1-b)^2$, or it it could be that neither started out employed and both heard about jobs and then both kept those jobs, which happens with probability $\mu_0 a^2(1-b)^2$. Similar reasoning applied to the other states, and we can characterize the steady states as the solutions to:

$$\begin{pmatrix} \mu_0 \\ \mu_1 \\ \mu_2 \end{pmatrix} = \begin{pmatrix} (1-a+ab)^2 & (1-a)^2 b(1-b)+b^2 & b^2 \\ 2a(1-b)(1-a+ab) & (1-b)\left((1-a)^2(1-2b)+2b\right) & 2b(1-b) \\ a^2(1-b)^2 & \left(1-(1-a)^2\right)(1-b)^2 & (1-b)^2 \end{pmatrix} \begin{pmatrix} \mu_0 \\ \mu_1 \\ \mu_2 \end{pmatrix}. \tag{10.5}$$

We solve this (noting that the vector μ is a unit eigenvector of the transition matrix) to find

$$\begin{pmatrix} \mu_0 \\ \mu_1 \\ \mu_2 \end{pmatrix} = \begin{pmatrix} b^2\left(1+(1-b)(1-a)^2\right)/X \\ 2ab(1-b)\left(1+(1-b)(1-a)\right)/X \\ a^2(1-b)^2\left((1-a)(3-a)(1-b)+1\right)/X \end{pmatrix} \tag{10.6}$$

where

$$X = b^2\left(1+(1-b)(1-a)^2\right)+2ab(1-b)\left(1+(1-b)(1-a)\right)+a^2(1-b)^2\left((1-a)(3-a)(1-b)+1\right).$$

If we let $a = 1$, so that workers are sure to hear about jobs in any period, then the probability of having nobody employed goes to b^2, the probability of having one employed goes to $2b(1-b)$, and the probability of having both employed goes to $(1-b)^2$, as we should expect. As b goes to 0, μ_2 goes to 1, and as b goes to 1, μ_0 goes to 1.

As these expressions are cumbersome, we can also examine the model when the time between periods becomes small. Then, a and b both go to zero, and it is only the relative rates that matter. In particular, the chance that more than one change happens in a period, in terms of having more than one piece of information and/or loss of a job, goes to 0 relative to the probability that one change happens in a period. For instance, let us replace a and b with $\frac{a}{T}$ and $\frac{b}{T}$. As T becomes large, second order and larger terms become negligible relative to single changes and then (10.5) is approximated by

$$\begin{pmatrix} \mu_0 \\ \mu_1 \\ \mu_2 \end{pmatrix} = \begin{pmatrix} 1-\frac{2a}{T} & \frac{b}{T} & 0 \\ \frac{2a}{T} & 1-\frac{2a}{T}-\frac{b}{T} & \frac{2b}{T} \\ 0 & \frac{2a}{T} & 1-\frac{2b}{T} \end{pmatrix} \begin{pmatrix} \mu_0 \\ \mu_1 \\ \mu_2 \end{pmatrix}. \tag{10.7}$$

The solution to (10.7) is[10]

$$\begin{pmatrix} \mu_0 \\ \mu_1 \\ \mu_2 \end{pmatrix} = \begin{pmatrix} \frac{b^2}{b^2+2ab+2a^2} \\ \frac{2ab}{b^2+2ab+2a^2} \\ \frac{2a^2}{b^2+2ab+2a^2} \end{pmatrix}. \tag{10.8}$$

From this we can deduce a few things. First, the probability that a given agent is employed in any period is

$$\mu_{dyad} = \mu_2 + \frac{\mu_1}{2} = \frac{2a^2+ab}{b^2+2ab+2a^2}.$$

If we compare this to the same limit for (10.4) which is $\mu_{isolate} = \frac{a}{a+b}$, we see that it is larger. Indeed, simplifying the above expression leads to

$$\mu_{dyad} = \frac{a}{a+b-\frac{ba}{2a+b}} > \mu_{isolate} = \frac{a}{a+b}. \tag{10.9}$$

It is clear that this should hold, since having a neighbor increases the opportunities for hearing about employment.

[10] We can also obtain this by examining the limits in (10.6) directly.

Figure 10.2.2. Correlation in Employment as a Function of $y = \frac{a}{b}$

We can also examine the correlation of employment across the two agents.

$$Corr_{dyad} = \frac{E[s_{1t}s_{2t}] - E[s_{1t}]E[s_{2t}]}{E[s_{it}^2] - E[s_{it}]^2} = \frac{\mu_2 - \mu_{dyad}^2}{\mu_{dyad} - \mu_{dyad}^2}.$$

Substituting from (10.8) and (10.9), the correlation is

$$Corr_{dyad} = \frac{ab}{3ab + 2a^2 + b^2} = \frac{1}{3 + 2\frac{a}{b} + \frac{b}{a}}. \tag{10.10}$$

This reaches a maximum when $\frac{a}{b}$ is $\frac{1}{\sqrt{2}}$, and is always positive. It is graphed in Figure 10.2.2 below as a function of $y = \frac{a}{b}$.

The correlation of two neighbors should clearly be positive, as one's probability of finding a job goes up when his or her neighbor is employed. It is less clear whether larger groups of agents should have positively correlated employment outcomes.

Complete Networks

Let us next examine settings where individuals live in cliques of n individuals who are all connected to each other. Here there is a full symmetry, so that we can keep track of

the state simply in terms of how many agents are employed. Let μ_k be the steady-state probability that exactly k agents are employed in a given period.

Again, let us examine situations where the time periods become small, so the arrival rates are a/T and b/T for some large T. This means that the probability of having two or more events occur in a period (for instance two people hearing about a job) becomes infinitely less likely than having just one event occur, as the former is on the order of $1/T^2$ and the latter is on the order of $1/T$. To calculate what happens at the limit as T grows, we only need to keep track of transitions between neighboring states. This permits us to solve in closed form for the steady-state probability of any state.

PROPOSITION **10.2.1** *Consider a complete network of n agents, with arrival rate a/T and breakup rate b/T. As T grows, the steady state probability of having k agents employed converges to*

$$\mu_k = \frac{\frac{n!}{k!}\left(\frac{b}{na}\right)^{n-k}}{\sum_{j=0}^{n}\frac{n!}{j!}\left(\frac{b}{na}\right)^{n-j}} = \frac{1}{\sum_{j=0}^{n}\frac{k!}{j!}\left(\frac{b}{na}\right)^{k-j}}. \tag{10.11}$$

And, for $k' > k$,

$$\frac{\mu_{k'}}{\mu_k} = \left(\frac{na}{b}\right)^{k'-k}\frac{k!}{k'!} \tag{10.12}$$

The proof is straightforward, but helps in illustrating how to derive properties of such a Markov chain.

Proof of Proposition 10.2.1: In steady state, for $1 < k < n$, we can end up in a state with exactly k employed agents from three different states in the previous period. It could be that the previous period had $k-1$ agents employed, and then the probability of transitioning to having k employed agents is the probability that some agent heard about a job (as then it certainly reaches an unemployed agent in a completely connected clique), which is approximately na/T for large T. It could be that the previous period had $k+1$ agents employed and then an agent lost a job, which happens with probability approximately $(k+1)b/T$. It could also be that the previous period had k agents employed and nobody heard about a job or lost a job, which happens with probability $1 - na/T - kb/T$

Thus, for large T we approximate the steady-state probability of being in state k by

$$\mu_k = \mu_{k-1}n\frac{a}{T} + \mu_k(1 - n\frac{a}{T} - k\frac{b}{T}) + \mu_{k+1}(k+1)\frac{b}{T}. \tag{10.13}$$

The zero employment state satisfies

$$\mu_0 = \mu_0(1 - n\frac{a}{T}) + \mu_1\frac{b}{T},$$

or

$$\mu_0 = \frac{b}{na}\mu_1. \tag{10.14}$$

If we substitute (10.14) into (10.13) with $k = 1$ we can solve to find

$$\mu_1 = \frac{2b}{na}\mu_2. \tag{10.15}$$

Iterating, we find that for any $k < n$

$$\mu_k = \frac{(k+1)b}{na}\mu_{k+1}. \tag{10.16}$$

This implies that

$$\mu_k = \frac{n!}{k!}\left(\frac{b}{na}\right)^{n-k}\mu_n. \tag{10.17}$$

(10.12) then follows.

Noting that $\sum_{j=0}^{n}\mu_j = 1$, (10.17) implies that

$$\mu_n = \frac{1}{\sum_{j=0}^{n}\frac{n!}{j!}\left(\frac{b}{na}\right)^{n-j}}. \tag{10.18}$$

and more generally that

$$\mu_k = \frac{\frac{n!}{k!}\left(\frac{b}{na}\right)^{n-k}}{\sum_{j=0}^{n}\frac{n!}{j!}\left(\frac{b}{na}\right)^{n-j}} = \frac{1}{\sum_{j=0}^{n}\frac{k!}{j!}\left(\frac{b}{na}\right)^{k-j}}. \tag{10.19}$$

Thus, we have the claimed expression for the probabilities of the states. ∎

Having these expressions for the steady-state probabilities allows us to compute average employment rates as well as correlations, as in Table 10.1.

Although the correlation is decreasing between any two agents as we increase the network size, that does not mean that the network effect is decreasing. In fact, quite the contrary is true. The society swings more to situations where many agents are employed or many agents are unemployed at the same time. Although any two of them in a large society will have low correlations, there is still a large overall effect. One way of measuring the impact of the network effect is to examine the variance of the total employment under the steady-state distribution of the network and then normalize it

Figure 10.2.2. The Variance of Steady-State Total Employment Divided by the Variance of Total Employment if Each Agent were Independently Employed with the Same Average Probability, as a function of Network Size with $a = .5 = b$

Table 10.1: Average Employment and Correlation in Employment in Complete Networks

	Ratio of job arrival to breakup: a/b		
size n:	1/2	1	2
1	avg=.333, corr=—	avg=.500, corr=—	avg=.667, corr=—
2	avg=.400, corr=.167	avg=.600, corr=.167	avg=.769, corr=.133
4	avg=.452, corr=.135	avg=.689, corr=.139	avg=.851, corr=.099
8	avg=.485, corr=.099	avg=.764, corr=.111	avg=.910, corr=.067
16	avg=.498, corr=.061	avg=.825, corr=.087	avg=.948, corr=.043
32	avg=.500, corr=.032	avg=.871, corr=.066	avg=.972, corr=.025
64	avg=.500, corr=.016	avg=.907, corr=.049	avg=.985, corr=.014
128	avg=.500, corr=.008	avg=.933, corr=.036	avg=.992, corr=.007
256	avg=.500, corr=.004	avg=.952, corr=.026	avg=.996, corr=.004
512	avg=.500, corr=.002	avg=.966, corr=.019	avg=.998, corr=.002

to see how it compares to the variance of a society with the same average employment but where each agent's employment follows a binomial distribution, independent of the employment other agents. This is pictured in Figure 10.2.2.[11]

Figure 10.2.2 shows how the normalized variation in steady-state total employment increases with network size.

Other Networks and Correlation in Employment

When moving beyond simple network structures, solving for the steady-state employment rates and correlations in employment becomes difficult analytically, but is still possible numerically through simulations. To get a feeling for some comparative statics, Calvó-Armengol and Jackson [119] present a few examples. All of the following examples use an arrival rate of $a = 0.100$ and a breakup rate of $b = 0.015$. Based on a time period being a week, then an agent loses a job about once every 67 weeks, and hears about a job directly on average once every ten weeks. Figure 10.2.2 presents unemployment rates and the correlation in employment for four different four-person networks.

[11] I thank Toni Calvó-Armengol for suggesting this illustration.

Figure 10.2.2. Calvó-Armengol and Jackson [119]: Unemployment Rates and Correlation in Employment with $a = .100$ and $b = .015$

As the network becomes more connected, the unemployment rate falls as the information about jobs has a lower probability of being lost. The correlation is higher for agents who are directly connected than for those who are indirectly connected. The correlation between the employment of any two agents falls as the number of ties that they have increases, as there are more sources of information affecting their employment.

Figure 10.2.2 shows that asymmetries in network position can lead to differences in steady-state employment rates even when the degree of agents is identical.

In Figure 10.2.2, the agents whose link forms a bridge (agents 1 and 6) have higher employment rates. The effect here is due to the fact that those two agents are more diversified in their social connections than the other agents: none of their neighbors are linked to each other. In contrast, each of the other agents has some clustering in their neighborhoods, and has higher correlation in their neighbors employment. The correlation in the employment of neighbors makes it more likely that an agent will end up hearing about either no jobs or multiple jobs at once, while an agent would rather instead have a higher probability of hearing about (at least) one job.

Figure 10.2.2. Calvó-Armengol and Jackson [119]: Unemployment Rates as a Function of Position in a Network with $a = .100$ and $b = .015$

The correlation observed in the above networks is not unique to these examples, but holds more generally. In fact, Calvó-Armengol and Jackson [119] show that as a and b each converge to 0, but a/b converges to some positive limit, the correlation in the employment of any two path-connected agents is positive. The interpretation of this limit is that the time between periods is shrinking.[12]

10.2.3 Duration Dependence

An important aspect of networked interaction models of this type is that they generate specific correlation patterns over time and can help us to understand time-series patterns of behavior that are observed in various data that have not been very well understood in the absence of the social setting.

A good example of this is what is called "duration dependence" in the labor economics literature. This refers to the fact that if we examine an unemployed worker

[12]In the short run, two indirectly connected agents might be competitors for a mutual neighbor's job information and so might have negatively correlated employment conditional on some states (see Exercise 10.7). Looking at this limit allows one to look more directly at longer-term effects.

and ask what the probability is that the worker will be employed in the next month, that probability goes down conditional on the worker having a longer history of unemployment, holding all else equal. This has been found in a variety of studies including Schweitzer and Smith [553], Heckman and Borjas [306], Flinn and Heckman [233], and Lynch [421]. As an illustration, Lynch [421] finds average probabilities of a typical worker finding employment on the order of 0.30 after one week of unemployment, 0.08 after eight weeks of unemployment, and 0.02 after a year of unemployment, after correcting for other observable characteristics like skill level, local employment rates, and so forth.

A standard explanation for duration dependence is that there must be some features of workers that we cannot observe in the data but that are observable to firms, and the workers who are unemployed for long time periods have unattractive features from firms' perspectives or other characteristics that make them less likely to become employed. However, the magnitude of the residual effects on employment (e.g., a 15-fold difference in the probability of becoming employed after one week of unemployment compared to one year above) even after including a wide variety of characteristics, has been a puzzle. As pointed out by Calvó-Armengol and Jackson [119], such a networked model of employment generates duration dependence as a general proposition. Let us illustrate this effect with some examples.

While the networks in Figure 10.2.3 are small, they show that understanding a worker's social context can account for some of the observed duration dependence. The idea behind a networked labor market exhibiting duration dependence is as follows. The longer that a worker has been unemployed, the greater the probability of the worker's neighbors being unemployed. This reflects both that the worker has not been able to pass the neighbors any job information, and also that the worker has not heard about a job from the neighbors and so it is less likely that the neighbors are employed. As more of a worker's neighbors are unemployed, it becomes less likely that the worker will hear about a job in the coming period. For instance, if a worker has been unemployed for only a week, it is still quite possible that many of the worker's neighbors are employed and so the worker will hear about a job shortly. However, if a worker has been unemployed for a year, then that suggests that many of the worker's neighbors are also unemployed, and makes it unlikely that the worker will will hear about a job from a neighbor. Thus, if an unobserved feature of a worker is the status of his or her neighbors, then could affect the employment probability of a worker. This presents a complementary explanation of duration dependence to the usual unobserved

Probability Employed Next Period
If unemployed for at least:

1 period	2 periods	10 periods
.099	.099	.099
.176	.175	.170
.305	.300	.278

Figure 10.2.3. Calvó-Armengol and Jackson [119]: Probability of Becoming Employed as a Function of Network and Previous Periods Unemployed, with $a = .100$ and $b = .015$

characteristics explanation.

This feature is not unique to networks in a labor market context, but also appears in other settings where behaviors across individuals are complementary. Observing the behavior of one individual tells us something about the likely behavior of the neighbors and vice versa. When we look at the time series of individual behavior in isolation, it will take on greater history dependence than one would otherwise expect.

10.2.4 Education and Drop-Out Decisions

Networked labor markets also provide interesting incentives for investment in education and human capital. This ties back to our discussion of strategic complementarities and graphical games from Chapter **??**.

Suppose that agents start out in a network g. Each agent has an idiosyncratic cost c_i of investing in education. If the agent invests in education then he or she becomes eligible for jobs, and otherwise simply gets a payoff of 0.[13] Let $x_i \in \{0, 1\}$ be 1 if agent i invests in education and 0 if not. If an agent is educated then the labor market described in the previous sections applies, and the agent can hear about jobs directly and also from an employed neighbor j who has also chosen to be educated.

Thus, we start with a network g and end up with a network $g(x)$, which is the subnetwork of g restricted to the nodes i such that $x_i = 1$. Based on $g(x)$, each agent will then have a long-run employment rate. We can then examine Nash equilibria of the game where the payoff to investing in education is the long run expected employment rate minus the cost, c_i. If this is greater than 0, then the agent invests.

Note that this is a graphical game of strategic complements. To get a feeling for the structure of the game, consider a dyad. Let us consider a situation where $a = b$ and look at the limiting process as in Proposition 10.2.1.

Figure 10.2.4 illustrates the complementarities well. The employment probability, and hence the payoff, of an agent goes up as he or she has more neighbors, since they pass job information. This leads to multiple equilibria and also to contagion effects in actions. To see the possibility of multiple equilibria explicitly, consider 4 agents and the payoffs pictured in Figure 10.2.4. If each agent has a cost c_i of .6, then it is an equilibrium for no agent to get an education, and it is also an equilibrium for all

[13] This is clearly a simplification. It could be that if one does not invest, then one gets information about unskilled jobs from neighbors who did not invest, while if one invests then one gets information about skilled jobs from neighbors who also invested. The important thing is that neighbors' decisions to invest affect one's own decision.

Figure 10.2.4. Expected Payoffs for Agents who Become Educated as a Function of the Job Network with $a = b$.

agents to get an education. There is a complementarity in their incentives. The better equilibrium for all involved is for all of them to get an education, but it is possible to end up at the other equilibrium.

We can also see contagion effects here. Suppose that the 4 agents have costs of education that are $c_1 = .51$, $c_2 = .61$, $c_3 = .66$ and $c_4 = .70$. Then we end up with a unique equilibrium such that no agents become educated. Agent 4 would not find it worthwhile no matter what the other agents do. This leaves at most three agents to become educated. Under that circumstance, agent 3 does not find it worthwhile to become educated, and so forth. So, Agent 4's decision has wide consequences. If we change costs so that $c_4 = .68$, so that we lower agent 4's cost just slightly, then suddenly it is an equilibrium for all four agents to become educated.[14]

This also provides some intuition for "poverty traps". The idea is that initial conditions can be very important, especially if there is even the slightest sequentiality in agents' decisions. For instance, if historically no agents have become educated, and then we ask whether some agent wants to become educated, he or she has to be willing to do

[14]It still remains an equilibrium for none of them to invest. One can also create examples where slight changes lead that equilibrium to disappear.

so without any neighbors having invested. This can lead whole groups to stay under-invested relative to what the best equilibrium would be. This complementarity can lead to dramatic differences in behavior between different groups of agents embedded in highly segregated networks; similar to what we saw in Section [**?**], so that some subgroup invests highly while another does not. When we bring homophily into the picture, then we can see how these ideas can help explain dramatic differences in pursuit of higher education across different ethnicities. If most of one's friends are of the same ethnicity and almost none go on to higher education then that will tend to be a best response, while if almost all go on to higher education then that will tend to be a best response. This has feedback effects and can exacerbate effects that arise in part from other socio-economic factors.

10.2.5 A Labor Market in a Homophilous Network

The model of networked labor markets of Calvó-Armengol and Jackson [119] discussed above only analyzes half of the market. That is, firms play no role in the analysis, as jobs simply appear at an exogenous rate.

A model of labor markets where firms play a richer role (and the structure of workers' networks plays a lesser role) was developed by Montgomery [455]. This model provides a reason for firms to use referrals as a means of hiring, as workers' social ties are homophilous in a sense associated with their productivity; it also provides different insights into wage dispersion than those we found in the Calvó-Armengol and Jackson [119], [120] model discussed above. Montgomery's [455] model is described as follows.

- The economy lasts two periods.
- There are N workers in each period and they live for only one period.
- Half of the workers produce no output and half produce one unit of output.
- Firms cannot observe the workers' types until output is delivered.
- Firms employ at most one worker in any period.
- A firm's profit is the output minus any wage paid.
- Wages are paid upon the hiring of the worker and cannot be contingent on the output.

- There is free entry into the market so that firms can enter the market in either period.

The potential workers are connected in a network which is formed as follows.

- Each worker from the first period knows one second-period worker with probability τ and does not know any second-period worker with probability $1 - \tau$.
- If a first-period worker knows a second-period worker, then it is a worker of the same "type" (productivity) with a probability $a > 1/2$.
- Each first-period worker who gets a link has that tie assigned to a second period worker by first choosing whether it will be a same or different type worker (with probability a and $1 - a$, respectively) and then choosing uniformly at random from workers of the selected type. This means that second period workers can have multiple ties.

The timing of decisions is as follows.

- Firms hire first-period workers at an (equilibrium) wage w_1.
- A firm that hired a first-period worker observes that worker's (and only that worker's) first-period output. If that firm desires, it may then make a "referral" wage offer to its worker's social tie (if the worker has a social tie).
- Second-period workers who receive offers from the firms of their first-period friends may accept one of those offers or decide to go on the second-period market.
- The second-period market is such that any second-period workers who have not accepted a job through the referral process are hired at an (equilibrium) wage of w_2.

The equilibrium notion that Montgomery employs is a variation on a competitive equilibrium, requiring that no firm want to enter or exit, that firms optimize given their information, and workers take the best offer they get. It also involves aspects of Nash equilibrium, since in offering a referral wage a firm is entering an auction against other potential employers who might also be making a referral offer to the same worker. The result that Montgomery proves is as follows.

PROPOSITION **10.2.2** *[Montgomery [455]] A firm makes a referral offer if and only if it has a productive worker in the first period, and it then randomly picks a wage to offer from an interval with lower bound of w_2 and an upper bound below 1.*[15]

The idea behind the proposition is as follows. Let us work backwards from the second period. In the second period market for the workers who have not accepted an offer, the wage will be equal to the expected value of those workers, given their distribution of types in equilibrium. Firms all have the same information about those workers' values, and will not over pay, and cannot under pay given that new firms can enter the market. Given the claim in Proposition 10.2.2, we will eventually be able to conclude that the expected value of such a worker is below 1/2, as those will be workers who have not received and accepted an offer, and so are conditionally more likely to either be connected to a low output first-period worker or to lack connections. Given that a second-period worker can get a wage of w_2 by waiting for the open market, any non-degenerate referral offer has to be at least w_2. The fact that the equilibrium involves a mixed strategy can be understood from the fact that offering a wage through a referral is like bidding in an auction with an unknown number of other bidders. The second-period worker could have other ties to first-period workers and thus could be receiving other wage offers. The worker's expected value will generally be above w_2, given that the worker is tied to a high-output first-period worker, and given that the wage w_2 will be below 1/2. If referrals were all hired at a given fixed wage below the expected value of the worker, then by slightly raising the wage one would hire the second-period worker for certain. If the wage were at or above the expected value of the worker, then one could lower the offer and still win in situations where there turn out not to be any other bidders.

The important aspects of the equilibrium can be summarized as follows.

- Having more social ties leads to higher expected wages for second-period workers.

  This is true since each additional tie has some chance of being a high-output worker and thus resulting in an extra wage offer.

- A low-output second-period worker with social ties has a higher expected wage than a high-output second-period worker who has no social ties.

[15] In fact, one can reason that the upper bound on bids will be no more than a, which is the expected value of a second-period worker conditional on having a tie to a first-period worker. Conditional on the worker accepting the wage offer, it is less likely that the worker has ties to other high-output first period workers, and so the conditional expectation of the worker's value will generally be less than a.

This follows from the observation that the high-output worker without social ties has to go on the second-period market, while any worker (regardless of actual productivity) with social ties has some probability of being connected to a high-output first-period worker and getting a wage offer above the second-period open-market wage.

- There is a dispersion of wages in the second period.

  This follows from the randomization in referral wages and the fact that workers differ in the number of social connections that they have.

- Firms earn positive profits in the second period from using referrals.

  This happens since firms have a higher chance of finding high-output workers through referrals, and as a lower bound, there is at least some chance that they can hire the worker with a wage just above w_2 in cases where the worker ends up having no other social ties.[16]

While highly stylized, this model provides insights into several aspects of networks in labor markets: why referrals can be attractive for firms, why they can lead to dispersion in wages,[17] and how workers who are more connected can fare better.

10.2.6 Evidence and Effects of Networked Labor Markets

Topa [595], Conley and Topa [156], and Bayer, Ross, and Topa [**?**] fit models of social interactions and employment which have some features similar to that described in Section [**?**], where networked workers should exhibit correlated employment and wages. Topa [595] and Conley and Topa [156] examine census-tract data in Chicago, focusing on data from the 1980 and 1990 censuses. As a proxy for network neighborhood relationships, Topa uses geographic neighborhood relationships. He examines the correlation of unemployment across census tracts and finds statistically significant

[16] The full argument here is a bit tricky, as the conditional expectation of a worker's value depends on what wage is offered and accepted. Hiring the worker with a lower wage provides some indication that the worker received fewer other offers. But in equilibrium, the expected profit is the same at all wages that are offered, and the workers who do receive offers are biased towards being of higher output.

[17] See Arrow and Borzekowski [18] for another model of wage dispersion based on the number of ties and a calibration to wage data.

correlation patterns between adjacent census tracts. He also finds significantly positive correlation between tracts that are not immediately adjacent, but are still both adjacent to a common tract.

As it is possible that social connections are not simply related to geographic proximity, Conley and Topa also examine a series of other distance measures. In addition to census tract distance measures, they examine travel time distance, ethnic distance, occupational distance, and education measures, as well as some other socio-economic co-variates. However, it could be that these measures are related to other characteristics that relate to employment patterns, and so the similar outcomes in employment which seem to indicate the role of some social relationships along these dimensions might simply be related to the fact that being close on these measures is related to other characteristics which account for common employment outcomes. To deal with this issue, they perform different exercises. First, they examine how the raw unemployment rate correlations depend on some combinations of these proximity measures. When combining various measures, being close on the ethnic dimension seems to explain the majority of covariation in unemployment rates. In view of this, they examine the residual employment rates when adjusting for a number of observable tract level characteristics. So, these residuals are obtained by subtracting out the variation in employment that can be explained directly by tract level characteristics. They then examine how these residuals correlate with the distance measured in tracts or some other characteristic (ethnicity, occupation, etc.). When they do this, the correlation patterns across these measures largely disappear. This seems to indicate that it is not that people have similar outcomes because they are nearby and thus socially related; but instead it could be that nearby tracts are quite similar in their characteristics and hence their workers tend to be employed or unemployed at the same time for other reasons.

The Conley and Topa [156] study could cast significant doubt on social proximity being important in employment outcomes. However, not finding a relationship when looking at census tract data does not imply that social relationships do not affect employment. Social relationships are not so obviously related to census tracts, especially when aggregated. Here a study by Bayer, Ross and Topa [**?**] cuts one level deeper. They examine census data from Boston where they can pinpoint residence down to the block level. This allows them to examine whether people living on the same block have more correlated employment outcomes than people living on nearby blocks that have similar characteristics. First, they find that living on the same block compared to

a nearby block with similar demographics significantly increases the probability that two individuals work together, and this effect is magnified when the individuals are of similar ages and backgrounds. Then, examining pairs of individuals who have a strong predicted referral effect, they find a substantial effect on employment and wages. They also examine other questions. For instance, they find that there is assortative matching along education, income and age, so that similarity along these dimensions with those in one's city block improves labor market outcomes significantly. The study is also careful to examine "reverse causation" explanations, where people end up on the same block because they are similarly employed.

There are other ways of studying social network effects on labor outcomes, such as examining immigrant populations and the social networks that they move into, or other exogenous factors that affect social networks. The difficulty is in finding extensive social network data together with rich measures of employment outcomes. Some examples of clever proxies for social networks appear in Munshi [470], Laschever [401], and Beaman [46]. Laschever [401] examines the formation of military units via the U.S. draft in World War I. He examines units that were formed at random, and then examines subsequent employment outcomes via the 1930 census. If the friendships formed within a given military unit did not matter, then there would not be any correlation among employment outcomes in the later period (after correcting for other factors). He finds statistically significant effects, so that a ten percent increase in the employment rate of a veteran's unit's unemployment rate decreases that veteran's employment rate by over three percentage points. Munshi examines Mexican immigrants to the U.S., using rainfall in Mexico to estimate the number of immigrants during various time periods[18] and then shows that having a larger number of immigrants arrive more than three years prior to one's own arrival leads to a significant increase in the probability of one's employment. Beaman [46] finds a more direct measure of the size of waves of specific immigrant groups, with a rich variation in sizes, countries of origin, and locations, as she examines the assigned relocation of political refugees into the U.S. The network size proxy is the number of refugees from the same country who did not have prior family members in the US and who are relocated to the same city. She finds several effects. First, the larger the number of political refugees relocated to a particular location at

[18] This might, at first, seem to be a strange method; but one wants something which influences immigration but is not correlated with employment possibilities within the U.S. This is something which can lead to emigration from Mexico, and yet is unlikely to be correlated with job opportunities in the U.S.

the same time or within a year of each other, the lower their average employment rate; which is consistent with the new arrivals competing for jobs and job information. More pointedly in terms of evidence of the effect of social networks, the larger the number of refugees who were relocated to a given area at least two years prior, the higher the employment rate and wages. For instance, a standard deviation increase in the number of refugees arriving two years prior leads to an increase in the probability of becoming employed by 4.6 percent along with a fifty cent increase in the average hourly wage, while a similar increase in the number of refugees arriving in the prior year leads to a decrease of 4.9 percent in the probability of becoming employed and a seventy cent decrease in the average hourly wages.

10.3 Models of Networked Markets

The above studies were tailored to labor markets. Beyond labor settings, it is important to have a more general understanding how the structure of the network of interactions affects the terms of trade.

10.3.1 Exchange Theory

An area of research known as "exchange theory" (see Cook and Whitmeyer [162] for an overview) concerns how the structure of relationships among agents affects "exchanges" between them. Such exchanges could be economic transactions of goods and services, the trading of favors, communication of information, or a variety of social interactions which convey direct benefits and costs to the involved agents. The term "exchange theory" has its origins in work by Homans [318], [**?**] on "social behavior as exchange," which initiated a theory of socially embedded behavior based on psychological reinforcement ideas applied to dyadic exchanges. This view was complemented by work by Thibaut and Kelley [594], and more direct connections to economic ideas of exchange were brought into the picture by Blau's [68] influential work. The ideas have been extensively developed and applied to a range of economic interactions that involve explicit relationships, such as decentralized markets, the formation of corporate boards, and international relations. Networks have played an increasing role in exchange theory, especially since the work of Emerson [209]. Emerson considered explicitly networked interactions to understand the power and dependencies that underly exchange. Critical to Emerson's theory is the idea that the exchange that occurs be-

tween two agents depends on their outside options and influences, and thus on their other relationships. Thus, one cannot examine an exchange between two individuals without understanding the influences of the network on their behavior.

To get a feeling for this theory, it is useful to discuss the work of Cook and Emerson [161] who laid out hypotheses about how power derives from social network structure. They also examined the role of equity considerations in exchanges and conducted some of the first experiments on this subject. Some of these ideas provide a nice background for the predictions and observations that we will see below when considering models of economic transactions in social networks.

Cook and Emerson [161] operationalize the idea of equity through a condition that two agents involved in an exchange should equilibrate their respective profits or net gains from a given transaction. They examine this in a context where agent 1 holds good X and agent 2 holds good Y, agent 1 has a higher per unit value for Y than X, and agent 2 has a higher value for X than Y. The idea is that if x units of good X are given from agent 1 to 2 in exchange for y units of good Y, and v_{iz} represents the marginal value to agent i for good z, then equity requires that

$$v_{1y}y - v_{1x}x = v_{2x}x - v_{2y}y.$$

Cook and Emerson define the power of 1 over 2 as "the potential of agent 1 to obtain favorable Y minus X outcomes at agent 2's expense."[19] They do not provide a formal recipe for how to evaluate this as a function of the network, but they do distinguish between how relationships affect each other. Consider agent 1 who has links to both agent 2 and agent 3 in a social network. They say that these relationships have a positive connection if a transaction across one link is contingent upon a transaction across the other, and have negative connection if a transaction on one link precludes a transaction on the other. To analyze how power depends on the network of relationships and potential exchanges, Cook and Emerson examine the networks in Figure 10.3.1.

Here, Cook and Emerson say that A has power over each B, but the B's have equal power relative to each other and the C's have equal power relative to each other. In terms of a specific measure of the power that A has over a B, Cook and Emerson reason based on the "comparison levels" that the agents will have. In particular, they argue that A's comparison level, in terms of the expected value of the transaction, should be 20 units. The idea is that A can trade with any of the B's. The B's that do not trade with A are balanced and so should end up splitting their 8 units equally for a value of

[19] This quote substitutes "agent 1" for "A" and "agent 2" for "B" in the original quote.

Figure 10.3.1. Exchange Networks from Cook and Emerson [161]. The solid lines indicate a potential transaction worth 24 units and a dashed line indicates a potential transaction worth 8 units.

4 units, which is their comparison level. Thus, if the B who transacts with A gets more than 4 units, then another B would have an incentive to offer to split 24 with A in a more favorable way.[20] Cook and Emerson then think of the comparison levels as some indication of power used, and then the excess of the power of an A with comparison level of 20 over a B with comparison level of 4 is 16 units. So here power is a measure of how much extra resources A can extract from the transaction with B compared to what B gets.

Cook and Emerson [161] ran a series of experiments on these networks, working with human subjects playing the roles of the above agents for cash earnings in proportion to the units of transaction. The subjects interacted through computers and were not aware of the identities of the other agents. The bargaining protocol was such that players could make direct offers of units (up to 8 between two B's and up to 24 between any other pair) to agents in their network, and if that agent agreed then they would complete that transaction, with the offering player keeping the total less the offer. Subjects played the game (in a fixed position) forty times. For the first twenty, players were only aware of the values of their potential transactions, and not of the transactions of the other players other than those that they were involved with. For the next twenty times, players observed each other's cumulative earnings. Cook and Emerson hypothesize that having knowledge of others' payoffs will lead to more equitable behavior and less exercise of power. The Cook and Emerson [161] data provides insight into several different things: first, whether or not there was an exercise of power so that A's earned more than B's; next, how this compared with the behavior of the evenly balanced C's; and, also how the knowledge of others' payoffs affected behavior. Furthermore, Cook and Emerson had an even pool of 56 male and 56 female subjects, and so compared behavior across genders. A brief summary of the results is that the A's did exercise power, beginning by earning between 2 and 4 units more than B's and tending up to 10 to 12 units more than B's just before the cumulative earnings were shown, but exercising less than the full 16 units of power that they had.[21] Among the C's, there were imbalances between the even partners, with the average imbalances beginning at 7 to 8 units (out of 24) and tending downwards to end up at 4 to 5 units by the end of the 40 periods. When looking across genders, Cook and

[20] This (20 to A and 4 to each B) turns out to be the unique core allocation in this problem, as defined via a standard cooperative game theory concept. See Section **??** and Exercise 12.3. This differs from the Shapley Value or Myerson Value allocations for this problem.

[21] These numbers actually look more consistent with the Myerson Value predictions than the core predictions for this network. See Exercise 12.3.

Emerson found significant differences between how males and females act in position A in the periods after the cumulative histories of payoffs are revealed. Males exhibit a short term lowering in their exercise of power, but eventually return back to about 12 units, while the females (significantly) lower their power usage to around 4 units by the end of the experiment. These experiments provide evidence that network position matters in bargaining and in helping to operationalize notions of "power." The data show that network-based bargaining power ends up being exercised even in situations where agents are not fully aware of the values of the possible transactions that can occur, but also that some equity concerns can mitigate the exercise of power. The differences between female and male behavior provide some interesting puzzles.

10.3.2 Bilateral Trading Models

The Cook and Emerson [161] exchange studies provide some insight into how bargaining power might be exercised, and suggest that agents are sensitive to the network of potential transactions that they are embedded in. To examine this in more detail, let us consider models networks of buyers and sellers. The following analyses use game theoretic models of the bargaining on networks to make predictions about which networks will form as agents try to maximize the value of their transactions.

A Networked Trading Model Based on Alternating Offers Bargaining

A natural starting point is a simple model of networks with bilateral bargaining that is due to Corominas-Bosch [167].

Each seller has a single object to sell which has no value to the seller. Buyers have a valuation of 1 for an object and do not care from whom they purchase it. If a buyer and seller exchange at a price p, then the buyer receives a payoff of $1-p$ and the seller a payoff of p. A link in the network represents the opportunity for a buyer and seller to bargain and potentially exchange a good.

Corominas-Bosch models the bargaining process explicitly via an alternating move game between the various buyers and sellers. That game leads to a particular solution. A link is necessary between a buyer and seller for a transaction to occur, but if an individual has several links then there are several possible trading patterns. Thus, the network structure essentially determines bargaining power of various buyers and sellers.

The game that Corominas-Bosch examines to predict the prices and transactions is

described as follows. In the first period sellers simultaneously call out prices. A buyer can only select from the prices that she has heard called out by the sellers to whom she is linked. Buyers simultaneously respond by either choosing to accept some single price offer they received, or to reject all price offers they received. If there are several sellers who have called out the same price and/or several buyers who have accepted the same price, and there is any discretion under the given network connections as to which trades should occur, then there is a careful protocol for determining which trades occur (which is designed to maximize the number of eventual transactions). At the end of the period, trades are made and buyers and sellers who have traded are cleared from the market. In the next period the situation reverses and buyers call out prices. These are then either accepted or rejected by the sellers connected to them in the same way as described above. Each period the roles of proposer and responder switch, and this process repeats itself indefinitely until all remaining buyers and sellers are not linked to each other. Buyers and sellers are impatient and discount according to a common discount factor $0 < \delta < 1$. So a transaction at price p in period t is worth $\delta^t p$ to a seller and $\delta^t(1-p)$ to a buyer.

In an equilibrium with very patient agents (so that δ is close to 1), there are effectively three possible outcomes for any given agent: either he or she gets most of of the available gains from trade, or roughly half of the gains from trade, or a small portion of the available gains from trade. Which of these three cases ensues depends on that agent's position in the network. Some easy special cases are as follows. First, consider a seller linked to two buyers, who are only linked to that seller. Competition between the buyers to accept the price will lead to an equilibrium price of close to 1 if agents are sufficiently patient. So the payoff to the seller in such a network will be close to 1, while the payoff to the buyers will be close 0. This is reversed for a single buyer linked to two sellers.

More generally, which side of the market outnumbers the other is a bit tricky to determine as it depends on the overall link structure, which can be much more complicated than that described above. Quite cleverly, Corominas-Bosch describes an algorithm which has some roots in Hall's Theorem (recall Theorem **??**) and subdivides any network into three types of sub-networks: those where a set of sellers are collectively linked to a larger set of buyers, sellers get payoffs of close to 1, and buyers get payoffs of close to 0; those where the collective set of sellers is linked to a same-sized collective set of buyers and each get payoff of around 1/2; and those where sellers outnumber buyers, sellers get payoffs close to 0, and buyers get payoffs close to 1. The limiting

payoffs, as the discount factor approaches 1, are found via the following algorithm.

- [1a.] Identify groups of two or more sellers who are all linked only to the same buyer. Regardless of that buyer's other connections, take that set of sellers and buyer out, and that buyer gets a payoff of 1 and the sellers all get payoffs of 0.
- [1b.] On the remaining network, repeat this process but with the role of buyers and sellers reversed.
- [k] Proceed, inductively in k, each time to identify subsets of at least k sellers who are collectively linked to some set of fewer than k buyers, or some collection of at least k buyers are collectively linked to some set of fewer than k sellers.
- [Stop] When all such subgraphs are removed, the buyers and sellers in the remaining network are such that every subset of sellers is linked to at least as many buyers and vice versa, and the buyers and sellers in that subnetwork earn payoffs of 1/2.

The limiting payoffs found by this algorithm are illustrated in Figure 10.3.2 .

To see how the algorithm works on the last network, consider Figure 10.3.2.

First, step 1a is concluded with no sets identified. Next, at step 1b, the set of two buyers linked to just one seller are eliminated. The remaining two buyers and two sellers are each linked to the same number on the other side and so the algorithm concludes by stopping with the remaining subset of 4 agents each getting a payoff of 1/2.

The intuition behind why the algorithm identifies the unique equilibrium outcome is as follows. If there are two or more sellers who are linked to just one buyer, they will compete in bargaining and the buyer can obtain a price of 0 (in the limit with high patience). This then implies that any other sellers linked to that buyer cannot expect that buyer to bid for their goods. At a later step, when we find three sellers linked to just two buyers, then it must be that each of the buyers is linked to at least two of the sellers (as otherwise two of the sellers would have been linked to just one buyer and removed at an earlier step). In this case, it is sort of a game of "musical chairs" among the sellers. At most two can sell an object, and so sellers who are quoting the highest price in some round have an incentive to cut their price slightly to avoid being left with an object; if it is the buyers who are quoting prices then no seller wants to be the only one not accepting as he or she would be left without selling an object. Again,

Figure 10.3.2. Limit Payoffs in the Corominas-Bosch [167] Model for Selected Networks

Figure 10.3.2. An Illustration of the Algorithm in the Corominas-Bosch [167] Model.

this leads to an unraveling of the price and so the buyers obtain all of the gains from trade.

For quite involved networks, the logic of this derivation pushes quite heavily on induction. However, the process itself naturally involves induction just as the algorithm does. That is, with some patience, several sellers linked to just one buyer will tend to compete away their surplus. As such transactions occur, the more complicated games of "musical chairs" begin to play out. A series of experiments by Charness, Corominas-Bosch, and Frechette [135] examine the extent to which human subjects play as predicted in such games. They examine a game of bargaining on a fixed network that proceeds just as the Corominas-Bosch model except that there are only a finite (but uncertain) number of rounds. While the payoffs in those experiments rarely reach the extremes that are predicted under the limit of full patience and potentially infinitely many periods of bargaining, the payoffs do share patterns that are similar to those predictions. Figure 10.3.2 pictures the predicted payoffs for one of the networks that was tested. This figure reports the percentage of potential pies to be split that each role received (so the total sums to 3 as there were three possible transactions in total), and also provides the benchmark prediction for the same network in the case with infinite patience and repetition.

Critical aspects of limiting payoffs under the bargaining can be summarized as follows.

(i) if a buyer gets a payoff of 1, then some seller linked to that buyer must get a payoff of 0, and similarly if the roles are reversed;

(ii) a buyer and seller who are only linked to each other get payoffs of 1/2; and

(iii) the subnetwork when restricting to the set of agents who get payoffs of 1/2 is such that any subgroup of k buyers in the subnetwork is linked with at least k distinct sellers in the subnetwork and vice versa for any k.

These observations about the payoffs, coupled with a cost per link, lead to the following sharp predictions concerning network formation using pairwise stability (see Section **??**).

PROPOSITION **10.3.1** *Consider a version of the Corominas-Bosch model where agents get the limiting payoffs as described just above. If the cost of a link for each agent*

Figure 10.3.2. Predicted and Observed Payoffs from Charness, Corominas-Bosch, and Frechette [135].

involved lies strictly between 0 and 1/2, then the pairwise stable networks coincide with the set of efficient networks.[22]

The proof of Proposition is straightforward so I sketch it here and the details are left for Exercise 10.1. An individual getting a payoff of 0 cannot have any links, as by severing a link he or she could save the link cost and not lose any benefit. Thus, all individuals who have links must get payoffs of 1/2. Then, one can show that if there are extra links in such a network (relative to the efficient network, which consists of a maximal number of disjoint linked pairs) that some could be severed without changing the bargaining payoffs, thus saving link costs. This builds on the fact that for payoffs to be 1/2, then it must be that buyers and sellers are evenly balanced. It cannot be that there is a buyer and seller who each have no links, as by linking they could both be made better off. So it must be that the network consists of pairs and that the maximum number of potential pairs forms.

[22] This contrasts with Corominas-Bosch's [167] analysis, which considers a formation process where no cost is saved by severing a link. That can lead to players having links even when they know that they receive a 0 payoff from the bargaining and trade.

The conclusion of an equitable split of the value in each transaction contrasts with the conclusion from a supply and demand model. If there are more buyers than sellers, then in a competitive model would have the sellers collect all of the surplus. What is it that accounts for the difference? Here there is a cost to connecting, and connecting occurs *before* the bargaining. Buyers and sellers only enter if they expect that they will have a positive payoff. The model is extreme, so that slight imbalances in the network of matchings of buyers to sellers leads to extreme outcomes and zero payoffs to some agents. Thus, the equilibrium entry into the market results in a balanced set of buyers and sellers. The limited set of outcomes, so that transactions are either even splits or completely favor one side of the exchange, is critical to the result. As we shall now see, if we enrich the set of possible transaction outcomes, we will see richer networks emerge.

A Networked Trading Model Based on Auctions

While the model above provides a benchmark, the conclusion that agents will form an efficient network relies on the complete information setting and the fact that buyers are identical as are sellers. In situations where there can be some heterogeneity and uncertainty in valuations, there can be benefits from having a more connected network so that the set of potential transactions is larger. This leads to a more complicated analysis and can lead to inefficient networks being stable. To see this, let us consider a simple example, based on a model of Kranton and Minehart [390]. It is similar to the Corominas-Bosch model described above except that the valuations of the buyers for an object are random and the determination of prices is made through an auction.[23]

The potential sources of inefficiencies can be seen from a situation with one seller and two buyers; and so I focus on that setting, and refer the reader to Kranton and Minehart [390] for a fuller analysis. The buyers each have a valuation for the good which is uniformly and independently distributed on $[0, 1]$. The good is sold via a second-price auction.[24] This is an auction where the highest bidder obtains the object and pays the highest bid among the bidders who are not getting the object (with ties in

[23] In many applications one would also see random and heterogeneous valuations for the sellers, but the main ideas can be seen without introducing such complications.

[24] Any of a variety of auctions will have the same property in this example, as there is an equivalence between any two different auctions and corresponding equilibria, provided that the equilibrium lead to the same allocation of the good as a function of valuations are are such that buyers with 0 values pay 0 if they "win."; The equivalence is that each buyer has the same expected payment in the two auctions, and the seller expects the same revenue.

the highest bid broken uniformly at random). If only one buyer links to the seller, then he or she gets the object for a price of 0. If both buyers are linked to the seller, then it is a dominant strategy for each buyer to bid his or her value, and the corresponding revenue to the seller is the minimum value of the two buyers.

In this model the potential value of a transaction is random, depending on the realized valuations of the buyers. The auction on the network with just one link has an expected value of a transaction of 1/2, and an equilibrium price of 0 so that the full expected gains from trade go to the buyer. In the auction with two links, the ex ante expected payoff to each buyer (before he or she sees his or her value for the object) is $\frac{1}{6}$. Each buyer has a $\frac{1}{2}$ chance of having the high value, an the expected valuation of the highest bidder out of 2 draws from a uniform distribution on [0,1] is $\frac{2}{3}$, and the expected price is the expected second highest valuation, which is $\frac{1}{3}$. So, the ex ante total gains from trade in the two-link network is 2/3, with 1/3 going to the seller and 1/6 to each buyer.

Now consider a situation where there is a cost of links of c to each individual. Efficient network structures are an empty network if $c \geq 1/4$, a one-link network if $1/4 \geq c \geq 1/12$, and a two-link network if $1/12 \geq c$.

Let us consider whether or not the pairwise stable networks are efficient. Given the seller's payoffs as a function of the network, the seller will only link to both buyers or else to neither. Thus, if link costs lie between 1/12 and 1/4, then the efficient network will not be pairwise stable. If the cost is above 1/6 and below 1/4, then the only pairwise stable network is empty as buyers do not expect a high enough payoff to maintain a link in a two-link network and the seller will not maintain a link in a one-link network. If the cost is between 1/12 and 1/6, then the two-link network will be pairwise stable, but it is over-connected relative to the efficient network. Thus, an efficient network is only pairwise stable in the cases where costs are below 1/12 or above 1/4.[25]

To see the intuition for the inefficiency in this setting note that the increase in expected price to the seller from adding a link comes from two sources. One is the expected increase in willingness to pay of the winning bidder, since the sale is to the highest valuation out of a set of independent draws from the same distribution, and

[25] This conclusion contrasts with that in Kranton and Minehart [390]. However, they analyze a case where link costs are 0 for sellers and positive for buyers. If sellers bear no costs of links, then the efficient networks are pairwise stable. Kranton and Minehart do discuss the fact that costly investment by the seller can lead to inefficiency.

we get one more draw when a link is added. This increase is of social value, as it means that the good is going to someone who values it more. The other source of price increase to the seller from adding a link comes from the increased competition among the bidders in the auction. This source of price increase is not of social value since it only increases the proportion of value which is transferred to the seller.

While the pairwise stable networks in this example are not efficient (or even constrained efficient), they are Pareto efficient. This is not true with more sellers as shown in Exercise 10.3, which shows pairwise stable networks that are Pareto inefficient.

10.3.3 Price Dispersion on Networks

Beyond the strategic formation of networks in exchange settings, there are also studies which examine how the terms of trade depend on network structure, when networks are (exogenously) generated via random graph models. For instance, Kakade et al [357] (as well as Kakade, Kearns and Ortiz [356]) examine a model of exchange on random graph-generated networks.

Buyers have cash endowments and a constant marginal value for a consumption good. Sellers have unit endowments of the consumption good (which they do not value) and desire cash. Buyers buy from the least expensive seller(s) with whom they are connected until they have exhausted their cash budgets. Prices are seller-specific and determined to clear markets. An equilibrium is a set of prices and transactions such that the market clears. In this setting, market clearing implies that each buyer who is connected to at least one seller exhausts his or her budget and each seller that is connected to at least one buyer sells all of his or her endowment.

The simplest version of this model is such that all buyers have the same marginal valuation and endowments, say each normalized to 1. In that case, there is an equilibrium of the following form.

- A buyer buying from multiple sellers sees the same price from each seller.
- The price of a given seller can be found by computing, for each buyer, the fraction of the buyer's total purchases that come from that seller, and then summing across buyers.
- The price of a given seller is no higher than the seller's degree and no lower than the minimum degree of the buyers connected to the seller.

Figure 10.3.3. Equilibrium Prices and trades for Some Network Configurations in the Competitive Model of Kakade et al [357]. The number under each seller is the price that the seller charges and also the total cash that the seller ends up with. The number above each buyer is the amount of the consumption good that the buyer purchases. The solid links involve trades, whereas there are no trades along the dashed links.

The outcomes for a few networks are pictured in Figure 10.3.3.

The pattern of trades in Figure 10.3.3 turns out to be very similar to that in the model of Corominas-Bosch and Figure 10.3.2. There is a richer variation in prices in the competitive model, but the basics of which buyers and sellers do well and which do poorly are qualitatively similar. The richer variation in prices reflects that buyers and sellers are assumed not exercise any monopoly power they might have; instead they adjust prices to clear markets. This also results in differences if one examines the networks that are pairwise stable, as shown in Exercise 10.5. In this competitive model, there are still gains from trade to be earned by both sides of the market, even when there are large imbalances among buyers and sellers. This leads too many agents to connect to each other relative to the efficient network, which involves pairing agents.[26]

Figure 10.3.3 already demonstrates that the configuration of prices that emerges as a function of the network is very network specific, and so deriving general conclusions for complex networks is difficult. There are simple observations, such as the fact that adding (costless) connections will weakly benefit the agents involved with that connection, but there is no general relationship between degree and welfare, as terms of trade depend on the full network configuration. Even though the model is difficult to solve analytically, Kakade et al [357] show that if links are formed uniformly at random, and the probability of forming a link is high enough and the number of agents grows, then there is no limiting price dispersion. In the case of a network formed via preferential attachment, there is a greater asymmetry in the degrees of nodes and such networks can maintain some price dispersion.[27]

10.3.4 Collaboration Networks Among Firms

Most of the discussion in this chapter has been either about labor markets and information transmission or about exchange networks, where trades occur between linked agents. There are also a number of other ways in which networks play a role in markets. For example, firms collaborate in research and development, firms merge, firms produce joint products and ventures, firms contract on specific supply relationships, and so forth.[28]

[26] This reflects the linear utility functions. With concavities, more interesting architectures emerge as being efficient.

[27] For more on how network shape affects trading behavior, see Judd and Kearns [351] for a set of experiments of networked trade.

[28] See Bloch [70] for an overview of some related literature.

To get some feeling for how various relationships among firms might affect how they act in the market, let us examine an example due to Goyal and Joshi [**?**]. They examine a setting where a link between two firms lowers their respective costs of production. Since firms eventually compete in the market, the costs of production affect the overall market outcome and profits.

In particular, each firm produces identical goods. If firm i produces q_i units of the good and the network structure is g, then firm i's cost is

$$q_i \left(a - bd_i(g)\right). \tag{10.20}$$

where $a > (n-1)b > 0$ and n is the number of firms, so that costs are always positive. So, a firm's marginal cost of production is decreasing in the number of collaborative links it forms with other firms, which in this model is its degree.

The profits to a firm then depend on how much each firm produces and what the resulting price in the market is. To model this, let us consider the textbook-case of "Cournot competition," which works as follows. The market price is described by an (inverse) demand function, such as

$$p = \alpha - \sum_j q_j,$$

where $\alpha > 0$ is scalar. Thus, the price decreases as firms produce more.

So firm i's profits are

$$q_i p - q_i \left(a - bd_i(g)\right) = q_i \left(\alpha - \sum_j q_j - a + bd_i(g)\right).$$

If q_i maximizes this, then it must be that the derivative with respect to q_i is 0, or

$$-q_i + \alpha - \sum_j q_j - a + bd_i(g) = 0. \tag{10.21}$$

Solving this simultaneously across i leads to[29]

$$q_i = \frac{\alpha - a + nbd_i(g) - b\sum_{j\neq i} d_j(g)}{n+1}.$$

A firm's profits are $(p - c_i)q_i$ (where $c_i = a - bd_i(g)$ is the marginal cost of firm i), and so noting from 10.21 that $q_i = p - c_i$ it follows that each firm's Cournot equilibrium profits are q_i^2, where q_i is given above.

[29] A sufficient condition for all quantities to be positive is that α is large, or that $\alpha - a - (n-1)(n-2)b > 0$.

This makes it easy to deduce pairwise stable networks. The profits of a firm are increasing in the equilibrium q_i, and the network enters q_i in proportion to $nd_i(g) - \sum_{j \neq i} d_j(g)$. Thus, firm i gains $n-1$ (noting that d_j increases for some j) with each link that it adds. If the link costs are the same across links, then the set of pairwise stable networks falls in one of two extremes: it is either the complete network or the empty network, depending on the cost of a link. In the case where the link costs are heterogeneous across firms, then the pairwise stable network would be a complete network among the subset of firms whose costs are lower than $n-1$ (presuming no firm has costs exactly at $n-1$). More interesting configurations would require some nonlinearities in link costs.

In terms of efficiency, there are a variety of different benchmarks to consider. In particular, it matters whether one just considers firm profits or also considers the welfare of the consumers buying the firms' products; and it also matters whether competition is restricted to Cournot equilibrium or can take some other form (see Exercise 10.6). From the industry profit standpoint, in most cases the highest industry profits would actually involve a star network where the center firm enjoys a low cost and also sees higher costs, and thus prices, from its competitors. This would be the efficient network structure if link costs are small and only firms' profits are considered. If we also include the consumers' welfare, and link costs are small enough, then it is best to see a low price and high production, which emerges when the complete network forms.[30]

10.4 Some Concluding Remarks

The above-described models, empirical analyses, and experiments on networked markets offer some insights that are fairly general. In the context of labor markets, we saw how links lead to correlated outcomes across neighbors, at a given time and across time. Such linked outcomes lead to complementarities in incentives to make investments in things like education. These patterns are not unique to labor markets, but also hold for some other economic transactions and behaviors where there are complementarities between the states of neighbors. In the context of exchange, we saw that the relation

[30] This conclusion, however, depends on how firms compete. If they compete via prices, then it can be enough to have two low-cost firms to push prices down (again, see Exercise 10.6). In such a case, the efficient network is what Goyal and Joshi [**?**] call "interlocking stars," such that two firms, i and j, are each linked to every other firm, and firms other than i and j are only linked to i and j.

between network structure and the terms of trade can be complex, but that an important determinant of favorable terms of trade is having connections to other agents whose other trading options are somewhat limited. So it is not simply direct connections that are important for terms of trade, but having connections to others who have more limited connections. This contrasts with other sorts of applications, such as information networks, where having well connected neighbors is desired. Moreover, high connection to low-degree neighbors leads to good outcomes for an agent not only in the exchange setting, but also in settings of collaboration among firms, and other settings where there is some sort of competition among agents.

While we have seen that networked labor markets are pervasive, and seen that there are some general insights to be gained from observing and modeling networked markets, there is much still left to be learned in this extensive area of application where networks play such a central and critical role.[31]

10.5 Exercises

EXERCISE **10.1** *Proof of Proposition 10.3.1.*

Provide a full proof of Proposition 10.3.1.

EXERCISE **10.2** *Payoffs in the Corominas-Bosch [167] Model.*

Find the predicted payoffs in the networks in Figure 10.5 under the Corominas-Bosch [167] model.

EXERCISE **10.3** *Pareto Inefficient Pairwise Stable Networks with Trade by Auction*

The following example from Jackson [329] shows that it is possible for (non-empty) pairwise stable networks in the Kranton-Minehart model to be Pareto inefficient. For this we need more than one seller. In that case, the auction works as follows. Prices rise simultaneously across all sellers. Buyers drop out when the price exceeds their valuations. As buyers drop out, there emerge sets of sellers such that the set of buyers

[31] This is not to say that this chapter provides an exhaustive survey of the literature, as there are a number of areas that I did not cover, including international trade (e.g., Furusawa and Konishi [246]), financial contagion and the role of networks in financial markets (see Allen and Babus [12]), collusion and market-sharing agreements among firms (e.g., Belleflamme and Bloch [48]), and models of competition among buyers and sellers with added heterogeneity (e.g., Wang and Watts [612]).

Figure 10.5. Find the payoffs under the Corominas-Bosch [167] Model

still linked to those sellers is no larger than the set of sellers. Those sellers transact with the buyers still linked to them. (The exact matching of who trades with whom given the link pattern is done carefully to maximize the number of transactions.) Those sellers and buyers are cleared from the market, and the prices continue to rise among remaining sellers, and the process repeats itself.

Consider a population with 2 sellers and 4 buyers. Let individuals 1 and 2 be the sellers and 3,4,5, and 6 be the buyers. Let the cost of a link to a seller be $c_s = \frac{5}{60}$ and the cost of a link to a buyer be $c_b = \frac{1}{60}$.

Expected payoffs to buyers in sellers in some of the relevant network configurations are:

$g^a = \{13\}$: $u_1(g^a) = -\frac{5}{60}$ and $u_1(g^a) = \frac{29}{60}$.

$g^b = \{13, 14\}$: $u_1(g^b) = \frac{10}{60}$ and $u_3 = u_4(g^b) = \frac{9}{60}$.

$g^c = \{13, 14, 15\}$: $u_1(g^c) = \frac{15}{60}$ and $u_3 = u_4 = u_5(g^c) = \frac{4}{60}$.

$g^d = \{13, 14, 15, 16\}$: $u_1(g^d) = \frac{16}{60}$ and $u_3 = u_4 = u_5(g^d) = \frac{2}{60}$.

$g^e = \{13, 14, 25, 26\}$: $u_1 = u_2(g^e) = \frac{10}{60}$ and $u_3 = u_4 = u_5 = u_6(g^e) = \frac{9}{60}$.

$g^f = \{13, 14, 15, 25, 26\}$: $u_1(g^f) = \frac{13}{60}$, $u_2(g^f) = \frac{8}{60}$, and $u_3 = u_4(g^f) = \frac{6}{60}$, while $u_5(g^f) = \frac{10}{60}$ and $u_6(g^f) = \frac{11}{60}$.

$g^g = \{13, 14, 15, 24, 25, 26\}$: $u_1 = u_2(g^g) = \frac{9}{60}$ and $u_3 = u_4 = u_5 = u_6(g^g) = \frac{8}{60}$.

Figure 10.5. Find the Equilibrium Prices and Trades for These Network Configurations in the Competitive Model of Kakade et al [357].

Show that out of these networks and the empty network, the pairwise stable networks are the empty network, g^d, and g^g. Show that that none of the pairwise stable networks is efficient. Show that g^g is not Pareto efficient.

EXERCISE **10.4** *Competitive Trades on a Network.*

Find the equilibrium prices and allocations for the networks in Figure 10.5 under the competitive model of Kakade et al [357] in Section 10.3.3.

EXERCISE **10.5** *Pairwise Stable Networks with Competitive Trades.*

Consider the competitive trading model of Kakade et al [357] as discussed in Section 10.3.3, when there are N_B buyers and N_S sellers. Each seller has a single unit for sale, and buyers have valuations of 1 and endowments of 1. Show that if N_B is an integer multiple of N_S then there is a pairwise stable network where each buyer links to one seller and each seller links to N_B/N_S sellers, and the reverse is true if N_S is an integer multiple of N_B. Assume that there is a cost $c > 0$ per link, which is less than the inverse of the integer multiple and is paid out of the final goods (so in cash for sellers and in the consumption good for buyers).

Is such a network structure Pareto efficient when $N_B > N_S$? Show that no efficient network is pairwise stable when $N_B > N_S$.

[

EXERCISE **10.6** *Collaboration Networks Among Firms with Bertrand Competition.*

Consider a collaboration network among firms as in Section 10.3.4 where production costs are given by (10.20). Let firms compete for the sale of their products via pure "Bertrand competition," where each firm simultaneously quotes a price and the firms charging the lowest price evenly split the market. Consider a situation where the total amount purchased is Q independently of the price.[32] If there are at least two firms who have the lowest cost level (highest degree), then there is a Nash equilibrium of the Bertrand game where all firms quote prices equal to their per unit costs, and do not make any profits. If there is a single firm with the lowest cost, then there is an equilibrium where that firm charges the second lowest per unit cost and sells Q.[33]

If there is a positive cost to a link, show that the empty network is the only pairwise stable network.

EXERCISE **10.7** *Negative Correlation in Short-Run Labor Networks.*

Consider a triad (three-agent completely connected network) in model of Section [**?**]. Suppose that at the end of one period agents 1 and 2 are unemployed and agent 3 is employed. Show that the next-period employment states of agents 1 and 2 are negatively correlated.

EXERCISE **10.8** *Association**

Consider a network where each agent has an employment state $s_i \in \{0, 1\}$. Suppose that state of i in period t is a function of the previous vector of all agents' states and an undirected network g. In particular, the probability that $s_{it} = 1$ depends on the states $s_{j,t-1}$ for $j \in N_i(g) \cup \{i\}$, it lies strictly between 0 and 1 and is increasing in $s_{j,t-1}$ for each $j \in N_i(g) \cup \{i\}$ holding the other agents' states constant, and it is independent

[32] The shape of the demand curve is not important for this exercise.

[33] The precise equilibrium with asymmetric costs in Bertrand competition involves mixed strategies where the firm with the lowest cost charges the second lowest cost, and then the firm(s) with the second lowest cost employ a mixed strategy that has some atomless weight on prices just above the second lowest cost. See Blume [**?**] for details.

of the states $s_{j,t-1}$ for each $j \notin N_i(g) \cup \{i\}$.[34] Show that the steady-state distribution of the vector $(s_1, \ldots, s_n)$ exhibits strong association (see Section 4.5.7) relative to the components of the network.

[34]The same conclusion holds under weaker conclusions, but involves substantial complications in the proof. See Calvó-Armengol and Jackson [119] for details.

Chapter 11

Game-Theoretic Modeling of Network Formation

Chapter 6 showed the importance of understanding strategic network formation, highlighting a tension between social welfare and individual incentives to maintain relationships. As discussed in the introduction to that chapter, there are many settings where links are formed in a cognizant manner, especially in applications where the individual nodes are firms, organizations, or countries, which have explicit objectives when it comes to their relationships. And, even friendships and other more purely social relationships exhibit costs and benefits that influence which ones emerge and endure. This leads to a rich set of questions regarding the modeling of network formation.

- There are issues of how to define equilibrium and stability notions: Can players adjust many relationships at a time? Can players coordinate their choices?
- There are issues of sophistication: Are players farsighted or myopic? Do players take into account how the links that they form influence others? Do they make errors?
- There are issues of dynamics: Can players revise links over time? Are there evolutionary pressures on their choices? Are there random forces of opportunity that determine which relationships can be formed?
- There are issues of bargaining and transfers: Can players compensate others for the relationships that they do (or do not) maintain, either through negotiated payment or through favors? Is this bargained over at the time of network formation?

- There are issues of the formation of directed networks: How should we model network formation if links can be formed unilaterally? How does it depend on whether one or both players involved in a directed link benefit from its presence?

- There are issues associated with the strength of links: How do we model strength of links? What happens if players can allocate effort or resources to maintaining different links? How will the outcome depend on the context?

Given the diversity of questions above, there is no simple message emerging this chapter. Instead, this chapter examines foundational questions concerning network formation. There is, however, a pervasive question that ties things together: "Under what circumstances do incentives lead to the formation of efficient networks?"

11.1 Defining Stability and Equilibrium

In Chapters 1 and 6 we saw the concept of pairwise stability as a method of modeling network formation. Why should we use that concept rather than an explicit game? This was discussed briefly in Section 6.1, but let us re-examine that question while examining possible non-cooperative games of network formation and alternative notions of equilibrium and stability.

11.1.1 An Extensive Form Game of Network Formation

Aumann and Myerson [20] provided an early model of network formation. More specifically they were interested in the formation of a communication graph that served as a basis for a cooperative game (as discussed in Section 12.2). The formation game they examined extends to serve as a model of network formation and is described in our setting as follows.

Players move sequentially and propose links which are then accepted or rejected. The extensive form game is based on an ordering over all possible links, denoted $(i_1j_1, \ldots, i_Kj_K)$. When the link i_kj_k appears in the ordering, the pair of players i_kj_k decide on whether or not to form that link, knowing the decisions of all pairs coming before them and forecasting the play that will follow them. Player i_k moves first and says "yes" or "no," and then player j_k says "yes" or "no," and the link forms if both say "yes". A decision to form a link is binding and cannot be undone. However, if a pair i_kj_k decide not to form a link, but some other pair coming after them forms a link,

then $i_k j_k$ are later allowed to reconsider their decision. This feature allows a player 1 to make a threat to 2 of the form "I will not form a link with 3 if you do not. But if you do form a link with 3, then I will also do so." The way in which this is captured is that the game moves through all the links a first time. If at least one link forms, then the game starts again with the same ordering, moving this time only through the links that have not yet been formed. The game continues to move through the remaining unformed links in order, until either all links are formed or there is a round such that all of the links that have not yet formed have been considered and no new links have formed.

This approach has the advantage of always having a pure strategy subgame perfect equilibrium.[1] Its main drawbacck is that the game can be very difficult to solve, even in very simple settings with only a few players. Moreover, the ordering of links can have a substantial impact on which networks emerge, and it is not so clear what a natural ordering is.

11.1.2 A Simultaneous Link-Announcement Game

Given the intractability of the sequential ordering and its inherent asymmetries, Myerson [473] suggests another game in the context of the formation of communication graphs, which also extends to the formation of networks. It is probably the most "natural" simultaneous move game of network formation. I will refer to it as the *link-announcement game*. Each player simultaneously announces the set of players with whom he or she wishes to be linked. The links that are formed are those such that both of the players involved in the link named each other.

More formally, the strategy space of player i is $S_i = 2^{N\setminus\{i\}}$.[2] If $s \in S_1 \times \cdot \times S_n$ is the profile of strategies played, then link ij forms if and only if both $j \in s_i$ and $i \in s_j$. The network that forms is

$$g(s) = \{ij | i \in s_j \text{ and } j \in s_i\}.$$

In modeling the networks that emerge from the link announcement game, we can use any of a variety of game theoretic solutions, such as Nash equilibrium.

The payoffs in the link formation game are described by a profile of utility functions, $u = (u_1, \ldots, u_n)$, which indicate the payoffs of each player as a function of the network.

[1] It is a finite game of perfect information, and so has at least one solution found by backward induction.

[2] 2^A is a notation for the set of all subsets of A, also known as the power set of A.

Figure 11.1.2. Both Networks are Nash Equilibria of the Link Announcement Game

A network $g \in G(N)$ is *Nash stable* if it results from a pure strategy Nash equilibrium of the link-announcement game, where player i's payoff as a function of the profile of strategies is $u_i(g(s))$.

This game is much easier to describe than the Aumann and Myerson extensive form, and it avoids inducing a priori asymmetries between the players or links. Arguably, any network that will be stable over time in the sense that no players would like to delete any links would have to be an equilibrium of this game. The main drawback of the game that it has too many Nash equilibria, including some which are easily seen to be unreasonable. In particular, $s_i = \emptyset$ for all i is *always* a Nash equilibrium, regardless of the payoffs. Each player refuses to link with any other player, because he or she correctly forecasts that the other players will do the same. This is seen most starkly in the dyadic case, as pictured in Figure 11.1.2. Here both networks are equilibria, although clearly the network where the link forms is the only reasonable one.

Thus, while the link formation game may at first seem to be a natural way to model network formation, it is not reasonable when using Nash equilibrium alone as a solution concept. Basically, Nash equilibrium allows players to refuse to form links, and thus effectively to "delete" links, but it does not capture the fact that it may be mutually advantageous for two players to form a new relationship. We need to move beyond

Figure 11.1.2. All Networks except Two-Link Networks are Nash Stable and all Strategies in the Link-Announcement Game are Undominated.

Nash equilibrium to capture this.

In the example pictured in Figure 11.1.2, it is a dominant strategy for each player to propose to link with the other player. This suggests that one way around the shortcoming of Nash equilibrium in modeling network formation might be to use a refinement of Nash equilibrium where players do not play weakly dominated strategies. However, a slight enrichment of the example in Figure 11.1.2 shows that this will not work. Consider a triad such that the empty network leads to a payoff of 0 for all players, a single link leads to a payoff of 1 for each of the linked players (and 0 for the other), a two-link network leads to a payoff of -1 for all players, and the complete network leads to a payoff of 1 for all players. This pictured in Figure 11.1.2.

In this example, all strategies in the link-announcement game are undominated. This means that the empty network is an outcome of a Nash equilibrium that only uses undominated strategies, where every player announces the empty set of players.[3]

In order to address the fact that it takes the consent of both players to form a link

[3]This is also a trembling hand perfect equilibrium. It is not a strict Nash equilibrium. However, requiring strictness in this game leads to very general existence problems, as outlined in Exercise 11.3.

Figure 11.1.3. An Over-Connected Pairwise Stable Network. Payoffs on permutations of these networks are the permuted payoffs.

in an undirected network, one has to explicitly consider coordinated actions on the part of pairs of players. This forces one to move beyond Nash equilibrium, and standard refinements of it, and somehow coalitional considerations (at least for pairs of players) have to be considered. That is the reasoning behind pairwise stability.

11.1.3 Pairwise Nash Stability

Although pairwise stability overcomes the difficulties inherent in examining Nash equilibria of the link-announcement game, it restricts attention to changes of one link at a time. This can lead to over-connected networks being pairwise stable, even when some player would benefit from deleting multiple links at once, as is pictured in the example in Figure 11.1.3.

In the example in Figure 11.1.3, the "reasonable" network is the one that is both Nash stable and pairwise stable. This has led to a concept of pairwise Nash stable networks.

A network is *pairwise Nash stable* if it is Nash stable and pairwise stable.[4]

[4]This refinement was first discussed by Jackson and Wolinsky [343] and has been used in various

As people who have worked with game theoretic solution concepts are aware, given any equilibrium or stability concept one can find some setting where it makes a questionable prediction or is deficient in some way. This reflects the fact that as applications vary, so do the sorts of deviations that are feasible or salient. Can players communicate and coordinate their actions? Can they make multiple changes at once? Can more than two players coordinate at a time? Is the application one where players move simultaneously, or are we really just looking for stable points of some process where the timing might be sequential? Can players revise their actions? Although this means that finding a single solution concept that works well in all settings is a futile activity,[5] it does not mean that we should give up on studying variations of solutions, since different ones can be more appropriate and/or useful in different settings, and we should not give up modeling simply because a universal solution concept is not available.

A number of variations on stability concepts are discussed in the exercises of this chapter, but let me push a bit further to discuss a few of the basic considerations and some solutions that have been used to capture them.

11.1.4 Strong Stability

In some settings, players have open lines of communication and more than two players can coordinate their link formation decisions at the same time. Alternatives to pairwise stability and pairwise Nash stability that consider larger coalitions of players were first considered by Dutta and Mutuswami [200].[6] The following is a slight variation on Dutta and Mutuswami's definition, from Jackson and van den Nouweland [338]. It always selects from among the pairwise Nash stable networks.

A network $g' \in G$ *is obtainable from* $g \in G$ *via deviations by* $S \subset N$ if

(i) $ij \in g'$ and $ij \notin g$ implies $\{i, j\} \subset S$, and

(ii) $ij \in g$ and $ij \notin g'$ implies $\{i, j\} \cap S \neq \emptyset$.

studies (e.g., Goyal and Joshi [283] and Belleflamme and Bloch [48]). For more detailed studies of the relationships between Nash stability, pairwise Nash stability, and pairwise stability, as well as refinements of Nash equilibria that justify pairwise Nash stability for a wide class of settings, see Calvó-Armengol and Ilkilic [118], Gilles and Sarangi [266], Bloch and Jackson [75], and Ilkilic [323].

[5] This view is not universally held among game theorists.

[6] There was some also some early discussion of core-based allocations in the exchange network literature; e.g., by Bienenstock and Bonacich [58].

The above definition identifies changes in a network that can be made by a coalition S without the consent of any players outside of S. Part (i) requires that any new links only involve players in S, in line with the consent of both players being needed to add a link. Part (ii) requires that at least one player of any deleted link be in S, in line with the idea that either player in a link can unilaterally sever the relationship.

A network g is *strongly stable* with respect to a profile of utility functions $u = (u_1, \ldots, u_n)$ if for any $S \subset N$, g' that is obtainable from g via deviations by S, and $i \in S$ such that $u_i(g') > u_i(g)$, there exists $j \in S$ such that $u_j(g') < u_j(g)$.

The relationship between this definition and the definition of Dutta and Mutuswami [200] is examined in Exercise 11.5, and relates to whether or not a blocking coalition has to just have some members be strictly better off and others be weakly better off, as above, or have all members of a blocking coalition be strictly better off. The definition given here is consistent with pairwise stability, as the strongly stable networks are always a subset of pairwise stable networks, and in fact a subset of the pairwise Nash stable networks.

We see an example of the implications of strong stability in Figure 11.1.4. In that example, a one link network is pairwise Nash stable, as is the complete network. However, only the complete network is strongly stable.

Strongly stable networks are necessarily Pareto efficient, as one of the groups that can potentially deviate to form a better network is the society as a whole. Thus, if some network is Pareto dominated by another network, so that the second network is weakly better for all players and strictly better for some, then that will provide a viable deviation and so the dominated network will not be strongly stable. In addition to this efficiency property, strongly stable networks are immune to all sorts of coordinated deviations by players, and so are very robust. However, they only make sense as a predictive tool in situations where such coordination is feasible, and thus might be limited to situations where players have substantial knowledge about the opportunities for network formation and the payoffs, and can also readily communicate with each other. Also, while strongly stable networks are very robust and are Pareto efficient, there are many contexts where they fail to exist. The issue of existence of various sorts of stable networks is an important one to which I now turn, before returning to discuss other ways of modeling network formation.

Figure 11.1.4. Strong Stability: An example with multiple pairwise stable, Nash stable, and pairwise Nash stable networks, but a unique strongly stable network. Permutations of these networks lead to permuted payoffs.

11.2 The Existence of Stable Networks

While the the link-announcement game always has an equilibrium, this is due to the fact that there is always a trivial equilibrium where no links form because no player expects any other player to be willing to form a link. Once we move to refinements for which the empty network is not always stable, such as pairwise stability, pairwise Nash stability, strong stability, or other such refinements, existence is not always guaranteed. Let us explore when stable networks exist.

11.2.1 Improving Paths, Dynamics, and Cycles

In studying the existence of various forms of stable networks, it is useful to consider some simple dynamics. The idea is to examine the sequences of networks that might emerge as players add or delete links to improve their payoffs. The resting points of these processes will be stable points, and so understanding these sequences helps in understanding when stable networks exist and what might happen when stable networks do not exist.

Let us say that two networks are *adjacent* if they differ by only one link. That is, g and g' are adjacent if either $g' = g + ij$ for some $ij \notin g$ or $g' = g - ij$ for some $ij \in g$.

A network g' *defeats* an adjacent network g if either

- $g' = g - ij$ and $u_i(g') > u_i(g)$, or if
- $g' = g + ij$ and $u_i(g') \geq u_i(g)$ and $u_j(g') \geq u_j(g)$, with at least one inequality holding strictly.

A network is pairwise stable if and only if it is not defeated by an (adjacent) network.

The following definition from Jackson and Watts [340] captures this notion of sequences of networks where each network defeats the previous one.

An *improving path* is a sequence of distinct networks $\{g_1, g_2, \ldots, g_K\}$, such that each network g_k with $k < K$ is adjacent to and defeated by the subsequent network g_{k+1}.

This usage of "path" refers to a sequence of networks and should not be confused with a path inside a network. The idea here is to examine the sequences of networks that can emerge as players add and delete links in a way that makes them better off. Clearly, the resting points of such a process are the pairwise stable networks. That is,

Figure 11.2.1. Improving Paths: The payoffs are listed in the nodes and the arrows point towards a network that defeats the one from which the arrow emanates. Following the arrows provides improving paths. There is a unique pairwise stable network.

a network is pairwise stable if and only if it has no improving paths emanating from it. Improving paths are illustrated in Figure 11.2.1.

The notion of improving paths is a myopic one, in that the agents involved in adding or deleting links are doing so without forecasting how their actions might affect the evolution of the process. This is a natural variation on best response dynamics, and has some experimental justification (e.g., see Pantz and Ziegelmeyer [497]), but nevertheless exhibits some forms of bounded rationality. I return to discuss farsighted network formation in Section **??**.

If there does not exist any pairwise stable network, then there must exist at least one *improving cycle* – that is, a sequence of adjacent networks $\{g_1, g_2, \ldots, g_K\}$ such that each defeats the previous one and such that $g_1 = g_K$. The possibility of cycles and non-existence of a pairwise stable network is illustrated in the following example from Jackson and Watts [340].

EXAMPLE **11.2.1** *Non-existence of a Pairwise Stable Network*

There are $n \geq 4$ players who obtain payoffs from trading with each other. The players have random endowments and the benefits from trading depend on the realization of these random endowments. The more players who are linked, the greater the gains from trade, but with diminishing marginal returns.

In particular, there is a cost of a link of $c = 5$ to each player involved in the link. The utility of being alone is 0. Not accounting for the cost of links, the benefits to each player in a dyad is 12, the benefits for being connected (directly or indirectly) to two other players is 16, and of being connected to three other individuals is 18.[7]

The resulting payoffs for several of the key network configurations are pictured in Figure 11.2.1.

[7] In terms of the economic background behind these payoffs, they can be derived as follows. There are two consumption goods and players each have a Cobb-Douglas utility function for the two goods of $u(x, y) = 96xy$, where x is the consumption of the first good and y is the consumption of the second good. A player's endowment is either (1,0) or (0,1), each with probability 1/2, and the realizations are independent across players. Players within each component trade to a Walrasian equilibrium within their component, regardless of the precise set of links in the component. For example, the networks $\{12, 23\}$ and $\{12, 23, 13\}$ lead to the same expected trades, but different costs of links. In a dyad there is a $\frac{1}{2}$ probability that one player has an endowment of (1,0) and the other has an endowment of (0,1). They then trade to the Walrasian allocation of $(\frac{1}{2}, \frac{1}{2})$ each and so their utility is 24 each. There is also a $\frac{1}{2}$ probability that the players have the same endowment and then there are no gains from trade and they each get a utility of 0. Expecting over these two situations leads to an expected utility of 12. Similar calculations for more players lead to the claimed payoffs.

Figure 11.2.1. Nonexistsence of a Pairwise Stable Network: Payoffs pictured for one, two and three link networks and an improving cycle including the four networks. Networks with more than three links are defeated by networks with fewer links.

Any network with more than three links in this example is defeated by a network with fewer links, as some players will save the link cost by severing the link, and yet the full trading benefits are already realized with just three links. The critical aspect of the example is that two separate dyads gain by forming a link between them, expanding the network from two to four players. However, in any network of four players that has just three links, one of the players who has more than one link will save 5 utils in cost by severing a link and only lose 2 utils in trading benefits.

Clearly, the nonexistence of pairwise stable networks also implies the nonexistence of pairwise Nash stable networks. Moreover, pairwise Nash stable networks can fail to exist even when the sets of pairwise stable networks and Nash stable networks are both nonempty (see Exercise 11.8).[8]

While the above example shows that pairwise stable networks may not exist in some settings, there are settings where pairwise stable networks always exist. We have already seen several including distance-based generalizations of the connections model, the co-author model of Section 6.4, and a variety of market settings from Chapter 10.

A set of sufficient conditions for the existence of pairwise stable and pairwise Nash stable networks comes from ruling out improving cycles. Having no improving cycles also means that any dynamics that follow improving paths will find stable networks. The absence of improving cycles is related to the existence of what is known as what is known as an (ordinal) potential function.

An *ordinal potential function* for a society N with payoff functions $u = (u_1, \ldots, u_n)$ is a function $f : G(N) \to I\!R$ such that g' defeats g if and only if $f(g') > f(g)$ and g' and g are adjacent.[9]

For a society N, the payoff functions $u = (u_1, \ldots, u_n)$ *exhibit no indifference* if for any two adjacent networks, one defeats the other.

PROPOSITION **11.2.1** *[Jackson and Watts [339]] If a society (N, u) has an ordinal potential function then there are no improving cycles. Conversely, if a society is such*

[8] The existence of Nash stable networks is guaranteed by the observation that the empty network is always Nash stable. As argued above, that is not an interesting existence property as it simply derives from a coordination failure. The more interesting existence issue deals with pairwise stable and Nash stable networks.

[9] Ordinal potential functions were defined by Monderer and Shapley [451] for non-cooperative games, based on better responses. This definition is similar in spirit, but adapted to network formation settings and pairwise stability. For a more detailed look at the relationship between various sorts of potential functions and existence of equilibria in network formation games, see Gilles and Sarangi [270].

that payoffs exhibit no indifference, then there are no improving cycles only if there exists an ordinal potential function.

This result echoes results on ordinal potentials in non-cooperative games, and a corollary is that if society admits an ordinal potential function then there exists a pairwise stable network. This follows since any network that maximizes f must be undefeated.

Proof of Proposition 11.2.1: The proof that there are no improving cycles if a society has an ordinal potential function is straightforward and left to the reader. So, let us show that the converse holds when payoffs exhibit no indifference.

Suppose that there are no improving cycles and payoffs exhibit no indifference. Define $f(g)$ to be the number of networks g' such that there exists an improving path from g' to g.[10] We need to show that this is an ordinal potential function. Consider two adjacent networks g and g'. If g defeats g', then every network that has an improving path leading to g' also has an improving path leading to g. Moreover, g' has an improving path leading to g, but the reverse is not true, as otherwise there would be an improving cycle. Therefore $f(g) > f(g')$. Conversely, if $f(g) > f(g')$ and g' defeated g then we reach a contradiction by a similar argument. Thus, $f(g) > f(g')$ implies that g' does not defeat g, which by the no indifference condition implies that g defeats g'. Therefore, f is an ordinal potential function. ∎

The no indifference condition is needed for the proposition's conclusions, and is the subject of Exercise 11.10.

We can easily extend this analysis to the case of pairwise Nash stability, with some proper modifications to the definitions above. Let us say that the networks $g \neq g'$ are *weakly adjacent* if g' is either obtained from g by the addition of a single link or obtained by the deletion of some set of links such that there is some agent involved in all of the deleted links. If we then redefine "defeats," "improving path," "improving cycle," and "ordinal potential function" accordingly, Proposition 11.2.1 still holds, and the existence of an ordinal potential function with those definitions implies the existence of pairwise Nash stable networks.

The existence of an ordinal potential function is a demanding condition, and this emphasizes that the absence of improving cycles is also a demanding condition. Nevertheless, there exist situations where this is satisfied. In fact, there are always transfers that lead to payoffs for which there exists an ordinal potential function (see Section **??**).

[10] The idea behind this construction for finding ordinal potential functions is due to Milchtaich [443].

In some cases, simply examining the sum of all payoffs leads to an ordinal potential function. This works in the case of the Corominas-Bosch's [167] model of buyer-seller networks from Section **??** (see Exercise 11.11). It also works for the symmetric connections model when $\delta > c > n(\delta - \delta^{n-1})$ or when c is very large or small. More generally, in cases where potential functions exist, the analysis can be greatly simplified.

11.2.2 The Existence of Strongly Stable Networks

Let us now turn to examine the existence of strongly stable networks. Let us start by showing that strong stability demands that certain patterns in payoffs be present.

A profile of utility functions or payoff functions $u = (u_1, \ldots, u_n)$ is *anonymous* if for every permutation π on N (a one-to-one function mapping the set of agents N to N), it follows that $u_{\pi(i)}(g^\pi) = u_i(g)$, where $g^\pi = \{\{\pi(i), \pi(j)\} | ij \in g\}$ is the network obtained from g by permuting the positions of agents according to π.

Anonymity requires that payoffs depend only on players' positions within the network and not their labels. Payoff relevance is captured through the network structure and not through other innate characteristics of the players.

Recall the definition of component decomposability from Section 6.6.2: A profile of utility functions or payoff functions $u = (u_1, \ldots, u_n)$ is *component decomposable* if $u_i(g) = u_i(g')$ whenever $C_i(g) = C_i(g')$.

Component decomposability requires payoffs to players to depend only on the structure of their components and not to depend on the structure of other components. This allows for externalities within components, but precludes externalities across components. It holds in some settings, such as those where payoffs only depend on communication patterns within components, but not in ones where separate components interact with each other.

PROPOSITION **11.2.2** *[Jackson and van den Nouweland [338]] Consider a society with anonymous and component decomposable payoffs. If there exists a strongly stable network $g \in G(N)$ that is not connected, then all players must get an equal payoff.*

This is a variation on what is known as an "equal treatment" condition, which is implied in a wide variety of settings when requiring stability with respect to deviations by groups of agents. The proof is straightforward and only sketched here. The idea is that if all players do not get the same payoff, then there is a player in one component who gets less than the payoff of a player in another component. By replacing the higher

payoff player j with the lower payoff player i, the payoffs to the other players in the new component of player i do not change, but i's payoff goes up (as implied by the anonymity and decomposability of payoffs when ensure that i's new payoff is j's old payoff), which is an improving deviation.

Proposition 11.2.2 shows that the existence of strongly stable networks imposes stringent requirements. For instance, in the symmetric connections model it implies that (for generic choices of parameters) the only networks that could possibly be strongly stable are networks with strong symmetry properties: those such that the cardinality of each extended neighborhood of every player is identical.

It is clear that if payoffs are equal across all players at every network, then strongly stable networks exist and coincide with the efficient networks. In that case, players' payoffs are perfectly aligned with society's total payoff. However, that demands that transfers be made across components in many contexts. Sufficient conditions for existence of strongly stable networks when there are no transfers across components require some definitions from the next chapter and are explored in Exercise 12.8.

11.3 Directed Networks

The modeling of network formation with directed networks differs from that with undirected networks, as links can be formed unilaterally, and the Nash equilibrium of a formation game becomes an appropriate modeling tool.

Clearly, whether a network is directed or undirected is not just a modeling choice, but instead depends on the application. Although many social and economic relationships involve some consent of both parties, there are some applications where links can be formed unilaterally. For example, one article can cite another without the consent of the first, and a web page can link to another without its consent. In those applications, one needs to adjust the network formation model to account for the unilateral nature of the formation process.[11]

In the case of directed networks, we can still write the payoffs as a function of the network that is formed, where now (fixing a society N) g is a directed network and

[11] A temptation is to mention things like phone calls or other sorts of broadcasting as falling into the directed case. However, those fall into a different category altogether. A phone call involves an asymmetry in the process since one person initiates the action, but it also requires that the both people be willing to hold a conversation, which is a costly activity. Access to many people and organizations is guarded.

$u_i(g)$ represents the utility to player i if g is the directed network that is formed. In the case where players can form a directed link unilaterally, one way to model network formation is to have each player list the set of directed links that he or she wishes to form (and the player can only list links from him or herself to another player), and then have the resulting network be the union of the listed links. This was suggested by Bala and Goyal [28]. More formally, we model this as follows.

A network g' is *obtainable from a network g by player i* if $g'_{kj} \neq g_{kj}$ implies that $k = i$.

Thus, a network g' is obtainable from a network g by player i if the only changes in the network involve links that are directed from i to other players.

A directed network g is *directed Nash stable* if $u_i(g) \geq u_i(g')$ for each i and all networks g' that are obtainable from network g by player i.

In cases where it is clear that we are discussing directed networks, I omit the "directed" from "directed Nash stability" and simply refer to a network as being Nash stable. Thus, a directed network g is Nash stable if and only if it is the outcome a Nash equilibrium of a game where the players simultaneously announce lists of directed links from themselves to other players and the network that forms is the union of those lists.

11.3.1 Two-Way Flow

There are several things to consider in a directed network in terms of how benefits accrue. For instance, in the case of a citation network, different values come from being cited as opposed to citing. That is similar in the case of web pages. Having links to other web sites can enhance the value of a web page and make it more attractive to visit, and being linked to by other sites makes a site easier to find and thus more likely to be visited. In this way, it might be that one side initiates a link, and yet both sides benefit from the link being present. As a first approximation of this, we can keep track of who forms the link, as that might involve specific costs (for instance space on a web page, time, etc.), but then allow the benefits of a link to be bilateral. This is what Bala and Goyal [28] term *two-way flow*.

11.3.2 Distance-Based Utility

To get some feeling for the formation of directed networks, let us start by considering a variation on the distance-based utility model from Section 6.3, but adjust this to allow for two-way flow and directeds.

Given a directed network g, let $\widehat{g}$ denote the undirected network obtained by allowing an (undirected) link to be present whenever there is a directed link present in g. That is, let $\widehat{g}_{ij} = \max(g_{ij}, g_{ji})$.

Recall that in the distance-based model, players get benefits from connections and indirect connections to other agents, where the value that they obtain from indirect connections is a decreasing function of the distance to the other player.

Let $b : \{1, \ldots, n-1\} \to I\!R$ denote the net benefit that a player gets from indirect connections as a function of the distance between the agents. The *distance-based utility model* is one where an agent's utility can be written as

$$u_i(g) = \sum_{j \neq i : j \in N^{n-1}(\widehat{g})} b(\ell_{ij}(\widehat{g})) - d_i(g)c,$$

where $\ell_{ij}(\widehat{g})$ is the shortest path length between i and j in the undirected network obtained from g and $d_i(g)$ is i's *outdegree*. Let $b(k) > b(k+1) > 0$ for any k and $c \geq 0$.

Again, this embodies the idea that a player sees higher benefits for being closer to other players. A special case of the distance-based utility model, analyzed by Bala and Goyal [28], is a directed adaptation of the symmetric connections model, where $b(k) = \delta^k$.

Proposition 6.3.1, characterizing the efficient networks in the undirected distance-based utility model, generalizes directly and shows that efficient networks in a directed version of the distance-based utility model share the same features as the symmetric connections model. The only difference is an adjustment that reflects the fact that only one player bears the cost of a link instead of two.

Let us say that a directed network g is a *directed star* if the associated undirected network $\widehat{g}$ is a star and if $g_{ij} = 1$ then $g_{ji} = 0$, so that links between two players only go in one direction.

PROPOSITION **11.3.1** *The efficient networks in the (directed version of the) distance-based utility model*

(i) consists of one directed link between each pair of players if $c < 2(b(1) - b(2))$,

(ii) is a directed star encompassing all nodes if $2(b(1)-b(2)) < c < 2b(1)+(n-2)b(2)$, *and*

(iii) is the empty network if $2b(1) + (n-2)b(2) < c$.

PROPOSITION **11.3.2** *Consider the directed version of the distance-based utility model.*

(i) *If* $c < b(1) - b(2)$*, then the directed Nash stable networks are those that have one directed link between each pair of players.*

(ii) *If* $b(1) - b(2) < c < b(1)$*, then any directed star encompassing all nodes is directed Nash stable and for some parameters there are other directed Nash stable networks.*

(iii) *If* $b(1) < c < b(1) + \frac{(n-2)}{2}b(2)$*, then peripherally sponsored stars*[12] *are Nash stable and so are other networks (e.g., the empty network),*

(iv) *If* $b(1) + \frac{(n-2)}{2}b(2) < c$*, then only the empty network is directed Nash stable.*

The proof is straightforward and the subject of Exercise 11.13.

Here we see very similar results to those of the nondirected case. With very high or very low costs to links, the efficient and stable networks coincide, while otherwise they may not. Again, efficient networks take the form of variations on stars or the complete network. The most interesting difference arises in the case of a peripherally-sponsored stars. Instability of stars in the undirected case can stem from the fact the hub of the star has to bear some costs and only sees direct benefits from connections and not any indirect benefits. With directed links, it is possible for only the outside players to direct the links, so that the hub does not have to bear any costs. Nevertheless, there are still inefficiencies, and most notably this arises since only one player bears the cost of a link while many players can benefit from its existence. Indeed, even when one can impose transfers, for a variety of settings there still exist conflicts between stability and efficiency. That is, variations on the results that we saw in Section **??** hold in the directed case, as explored by Dutta and Jackson [197].

11.3.3 One-Way Flow

While the two-way flow directed setting has much in common with the undirected setting, a "one-way flow" directed setting introduces some twists.

If we look at one extreme of the distance-based model, then a simple and intuitive characterization of both efficient and stable networks emerges. In particular, consider a one-way flow directed version of the symmetric connections model where we set $\delta = 1$. This is the benchmark where an arbitrarily distant connection provides the same benefit as a direct connection, and was analyzed by Bala and Goyal [28].

[12] This is a directed star where no link is formed by the center.

Figure 11.3.3. Payoffs in a One-Way Flow Model with no Decay.

In particular, let $R_i(g)$ denote the number of other players who can be reached from i via a *directed*-path in g. Then i's payoff is

$$u_i(g) = R_i(g) - cd_i(g) \tag{11.1}$$

where $d_i(g)$ is i's out degree.

While this model is clearly extreme since a player at a great distance is just as beneficial as a direct neighbor, it still provides some insight into the one-way flow setting. The payoffs are illustrated in Figure 11.3.3

In this setting, the characterizations of efficient networks and strict Nash stable networks are simple. First, we need a couple of definitions.

A network is an n-player *wheel* if it consists of n directed links and has a single directed cycle that involves n players. A wheel is illustrated in Figure 11.3.3.

A directed Nash stable network is *strictly Nash stable* if any change in the directed links from some player leads to a strictly lower payoff for that player.

PROPOSITION **11.3.3** *[Bala and Goyal [28]] The unique efficient network structure in a one-way flow model where there is no decay and payoffs are as in (11.1) is an n-player wheel if $c < n-1$ and an empty network if $c > n-1$. Moreover, if $c < 1$,*

Figure 11.3.3. A Wheel on Five Nodes

then n-player wheels are the (only) strictly Nash stable networks, if $1 < c < n-1$ then n-player wheels and empty networks are the (only) strictly Nash stable networks; and if $c > n-1$, then the empty network is the unique strictly Nash stable network.

Proof of Proposition 11.3.3: First, let us show that a k player wheel is the unique total payoff maximizing network among those that are nonempty, involve at least k links and exactly k players have a link in or out. The cost is at least kc for any such network, which is the cost of a wheel. In order to have at least as high a payoff as a wheel, it must be that $R_i(g) = k-1$. Thus, there is a directed cycle containing all k players. If the network is not a wheel, and it contains a directed cycle with k players, it has more than k links, and so leads to a lower payoff than the k-player wheel. Thus, the only possibilities besides wheels for efficient networks are the empty network and networks that involve k players but have fewer than k links. In the latter case, it must have $k-1$ links to include k players in a component. Here thus must be a player i who has at least one link in but no links out and another player j who has at least one link out but no links in. Given that it is efficient for j to link to some k (and since j has no links in, only j benefits from that link), adding a link from i to j would increase payoffs by even more than the link from j to k does on the margin

(since $R_i(g+ij) - R_i(g) \geq 1 + R_j(g) - R_j(g-jk)$ which follows since i reaches j and $R_i(g) = 0$), which is a contradiction.

Thus, different wheels (and combinations of wheels) and the empty network are the possible efficient networks. The remainder of the claim is straightforward, noting that if the value of a wheel with less than n players is positive, then the value of a wheel involving all players generates a higher per capita payoff.

Next, let us characterize the strictly Nash stable networks.

First, in the case where $c > n-1$ it follows directly that the only (strict) Nash network is the empty network, since a link can lead to a marginal payoff of at most $n-1-c$. Next, in a case where $1 < c < n-1$, the empty network is still a strict Nash equilibrium, as each link that a player adds will changes that player's payoff by an amount $1-c < 0$. In the case where $c < 1$ it is clear that the empty network is not Nash stable. The proof is then completed by showing that whenever $c < n-1$ any nonempty strictly Nash stable network must be a wheel involving all players, as it is clear that such a network is strictly Nash stable.

So, let $c < n-1$ and consider a nonempty strictly Nash stable network. First, note that all players have at out degree of at least one. Suppose not. There is at least one player j who strictly benefited from a link ij, since the network is nonempty. By duplicating that link, a player with no out links would also strictly benefit, which contradicts equilibrium. Next, note that each player must have at most one link coming in. Suppose to the contrary that players i and j both have links to player k. By deleting the link to k and adding a link to j (or keeping the link to j if i already has one), i's payoff can only increase as there is still a path to k (and hence to all other players reached through k) and i has not increased the number of links. Thus, i benefits weakly from such a change and so the network cannot have been a strictly Nash stable network, which is a contradiction. Hence we have a network such that every player has at least one link out and at most one link in, and hence every player has one link in and one link out. This must be a wheel including all players. ∎

The strict aspect of equilibrium is a useful device here as it really narrows down the set of stable networks dramatically. Moreover, in some experiments on this sort of model, Callendar and Plott [112] find evidence that strictness is a useful predictor of behavior. Part of the reason for the predictive power is the absence of any decay (since $\delta = 1$), which leads to lots of indifferences over which links form. More generally, when there is decay, many indifferences are naturally eliminated and a refinement to strict equilibrium does not make much difference.

Figure 11.4. An Example with Two Pairwise (Nash) Stable Networks, where Improving Paths can get Stuck at the Empty Network.

11.4 Stochastic Strategic Models of Network Formation

Recall that in Section 6.3.2 we considered the following process for growing a network. At each point in time a link is randomly chosen, with equal weight on all links. If the link is not in the network, then the two players involved in the link have the choice to add it to the network and they add it if it makes each of them weakly better off in terms of payoffs and makes at least one of them strictly better off. If the link is already in the network, then either of the players involved in the link can choose to delete it, and it is deleted if that would increase the payoff for either player. If this process comes to rest then it will come to rest at a pairwise stable network. If there do not exist any pairwise stable networks, then it will keep cycling.

While such a process models the dynamics of network formation, it can get stuck at networks that are pairwise stable, but such that we would expect players to find their way around. To see this issue more starkly, consider a three-player society where the payoffs to different networks are as pictured in Figure 11.4.

For the payoffs pictured in Figure 11.4, the empty network and the complete network are both pairwise stable. However, a process simply following improving paths, as indicated below, can get stuck at the empty network. There are two different ways in which this process might get "unstuck". One variation would be to allow for trembles or some exogenous events that cause links to be added or deleted with some (small) probability ε. Once one link forms, then there is a good chance that another will be formed, and then the process would reach the complete network. Another variation is to consider "farsighted" players. Players might realize that if they add one link then other links would subsequently form. Thus, even though a single link would lead to negative payoffs, they might add it, anticipating that it will lead other links to form. These are both quite natural variations on the process described before, but from very different perspectives.[13] One simply introduces some randomness into the process, while the other relies on rational and forward-looking players. These also rely on different knowledge on the part of the players. In a farsighted process, players understand the incentives of other players and they forecast the subsequent evolution of the network, while the perturbed myopic process does not require knowledge on the part of the players other than whether a given link is beneficial on the margin. These are different types of arguments and thus might be more or less appropriate depending on the setting. Let us consider each in turn.

11.4.1 Random Improving Paths and Stochastic Stability*

Eexogenous randomness in the network formation process, so that links occasionally are added or deleted even though the benefits do not outweigh the costs, leads to a network formation process that can yield sharp predictions about which networks are likely to emerge. Such a variation on the improving path process was introduced by Jackson and Watts [**?**].

The process can be described starting at any network $g \in G(N)$. At each time $t \in \{1, 2, \ldots\}$ a link ij is randomly identified, with each link having an equal probability of being identified and with the randomness being independent across time.[14] Again, as in an improving path, if the link is not in the network and the players in question

[13] There are other perspectives, including that of strong stability. The arguments here are most pertinent to settings where such coordination between larger coalitions of players is not possible.

[14] The results described below extend to some more general processes where several links are identified at once, or which links are identified depend on the current network or the history of links that have been considered. However, this process is a useful one for the purposes of illustration.

would like to add the link (both weakly and at least one strictly), then the link is added, while if the link is already in the network then it is deleted if either of the two players strictly prefers to delete it. There is an added randomness to the process. With a probability of $1 - \varepsilon$ the intent of the players (to add a link, to delete a link, or to leave the network as it is) is carried out, and with probability $\varepsilon > 0$ the reverse occurs.

Thus, at each time some link is examined and with some probability the link is added, deleted, or ignored, depending on what the players would like to do under the concept of an improving path; and with some probability there is a "perturbation" and exactly the opposite occurs. Effectively, this process has small probabilities that some exogenous events happen, which might be errors on the part of players or some other interventions that break up beneficial relationships or introduce relationships that are not beneficial. There are many possible perturbations that could account for such randomness.

Given these random perturbations in the process, the process will now continue (with probability one) to have the network change indefinitely. Moreover, it will continue to visit each network over time. In fact, this process is now a finite state, aperiodic, irreducible Markov chain (recalling definitions from Section 4.5.8).[15] Thus, it has a steady-state distribution.

To get a feeling for this process, let us reconsider the example pictured in Figure 11.4.

If the process is at the empty network at some time, then it will only change to another network if there is an error. Thus, there is a ε chance that it will lead away from the empty network.

If the process is at a one-link network, then regardless of which link is identified, the players will wish to change the network, either adding a new link or deleting the new link. Thus, there is a $1-\varepsilon$ chance that it will change networks and only a ε chance that it will stay at a one link network. When it does change networks, it is twice as likely to lead to a two-link network as to lead to the empty network.

Once we get to a two-link network, then the players would choose to change the network only if the missing link is the one identified. In this case, there is a $1/3$ chance that the probability of leaving the network will be $1 - \varepsilon$ and a $2/3$ chance that the probability of leaving the network will be ε. In particular, there is a $(1-\varepsilon)/3$ chance of changing to the complete network, a $(2 - \varepsilon)/3$ chance of staying at the same network,

[15] Players behavior, and that of the system, depend only upon the current network and not on the history of how they got there.

and a $2\varepsilon/3$ chance of changing to a one-link network.

At the complete network, no player will wish to make any changes. So, the process will only change networks if an error occurs, and so changes to a two-link network with probability ε and stays put otherwise. Viewing this as a Markov chain, let the "state" of this system simply keep track of how many links the network has and consider the probability of transitioning from one "state" to another. The transition probabilities are described in the following matrix, where the ij-th entry is the probability that the network will change from a network with i links to one with j links.

$$\Pi(\varepsilon) = \begin{pmatrix} 1-\varepsilon & \varepsilon & 0 & 0 \\ \frac{1-\varepsilon}{3} & \varepsilon & \frac{2(1-\varepsilon)}{3} & 0 \\ 0 & \frac{2\varepsilon}{3} & \frac{2-\varepsilon}{3} & \frac{1-\varepsilon}{3} \\ 0 & 0 & \varepsilon & 1-\varepsilon \end{pmatrix}.$$

From this, it is easy to deduce the steady-state distribution of this process. It is a 1×4 vector μ such that $\mu\Pi = \mu$. This is the left-hand unit eigenvector, which in this case is described as follows.

$$\mu(\varepsilon) = \left(\frac{\varepsilon(1-\varepsilon)}{1+2\varepsilon}, \frac{3\varepsilon^2}{1+2\varepsilon}, \frac{3\varepsilon(1-\varepsilon)}{1+2\varepsilon}, \frac{(1-\varepsilon)^2}{1+2\varepsilon} \right).$$

Let us examine the properties of this process. As we let ε go to 0, $\mu(\varepsilon)$ tends to $(0,0,0,1)$ and the time that the process spends in the complete network tends to 1 while the time that the process spends in any other network tends to 0.

To understand this process, note that for very small ε, once the process reaches the empty network, it stays there until an error occurs, and so it can stay there for a very long time as ε becomes small. In contrast, if it is either at a one or two link network, it will leave that state with very high probability. When it is at the complete network, it will stay there with very high probability. To see why the process spends almost all of its time in the complete network rather than the empty network when ε is small, note the following. If it is at the complete network, even if an error occurs it ends up at a two-link network. All two-link networks lead back to the complete network with very high probability. It actually takes an error to transition from a two-link network to a one link network. Thus, moving from the complete network to the empty network takes at least two errors to occur, which happens on the order of ε^2. In contrast, moving from the empty network to the complete network only takes one error. In particular, once a one-link network is reached, then there is a nontrivial probability of transitioning to a two link network and then to the complete network. Thus, the probability of

transitioning from the empty network to the complete network is on the order of ε. As ε becomes small, the process is much more likely to transition from the empty network to the complete network than the other way around. Although the process can still stay at the empty network for many periods in a row upon reaching it, asymptotically it will spend much more time at the complete network.

Note that it is necessary to look at the limit of the $\mu(\varepsilon)$'s to find μ. If we examine the limiting improving path process directly without any errors, then that process is described by the transition matrix

$$\Pi = \begin{pmatrix} 1 & 0 & 0 & 0 \\ \frac{1}{3} & \varepsilon & \frac{2}{3} & 0 \\ 0 & 0 & \frac{2}{3} & \frac{1}{3} \\ 0 & 0 & 0 & 1 \end{pmatrix}.$$

While $\mu = (0, 0, 0, 1)$ is a steady-state of that system, so is $(a, 0, 0, 1 - a)$ for any $a \in [0, 1]$. That is, the process without any mutations does not discriminate between the empty and complete networks. One needs the error process to really discover how stable various networks are to perturbations.

11.4.2 Stochastically Stable Networks*

With more than a few players, working directly with the perturbed improving path process $\Pi(\varepsilon)$ can be cumbersome, and so it is important to discover the set of stochastically stable networks more directly and generally. Here, we make use of a powerful theorem by Freidlin and Wentzell [239] that characterizes the steady-state distribution of Markov processes, which was adapted by Kandori, Mailath, and Rob [358] and Young [632] to understand how perturbed Markov chains behave as the probability of an error, ε, tends to 0. Jackson and Watts [340] show how such a general "stochastic stability" analysis can adapted to a network setting to derive insights about the evolution and dynamics of network formation. Let me outline some of the central tools and techniques.

Consider an improving path process with added errors as described above. Let $\mu(g, \varepsilon)$ be the steady-state probability that process is at network g when the process has error rate ε.

A network $g \in G(N)$ is *stochastically stable* if its steady-state probability is bounded below as the error rate, ε, tends to zero; that is, g is stochastically stable if $\mu(g, \varepsilon) \to_\varepsilon a > 0$.

When pairwise stable networks exist, any stochastically stable network must be pairwise stable. This is clear since the process will leave any non-pairwise stable network with a probability that is bounded below as ε goes to 0, while a pairwise stable network is only left if an error occurs.[16] When pairwise stable networks do not exist, the stochastically stable networks only include networks that sit on improving cycles of networks which are randomly visited over time. It could pick certain cycles and not others, as it might take many more errors to leave one cycle than another.

Thus, stochastic stability selects from among the pairwise stable networks, when they exist, and thus can provide a more refined prediction based on a sort of robustness argument. We already saw such a selection in the example above, where there were two pairwise stable networks and only one stochastically stable network. Stochastic stability identifies the most "robust" or easy to reach networks in a particular sense. The disadvantage of this approach is that the limit points of the dynamics can be difficult to identify in some applications. Nevertheless, there are many settings where it provides a meaningful refinement, as discussed below.

The characterization of stochastically stable networks follows from results characterizing the limiting properties of perturbed Markov chains, as I now outline.

Consider a Markov chain on a finite state space S with transition matrix Π. In the application to networks, the state space is the set of networks and the transition matrix is determined by the random identification of a link and then following an improving path (adding or deleting the link).

A set of mutations of Π is a set of transition matrices $\Pi(\varepsilon)$, one for each ε in a range $a > \varepsilon > 0$ for some $a > 0$, such that

(i) $\Pi(\varepsilon)$ is aperiodic and irreducible for each ε

(ii) $\Pi(\varepsilon)$ converges to Π as $\varepsilon \to 0$, and

(iii) $\Pi(\varepsilon)_{ss'} > 0$ implies that there exists $r \geq 0$ such that $0 < \lim_{\varepsilon \to 0} \frac{\Pi(\varepsilon)_{ss'}}{\varepsilon^r} < \infty$.

Part (i) ensures that the mutations add noise in a way such that any state can eventually be reached from any other state, and in an aperiodic way. Part (ii) ensures that for small ε the mutated matrix is close to the original matrix. The number r in (iii) is the *resistance* of the transition from state s to s', and roughly can be thought of as quantifying the level of error or mutation needed to get from state s to s'.

[16] It is possible for a (unique) stochastically stable network to be pairwise stable but not pairwise Nash stable. See exercise 11.14.

In the application to networks, the perturbations are found by including an ε error in the addition or deletion of the randomly identified link. Since this means that any network can lead to any adjacent network, as well as back to itself, the process satisfies (i), and (ii) is also clearly satisfied. To verify that (iii) is satisfied, first note that $\Pi(\varepsilon)_{gg'} > 0$ implies that g and g' are adjacent. There is a resistance of 0 in the case where g' defeats g (lies on an improving path with only one link), and so $\Pi_{gg'} > 0$ and setting $r = 0$ satisfies (iii). Otherwise, the transition only occurs if there is an error, and so $\Pi(\varepsilon)_{gg'}$ is simply ε divided by the number of links which could be identified by the process. Thus, $\Pi(\varepsilon)_{gg'}$ goes to 0 at the rate of ε and so $r = 1$ satisfies (iii).

Let me now state a theorem from Young [632] that characterizes the states that have positive probability under the limit of the steady state distributions of the mutations of the process.

Given any state s, an s-tree is a directed graph with a vertex for each state and a unique directed path leading from each state $s' \neq s$ to s. The *resistance* of s is the minimum across all s-trees of the summed resistance over directed edges in that tree.

THEOREM **11.4.1** *(Young [632]) Let Π be the transition matrix associated with a Markov chain on a finite state space with an associated set of mutations $\{\Pi(\varepsilon)\}$ and with corresponding (unique) stationary distributions $\{\mu(\varepsilon)\}$. Then the steady state distributions $\mu(\varepsilon)$ converge to a stationary distribution μ of Π. Moreover, a state s has positive probability under μ (and is thus stochastically stable) if and only if s has minimum resistance.*

From Theorem 11.4.1 it is easy to see that if a state s has positive probability under μ and there is an adjacent state s' that can be reached from s with no resistance, then the state s' will also have minimum resistance and thus will also have positive probability under μ. To see this, simply start with an s-tree with minimum resistance, and construct an s'-tree with at least as low a resistance as follows. Cut the directed link out from s' and form a directed link from s to s'. The new link has resistance 0, and so this tree has at least as low a resistance, and since s has minimum resistance, then s' must also.

By this reasoning, we can consider whole sets of states that can reach each other. The stochastically stable networks will either be pairwise stable networks or lie on cycles, where they can reach (and be reached by) other stochastically stable networks via an improving path. In terms of the results on stochastic stability of Markov chains, this is stated as follows.

The *recurrent communication classes* of Π, denoted $S_1, \ldots, S_J$, are disjoint subsets of states (not necessarily including all states) such that

- from each state there exists at least one path of zero resistance leading to some state in one of the recurrent communication classes,
- any state in a recurrent communication class can reach any other state in the same recurrent communication class by a path of zero resistance, and
- for any recurrent communication class S_j and states $s \in S_j$ and $s' \notin S_j$ such that $\Pi(\varepsilon)_{ss'} > 0$ for some ε, the resistance of the transition from s to s' is positive.

In the application to networks, the recurrent communication classes are either singletons consisting of a pairwise stable network, or a closed improving cycle, where closure refers to the third item above and means that there is no improving path leading out from a network in the cycle to a network that is not part of the cycle.

For two recurrent communication classes S_i and S_j, since $\Pi(\varepsilon)$ is irreducible for each ε, it follows that there is a sequence of states $s_1, \ldots, s_k$ with $s_1 \in S_i$ and $s_k \in S_j$ such that the resistance of transition from each consecutive state to the next in the sequence (e.g., from s_h to s_{h+1}) is defined by (iii) and finite. Let this be denoted by $r(s_h, s_{h+1})$. The resistance of transition from recurrent communication class S_i to recurrent communication class S_j is the minimum over all such sequences of $\sum_h r(s_h, s_{h+1})$, and is denoted $r(S_i, S_j)$.

Given a recurrent communication class S_i, an S_i-tree is a directed graph with a vertex for each communication class and a unique directed path leading from each recurrent communication class $S_j \neq S_i$ to S_i. The *stochastic potential* of a recurrent communication class S_i is then defined by finding an S_i-tree that minimizes the summed resistance over directed edges, and setting the stochastic potential equal to that summed resistance.

With these definitions in hand, we can relate resistance to stochastic stability.

THEOREM **11.4.2** *(Young [632]) Let Π be the transition matrix associated with a Markov chain on a finite state space with an associated set of mutations $\{\Pi(\varepsilon)\}$ and with corresponding (unique) stationary distributions $\{\mu(\varepsilon)\}$. Then the steady state distributions $\mu(\varepsilon)$ converge to a stationary distribution μ of Π, and a state s has positive probability under μ (and thus is stochastically stable) if and only if s is in a recurrent communication class of Π which achieves the minimal stochastic potential. This is equivalent to s having minimum resistance.*

This is similar to the previous theorem, except that it says that to identify the stochastically stable states, we need only work with the stochastic potential of the recurrent communication classes rather than keeping track of the resistance state-by-state. Thus, in identifying the stochastically stable networks, one needs only focus on pairwise stable networks and closed improving cycles of networks. This can substantially simplify the analysis. To get a feeling for this, and to see an example of how stochastic stability can refine the set of pairwise (Nash) stable networks, consider the co-author model from Section 6.4.

Recall that the payoff to player i in network g is

$$u_i(g) = \sum_{j:ij \in g} \left(\frac{1}{d_i(g)} + \frac{1}{d_j(g)} + \frac{1}{d_i(g)d_j(g)} \right)$$

for $d_i(g) > 0$, and $u_i(g) = 1$ if $d_i(g) = 0$.

When $n = 7$ there are 22 different pairwise (Nash) stable networks: the complete network and each network such that there are five completely connected players and a separate dyad. As Jackson and Watts [340] point out, only the complete network is stochastically stable. This is seen as follows. Each pairwise stable network other than the complete network has a resistance of 1 to the complete network. Indeed, it is easily checked that deleting the link in the dyad leads to a network that lies on an improving path to the complete network. Thus, when g is the complete network, we can construct a g-tree that has stochastic potential of 21, by pointing each other network directly to the complete network. In contrast, it takes several errors to get from the complete network to a network that lies on an improving path to some other pairwise stable network. If just only link in the complete network is severed, then the only improving path leads back to the complete network. Thus the resistance from the complete network to any other pairwise (Nash) stable network is more than 1. Constructing a g-tree for any other network leads to a stochastic potential of more than 21.[17]

Interestingly, the complete network is Pareto dominated by any of the other pairwise (Nash) stable networks, yet is the unique stochastically stable network, which offers a further illustration of the tension between efficiency and stability.

In some cases, there are weakenings and generalizations of stochastic stability that can be easier to work with, as shown by Tercieux and Vannetelbosch [589].

[17] There are no improving cycles, so the only recurrent communication classes are the ones that each consist of a different pairwise stable network.

11.4.3 Stochastic Stability Coupled with Behavior

It is possible to extend the apparatus of stochastic stability to include other considerations. For instance, Jackson and Watts [341] examine a graphical game in a setting where strategies co-evolve with the network. That is, players are choose between two actions in a coordination game where their payoffs depend on the play of their neighbors. At the same time as choosing their actions, they can also decide on adding or deleting links. With costs to links, they prefer to be linked to other players with whom they coordinate their play. Their payoffs are thus affected both by whom they link to and what strategies they play. Analyzing these things together provides for interplay between the network structure and play of the game. This can lead to stochastically stable outcomes that differ from the behavior that predicted when simply fixing the network structure (players who play more efficient actions can be more attractive), and can also lead to different predictions in terms of network structure than having fixed play. It can also lead to differences in the speed of convergence of play, as the evolving network structure can lead to the diffusion of certain types of play in a more rapid fashion than with a static network. The analysis ends up being sensitive to the details of the setting, but shows the importance of analyzing the co-evolution of behavior and network structure.[18]

11.5 Farsighted Network Formation

A very different perspective on network formation from that of random errors and myopic behavior is one where players are forward-looking and make no errors. This applies in very different circumstances, where players have a good idea of the setting and the relevant incentives that various players have to form and sever links. This has been explored from various vantage points, some of which involve explicit variations on network formation games (see Dutta, Ghosal and Ray [**?**]) as well as other approaches that capture farsightedness directly through variations on improving paths (e.g., Page, Wooders, and Kamat [494]). Let us examine this latter approach in more detail.

In the definition of improving path changes from one network to the next are improving for the players involved, but without anticipating the subsequent changes that

[18] That analysis has been extended to directed networks by Goyal and Vega-Redondo [288], Hojman and Szeidl [314], to anti-coordination games by Bramoullé et al [94], and to settings with geography by Droste, Gilles and Johnson [193]. See also Skyrms and Pemantle [563] for a reinforcement based evolutionary analysis of games played on networks.

will occur along the path. In contrast, the idea of a farsighted improving path captures the notion that the players anticipate the further changes along the path and compare the ending network and the current one.

Let us say that a network g' is *improving* for S relative to g if it is weakly preferred by all players in S to g, with strict preference holding for at least one player in S.

Next, consider a sequence of networks $g_1, \ldots, g_K$, and a corresponding sequence $S_1, \ldots, S_{K-1}$, such that g_{k+1} is obtainable from g_k via deviations by S_k. Such a sequence is a *farsighted improving path* if, for each k, the ending network g_K improving for S_k relative to g_k.

In the case where consecutive networks in the sequence are required to be adjacent, then this is a farsighted analogue of an improving path, while more generally it allows for large coalitional deviations.

Now we can say that a network g is *farsightedly pairwise stable* if there is no farsighted improving path from g to some other network g', such that each pair of consecutive networks along the sequence are adjacent.

Similarly, we can say that a network g is *farsightedly strongly stable* if there is no farsighted improving path from g to some other network g'.

These are both demanding requirements. They refine the set of pairwise stable and strongly stable networks, respectively. That is, any network that is farsightedly pairwise stable is necessarily pairwise stable and a network that is farsightedly strongly stable is necessarily strongly stable. These definitions require that networks be immune to both immediate deviations and farsighted sequences of deviations of arbitrary length.

In the example in Figure 11.1.4 the complete network is farsightedly strongly stable and thus farsightedly pairwise stable. But more generally, such definitions are difficult to satisfy. An aspect of the definitions that is too strong is that it does not require that a farsighted improving path end at a network that is stable itself. That is, if players are really farsighted, then they would not follow some farsighted improving path unless they really anticipated that the endpoint is justified as the stopping point of the process. Such a definition, however, becomes circular as it requires the endpoint to be farsightedly stable. This sort of existence problem is nicely handled through a concept developed by [148] and adapted to the network setting by Page, Wooders and Kamat [494].

The idea is based on a self-consistent set-based definition. In particular, a set of networks is said to be consistent if all deviations away from the network are expected to lead (in a farsighted manner) back to some network in the set, and one that is not

improving for the original deviating coalition.

More formally, a set $A \subset G(N)$ is *consistent* if for each $g \in A$, and g' obtainable from g via deviations by some $S \subset N$, either $g' \in A$ and g' is not improving for S, or there exists a farsighted improving path from g' to some $g'' \in A$ such that g'' is not improving for S.[19]

It is easily checked that a union of consistent sets is consistent. Thus, Chwe suggests examining the largest consistent set, which he shows is always nonempty.

The idea of a consistent set A is that any network in the set is justified as being "stable" as follows. Consider $g \in A$, and g' obtainable from g via deviations by some $S \subset N$. If g' is improving for S, then there must be some expectation that discourages S from deviating to g'. In particular, there must exist a farsighted improving path moving away from g' that S anticipates will be followed and will lead to some $g'' \in A$ such that g'' is not improving for S. The presence of g'' in A implies that this is also a justifiable resting point, and so S can expect the process to stay there. This anticipation then deters the original deviation. If every deviation away from g can be deterred in this way, then it is a viable resting point, and the set is consistent in that its various elements are used in justifying each other as resting points.

To see how the largest consistent set can make different predictions from other solutions, let us re-examine a variation on the example from Figure 6.2.2, which involved a bargaining network. Allowing for coalitional deviations, we find that no network is strongly stable. The difficulty is that the efficient network is defeated by a network where a link is added. This in turn is defeated by the addition of another link, but then all players would be better off moving back to the efficient network.

The largest consistent set relative to the payoffs in Figure 11.5 includes the efficient network and two other networks. Without going through the full set of calculations needed to verify that this is the largest consistent set, let us examine a few of the key deviations to check that the set is consistent. The reasoning is a bit subtle, but holds together as follows. Suppose that we start at the efficient network. In order to check that this is part of a consistent set, we need to check that if some group deviates to change the network, that they could then anticipate some farsighted improving path that leads away from the deviation and to another network in the consistent set that would not be improving. A possible problematic deviation is players 1 and 2 threatening

[19] The definitions here differ slightly from Chwe's definitions, as here the definition of improving only requires weak improvement for some players and strict for at least one, while Chwe's definition requires improvement for all players.

Figure 11.5. No Network is Strongly Stable, Pairwise (Nash) Stable Networks are Inefficient, while the Largest Consistent Set is Efficient

to add the top link, which would lead them to a higher payoff of 3.25 each. To check the condition for this to be a consistent set, we need to find a farsighted improving path away from this network leading to another network in the consistent set that is not improving for 1 and 2 relative to their original payoffs of 3. Indeed, players 3 and 4 could add a link, which would be improving for players 3 and 4 and lead to another network in the consistent set which offers a lower payoff to players 1 and 2 (2.5 each). Thus, this possible anticipated continuation reasoning deters 1 and 2 from adding a link in the first place, and thus is one way to justify the original efficient network being in the set. Next, let us consider the network with the three links where players 1 and 2 get a payoff of 3.25. Suppose that players 3 and 4 deviate to add a link resulting in a network where all players get 2.5. In order for the network with three links to be in the consistent set, we need to check that there is a farsighted improving path that leads to a consistent network with a payoff for players 3 and 4 that deters them from making this initial change. Here, there is a farsighted improving path which goes to the three link network at the bottom left of the figure, which then leads to payoffs of 0 for all players and then continuing on a farsighted improving path back to the original three-link network at the top right where players 3 and 4 have a payoff of 2

each. Thus, again, we find a subsequent farsighted improving path which can deter the original deviation. Finally, we need to check that the network at the bottom left is in the consistent set. An obvious deviation is to the efficient network. From that network there is a farsighted improving path which leads to the three link network at the top right, which is in the consistent set an leads to a lower payoff for players 3 and 4, thus deterring their original deviation.

This example shows the reasoning behind the consistent set, and why it is a set-based notion. Various networks in the set are sustained because of anticipated deviations leading to other consistent networks. The consistency refers to the fact that various networks in the set are used to sustain others, and the reasoning has to be fully consistent. Considering the largest such set implies that nothing outside of the set could be sustained via such reasoning.

PROPOSITION **11.5.1** *[Chwe [148]] Consider any N and profile of preferences. There exists a unique largest consistent set (so that every consistent set is a subset of it and it is consistent), and this set is nonempty.*

The ideas behind the proof are relatively straightforward. First, it is easily checked that the union of consistent sets is consistent, as there are fewer potential deviations to worry about that move outside of the set and more things that can deter those deviations. Thus, given the finite setting there will exist a largest consistent set simply by taking the union of all consistent sets. Showing that the largest consistent set is nonempty is the harder part of the proof. It relies on showing that a sequence of networks such that there is a farsighted improving path from any network to any subsequent network in the sequence, must be finite in length. This follows in our setting since an infinite path must repeat some networks, which cannot be improving relative to themselves.

The basic ideas behind the largest consistent set are not particular to the specific notions of "improvement" or "deviation" that we have been working with. Indeed, Chwe's original definitions do not mention networks at all. It is a quite versatile idea, that can be adapted to other settings, including networks with multiple relations between pairs or groups of players, directions, and other sorts of considerations. Such extensions are explored by Page, Wooders and Kamat [494] and Page and Wooders [493].[20]

[20] See Dutta, Ghosal, and Ray [**?**] and Herings, Mauleon, and Vannetelbosch [310] for other approaches to defining farsighted stability.

11.6 Transfers and Network Formation

As discussed in Chapter 6, the tension between efficiency and stability in network formation stems from externalities. Players do not take into account the indirect impact that their link-formation decisions have on others. At least in some contexts, this can be rectified if transfers are allowed so that players can pay each other for forming or severing links, or if players can bargain over how the value of relationships is allocated when forming links. Such transfers are applicable in many settings where links represent economic or business relationships, and transactions are occurring as part of the relationship. If the relationship is more advantageous for one party, then that can be contracted upon at the time of the relationship formation. One not only sees such agreements in purely economic relationships, but also in social ones. For instance, we even see transactions in some marriages in the form of dowries. Even with no wealth or goods exchanged, there can be an allocation of tasks or favors that is either implicitly or explicitly agreed to in order to maintain a relationship.

11.6.1 Forming Network Relationships and Bargaining

The fact that transfers can affect the network that forms means that it can be important to model the use of transfers as part of the network formation process. Such a process was first investigated by Currarini and Morelli [172] by examining a sequential network formation game that is described as follows.[21] The game is defined for cases where the utilities are component decomposable (recalling the definition from Section 6.6.2), so that the payoffs to a given component depend only on that component's configuration and not on the remainder of the network. Players are ordered exogenously, labeled in the order of their moves so that player 1 moves first, then player 2 and so forth. At his or her turn, player i announces the set of players with whom he or she is willing to be linked ($S_i \subset N \setminus \{i\}$), and a payoff demand $v_i \in I\!R$ – which is interpreted as the net payoff that the player wishes to get. The outcome of the game is then as follows. First one examines the network that could potentially form by including the links such that both players involved in the link announced each other. That is, the potential network that might form is $g(S)$ where $ij \in g(S)$ if and only if $j \in S_i$ and $i \in S_j$. This is not the final network, as one has to check to see whether the payoff demands that the agents made can all be satisfied. The network that is eventually formed is

[21] See Mutuswami and Winter [471] for elaboration on a similar model.

determined by checking which components of $g(S)$ are actually feasible in terms of the demands submitted. That is, if g' is a component of g, then g' is actually formed if $\sum_{i \in N(g')} v_i \leq \sum_i u_i(g)$, and otherwise *none* of the links in g' are formed.

The presumption is that if a component forms, then players in that component get payoffs of the v_i's that they demanded. Exactly how transfers are made, or what needs to be done to convert the initial utilities into this final allocation of payoffs is not specified and might involve some complicated transfers that travel some distance in the network.

Currarini and Morelli then show the following result, for a class of settings where payoffs satisfy a condition that they name size monotonicity.

Payoffs $u = (u_1, \ldots, u_n)$ satisfies *size monotonicity* if $\sum_i u_i(g) > \sum_i u_i(g - kj)$ for every g and every bridge $kj \in g$ (such that $g - kj$ has more components than g).

PROPOSITION **11.6.1** *[Currarini and Morelli [172]] If payoffs satisfy size monotonicity, then every (subgame perfect) equilibrium of the Currarini and Morelli bargaining and network formation game leads to an efficient network.*

The intuition behind the result is as follows. It is helpful to consider a simple dyad to see the idea. Suppose that if the dyad is formed, player 1 will get a utility of 2 while player 2 will get a utility of -1. This is a beneficial relationship for player 1, but a costly one for player 2. There is a total utility of 1 to be had, and so it is efficient for the link to form; however, without any reallocation of value, player 2 would not be willing to form the relationship. Given that player 1 moves first, the equilibrium here is easy to see: player one states $S_1 = \{2\}$ and sets $v_1 = 1$; and then 2 responds with $S_2 = \{1\}$ and $v_2 = 0$.[22] This is the only subgame perfect equilibrium outcome. Effectively, player 1 pays player 2 a unit of utility in order to form the link. If the player roles were reversed and player 2 moved first, then player 2 would demand $v_2 = 1$ and leave player 1 with no value. The important aspect is that the players are now able to ensure that each gets enough value to form the efficient network. When there are more than two players the analysis becomes a bit more complicated, as the first movers have to forecast how much utility they can extract from the network, how much will be left, and what options the later players will have in terms of forming links; but the basic idea is that they will correctly forecast exactly how much they can extract

[22] In terms of the full specification of how 2 behaves, he or she with $S_2 = \{1\}$ and $v_2 = 1 - v_1$ whenever $v_1 \leq 1$ and otherwise says $S_2 = \emptyset$.

in equilibrium by maximizing with respect to the foreseeable equilibrium strategies of the subsequent players.[23]

This game has features that are important in the result, but are also a bit artificial. In particular, the fact that players move in a fixed, forecastable order and exactly once is important in backward induction and getting efficiency. The idea behind efficiency comes from the fact that suggesting links leading to an efficient network maximizes the payoff that each player is able to extract at his or her turn, given the previous demands of the other players and given how the remaining players will be forced to react. It is clear that it can provide some players with big advantages or disadvantages in terms of the network and payoffs that eventually emerge, and that this hinges on the fixed sequential ordering.

11.6.2 A Network Formation Game with Transfers

As an alternative to the above game, Bloch and Jackson [74] suggest a simultaneous move game where players can directly offer transfers to each other in order to form links. The motivation behind this is not that a simultaneous move game is how networks are formed. To the contrary, the idea is that if one models a richer setting where players can go back and forth and bargain, it will have to be that in the end they come to a point where none of them would want to change their proposed transfers or links. Thus the resting point of a more open and dynamic process will have to reach an equilibrium point where no player would gain from changing his or her action given the actions of the others. This is modeled as follows.

Let each player i announce a vector $t_i = (t_{i1}, \ldots, t_{in}) \in I\!R^n$ such that $t_{ii} = 0$ and with the interpretation that t_{ij} is the amount that i is willing to transfer to j to form a link, or, if this is a negative number, the amount that i requests in order to form the link.

A link ij is formed if and only if $t_{ij} + t_{ji} \geq 0$. In equilibrium this will hold with equality.

Let $g(t) = \{ij | t_{ij} + t_{ji} \geq 0\}$ denote the network that forms. Player i's payoff is then

$$\pi_i(t) = u_i(g(t)) - \sum_{j:ij \in g(t)} t_{ij}.$$

To solve this game, one can use Nash equilibrium; however, one then runs into the

[23] To see how this works in some richer examples, see Jackson [?] and the proof is provided in Currarini and Morelli [172].

same difficulties that are faced with Nash equilibrium in the basic network formation game. Tor instance, if a player expects all other players to demand enormous amounts to form a link (that is, to state very negative t_{ij}'s), then it is in his or her interest to do the same. Thus, the empty network is always an equilibrium, regardless of how attractive other networks are. Thus, one runs into the problem that nobody forms any links since they all correctly forecast that no one else will form a link.

To deal with this issue, Bloch and Jackson [74] adapt pairwise Nash equilibrium to this setting.

A *pairwise transfer equilibrium* is a profile of vectors of proposed transfers $(t_1, \ldots, t_n)$ such that t is a Nash equilibrium, that is

$$\pi_i(t) \geq \pi_i(\widehat{t}_i, t_{-i})$$

for all i and $\widehat{t}_i \in I\!R^n$ (such that $\widehat{t}_{ii} = 0$); and, for any $ij \notin g(t)$

$$u_i(g(t) + ij) + u_j(g(t) + ij) \leq u_i(g(t)) + u_j(g(t)).$$

Note that this latter requirement is equivalent to requiring that there does not exist any $\widehat{t}_{ij}$ and $\widehat{t}_{ji}$ such that $\widehat{t}_{ij} + \widehat{t}_{ji} \geq 0$ and such that both i and j would be weakly better off with these new announcements and the addition of the link between them with at least one strictly better off. Thus, this is a parallel definition to pairwise Nash equilibrium, but allowing for transfers between the players.[24]

PROPOSITION **11.6.2** *[Bloch and Jackson [74]] In the distance-based utility model, for each efficient network, there exists a pairwise transfer equilibrium which results in that network and balanced transfers (so that the total transfers sum to 0).*

Bloch and Jackson do not prove this directly, but instead as part of a more general characterization which provides the necessary and sufficient conditions for a network to be supportable as an equilibrium of this transfer game. The direct proof in the case of the distance-based utility model is quite intuitive as it deals mainly with the star, and works by showing that the peripheral players can offer sufficient transfers to the center player to sustain the star as an equilibrium whenever it is efficient. That proof is left as Exercise 11.15.

The pairwise transfer equilibria in the transfer game above do not necessarily always include efficient networks. There are various reasons for this. One is that there

[24] For a notion of equilibrium incorporating transfers for the case of directed network formation see Johari, Mannor and Tsitsiklis **??**.

can be indirect externalities, so that the efficient network involves relationships that affect players who are not directly involved. A player might like to pay a neighbor to undertake more or fewer other relationships, but cannot as the types of transfers described above only affect the given link in question. For example, a player might benefit from having friends with more contacts, or else from having friends who are less distracted. Also, it could be that players would like to subsidize links that are far away in the network, so that they need to make transfers to players who are not even their neighbors. Furthermore, it might be that players are hurt by (distant) links that others wish to form. Here one would like to pay other players not to form relationships. For example, this is the case in some research and development settings, where a firm would like to be able to pay other firms not to collaborate with each other. Bloch and Jackson [74] also consider two other variations of such transfer games, one where players can offer to subsidize links that they are not involved with, and also can make transfers contingent on the network. They provide characterizations as to which types of externalities can be overcome by which sorts of transfers.

11.7 Weighted Network Formation

Most of the strategic network formation literature has looked at discrete linking decisions. That is, relationships are modeled as either being present or not, or either weak or strong, but without much richer choices. In many contexts decisions are much richer: for instance, we decide how much time to spend with different friends and how much effort to devote to various collaborations. Allowing for richer choices leads to new insights into how relationships form and what incentives players have to maintain efficient relationships. This is illustrated in the following model due to Rogers [537].

There is a finite society of $n \geq 3$ players who form a weighted and directed network. Each player has a budget of time that he or she can spend with other players. Let the budget for player i be denoted $B_i > 0$.

A feasible strategy for player i is a vector $(g_{i1}, \ldots, g_{in})$ such that $\sum_{j \neq i} g_{ij} = B_i$, $g_{ij} \geq 0$ for all $j \neq i$, and $g_{ii} = 0$. The interpretation is that g_{ij} is the amount of time that i spends with j. This is a directed network and these need not be reciprocal.

Each player i has some natural intrinsic base utility $v_i > 0$ that would be his or her payoff in the absence of any network interactions. In addition to that natural utility, the player benefits from other players' payoffs in an amount that depends on the time that is spent with other players times their payoffs. So spending time with a "happier"

player leads to greater utility, all else held equal. However, there is a diminishing return to the time spent with any given other player.

In particular, in Rogers' [537] model, the payoff to player i is

$$u_i = v_i + \sum_{j \neq i} f(g_{ij}) u_j \tag{11.2}$$

where f is a nonnegative and continuously differentiable function such that $f(0) = 0$ and $\lim_{x \to 0} f'(x) = \infty$.

Here payoffs are self-referential, as the payoff to a given player depends on the payoffs to others, which in turn depend on the given player's payoff. This relates back to the sorts of eigenvector-based centrality measures we have discussed earlier, which had a similar self-referential formulation. So, this can also be thought of as an network formation problem in the face of endogenous centrality measures. The last condition on the derivative of f ensures that $g_{ij} > 0$ for all i and $j \neq i$, which makes the model easier to work with.

Letting $f(g)$ denote the $n \times n$ matrix with ij-th entry $f(g_{ij})$, we can write

$$u(g) = v + f(g)u(g),$$

where $u(g)$ and v are $n \times 1$ column vectors. This has the solution

$$u(g) = (I - f(g))^{-1} v = A(g)v,$$

whenever $A(g) = (I - f(g))^{-1}$ is well-defined.

In this setting a natural notion of equilibrium is simply a Nash equilibrium, where each player i is choosing $g_i = (g_{i1}, \ldots, g_{in})$ to maximize $u_i(g)$.

The following is a strengthening of results by Rogers [537].

PROPOSITION **11.7.1** *[Rogers [537]] Suppose that* $\max_i f(B_i)$ *is small enough so that* $A(g) = (I - f(g))^{-1}$ *is well-defined, continuous, and nonnegative for all feasible* g *(and described by* $A(g) = \sum_p f(g)^p$*).*

- *All Nash equilibrium are interior* ($B_i > g_{ij} > 0$ *for all* i *and* $j \neq i$*).*
- *Any best response for a player* i *to a feasible and interior* g_{-i} *(and thus a Nash equilibrium strategy) is such that for each* j *and* h

$$f'(g_{ij}) u_j(g) = f'(g_{ih}) u_h(g). \tag{11.3}$$

- *If for each i and feasible and interior g_{-i} there is a unique g_i that satisfies (11.3), then g is a Nash equilibrium if and only if it is feasible, interior, and satisfies (11.3) for each i, j and h.*

- *If for each i and feasible and interior g_{-i} there is a unique g_i that satisfies (11.3), then the network strategy g_i that maximizes $u_i(g_i, g_{-i})$ given a feasible and interior g_{-i} also maximizes $u_k(g_i, g_{-i})$ given g_{-i} for each k, and so g_i maximizes the total sum of utilities $\sum_j u_j(g_i, g_{-i})$ given g_{-i}.*

Proof of Proposition 11.7.1: First, given that the limit, as x goes to 0, of the derivative of $f(x)$ is infinite, and that $u_j(g) \geq v_j > 0$ for each j, by (11.2) it follows that every Nash equilibrium (and every maximizer of the total sum of utilities) is such that $g_{ij} > 0$ for all i and $j \neq i$.

Consider any player i. Given that A is well-defined, given interior strategies of other players, it follows that regardless of i's strategy, all entries of A are strictly positive.[25]

In order to maximize u_i it must be that $\frac{\partial u_i}{\partial g_{ij}} = \frac{\partial u_i}{\partial g_{ih}}$ for each j and h other than i. For any k we can write

$$u_k = \sum_\ell A_{k\ell}(g) v_\ell.$$

Therefore

$$\frac{\partial u_k}{\partial g_{ij}} = \sum_\ell \frac{\partial A_{kl}(g)}{\partial g_{ij}} v_\ell.$$

To develop an expression for $\frac{\partial A_{kl}(g)}{\partial g_{ij}}$, we follow Rogers [537], who shows that differentiating $AA^{-1} = I$ leads to $\frac{\partial A(g)}{\partial g_{ij}} A(g)^{-1} = -A(g) \frac{\partial A(g)^{-1}}{\partial g_{ij}}$, and so $\frac{\partial A(g)}{\partial g_{\ell k}} = -A(g) \frac{\partial f(g)}{\partial g_{ij}} A(g)$. Therefore,

$$\frac{\partial A_{kl}(g)}{\partial g_{ij}} = f'(g_{ij}) A_{ki}(g) A_{j\ell}(g). \tag{11.4}$$

Substituting from (11.4), it follows that

$$\frac{\partial u_k}{\partial g_{ij}} = \sum_\ell f'(g_{ij}) A_{ki}(g) A_{j\ell}(g) v_\ell = f'(g_{ij}) A_{ki}(g) \sum_\ell A_{j\ell}(g) v_\ell = f'(g_{ij}) A_{ki}(g) u_j(g). \tag{11.5}$$

[25] We can write $A(g) = \sum_p f(g)^p$. Given that $g_{kj} > 0$ for all $k \neq i$ and $j \neq k$, it follows that for any i and j that the ij-th entry of $f(g)^p$ is positive for large enough p. To see this, recall that $f(g)^p$ will be positive if there is a directed walk of length p from i to j. Given that there are at least two other players, there is a path of some length from each other player to every player. Regardless of whom i connects to, i will also reach all other players.

Setting $k = i$ implies that $\frac{\partial u_i}{\partial g_{ij}} = f'(g_{ij})A_{ii}(g)u_j(g)$. This, and the facts that $A_{ii} > 0$ and $u_j(g) \geq v_j > 0$, implies that for every $j \neq i \neq h$:

$$f'(g_{ij})u_j(g) = f'(g_{ih})u_h(g).$$

Given that $A_{ki}(g) > 0$, (11.5) implies that the same condition characterizes the maximization of $u_k(g)$. The claims in the proposition follow directly. ∎

An important implication of the Proposition is that (when best responses are unique) any network that maximizes the total sum of utilities will be a Nash equilibrium network. The choice to maximize a given player's utility is the same choice as a society would make to maximize overall welfare.

What is special about this setting that leads to the congruence between efficiency and stability here, in contrast with the more general conflict between stability and efficiency that we have seen? There are several things which are important, and understanding them helps us to understand this conflict more generally. First, the problem faced by any given player in the Rogers' model is to allocate a given budget of "time" or "effort" on different relationships. Thus, the problem is solely one of allocating the budget across different relationships, rather than deciding on how much or many relationships to have in total. That is, generally we can think of a network formation problem faced by a player as having two main components: the total quantity of effort or relationships to maintain, and how to distribute that across the different relationships. The first part of the problem is missing here and is generally the problematic one. Usually the inefficiency of network formation stems from the fact that a given player does not properly account (with respect to social welfare) for the fact that his or her relationships also generate additional costs or benefits to others beyond his or her own private benefit. So the player either under or over invests in the total amount of relationships relative to what is socially valuable. The decision faced by players in the Rogers' model is solely allocative: Given the fixed budget of weight, how should a player spread it around? Here the player wants to spread it in a way that maximizes his or her payoff, and that would also be the same way that would maximize the indirect payoffs, since in this model indirect payoffs come through a given player's utility. That is, a player gets utility from his or her neighbors' utility, and so whatever makes them happy also makes him or her happy. This points to the second thing which is special about the model. A player gets indirect utility precisely through increases in neighbors' utility. To see how this is special, consider a network that has player 1 connected to both 2 and 3, who are each connected to player 4. In the Rogers model,

the benefits that player 1 obtains from the indirect connection to player 4 come from both the utility that player 2 gets from being connected to 4 (independently of whether 3 is connected) and the value that player 3 gets from being connected to player 4 (independently of whether 2 is connected). In many contexts, it might be the that the marginal benefit to player 1 of having a second indirect path to player 4 is lower than the marginal benefit of having the first path. Finally, there is also symmetry in that all players get the same direct or indirect utility from any given connection, and they do not have any heterogeneity in which connections they would prefer.

While this model has special features, and they are responsible for a congruence between equilibrium networks and efficient networks, the model still provides a nice benchmark in terms of understanding the tradeoffs that players face in deciding how to allocate their time or effort across different relationships. There are many variations on the model that one might consider, including some by Rogers [537], a model by Brueckner [102] where effort translates into the probability that a link forms, and a model by Bloch and Dutta [71] where players do not face a budget constraint.

11.8 Agent-Based Modeling

When modeling network formation (or behavior on networks, or some combination of the two), a difficulty faced is that quite complex networks and/or patterns of behavior can emerge from fairly simple specifications, especially when even minimal sorts of heterogeneity (geography, age, costs, preference types, etc.) are introduced. Although there are many insights that one can derive analytically, there are some things that cannot be seen so directly. In many cases, it is more expedient to examine the behavior of large computer-simulated societies.

Such analyses have become more extensively used in the literature and are often referred to as *agent-based modeling*. These techniques can be very useful for a variety of purposes. As mentioned above, they can be used to analyze systems where equilibrium or dynamics cannot be determined analytically. They can also be used as tools to illustrate systems, or for exploratory analyses that help form hypotheses and conjectures. Such techniques are also useful in empirical analyses, for generating distributions of behaviors that would emerge under a model, which can then be compared to or fitted to observed data.

As with any form of analysis, there are important considerations in terms of how sensitive or robust the conclusions are to the specification. In agent-based modeling

there are also issues of how many simulations to run, how long to run them for, how large a society to consider and so forth. As there are already a number of good sources on this subject, I will not discuss that here.[26]

11.9 Exercises

EXERCISE **11.1** *Nash Stability and Pairwise Stability.*

Provide an example of a society of individuals and utility functions such that the set of Nash stable networks is a strict subset of the set of pairwise stable networks. Provide an example where the reverse is true.

EXERCISE **11.2** *Pairwise Nash Stability*

Provide an example of a society of individuals and utility functions such that the set of pairwise Nash stable networks is a strict subset of the set of pairwise stable networks and also a strict subset of the set of Nash stable networks.

EXERCISE **11.3** *Strict Nash Equilibria in the Link-Announcement Game and Nonexistence*

Consider a potential dyad. Suppose that the payoff to having the link is negative for each player, while the payoff to not having the link is zero for each. Show that there is no strict Nash equilibrium of the link announcement game. Recall that a strict Nash equilibrium is a pure strategy Nash equilibrium where the actions played are the unique best responses to each other.

EXERCISE **11.4** *Strongly Stable Networks and the Connections Model.*

Consider the symmetric connections model (see Section **??**) with $\delta < c$ and $n \geq 4$. Identify a network that is pairwise Nash stable but not strongly stable for some choice of parameters. Find an example of a strongly stable network that is not efficient for a case where $n \geq 5$.

EXERCISE **11.5** *Deviations and Strongly Stable Networks.*

[26] Some starting references on this subject include: Axelrod [21], [22], Bonabeau [**?**], Brately, Fox, and Schrage [97], Epstein and Axtell [**?**], Gilbert and Troitzsch [262], Grimm and Railsback [296], Tesfatsion [592], and Tesfatsion and Judd [593].

The following definition follows one in Dutta and Mutuswami [200]. A network g is *strongly stable** with respect to if for any $S \subset N$ and g' that is obtainable from g via deviations by S, there exists $j \in S$ such that $u_j(g') \leq u_j(g)$.

Find an example of a network that is strongly stable* but not pairwise stable and hence not strongly stable.

EXERCISE **11.6** *Existence of Pairwise Stable Networks.*

Consider any N and profile of utility functions, one for each player. Show that either there exists a pairwise stable network or a closed cycle (as defined in Section **??**).

EXERCISE **11.7** *Improving Paths for Pairwise Nash Stability.*

Develop a definition of "improving path* that allows pairs of agents adding one link, or a single agent deleting multiple links and relate it to the existence of pairwise Nash stable networks. Provide an example where all improving paths* are part of cycles even though there exists a pairwise stable network.

EXERCISE **11.8** *Existence of Pairwise Stable and Pairwise Nash Stable Networks.*

Find an example where payoffs are anonymous,[27] and there exists a pairwise stable network, but there does not exist a pairwise Nash stable network. Does there exist such an example with $n = 3$ and where isolated players get a payoff of 0?

EXERCISE **11.9** *Simultaneous Stability.*

Consider the following variation on strong stability. A network g is *simultaneously stable* if for any $S \subset N$ such that $|S| \leq 2$, g' that is obtainable from g via deviations by S, and $i \in S$ such that $u_i(g') > u_i(g)$, there exists $j \in S$ such that $u_j(g') < u_j(g)$.

Thus, a network is simultaneously stable if no single player strictly prefers to delete some set of his or her links, and no two players would each weakly benefit (with at least one benefiting strictly) by deleting some of their links and/or adding a link between

[27] A profile of utility functions is anonymous if for every π that is a permutation on N (a one-to-one function mapping the set of agents N to N), it follows that $u_{\pi(i)}(g^\pi) = u_i(g)$, where $g^\pi = \{\{\pi(i), \pi(j)\} | ij \in g\}$ is the network obtained from g by permuting the positions of agents according to π.

them. This is a stronger requirement than Pairwise Nash stability, but weaker than strong stability because only coalitions of two players are considered.

Consider a setting where players come with "types" in some finite set Θ, and let player i's type be denoted θ_i. Suppose that payoffs are as follows. Let $s_i(g)$ be the number of players of i's same type to whom i is linked (so $\theta_i = \theta_j$ and $ij \in g$), and $o_i(g)$ be the number of players of types other than i's type whom i is linked to. Suppose that payoffs are as follows

- $u_i(g) = o_i(g) + 2s_i(g)$ if $o_i(g) + s_i(g) \leq d_i$, and
- $u_i(g) = 0$ if $o_i(g) + s_i(g) > d_i$,

where $d_i \geq 1$ is a capacity of links that i can maintain. So, players benefit more from links to their own types.

Show that the pairwise Nash networks are those such that: (i) no player exceeds his or her capacity and (ii) there is at most one player with fewer links than his or her capacity. Characterize the set of simultaneously stable networks. Show that if there are at least two players who have the same type, then the set of simultaneous stable networks is a strict subset of the set of pairwise Nash networks.

EXERCISE **11.10** *Ordinal Potential Functions and the Absence of Indifference*

Provide an example where the payoffs exhibit indifference and there are no improving cycles, but there does not exist an ordinal potential function (3 players will suffice).

EXERCISE **11.11** *An Ordinal Potential Function for a Buyer-Seller Network.*

Consider the Corominas-Bosch model from Section **??**. Show that the sum of all payoffs is an ordinal potential function.

EXERCISE **11.12** *Existence of Strongly Stable Networks and Top Convexity.*

Payoffs are *top-convex* if $\max_{g \in G(N)} \frac{\sum_{i \in N} u_i(g)}{|N|} \geq \max_{g \in G(S)} \frac{\sum_{i \in S} u_i(g)}{|S|}$ for all $S \subset N$.[28]

Suppose that payoffs are component decomposable and are such that any two players in the same component get the same payoff. Show that the set of strongly stable networks is nonempty if and only if payoffs are top-convex.

[28] This definition and result are due to Jackson and van den Nouweland [338].

Show that if we reallocate utility so that players within a component get an equal split of the total utility within a component, then payoffs in the symmetric connections model are top-convex.

EXERCISE **11.13** *Proof of Proposition 11.3.2 - Directed Nash Stable Networks in a Distance-Based Model.*

Prove Proposition 11.3.2.

EXERCISE **11.14** *A Stochastically Stable Network that is not Pairwise Nash Stable.*

Provide an example of a stochastically stable network that is pairwise stable but not pairwise Nash stable. Describe a variation on the random process that would instead select from Pairwise Nash Stable networks.

EXERCISE **11.15** *Proof of Proposition* **??**.

Prove Proposition **??**.

EXERCISE **11.16** *Complementarities in Link Efforts with Convexities.*

Consider the following variation of a model by Bloch and Dutta [71].

Each agent has a unit of effort to allocate on different relationships. In particular, agent i chooses a vector of efforts, where $x_{ij} \in [0,1]$ is the effort that i invests on a relationship with agent j and where $\sum_{j \neq i} x_{ij} = 1$. The "strength" of overall relation between i and j is then $s_{ij} = \phi(x_{ij}) + \phi(x_{ji})$, where ϕ is an increasing function.

The payoff to i as a function of s (the matrix of s_{ij}'s) is $u_i(s) = \sum_{k \neq i} v_{ik}(s)$ where $v_{ik}(s)$ is determined as follows. Let P_{ik} be the set of the potential paths between i and k that could occur in any network. For a path $p = i_1 i_2, i_2 i_3, \ldots, i_{m-1} i_m$ let $v(p,s) = s_{i_1 i_2} \times s_{i_2 i_3} \times \cdots \times s_{i_{m-1} i_m}$. Then $v_{ik} = \max_{p \in P_{ik}} v(p,s)$.

Show that if ϕ is a strictly convex function then any Nash equilibrium choice of x_{ij}'s is such that, for each i, $x_{ij} = 1$ for some j and $x_{ik} = 0$ for all $k \neq j$. What are the equilibrium configurations for a three agent system when ϕ is strictly convex?

EXERCISE **11.17** *Schelling's Tipping and Segregation Models: An Agent-Based Computation Exercise.*

Consider the following simple model of segregation due to Schelling [549], [550]. A finite set of agents live on a line segment.[29] Agents are either red or blue. Agents have preferences over their neighborhoods: an agent prefers to be in a neighborhood where at least half of his or her neighbors are of the same color. Other than this agents have no further preference. An agent considers his or her neighborhood to consist of the k nearest agents to his left plus the k nearest agents to his right. (For agents near the end of the segment, simply wrap the segment around to form a circle when defining closest neighbors.) At any point in time each agent can be labeled as either "content" or "discontent," depending on whether at least fifty percent of their neighbors are of their color.

Schelling describes the following algorithm

- Start with n agents randomly positioned on a line segment (without any two agents at the same point) and with their colors randomly assigned with independent and equal probability of red or blue.
- Identify the "discontent" agents and label this set $D(0)$.
- Starting with the leftmost "discontent" agent, move that agent to a point where the agent is content, and do so in a manner so that the agent needs to leapfrog the fewest other agents (and break ties by moving to the left).
- Next, if the second agent who was discontent is now content (due to the change induced by the first intially discontent agent's move) then leave that secon initially discontent agent in place. Otherwise, move that agent to a point where he or she will be content (again leapfrogging as few agents as possible and moving to the left in the case of a tie).
- Iterate on this process until all of the agents in $D(0)$ have been considered.
- Now begin the whole process over again, identifying a new set of discontent agents $D(1)$, and moving discontent agents as described above.
- Iterate on this process until all agents are content.

Write a program to run this algorithm when $k = 4$ and $n = 100$. Run this program 100 times. For each run, record how many changes in color there are as one moves

[29] There are two dimensional versions of the model, which are known as "Schelling's Checkerboard Model".

along the segment from left to right at the starting configuration and at the ending configuration. This gives an idea of how many different segmented groups of agents of the same color there are on the line. Also record the average fraction of neighbors of the same color at both the starting and ending configurations.

Chapter 12

Allocation Rules, Networks, and Cooperative Games

Throughout this book we have seen different sorts of predictions of how powerful or central different agents are, as well as how influential they are, what terms of trade they might get in an exchange, and what utility they might end up with in a game played on a network. These predictions were derived using a variety of tools, ranging from specific measures of power and centrality to models of the spread of information, bargaining on networks, or strategic interaction on a network. Beyond these tools that are directed at specific applications, there is a more general perspective that builds on properties of how the aggregate payoff behaves as a function of the network and then deduces allocations of payoffs from those properties. It is an offshoot of cooperative game theory, which examines how productive value is split among the members of a society based on the relative contributions of different coalitions of players. This approach has both normative (how the total payoff should be split) and positive (how value is split) sides to it.

In this chapter I examine how tools of cooperative game theory have been extended and adapted to network settings. I begin with a brief background discussion of cooperative game theory and then turn to the extension of various methods and concepts to network settings. As we shall see, the concepts provide a nice basis for making predictions about the outcomes of multilateral bargaining on networks, as well as more generally for analyzing the power or influence of various players in a network. We will also see that there are different ways to extend and adapt cooperative tools to network settings, and that what is the "right" extension will depend the context.

12.1 Cooperative Game Theory

Cooperative game theory starts with a society of players just as a network setting does, but instead of thinking of how the players might be structured in terms of social networks, the foundation is built on simpler structures. In particular, the primitives are how the players might be grouped into subsets or "coalitions".

There are several branches of the theory and an important distinction is made between "transferable utility" and "non-transferable utility (NTU)" games. In transferable utility games payoffs can be freely reallocated among players (so that payoffs are transferable), while in non-transferable utility games the payoffs can only come in given configurations. While both of these branches have natural cousins in the network setting, I focus on the more developed branch of transferable utility.[1]

Cooperative game theory provides a prediction (or prescription, depending on the interpretation) of how the total value generated in a society will (or should) be split among its members. It takes into account the relative values that every possible subset of players could generate, and then based on certain properties of how the allocation of value reacts (or should react) to these values. One interpretation is that the resulting allocation is a prediction of what the outcome will be if the players bargain over how to allocate the total value generated in the society, and when the values of various coalitions of players represent threat points of what they can earn by seceding from the society. As multilateral bargaining is difficult to model non-cooperatively, cooperative techniques can be quite useful in this regard. Another interpretation is that the resulting allocation is how a society should allocate its value, based on some principles.

[1] The terminology of "cooperative" and "non-cooperative games is perhaps no longer as useful as it was when first defined. The idea of a cooperative game began as an offshoot of a non-cooperative game. The value that could be generated by a group of players was what they could guarantee themselves by coordinating their strategies in the non-cooperative game. (See Luce and Raiffa [**?**] for a nice overview of these ideas.) That is, the value of a given coalition of players was derived by looking at the maximum value (in terms of the sum of their payoffs) that they could get across their choices of strategies when the remaining players react by collectively choosing their strategies minimize the coalition's payoff. The idea of a value of a group of agents extends far beyond the original cooperation in a non-cooperative game derivation, and so the terminology is no longer so pertinent. Also, in many applications there is a well-defined value generated by a group of agents without requiring them to "cooperate," especially when the theory is applied normatively. Nevertheless, the terminology remains from its historic roots.

12.1.1 Transferable Utility (TU) Cooperative Games

The society of players is denoted $N = \{1, \ldots, n\}$.

The productive values of different coalitions are are captured via a *characteristic function*, $w : 2^N \to I\!R$, where the value of a coalition $S \subset N$ is denoted $w(S)$. Let us normalize a characteristic function so that $w(\emptyset) = 0$.

Together (N, w) are referred to as a *transferable utility game* or a *TU game*. The set of all such games on a society N is denoted $W(N)$.

The term "transferable utility" refers to the idea that the value of a coalition can be transferred its members.

It helps to keep a few examples in mind.

EXAMPLE **12.1.1** *Divide the Dollar.*

Consider a legislature that operates by majority rule and has a budget to split among its members. Normalize the value of the budget to 1. A proposal of how to split the budget can be passed if it receives the votes of a majority of the legislature's members. Thus, any coalition of at least $\frac{n}{2}$ members, and only such coalitions, can generate a value of 1.

This is represented by a TU game such that $w(S) = 1$ if $|S| \geq \frac{n}{2}$ and $w(S) = 0$ otherwise.

EXAMPLE **12.1.2** *Simple Games.*

The divide-the-dollar game is an example of a more general class of games such that there are "winning" coalitions that can generate a value of 1. The divide the dollar setting is one where those coalitions are ones that contain a majority of the players. More generally, one can consider other possible rules for which coalitions can generate value.

A *simple game* is a TU game such that

- $w(S) \in \{0, 1\}$,
- $w(S) = 1$ and $S \subset S'$ implies that $w(S') = 1$,
- $w(N) = 1$,
- $w(S) = 1$ implies that $w(N \setminus S) = 0$.

Thus, a simple game specifies which coalitions generate a value of 1, is such that larger coalitions are at least as powerful as smaller coalitions, and is such that there cannot exist disjoint coalitions that each generate a value of 1 at the same time.

EXAMPLE **12.1.3** *A Quota Game with Veto Players.*

Another class of interesting TU games is a subset of the simple games where a specific player is needed in order to generate value. That is, a coalition is worthless unless it contains some specific player.

Let there be a quota $q \geq \frac{n}{2}$ and a set of veto players $C \subset N$ such that $w(S) = 1$ if and only if $|S| \geq q$ and $C \subset S$.

Thus, a coalition generates a value of 1 if and only if it meets the size quota and all of the veto players are included. An example of such a setting is the United Nations security council which has fifteen members and five veto players (the five permanent members: China, France, Russia, the U.S.A., and the U.K.). A resolution passes only if it receives "yes" votes of at least two thirds of its members and none of the five veto players vote "no".[2]

12.1.2 Allocating the Value

The values of different coalitions form the foundation for the analysis of a cooperative game, as they tell us the value there is to be split among the players and also the extent to which different groups of players are responsible for the generation of the value. The heart of the analysis is then how the value of the society is (or should be) allocated among its members. This is captured by an imputation.

An *imputation* is a function $\phi : W(N) \to I\!R^n$ such that $\sum_i \phi_i(w) = w(N)$.

An imputation thus indicates how much of the value generated by the full society is allocated to each player. Generally it is presumed that the grand coalition of the full society generates the maximum possible value.[3]

[2] The actual rules of the U.N. Security Council are a bit more complicated than a simple game as countries are allowed to abstain, and they sometimes do. In addition, different voting rules are used depending on the issue involved, but the basic structure is built on a quota game with veto players.

[3] There is a specification that examines more general settings where the value generated depends on how a society is partitioned and such that it might be efficient to have partitions other than the one where all players are grouped together. Such games are called games in partition function form, and can also be seen as special cases of the network setting discussed below.

An imputation can model different things. It might capture the result of a bargaining process or it might be a normative analysis of how the value should be allocated. It might also be a measure of the relative power of different members of the society.

A prominent imputation rule is the Shapley Value, introduced by Shapley [**?**]. It has a number of interesting properties, and can be seen as being based on the relative marginal contributions of players towards productive value.

12.1.3 The Shapley Value

The Shapley Value is an imputation defined by

$$\phi_i^{SV}(w) = \sum_{S \subset N \setminus \{i\}} (w(S \cup \{i\}) - w(S)) \left(\frac{\#S!(n - \#S - 1)!}{n!} \right).$$

A standard interpretation of the Shapley Value is as follows. Uniformly at random, choose an ordering of the players and let it be $\{i_1, i_2, \ldots, i_n\}$. Now, consider building the society up by adding one player at a time in this order. A player gets the marginal contribution that he or she makes to the society when added to the players who preceded him or her. So, a player i whose place in the order follows a coalition S gets $w(S \cup \{i\}) - w(S)$. There are $\#S!(n - \#S - 1)!$ such orderings, and averaging over all such orderings leads to the Shapley value.

In the divide-the-dollar game the Shapley Value allocates $1/n$ to each player given the full symmetry of the game. This is true of most any imputation. If instead we examine a simple majority game with a single veto player, then we see asymmetries and begin to get an impression of how the Shapley value operates.

EXAMPLE **12.1.4** *A Majority Game with One Veto Player.*

Consider a quota game with an three players and a single veto player, player 1. In particular suppose that $w(S) = 1$ if $|S| \geq 2$ and $1 \in S$, and otherwise $w(S) = 0$.

The Shapley value of this game can be calculated as follows. There are 6 possible orderings of the players: (1,2,3), (1,3,2), etc. Player 1 contributes a marginal value of 1 in 4 of these 6 possible orderings (whenever 1 is not the first player included). The other two players each contribute a marginal value of 1 in just 1 of the 6 possible orderings (the ordering where player 1 comes first and he or she comes second). Thus, the Shapley Value of this game is

$$\phi^{SV}(w) = \left(\frac{2}{3}, \frac{1}{6}, \frac{1}{6} \right).$$

Player 1 gets a larger value than the other two players because of the asymmetric roles in this game. Players 2 and 3 get some value due to the fact that they do contribute productive value in that player 1 cannot generate any value without at least one of them.

12.1.4 The Core

Instead of having an imputation, such as the Shapley Value, which makes a unique prediction for each cooperative game, we might instead make a set of predictions based on some principles. The most prominent such predictions are based on the "core." The idea is that the allocation of the value of the whole society must be such that no coalition could secede and improve each member's payoff by allocating the value it generates alone to its members.

The *core* of a TU cooperative game is the set of all allocations $x \in I\!R^n$ such that

- $\sum_{i \in N} x_i = w(N)$, and
- $\sum_{i \in S} x_i \geq w(S)$ for all $S \subset N$.

When the core is nonempty, it makes powerful predictions, as an allocation in the core cannot be blocked by any coalition.

The core is sometimes empty as seen, for instance, in the divide-the-dollar game as follows. Consider any allocation x such that $\sum_{i \in N} x_i = w(N)$. There must exist i such that $x_i > 0$. Thus, it must be that $\sum_{j \neq i} x_j < 1$, while $w(\{j : j \neq i\}) = 1$. Thus, this cannot satisfy the second requirement in the definition of the core, as the coalition of players other than i are not getting the value that they would obtain by excluding player i. The core of this game is empty.

This shows the inherent instability of majority rule, and also previews the difference between predictions made based on an imputation rule such as the Shapley Value which in the divide-the-dollar game gives an equal allocation to each player, and the core. To see further differences, let us re-examine a game with a veto player.

EXAMPLE **12.1.5** *The Core in a Majority Game with One Veto Player.*

Reconsider the quota game from Example 12.1.4 with three players and a single veto player, player 1, and recall that the allocation under the Shapley Value was $\phi^{SV}(w) = \left(\frac{2}{3}, \frac{1}{6}, \frac{1}{6}\right)$.

The core in this game consists of a single allocation: (1,0,0). To see this, note that a core allocation must satisfy $x_1 + x_2 \geq 1$, $x_1 + x_3 \geq 1$, $\sum_i x_i = 1$, and $x_i \geq 0$ (given that $w(\{i\}) = 0$) for each i.

This example shows us that the core and Shapley Value are capturing different things. The Shapley value is not necessarily in the core. The core is built on ensuring that no coalition could block the allocation with a better allocation for its members, while the Shapley Value is derived from calculations on relative contributions.

The Shapley Value always lies in the core in some cases, including a subclass of games called convex games. Thus, that class of games is such that the core is nonempty.

A TU game w is *convex* if

$$w(S \cup \{i\}) - w(S) \leq w(S' \cup \{i\}) - w(S'),$$

whenever $S \subset S'$ and $i \notin S'$.

The convexity here refers to the fact that the marginal contribution of a player (weakly) increases as the size of the coalition he or she is added to is increased. If the value of a coalition only depends on the number of members it has, then this requires that that value be a convex function of the number of players. In such games, the grand coalition generates enough value to allocate in a way such that each coalition is getting at least its value, and so the core is nonempty, and, in fact, contains the Shapley value.

PROPOSITION **12.1.1** *If a TU game is convex, then the Shapley Value of the game is in the core of the game.*

The proof is relatively straightforward and the subject of Exercise 12.1.

With a brief introduction to cooperative game theory in hand,[4] let us now begin to bring network structures into play.

12.2 Communication Games

Myerson [473] introduced an interesting subclass of cooperative games that are called communication games.[5]

[4]For a bit more background on cooperative game theory see Myerson [474] and Osborne and Rubinstein [489].

[5]Myerson referred to the network as a "cooperation structure" and such games are also referred to as games with cooperation structures.

Figure 12.2. *A Communication Network*

Given a network (N, g), recall that $g|_S$ is the subnetwork of g restricted to the nodes in $S \subset N$ and $\Pi(g|_S)$ is the partition of S generated by the components of g restricted to S (as defined in Section **??**).

Myerson's definition begins with a convex TU cooperative game $(N, w) \in W(N)$, and augments this by a network $g \in G(N)$ that describes who can communicate with whom.

The *communication game* (N, w, g) induces a cooperative game $(N, \widehat{w}_g)$ such that

$$\widehat{w}_g(S) = \sum_{C \in \Pi(g|_S)} w(C).$$

The idea is that coalitions can only function to the extent that they can communicate. To see how this works, consider the network pictured in Figure 12.2.

Here, the coalition $\{1, 4, 5\}$ can function because the players are path-connected to each other, each lying in the same component, and thus $\widehat{w}_g(\{1, 4, 5\}) = w(\{1, 4, 5\})$.

In contrast, the coalition $\{1, 3, 4\}$ can only partially function and

$$\widehat{w}_g(\{1, 3, 4\}) = w(\{1\}) + w(\{3, 4\}) = w(\{3, 4\}).$$

Here, even though 1, 3, and 4, are path-connected in g, player 1 cannot communicate with 3 or 4 without 5 being present.

The value of coalition $\{1, 2, 6, 7\}$ is 0, since they cannot communicate at all in g.

12.2.1 The Myerson Value

The Shapley value has a natural extension to communication games.[6]

Myerson [473] defined an allocation rule for a communication game (N, w, g), namely

$$\psi^{MV}(w, g) = \phi^{SV}(\widehat{w}_g)$$

Although one can view a communication game as a specific form of a cooperative game (basically, the induced $(N, \widehat{w}_g)$), it also works the other way around. In the case where g is the complete network, a communication game reduces to a cooperative game in that $\widehat{w}_g = w$. Moreover, as one varies the network structure, one can see how the allocation of value varies. That is, as the network structure is varied, $\widehat{w}_g$ varies and so does the allocation, even though the underlying cooperative game remains fixed.

To see this, consider the divide the dollar game with three players. In that case th Shapley value allocates 1/3 to each player. That would be the allocation under the Myerson value if g is the complete network. However, if instead the network had only one link, then the two agents involved in the link would each get a value of 1/2. The most interesting case occurs when there is a two-link game. This now looks like a cooperative game where the middle player is a veto player, since without that player a coalition cannot function. Thus, the middle player gets 2/3 of the value, while the end players each get 1/6. This is pictured in Figure 12.2.1

While the communication games introduced by Myerson [473] bring networks into the context of cooperative game theory, they stop short of allowing one to fully analyze the allocation of the values in network settings. The difficulty lies in the fact that the actual value that a society generates is still based on a characteristic function, and it is mainly the allocation of value that is affected by the network structure, rather than the overall productive possibilities. To see the issue, consider a society of $N = \{1, 2, 3\}$, and any underlying cooperative game. A network of two links, say $g = \{12, 23\}$, and the complete network, $g' = \{12, 23, 13\}$, both lead to the same overall productive value in a communication game since they allow all three agents to communicate. While the Myerson Value allocates value differently to the players in the game, it still requires that both networks have the same value to allocate. In most any productive situation,

[6] For more of an overview of the literature on communication games and other allocation rules see Slikker and van den Nouweland [**?**].

Figure 12.2.1. *The Myerson Value in a Communication Game: a 3-Player Divide-the-Dollar Game.*

including the structure of a firm or any sort of organization, links involve some costs and, more generally, network structure will affect productivity. Dealing with this issue requires a richer setting where the productive value is not based on a cooperative game, but is instead directly dependent on the network in place, as discussed next.

12.3 Networks and Allocation Rules

Jackson and Wolinsky [343] proposed a richer model than that of communication games, where the value that a society generates depends explicitly and directly on the network structure. This has as special cases both cooperative games and communication games, but uses networks as the primitive. It is described as follows.

Throughout, let a society N be given.

12.3.1 Value Functions

The productive value of a society is now determined directly by the network structure, and is captured via a value function.

A *value function* is a function $v : G(N) \to I\!R$.

Let us normalize the value of the empty network to be zero, so that $v(\emptyset) = 0$.

The set of all possible value functions for a society N is denoted $\mathcal{V}(N)$.

Note that any profile of utility functions $u = (u_1, \ldots, u_n)$ generates a value function defined by $v(g) = \sum_i u_i(g)$. Thus, the utility-based models of network formation that we have discussed, such as the connections model, distance-based utility models, the co-author model, and so forth, give rise to distinct value functions.

A prominent class of value functions is the set of component additive ones.

A value function v is *component additive* if $\sum_{h \in C(g)} v(h) = v(g)$.

Component additivity is a condition that rules out externalities across components, but still allows externalities within components. That is, the value of a given component does not depend on how other components are structured. It is quite natural in some contexts, for instance social interactions, but not in situations where different components interact with each other. If the value function is derived as the sum of a component decomposable profile of utility functions, then it will clearly be component additive.

Another prominent subclass of value functions is the set of anonymous ones.

Given a permutation of players π (a bijection from N to N) and any $g \in G(N)$, let $g^\pi = \{\{\pi(i), \pi(j)\} | ij \in g\}$.

Thus, g^π is a network that shares the same architecture as g but with the players relabeled according to π.

A value function is *anonymous* if $v(g^\pi) = v(g)$ for any permutation of the set of players π.

Anonymity says that the value of a network depends only on the structure of the network and not the labels of the players who occupy various positions. It requires that the critical productive determinant be social structure, and abstracts away from personal productive differences between individuals.

12.3.2 Allocation Rules

The analog of an imputation in the network setting is an allocation rule. It is a richer object because it not only depends on the value function, but also on the network structure that is in place.

An *allocation rule* is a function $Y : G(N) \times \mathcal{V}(N) \to I\!R^n$ such that $\sum_i Y_i(g, v) = v(g)$ for all v and g.

The definition of an allocation rule has a balance condition, $\sum_i Y_i(g,v) = v(g)$, built into it.

The idea of an allocation rule is to analyze how the total productive value or utility of a society ends up being allocated. It is the analog of an imputation, but now in the context of a network setting instead of a cooperative game. In many of the previous chapters, a profile of utility functions was taken as given. However, bargaining might occur about the terms of trade, or even about favors within a friendship or an allocation of chores. It could also be that there are taxes or subsidies imposed. An allocation rule keeps track of how the total value ends up being allocated after such a process.

An allocation rule depends on both g and v. This is important as it can then take account of a player i's role in productive value beyond the specific network in place. For instance, consider a network $g = \{12, 23\}$ in a situation where the value generated is 1 ($v(g) = 1$). Player 2's allocation might depend heavily on the values of other networks. For instance, if $v(\{12, 23, 13\}) = 0 = v(\{13\})$, then 2 is essential to the network and may receive a large allocation. If, on the other hand $v(g') = 1$ for all networks, then 2's role is not particularly special. This information can be relevant, especially in bargaining situations, which is why the allocation rule is allowed to depend on it.

12.3.3 Some Properties of Allocation Rules

There are some properties of allocation rules that are useful in studying extensions of the Shapley Value and Myerson Value to the network setting.

An allocation rule Y is *component balanced* if $\sum_{i \in S} Y_i(g,v) = v(g|_S)$ for each component additive v, $g \in G$, and $S \in \Pi(g)$.

Component balance requires that the value of a component of a network be allocated to the members of that component in cases where the value of the component is independent of how other components are organized. This would tend to arise naturally. It also is a condition that an intervening government would like to respect if it wishes to avoid secession by components of the network.

Given a permutation $\pi : N \to N$, let v^π be defined by $v^\pi(g) = v(g^{\pi^{-1}})$ for each $g \in G$ (recalling the definition of g^π from Section **??**). This is just value function obtained when agents' names are relabeled through π.

An allocation rule Y is *anonymous* if for any $v \in \mathcal{V}$, $g \in G$, and permutation of the set of players π, $Y_{\pi(i)}(g^\pi, v^\pi) = Y_i(g,v)$.

Anonymity of an allocation rule requires that if players are relabeled, then the allocation change accordingly.

12.3.4 Egalitarian Allocation Rules

An egalitarian allocation rule spreads value equitably among the members of a society. This can be done in different ways. One can simply spread value completely equally, or one might instead spread value the value of a component back to the members of that component.

The *egalitarian allocation rule* Y^e is defined by $Y_i^e(g,v) = \frac{v(g)}{n}$.

The egalitarian allocation rule has nice properties. Any efficient network will be pairwise (Nash) stable, and in fact strongly stable, if payoffs are given by the egalitarian rule since it maximizes the payoffs of all players. Moreover, there are no improving cycles, as we can see by setting $f(g) = \frac{v(g)}{n}$ and applying Proposition 11.2.1.

Despite these virtues, the egalitarian rule fails to satisfy component balance in component additive settings where not all components generate the same value. That is, there are many situations where it will makes transfers across components even though there are no externalities across the components. While this might be attractive from a normative perspective, it not as natural from a positive perspective (for instance, as the prediction of the outcome of a bargaining process), especially when the value function is component additive. Moreover, it can fail a basic stability property, as it could give incentives for components to secede, as they might end up being taxed as a whole. A natural variation on the egalitarian rule only equalizes allocations within components.

The *component-wise egalitarian allocation rule*, denoted Y^{ce}, is defined as follows. For a component additive v and network g, Y^{ce} is such that for any $h \in C(g)$ and each $i \in N(h)$

$$Y_i^{ce}(g,v) = \frac{v(h)}{\#N(h)}.$$

For a value function v that is not component additive, $Y^{ce}(g,v) = Y^e(g,v)$ for all g.

The component-wise egalitarian allocation rule only differs from the egalitarian rule in situations where it is clear that one can attribute a value to each component separately from the organization of the rest of the network; that is, in the situation of component additive value functions. Otherwise, there is no obvious value to attribute to a component, and then this allocation rule coincides with the egalitarian rule.

While the component-wise egalitarian rule is not quite as nice as the egalitarian rule in terms of all efficient networks being pairwise Nash stable and strongly stable, it still has some nice stability properties. For instance, when payoffs are given by the component-wise egalitarian allocation rule, there always exists a pairwise (Nash) stable

network, and one can be found by a simple algorithm as outlined by Jackson [?] for the case of a component additive v (as otherwise it is the same as the egalitarian rule).

- Find a component h that maximizes the payoff $Y_i^{ce}(h, v)$ over i and h, and if there is more than one such component then choose the one that has the most agents.

- Follow the same policy on the remaining population $N \setminus N(h)$, and iterate.

The collection of resulting components forms the network.[7] While this identifies a pairwise Nash stable network, it does not always find a strongly stable network, but it does always find networks that are nearly strongly stable (see Exercise 12.7).

In many contexts the component-wise egalitarian allocation rule is such that efficient networks are pairwise stable (see Exercise 12.9).

Beyond egalitarian type allocation rules, there are allocation rules based on very different approach, namely Shapley value-style marginal contribution calculations.

12.3.5 The Myerson Value in Network Settings

The Shapley and Myerson Values have a natural extension to the context of networks, as shown by Jackson and Wolinsky [343]. That allocation rule is expressed as follows.

$$Y_i^{MV}(g, v) = \sum_{S \subset N \setminus \{i\}} (v(g|_{S \cup i}) - v(g|_S)) \left(\frac{\#S!(n - \#S - 1)!}{n!} \right).$$

The Myerson Value in this full network setting again allocates value using Shapley Value-style calculations, now based on how the value changes as the players comprising the network are changed.

The Myerson Value has some nice properties that distinguish it from other rules, as I now discuss.

[7] This follows a argument similar to one used by Banerjee, Konishi and Sönmez [?] to establish existence of core-stable coalition structures in a class of coalition formation games called "hedonic games."

12.3.6 Equal Bargaining Power, Fairness, and the Myerson Value

An allocation rule satisfies *equal bargaining power* if for any component additive v and $g \in G(N)$

$$Y_i(g,v) - Y_i(g-ij,v) = Y_j(g,v) - Y_j(g-ij,v),$$

for any link ij.

Equal bargaining power is a variation on a condition called "fairness" by Myerson. The fairness name can be thought of as viewing the property from a normative perspective, while the equal bargaining name looks at the property from a more positive viewpoint. Note that equal bargaining power does *not* require that players split the marginal value of a link. It just requires that they equally benefit or suffer from its addition. It is possible (and generally the case) that $Y_i(g,v)-Y_i(g-ij,v)+Y_j(g,v)-Y_j(g-ij,v) \neq v(g)-v(g-ij)$, so that the marginal value of a link is not allocated only to the two involved players.

At first sight, equal bargaining power seems like a natural condition. Why shouldn't two players involved in a relationship each gain or suffer equally from the addition of that relationship? (There will be an answer given to this shortly.) The is a powerful condition that is not satisfied by many rules including egalitarian-style rules. In fact, equal bargaining power in conjunction with component balance uniquely ties down the allocation rule. The following proposition from Jackson and Wolinsky [343] is a direct extension of Myerson's [473] result from the communication game setting to the network setting.

PROPOSITION **12.3.1** *[Myerson [473], Jackson and Wolinsky [343]] Y satisfies component balance and equal bargaining power if and only if $Y(g,v) = Y^{MV}(g,v)$ for all $g \in G$ and any component additive v.*

The proof follows the logic of Myerson's proof, but adapted to a network setting. One can show that there is a unique rule that satisfies equal bargaining power and component balance when v is component additive, and that the Myerson value satisfies these conditions.

Without providing the proof here, let me illustrate the ideas behind why these two properties uniquely tie down the allocation. Start by considering a one link component. In that case, if the link were deleted, both players would get a 0 payoff (by component

balance) and the "normalization" that isolated nodes generate value 0.[8] Equal bargaining power then implies that the players get the same allocation, and component balance requires that the two players split the entire value of a single link, and so

$$Y_i(\{ij\}, v) = Y_j(\{ij\}, v) = \frac{v(\{ij\})}{2}.$$

Next, consider a two link component $h = \{ij, jk\}$. Component balance requires that

$$Y_i(h, v) + Y_j(h, v) + Y_k(h, v) = v(h). \tag{12.1}$$

Equal bargaining power requires that

$$Y_i(h, v) - Y_i(\{jk\}, v) = Y_j(h, v) - Y_j(\{jk\}, v),$$

and by component balance $Y_i(\{jk\}, v) = 0$, and so this implies that

$$Y_i(h, v) = Y_j(h, v) - \frac{v(\{jk\})}{2}. \tag{12.2}$$

Similarly,

$$Y_k(h, v) = Y_j(h, v) - \frac{v(\{ij\})}{2}. \tag{12.3}$$

Then from (12.1), (12.2), and (12.3) it follows that

$$3Y_j(h, v) - \frac{v(\{ij\})}{2} - \frac{v(\{jk\})}{2} = v(h),$$

or

$$Y_j(h, v) = \frac{v(h)}{3} + \frac{v(\{ij\})}{6} + \frac{v(\{jk\})}{6}.$$

Then (12.2) and (12.3) imply that

$$Y_i(h, v) = \frac{v(h)}{3} + \frac{v(\{ij\})}{6} - \frac{v(\{jk\})}{3},$$

and

$$Y_k(h, v) = \frac{v(h)}{3} - \frac{v(\{ij\})}{3} + \frac{v(\{jk\})}{6}.$$

These three expressions provide the Myerson Value for a component of the form $h = \{ij, jk\}$.

We see that the allocation for one and two link networks are unique under component balance and equal bargaining power. The idea is that we can derive the two

[8] This is implied by $v() = 0$ and component balance. We now see that this is more than a normalization, as it requires that all players generate the same value when isolated.

link network from two different one link networks, and so we have two different conditions tying down the allocation. Together with component balance, we then have three conditions tying down three allocations. As we continue to examine larger and larger components, an iterative logic can be used to determine the allocation uniquely at each step. The proof shows that there is at most one rule satisfying these conditions and so builds on this logic, but it does not work by explicitly deriving the allocation as in the exposition above.

There are also weighted versions of the Shapley and Myerson values, where the bargaining power is not equal but instead involves asymmetries among the players and some players receive systematically larger shares than other agents. Dutta and Mutuswami [200] extend the characterization to allow for weighted bargaining power and show that one obtains a version of a weighted Shapley (Myerson) Value.

12.3.7 Pairwise Stable Networks under the Myerson Value

A nice feature of the Myerson value is that pairwise stable networks always exist under it. In fact, the Myerson Value has an ordinal potential function, which then allows us to apply Proposition 11.2.1 to conclude that there are no improving cycles and that pairwise stable networks exist.

PROPOSITION **12.3.2** *[Jackson [?]] There exists a pairwise stable network relative to the Myerson Value allocation rule Y^{MV} for every value function v. Moreover, following improving paths relative to the Myerson value and any value function, and starting from any network, eventually leads to a pairwise stable network, and there are no improving cycles under the Myerson Value.*

Proof of Proposition 12.3.2: This is a corollary to Proposition 11.2.1. Let

$$f(g) = \sum_{S \subset N} v(g|_S) \left(\frac{(\#S-1)!(n-\#S)!}{n!} \right).$$

Then $Y_i^{MV}(g,v) - Y_i^{MV}(g-ij,v) = f(g) - f(g-ij)$, and so f is an ordinal potential function as required in Proposition 11.2.1. ∎

Although the Myerson Value leads to nice stability properties in terms of the existence of pairwise stable networks and the absence of cycles, it does not guarantee that the stable networks are even Pareto efficient. In fact, it can lead to systematic over-connection. This is illustrated by the following example and detailed in Exercise 12.6.

Figure 12.3.7. *Over-Connection and Pareto Inefficiency of Pairwise Nash Stable Networks under the Myerson Value: Dyads have Value 6 and Other Nonempty Components have Value 10.*

In Figure 12.3.7, we see the incentives for players to over-connect under the Myerson Value. In this example a dyad generates a value of 6 and any other nonempty component generates a value of 10. It is easy to check that the unique pairwise stable network is the complete network (which is verified via the improving paths pictured in the figure and a few that are not pictured), but this network is Pareto dominated by the efficient network. The reason for the inefficiency is that by having more links, there are more orderings under which a given player is important in contributing to the network. Thus, a player wishes to have more connections as they lead to increased bargaining power (as reflected in the Shapley value calculations).

12.4 Allocations Rules when Networks are Formed

If the network is something which can be formed at the players' discretion,[9] then one can argue that the Myerson Value it is correct neither from a normative standpoint, nor a positive standpoint, especially if the allocation rule is partly determined by the bargaining of players during the formation process. In particular, values of all networks, and not just sub-networks, should play some role in determining the allocation, as they are all viable alternatives. The Myerson Value takes into account subnetworks of a given network when calculating its value, but not other networks. To get a better feeling for this, let us examine some examples from Jackson [331].

EXAMPLE **12.4.1** *A Criticism of the Myerson Value*

There is a three person society. Consider the two different value functions pictured below.

One value function v is $v(\{12\}) = v(\{23\}) = v(\{12, 23\}) = 1$, while $v(g) = 0$ for all other networks.

The other value function v' is such that all nonempty networks generate the same value of 1.

The Myerson Value assigns the same allocation to the agents in the network $g = \{1, 2, 3\}$ regardless of which of the two value functions is in place. That is,

$$Y^{MV}(\{12, 23\}, v) = Y^{MV}(\{12, 23\}, v') = \left(\frac{1}{6}, \frac{2}{3}, \frac{1}{6}\right).$$

[9] Actually, if the network is something that is fixed and cannot be altered, then it is not clear why one would pay attention to marginal contributions to the network, or why just subnetworks would be important. So, the criticisms here apply more broadly.

Figure 12.4. *The Myerson Value on v.*

Figure 12.4. *The Myerson Value on v'.*

Player 2 is rewarded for being the central player in the network. Although the network is asymmetric, under the value function v', player 2 is not special in any way.

Let us consider the two main perspectives that might be taken. First, it could be that the network is something that can be adjusted and the allocation needs to take into account the fact that agents could rearrange themselves, or it might be that the allocation is the result of a bargaining process. From this perspective, the fact that player 2 is essential to generating value under v and not special under v', leads to very different disagreement points which should be reflected in the bargaining, but the Myerson value does not account for this. Second, it could be that the network is fixed and changing the network can only be relevant from normative perspective. If that were the case, then why should the allocation rule take into account subnetworks but not others? Basically, the criticism here is that the Myerson value takes into account how the value changes with respect to some but not all networks, and thus does not fully account for the roles of different players in generating value. This issue manifests itself here, but not in the cooperative game setting because the cooperative game setting generally views the grand coalition as forming, and so all other possible coalitional configurations are subsets. In a network setting, the efficient (or stable) networks will generally not be fully connected and thus the alternative networks include more than subnetworks.

A related issue can be seen when we examine the conditions that characterize the Myerson value. The next example from Jackson [331] shows some shortcomings of the equal bargaining power condition.[10]

EXAMPLE **12.4.2** *A Criticism of Equal Bargaining Power*

Let $v(\{12\}) = v(\{23\}) = 1$ and $v(g) = 0$ for all other networks. Thus, single link networks that include player 2 result in a value of 1, and other networks result in a value of 0.

Any allocation rule, including the Myerson Value, that satisfies equal bargaining power and allocates 0 to players on the empty network will result in $Y_1(\{12\}, v) = Y_2(\{12\}, v)$, as in Figure 12.4.

While there might be situations where the value will be split evenly despite the fact that player 2 is essential for generating value but neither of the other players is, *requiring* that player 2 get the same allocation as the other player in a link is quite

[10] For a discussion of shortcomings of the component balance condition, and other examples, see Jackson [331].

Figure 12.4. *A Critique of Equal Bargaining Power - Player 2 is required for to generate any value while other players are not, but the allocation is necessarily the same for all players under equal bargaining power.*

strong and should not be expected of a bargaining process. Indeed, this would be inconsistent with the sorts of outcomes we see in the exchange experiments of Cook and Emerson [161] as discussed in Section **??** or of Charness, Corominas-Bosch, and Frechette [135] as discussed in Section **??**. Even from a normative point of view, it is not entirely obvious that one should require that the allocation be symmetric in the dyad.

12.4.1 Defining Allocation Rules from Network Formation Possibilities

In order to account for the outside options that players and groups of players have available in constructing a network, Jackson [331] suggests the following alternative method of deriving allocation rules.

From any value function over networks we can define an associated cooperative game by[11]

$$w_v(S) = \max_{g \in G(S)} v(g).$$

The idea here is that $w_v(S)$ captures the value of a coalition S by measuring the maximal possible value that they could generate by forming a network among themselves when they are the only members of the society. This is a measurement of their threat value, or alternatively what they could generate for society without the help of any other agents.[12]

With these measures in hand, we can then allocate value based on Shapley value style calculations, now based on this auxiliary cooperative game that keeps track of the productive value of different groups of players.

So, in terms of allocating value, if g is efficient, then set

$$Y(g, v) = \phi^{SV}(w_v), \tag{12.4}$$

which is equivalently written as

$$Y_i(g, v) = \sum_{S \subset N \setminus \{i\}} (w_v(S \cup \{i\}) - w_v(S)) \left(\frac{\#S!(n - \#S - 1)!}{n!} \right).$$

[11] There is a slight abuse of notation here since v is defined on networks on N while g is a network on S, where S is a subset of N. This is easily translated to be a network on N where players outside of S are disconnected.

[12] I say "a measurement," as in cases where there are externalities across components of a network, it could be that the value generated by S depends on how other players are organized. This threat point is unambiguous if v is component additive, but is less clear otherwise.

Although this might appear to be similar to the Myerson value given its Shapley value-style calculations, it is a very different allocation rule. We see the differences immediately by noting that it gives different allocations for the two value functions given in Example 12.4.1. There it provides the same allocations under v as the Myerson value, but leads to a completely egalitarian allocation under v', while the Myerson value does not show any difference when the value function changes. It also leads to a higher allocation for player 2 in Example 12.4.2, in contrast to the Myerson value. This allocation rule violates both equal bargaining power and component balance, and is in turn characterized by conditions that are violated by the Myerson Value, as shown in Jackson [331].[13]

This way of defining allocation rules only ties down the allocation when an efficient network is chosen. There are many ways to then define the allocation on other networks. Jackson [331] suggests one possibility of simply adjusting allocations to be proportional to the allocation that would be obtained on an efficient network. That is, if some inefficient network generates 2/3 of the value of an efficient network, then each player would get 2/3 of the allocation that he or she would obtain under an efficient network. There are other ways to do this as well.[14]

12.4.2 The Core in Network Settings

Once we view the network as a flexible or changeable entity and see the associated cooperative game, then we can make more use of the cooperative game theoretic tool box. For example, there is a natural definition of the core in network settings.

A network-allocation pair $g \in G(N)$ and $y \in I\!R^n$ is in the *core* relative to (N, v) if

- $\sum_i y_i \leq v(g)$, and
- $\sum_{i \in S} y_i \geq w_v(S) = \max_{g \in G(S)} v(g)$ for all $S \subset N$.

The core includes the specification of both a network and an allocation of its value. The requirement is that no coalition could deviate, form a network on its own, and

[13] Jackson called this the player-based flexible network allocation rule. He also examined "link-based" variations on such a rule. There, one allocates value to links based on their importance in providing value, and then players get value from their links. Such an idea has roots in the communication game setting as studied by Meessen [441] and Borm, Owen, and Tijs [**?**].

[14] See Navarro [477] for further discussion and other allocation rules.

generate a higher value than what they are being allocated.[15]

So, analogously to its role in cooperative game theory, the core concept captures allocations which are stable to deviations from various groups, and can lead to allocations that differ from those derived from Shapley Value style calculations.

An allocation rule Y is *core consistent* if for any v such that the core is nonempty, there exists at least one g such that $(g, Y(g, v))$ is in the core.

While the Myerson value is not always in the core, and thus not core consistent, there are allocation rules which are core consistent. The nucleolus (of Schmeidler [**?**]) is an imputation defined on cooperative games that is core consistent relative to cooperative games. There is a natural analog of the nucleolus in a network setting, termed the networkolus by Jackson [331], that is core consistent in network settings.

Let $B(g, v) = \{y \in I\!R^n | \sum_i y_i = v(g)\}$ be the balanced allocations for g under v.

Let $e_S(y) = \sum_{i \in S} y_i - w_v(S)$ be the excess allocated to coalition S at an allocation y relative to their threat value under v, and let $e(y)$ denote the vector with entries indexed by a list of the nonempty S's, $S \subset N$.

Given an efficient g, let $Y^N(g, v) = y$ be the unique allocation such that $e(y)$ leximin dominates $e(y')$ for all $y' \in B(g, v)$.[16]

The networkolus examines how much various coalitions are getting relative to their threat values. In the case where the core is nonempty, so that there is some allocation that gives each coalition at least its threat value, then the networkolus equilibrates (to the extent possible) the excess value given to each coalition. More generally, even when the core is empty, it provides an allocation, and although in that case some of the excesses will be negative, the networkolus still minimizes the amount by which any coalition falls below its value.

[15] Again, this definition makes the most sense for component additive value functions, as otherwise the threat value generated by S in forming its network could depend on how the other players are organized. This is an issue that has resulted in various core definitions in cooperative settings, and appears here as well.

[16] A vector e leximin dominates a vector e' if there is some scalar x such that for any $x' < x$, e and e' have the same number of entries with value x', while e has fewer entries with value x. The calculation of the networkolus can be a difficult task without some underlying structure on v, but it can be shown that this is well-defined through a straightforward extension of results on the nucleolus.

12.5 Concluding Remarks

As we have seen here, tools from cooperative game theory can be adapted to provide insight into how the value of a network might be allocated among the players in a society and how this depends on the network in place and the values generated by alternative networks. T here are different perspectives that one might take, making this either a question of how value should be allocated or of how an allocation results from some process. Although we can adapt concepts from cooperative game theory to network settings, there are issues that arise in the network setting that lead to new questions regarding how value should be allocated. This is still a largely unexplored area.

12.6 Exercises

EXERCISE **12.1** *Convex TU Games.*

Prove Proposition 12.1.1.

EXERCISE **12.2** *A Convex 3-Player TU Game.*

Consider a three-player TU game where $w(\{1,2,3\}) = 2$ and $w(\{2,3\}) = 1$ while $w(S) = 0$ for all other S. Find the core allocations and Shapley value of the game.

EXERCISE **12.3** *The Core in an Exchange Network.*

Consider the society described in the left-hand network in Figure 10.3.1, where singletons are worthless, a coalition of any two "B" players is worth 8, a coalition of A with a B is worth 24, a coalition of three players is worth the same as the maximal value across its subsets of size 2, and the grand coalition is worth 32. Show that the unique core allocation is 4 for each B player and 20 for the A player. Find the Shapley Value for this game. Show that it differs from the core allocation.

EXERCISE **12.4** *Additivity of the Myerson Value.*

Let a value function v be such that $v(g) = v_1(g)+v_2(g)$ for two other value functions v_1 and v_2 and every $g \in G(N)$. Show that

$$Y^{MV}(v,g) = Y^{MV}(v_1,g) + Y^{MV}(v_2,g).$$

EXERCISE **12.5** *The Myerson Value in the Symmetric Connections Model*

Consider a star network comprising all players in the symmetric connections model. Find the Myerson Value allocation.

Consider a three player society and show that there exists a range of δ and c such that a star is efficient but only the complete network is pairwise stable under the Myerson value allocation rule.

EXERCISE **12.6** *Over-connection under the Myerson Value.*

Consider a value function v such that $v(g) = b(g) - c\sum_i d_i(g)$ where b represents benefits and $c > 0$ is a cost of maintaining a link.

$b(g)$ is *monotone* if

- $b(g') \leq b(g)$ if $g' \subset g$, and
- $b(\{ij\}) > 0$ for any ij.

The following is a special case of a result from Jackson [329].

PROPOSITION **12.6.1** *Let $n \geq 4$, and consider an anonymous and monotone benefit function b for which there is some efficient network g^* relative to b which is symmetric and not the complete network. There exists $\overline{c} > 0$ such that for any $c < \overline{c}$, any pairwise stable network relative to Y^{MV} and the value function $v(g) = b(g) - c\sum_i d_i(g)$ is Pareto dominated by some subnetwork.*

Prove Proposition 12.6.1.

Hint: first show that if $ij \notin g$ then $Y_i(g+ij, b) - Y_i(g, b) \geq b(\{ij\}) > 0$, and conclude that the complete network is the unique pairwise stable network under b. Then apply the additivity of the Myerson Value from Exercise 12.4 and work with small costs.

EXERCISE **12.7** *Possible Non-Existence of Strongly Stable Networks under the Component-Wise Egalitarian Rule.*

Show that there exists a component additive value function for which there is no strongly stable network under the component-wise egalitarian rule. Show that if we weaken strong stability to say that a network is stable if there is no deviation by a coalition of agents that is *strictly* improving for *all* members of the deviating coalition, then there will exist a strongly stable network under the component-wise egalitarian rule for any v.

EXERCISE **12.8** *The Existence of Strongly Stable Networks under the Component-wise Egalitarian Allocation Rule.**

The following condition and result are from Jackson and van den Nouweland [338].

A value function is *top-convex* if $\max_{g \in G(N)} \frac{v(g)}{|N|} \geq \max_{g \in G(S)} \frac{v(g)}{|S|}$ for all $S \subset N$.

Show that if the value function is component additive, then under this condition, the per capita value of each component of an efficient network is equal, and is at least as high as the per capita value of any component of any network.

Suppose that payoffs are governed by the component-wise egalitarian allocation rule and consider an anonymous and component additive value function. Show that the set of strongly stable networks is nonempty if and only if the value function is top convex. Moreover, show that in that case, the strongly stable networks are the efficient ones.

EXERCISE **12.9** *The Component-Wise Egalitarian Allocation Rule and Bridges.*

A pair of a network and a component additive value function, (g, v), is *bridge-monotonic* if,

$$v(C_i(g))/\#C_i(g) \geq \max\left[v(g^1)/\#N(g^1), v(g^2)/\#N(g^2)\right]$$

for every bridge ij in g such that $v(g) \geq v(g - ij)$, where $\#C_i(g)$ is the number of players in i's component of g, and g^1 and g^2 are the components of g bridged by ij.

Prove the following proposition.

PROPOSITION **12.6.2** *[Jackson and Wolinsky [343]] If g is efficient relative to a component additive v, then g is pairwise stable for Y^{ce} relative to v if and only if (g, v) is bridge-monotonic.*

EXERCISE **12.10** *The Shapley Value in the Connections Model.*

Consider the symmetric connections model with parameters such that a star is the unique efficient network structure. Let v be defined by $v(g) = \sum_i u_i(g)$, where u_i is from the symmetric connections model. Compare the Myerson value allocation for a star to the Shapley Value of w_v, as defined in (12.4), for a star.

EXERCISE **12.11** *Anonymity and the Shapley Value in Network Settings.*

Let v be an anonymous value function. Show that for any efficient network, the Shapley Value of w_v, as defined in (12.4), results in the same allocation as the egalitarian allocation rule.

EXERCISE **12.12** *The Monotonic Cover of a Value Function*

Given a value function v, Jackson [331] defines its *monotonic cover* $\widehat{v}$ by

$$\widehat{v}(g) = \max_{g' \subset g} v(g').$$

Consider an efficient g and a component additive v. Define an allocation rule Y so that the allocation at g, v is described by

$$Y_i(g, v) = \sum_{S \subset N \setminus \{i\}} (\widehat{v}(g^{S \cup i}) - \widehat{v}(g^S)) \left(\frac{\#S!(n - \#S - 1)!}{n!} \right).$$

where g^S is the complete network on the nodes S (viewed as network on N). Show that this is the same allocation as the Shapley Value of w_v, as defined in (12.4).

EXERCISE **12.13** *The Core in Example 12.4.1*

Determine the core networks and allocations (as defined in Section 12.4.2) under the value functions in Example 12.4.1.

EXERCISE **12.14** *The Networkolus and the Core.*

Consider a value function v for a three player society such that $v(\{12\}) = v(\{23\}) = 1$, $v(\{12, 23\}) = w$, and $v(g) = 0$ for all other networks, where $w > 0$.

Find the Myerson value, the player-based flexible network allocation, the networkolus, and all of the core allocations.

Chapter 13

Observing and Measuring Social Interaction

This book to this point has been focused on what we know about social and economic networks, as well as how we model and analyze social networks and their impact. I close with a chapter about measurement of social networks as well as inference from them. This is not meant to be a primer on empirical work, but rather to provide background on some important issues that are particularly acute when doing empirical analyses involving social networks. Whether or not one performs such analyses, understanding these issues is important in interpreting and evaluating empirical and experimental studies of social and economic networks.

A challenge in working with social network data relates to the fact that social structure is generally endogenous and related to many characteristics of the agents involved. People who are neighbors share many characteristics with their neighbors, as we saw in our discussion of homophily in Section **??**, and they might be choosing their neighbors not just with those characteristics in mind but also with feedback from the outcomes or behaviors that we might be interested in understanding. If we want to establish that a certain behavior is influenced by social network structure, then we have to be sure to properly account for many other related characteristics which could be the driver of the behavior, and to properly account for the fact that there can be feedback between the social structure, behavior, and the background characteristics. This not only relates to properly specifying a model to be able to sort out various effects, but also being sure that these different characteristics are "identifiable" and can really be sorted out given the data. In addition, there is also a somewhat related question of when it is that we can deduce that social structure "causes" behavior, and

not the other way around. I discuss how these difficulties manifest themselves, as well as some techniques for overcoming them.

I also discuss how we can use social network data to discover the latent social structures that underlie many social networks. This is not so much a challenge of social network analysis, but rather an aspect of analysis of social structure that involves some methods that are special to network settings. This includes (stochastic) block modeling, identifying community structures, as well as latent space estimation. The idea is that the nodes of a network belong to groups or organizations that are not directly observed, or are part of an unobserved "spatial" structure. These unobserved social structures determine social networks, and are interesting to understand in their own right. There are various techniques that have been developed for uncovering latent social structures based on social network data, and I provide an overview of some of the techniques and the ideas behind them.

13.1 Specification and Identification

A basic challenge arises in isolating the impact that social networks have on various behaviors, and is related to a more general quest to identify "peer effects". Social relationships are present for a variety of reasons, and social neighbors might display similar behaviors because they are influenced by common traits or experiences. It can be difficult to sort out whether individuals are behaving in a certain way because of the influence of their neighbors, or because of some influences are common to them and their neighbors, or because of other factors that are related to their network position.

13.1.1 Specification and Omitted Variables

To get a feeling for this, let us reconsider the study of Coleman, Katz, and Menzel [154] discussed in Section **??**. Van den Bulte and Lilien [600] criticize the study saying that it did not properly account for the effects that marketing and advertizing efforts by various pharmeceutical firms had on the diffusion process. To the extent that the direct effects of marketing or advertising, or other market forces, are correlated with the degree that Coleman, Katz, and Menzel measured, then it could be that these other factors are responsible for the diffusion and the degree ends up appearing to be the driver of diffusion because it is correlated with the other factors. Further studies (e.g., see Bhatia, Manchanda and Nair [56]) have found evidence of such effects after

controlling for marketing and other characteristics. Nevertheless, the point that one needs to include all the relevant factors in the analysis is an important one.

As a very simple example, suppose that degree in a network is correlated with age, so that older people have more connections. Now suppose that one hypothesizes that people with higher degree behave differently from people with lower degree. So, one estimates an equation of the form

$$Y_i = \alpha_d + \beta_d d_i + \varepsilon_i, \tag{13.1}$$

where Y_i is a measure of the behavior that we are interested in explaining, d_i is individual i's degree, and ε_i is an error term that captures unobserved idiosyncratic factors. However, suppose, for instance, that degree varies with age, so that

$$d_i = \delta + \gamma age_i + \eta_i, \tag{13.2}$$

where α_d is a base degree and η_i is an idiosyncratic term. If the true relationship is in fact of the form,

$$Y_i = \alpha_a + \beta_a age_i + \nu_i, \tag{13.3}$$

then when we fit (13.1), given (13.2), we can end up seeing an estimate for the coefficient on degree, β_d, that looks significant, but is really just a proxy for the effect of age, which is filtered through degree.

Suppose instead that the true relationship is of the form

$$Y_i = \alpha_d + \beta_d d_i + \beta_a age_i + \varepsilon_i, \tag{13.4}$$

so that both degree and age affect the variable in question. For example, suppose that we are examining a model of social capital, and so Y_i is some measure of wealth or power accumulation, and we are testing for how this is influenced by a measure of social connectedness. If we then fit (13.1), including degree but omitting age, then given that degree and age are related according to (13.2), we will end up with a biased estimate of β_d as it proxies for some of the effect of age. For instance, with positive relationships between each of the variables, by omitting age we would end up with an inflated estimate of how degree affects wealth.

While such specification and omitted variable problems are not unique to analysis of social networks, they are particularly acute in social network settings because of homophily. Recalling the discussion from Section **??**, we know that people tend to associate with others who are similar when examined from a wide variety of perspectives.

So, if we see that behavior of individuals tends to match patterns of the social network, we cannot attribute that behavior directly to network influence without being sure to properly account for all of the other factors that might be related to whom interacts with whom.

Instrumental Variables

It is generally difficult to be sure of all of the potential factors that might covary with both social relationships and behavior, and so there can always be a lurking issue with omitted variables and other sorts of misspecifications in estimating the impact of social structure on behavior. One way to view the bias that emerges in estimation is that the omission or misspecification leads the variables that we wish to estimate effects of to be correlated with the error term, and that can result in the bias in estimation (and can lead the estimator to be inconsistent so that even large data sets will not overcome the problem).

A standard approach to dealing with such problems is to work with instrumental variables. To develop an intuitive understanding of instrumental variable methods, let us understand what goes wrong in the case of an omitted variable. Ideally, to estimate the effect of degree on wealth, we would like to have a set of observations where degree is varied, and other variables are held constant in order to isolate the marginal effect of degree on wealth. If we design controlled experiment, this is how we would set things up. The difficulty is that we do not have such control, and when degree is high, the omitted variable of age also tends to be high, and when degree is low, the omitted variable of age also tends to be low. The idea of an instrumental variable is that it is one that is correlated with degree, but uncorrelated with the error term, or in this case, uncorrelated with the omitted variable of age. If we find a variable that covaries with degree, but is uncorrelated with the error term (and in this case with the omitted variables), then that serves as a substitute for the controlled experiment that we would have liked to design. For example, we might find some sort of factor that leads to changes in degree, such as a club that opens branches in some communities but not others (for exogenous reasons), but in a way that we expect to be uncorrelated with things like age or anything else that might lead to correlation with the error or omitted variables. This variable becomes the instrument. Effectively, it provides the sort of experiment that we would have liked to have set up, but causing variation in degree in ways that are independent of other possible explanatory factors.

One can then derive estimates based on the instruments using standard techniques

developed for this purpose or we can use two-stage least squares estimation. That is, we first regress degree on the instrumental variable, to develop estimated values of degree based on the instrument. Then in the place of degree in the original regression we use these estimated values of degree as predicted by the instrument, which are then independent of the error terms as they are conditional on the instrument. In this way we obtain a consistent estimator.

Endogeneity

Another problem that arises in working with estimation based on social structure is that social structure is often endogenous to the things that it impacts. For example, in estimating the impact of social connectedness on wealth, it could also be that wealth impacts connectedness; e.g., by providing additional access or opportunities.[1] While this is a distinct problem from the specification and omitted variables problem discussed above, it could also lead degree to be correlated with the error term, and can also lead to biased and inconsistent estimation.

Instrumental variables can also be helpful in sorting out endogeneity issues. Again, we want an instrumental variable that is related to degree, but will not be related to the error terms. Thus, it is a variable that avoids being endogenous, but is related to degree, and so when it leads to high or low degree we are sure that the high or low degree is coming about for exogenous reasons. For example, if a government came in and randomly chooses some villages to provide subsidized communication to (in the form of internet or telephone, etc.) which might enhance degree in some villages and not others, then we could examine how these changes in degree for exogenous reasons influence wealth. More specifically, we could measure the induced degree differences that we attribute to the government program and then see the extent to which it influences wealth, again using two-stage least squares, or other methods of working with instrumental variables.

While instrumental variables are a very useful tool for dealing with the omitted variable and endogeneity problems, they are not a panacea. First, finding "good" instruments, that are related to the problematic variable(s), but are not endogenous and not related to omitted variables and error terms, can be problematic. In fact, we can never really be sure of this as we never directly observe the "true" error terms. Second, even if we find instruments that we are reasonably confident in, it can still

[1] See Durlauf [**?**] for more discussion of some of the endogeneity issues associated with studying social capital.

be difficult to find ones that have a strong enough relationship with the problematic variables to be very useful in producing powerful estimates.

The example above of a government program that randomly selects certain villages for improvements that could lead to changes in social capital is a form of a "natural experiment." That is, it sets up nice control situations that provides us with just the sort of variation that is useful, so that we see what happens with and without the program, and thus with and without some exogenously determined increase in social capital.[2] Often ideal instrumental variables are related to such exogenous variation, when we are lucky enough to find them. We saw examples of such natural experiments in the discussion in Section **??** of the empirical analyses of how network connections shape labor market outcomes, where various exogenous variations in social structure, such as immigration due to rainfall in the home country, or random assignment to military units, or assignment to a city by an agency for exogenous reasons.

13.1.2 The Reflection Problem and Identification

Another problem in specifying a model social influence on behavior has to do with making sure that the specified relationship is properly "identified," meaning that the parameters of the model are uniquely determined by a data set. To caricature the identification problem in social influence: it arises from the fact that behavior is being determined by behavior, and so there is a sort of circularity, and under some specifications it can be difficult to sort out the influence of behavior on behavior. A well-known illustration of this is due to Manski **??**, [425].

Manski **??**, [425] describes an identification problem that is faced when examining social influences on individual behavior and provides an useful paradigm for understanding identification problems in such settings.

To see the identification problem that Manski [424] refers to as the reflection problem, let us consider it in its starkest form just to get a clear understanding of it. Consider a situation where the behavior of an agent is a linear function of the average level of the behavior taken by other members of his or her cohort. To be specific, let us suppose that an agent i has some characteristics x_i and that the agent's cohort is other people who have the same attributes. So, what determines i's behavior is what he or she expects his or her peers to do. Let Y_i denote i's behavior. His or her expectation

[2] For an interesting example of an analysis of social capital, based on the presence of television (which depends on some exogenous programs and geography) in rural Indonesian villages, see Olken [488].

of what people with the same attributes x_i will do is simply $E[Y_i|x_i]$ and so we write the relationship as

$$Y_i = a + bE[Y_i|x_i] + \varepsilon_i \tag{13.5}$$

where ε_i is a zero-mean random variable (conditional on x_i) which is a noise term capturing some unmeasured idiosyncracies. What will happen if we try to estimate this relationship? Note that if we take the expectation of both sides conditional on i's attributes x_i, then we end up with

$$E[Y_i|x_i] = a + bE[Y_i|x_i].$$

This has a unique solution (provided $E[Y_i|x_i]$ is nonzero) which is $a = 0$ and $b = 1$. Thus, when we fit (13.5) we end up with a tautological relationship of

$$Y_i = E[Y_i|x_i] + \varepsilon_i$$

which simply says that Y_i is its expectation plus noise, which tells us nothing about endogenous social interaction.

This is what Manski refers to as the "reflection problem:" i's behavior is a function of the expectation of the peers' behaviors which is just the expectation of i's behavior, which reflects i's behavior. Effectively, we have not specified a system that has any real bite in terms of tying down the relationship, and so it is not properly identified.[3]

Even if we enrich the specification, to allow Y_i to also depend on i's attributes x_i directly, we still have an identification problem. That is, suppose that we specify that

$$Y_i = a + b_1 E[Y_i|x_i] + b_2 x_i + \varepsilon_i. \tag{13.6}$$

Again, taking expectations,

$$E[Y_i|x_i] = a + b_1 E[Y_i|x_i] + b_2 x_i.$$

If $b_1 \neq 1$ (so we avoid having this parameter predetermined and tautological), then we can rewrite this as

$$E[Y_i|x_i] = \frac{a}{1 - b_1} + \frac{b_2}{1 - b_1} x_i.$$

[3]The identification problem is different from a multiple equilibrium problem, which can also result in settings with interdependencies in behaviors. As we have seen in graphical games with strategic complementarities, there can be multiple equilibria. The multiple equilibrium problem its own challenges.

Substituting this back into (13.6), we obtain

$$Y_i = \frac{a}{1-b_1} + \frac{b_2}{1-b_1} x_i + \varepsilon_i \tag{13.7}$$

Presuming that x_i is not constant, then we can estimate the two composite parameters $\frac{a}{1-b_1}$ and $\frac{b_2}{1-b_1}$. However, this does not identify the parameters a, b_1 and b_2, as there are many different values of these which lead to the same composites. We could set b_1 to any value (other than 1) and find values of a and b_2 that are consistent with the composite parameters. Adding in extra variables, does not help, as although there are more variables, there also more parameters to identify, as discussed in Exercise 13.1.

As Manski points out, one remedy is to use instrumental variables to sort out the identification, since part of the difficulty stems from the fact that behavior is endogenous, entering on both sides of the equations in the model. There are a variety of other ways around identification problems in social network settings. Let us examine several of them.

Social Structure and Identification

Note that the reflection problem stated above stems from the fact that i's peers are not identified directly, but just assumed to be similar to i. We are ignoring any real social structure and information that might be available about i's neighbors. If we explicitly track i's neighbors, then that information can identify a model.[4] To see one way that this works, let a possibly weighted and directed network matrix g govern interaction. Also, to make the technique as transparent as possible, ignore constant terms as well as any node-specific characteristics, so that we are just working directly with the interaction of behaviors, and let us stay with a linear relationship. In particular, suppose that

$$Y_i = b \sum_j g_{ij} Y_j + \varepsilon_i. \tag{13.8}$$

Thus, each individual's behavior is a weighted average of his or her neighbors' behavior. If the g_{ij}'s are not degenerate,[5] so that $(I - bg)$ is invertible, then we can express this as

$$Y = (I\!I - bg)^{-1} \varepsilon, \tag{13.9}$$

[4] The techniques here are common to the spatial econometrics literature, as outlined in Ansel [17]. The specifics of the derivation that follows in this section are due to Marcel Fafchamps, who showed me how this approach adapts to network settings and pointed me to the related references.

[5] This is relative to b, but generically in g the matrix will be invertible for any given b.

where Y and ε are the corresponding vectors, and $I\!I$ is the identity matrix. Letting ^{T} denote transpose, it follows that

$$E\left[YY^T\right] = (I\!I - bg)^{-1} E\left[\varepsilon\varepsilon^T\right] \left((I\!I - bg)^T\right)^{-1}. \tag{13.10}$$

If we have knowledge of the social network matrix g and of the covariance matrix of the error terms $E\left[\varepsilon\varepsilon^T\right]$, for instance, using a standard assumption that errors are independently and identically distributed with a finite variance, then b will be identified by equation (13.10). ident22).

This technique relies on some knowledge of the error terms. This can be a problem, especially in situations where we worry that omitted variables could influence behavior; for instance, resulting in positive correlation in the errors. This does not close the door on identification, as the above specification does not take advantage of other factors that influencing behavior.

In particular, in the reflection problem i's peers' behavior were not identified other than through i's characteristics. If we have explicit information about i's peers, and they differ from i in characteristics and the social relationships are not entirely symmetric, then this can overcome the "reflection" problem. As an extreme example, just to illustrate the point, suppose that there are different types of agents, say young and old. Suppose that older agents do not pay attention to the younger agents, but the younger agents pay attention to the older agents. In that case, a straightforward regression can estimate older agents' behavior, and then this can be used to estimate the younger agents' behavioral relationship. While this is an extreme example, where there are some agents who are not influenced by social interaction, more generally some asymmetries in the ways in which agents are influenced by each other is enough to provide identification. The reflection problem noted above was an extreme case where an agent was only influenced by agents whose actions were forecasted by the agent's own characteristics, and so variation in background characteristics were not helpful in identifying the relative behaviors and their impacts on each other.

Nonlinearities in Social Interaction

Beyond the fact that the reflection problem can be overcome with richer information in terms of interaction, it also is important to note that even without such information it derives from the linear-in-means specification. To see how linearity matters, let us modify the specification in (13.5) so that instead of having an agent's behavior be

proportion to the mean of his or her peers, where $Y_i = a + bE[Y_i|x_i] + \varepsilon_i$, let i's behavior be influenced by the maximal action by his or her peers. For example, let

$$Y_i = a + b_1 E[\max_{j \in N_i} Y_j | x_i] + b_2 x_i + \varepsilon_i, \tag{13.11}$$

where N_i are the neighbors of i, whose behavior might still be estimated based on x_i or observed more directly as a social network. Now, if we take the expectation of each side, we no longer have a tautology, but instead have

$$E[Y_i|x_i] = a + b_1 E[\max_{j \in N_i} Y_j | x_i] + b_2 x_i,$$

which is identified as long as we can deduce $E[\max_{j \in N_i} Y_j | x_i]$ in a way such that it and x_i are not constant nor linearly dependent.

Note that is was not essential that the specification be based on the max. There are a wide variety of specifications that avoid the identification problems (see Brock and Durlauf [100] for more discussion and specifications). In fact, the identification problems only arise for very particular specifications, such as the simple linear/average behavior specification.[6] This emphasizes the importance of building a model that properly captures the social interaction structure and incentives that are at the heart of the particular application. In fact, chapters **??** and **??** provide a base for modeling social interaction in ways that will generally be nonlinear and identifiable.

Timing

Another aspect of specification is timing. In the reflection problem, part of the difficulty stems from the contemporaneous interaction of the decisions. If decisions are repleatedly taken over time, then it could be that an agent's decision depends on the observations of *past* decisions of his or her peers. This can help identify the relationship, and can also help sort out causation. One can see if the current decisions of a given individual vary with the past decisions of his or her peers. For example, Conley and Udry [**?**] examine the timing of past neighbors' success in experimenting with fertilizer in pineapple production in Ghana to test for social learning. This is still quite challenging as there can still be omitted variables that are at the root of adoption. However, careful attention to the timing of behavior allows Conley and Udry to check whether increases in use by one agent are triggered by past successes of that agent's neighbor(s), after properly sorting out other potential causes.

[6] One does need to be careful however. Nonlinear models can also face identification problems as discussed in Exercise [**?**].

It is important to note that taking advantage of timing has been used not only to uncover whether an agent's behavior is influenced by his or her peers and social neighbors, but also to examine the endogeneity of social structure. For example is it that an agent acts in a certain way because his or her friends do, or is it that he or she selects friends that act in similar ways? This sort of endogeneity question is fundamental to social network analysis, especially when examining peer effects, and timing can be used to help sort out these effects. For example, Kandel [**?**] uses time series data on high school friendships together with data on individual drug use, delinquency, political opinion, and educational aspirations, to examine whether friendships tend to form among agents with similar behaviors, or whether agents' behaviors are influenced by that of their friends.[7] By examining the formation of new friendships and the deterioration of old friendships together with behavior over time, Kandel is able to identify whether either or both of these effects are present. The timing helps her show that both effects are present. Agents are relatively more likely to form new friendships with others whose past behavior matches their own, and to sever past friendships with others whose past behavior differs from theirs. In addition, when agents' behaviors change, it tends to be influenced by the past behavior of the agents who remain their friends. Moreover, the magnitude of the effects differs across behaviors. Such an analysis is demanding in terms of the richness of the data that is necessary, especially if one also wants to control for other variables which might be adjusting over time and co-varying with behavior and or social structure. Nevertheless, longitudinal (time series) data is a powerful tool for sorting out both social influence and endogeneity.

13.1.3 Laboratory and Field Experiments

As we have seen in the previous sections, many of the challenges in empirical analysis of social structure and social interaction are in separating out effects to see which factors and behaviors are related to which others, and to begin to understand which ones might cause which others. Various forms of experiments on behavior, where the particular values of some variables are carefully controlled and varied, allow one to track which conditions have been altered and thus uncover their impact. Given the power of experiments, they are a rapidly emerging tool of network analysis.[8]

Experiments can be used in various ways. First, an experimenter can examine

[7] For alternative methods of studying the co-evolution of networks and behavior see Snijders, Steglich, and Schweinberger [575].

[8] For a survey of parts of the literature see Kosfeld [388].

how social structure affects behavior, and how an agent's position within a network influences his or her behavior. For example, one can put agents in specific network contexts, such as in an exchange or bargaining network in the experiments of Cook and Emerson [161] and Charness, Corominas-Bosch, and Frechette [135]. Then comparing behavior across network position, as well as tracking changes in behavior as one changes overall network structure, allows one to explicitly track the impact of social network structure on behavior. There the idea is that the only variable that is altered is the social structure, which helps show whether or not agents behave differently when embedded in different positions within a network or in different networks. One can also examine something like how well agents are able to communicate and learn in social contexts, and how that depends on the network structure (e.g., see Bavelas [44], Leavitt [405], Choi, Gale and Kariv [141]), or how well agents are able to coordinate their actions in a social network (e.g., see Kearns, Suri, Montfort [365]). One can also investigate whether or not agents will behave differently if the network that they are part of is exogenously imposed or chosen by them (see Corbae and Duffy [165] and Riedl and Ule [**?**]). The control present in the experimental setting has proven to be a very useful tool for identifying network effects.

Second, one can test alternative theories of behavior in network contexts. Here one does not necessarily need to use variations in treatments within an experiment; instead one can simply find a setting where the predictions of different theories lead to different outcomes. For example, one can test models of network formation such as "myopic" ones like pairwise stability against a "farsighted" notion, as in Pantz and Ziegelmeyer [497]. There, the payoffs to network formation can be fixed, but are chosen by the experimenter so that one should observe different networks form if agents are farsighted in their link formation rather than myopic. Alternatively, one does not necessarily have to run a horse race of different theories against each other, but one can simply test whether a given theory's predictions hold. For example, one can examine variations on undirected or directed connections model and then see whether pairwise stable or nash stable networks form (e.g., see Callander and Plott [112], Falk and Kosfeld [224], Deck and Johnson [178], Vonin [**?**], and Goeree, Riedl, and Ule [276]).

While the first approach above was useful because it allows one to adjust some aspect of the social setting and then isolate its affect on outcomes, the advantage of the second approach is different. Under the second approach one only needs a single treatment, but one that distinguishes between different theories or hypothesized behaviors. Here the power of the experiment comes from being able to impose a certain

structure, and be sure that one has more or less complete knowledge of the network of interactions or of the relevant payoffs, etc. These can be difficult to observe from field data.

Beyond laboratory experiments, field experiments can be a very useful tool as well. One loses some of the control of a laboratory environment, but gains access to a social network in its natural setting. Milgram's small-world experiments, and those that have followed, are examples of this technique. There, the objective was to discover things about a real social network (and how people navigate it), and the controlled aspect was giving subjects a particular task to perform in a way to elicit information about network structure, such as the distance between two agents. Such field experiments can be useful not only for discovering social network structure, but also for seeing how it influences behavior. For instance, Goeree et al [277] examine how players behave in a dictator game (where a player has a choice of how much of a sum of money to keep and how much to give to another player) as a function of the social network distance between the players. One can also sort through various theories of social capital, altruism, and reciprocity, by examining specific behaviors as a function of social network (e.g., see Leider et al [407]). In such field experiments the control of a task, game, or information seeding, and so forth, placed in the context of a (measured) real social network helps uncover how behavior is related to social structure.

13.2 Community Structures, Block Models, and Latent Spaces

Another aspect of empirical investigation that is special to social network analysis is uncovering the latent social structure that underlies a network and led to its formation. Such structure is often not fully observable, and so needs to be constructed from what is observed. Uncovering such social structure can be useful for a variety of reasons. For example, coupling such implicit structure with other attributes can help to investigate whether there are specific biases in a society, such as in hiring or publishing. It can also help in classifying and categorizing political and other ideologies, as well as economic patterns of behavior.

The models that we have seen in earlier chapters for how networks are formed, when fitted to network data, can provide some insight into underlying structure, especially in terms of fitting some of the strategic models to data. But beyond these, there are also

various algorithmic and statistical methods which are specifically designed to discover underlying social structures or groupings. Let us examine those.

13.2.1 Communities and Blocks

There are various ways in which the structure underlying a social network can be modeled. One basic and standard way is to presume that the nodes of the network belong to different blocks or communities. The network that emerges depends on the underlying blocks or communities, which in turn can be recovered by examining the network. The early literature provided some definitions that can be used to capture underlying structures and the subsequent literature has provided a number of algorithms for recovering them.

One notion of a block or community is that it consists of nodes that are somehow comparable or equivalent. An early concept of this sort is structural equivalence, where two nodes are said to be structurally equivalent if their relationships to all other nodes are identical. This was first discussed by Lorrain and White [**?**] and further by White, Boorman and Breiger [628]. In particular, two nodes i and j are *structurally equivalent* relative to a network g if $g_{ik} = g_{jk}$ for all $k \neq i$, $k \neq j$ (and the same for g_{ki} and g_{kj}. This equivalence notion leads equivalence classes of nodes, so that we can partition the set of nodes into sets of equivalent nodes.

It is clearly rare to find networks where many pairs of nodes are structurally equivalent as many factors affect network formation, resulting in substantial noise both in actual and observed relationships. In view of this, the literature has moved beyond such a strict definition to develop a variety of methods of grouping nodes into equivalence classes and defining how nodes relate to each other, and also to develop methods of uncovering some basic blocks which underly the society but are not directly observed.[9]

In order to discuss such methods, I begin with a formal definition of such a grouping of nodes into equivalence classes, called a community structure.

A community structure is a partition of the set of nodes N, Π.[10] Thus, it groups the set of nodes into separate communities.

For example, consider the nodes in the network pictured in Figure 13.2.1.

One community structure of the example in Figure 13.2.1 is pictured in Figure 13.2.1, where the ovals collect the nodes considered to be in the same community.

[9] For an overview of blockmodeling see Doreian, Batagelj, and Ferligoj [190].

[10] Recall that a partition, π, is a collection of disjoint subsets of N whose union is N.

Figure 13.2.1. *A Sample Network.*

Figure 13.2.1. *A community structure for the network in Figure 13.2.1.*

There are many different ways in which the nodes of any network might be partitioned, and which community structure seems most appropriate can depend on the context and also on what we imagine a community to represent. Let us examine some of the more prominent methods for identifying community structures.

13.2.2 Methods for Identifying Community Structures

Just as we saw the proliferation of measurements of centrality and power, there are many different ways to think about what it means to say that two nodes are equivalent or belong in the same equivalence class or "community." I discuss a few prominent approaches of classifying nodes into equivalence classes, chosen to give a feel for the spectrum of potential viewpoints.[11]

Let me begin with a criticism of some of the literature, which is important to keep in mind when examining the techniques presented below. In order to make sense of a community structure, we should have a well-specified notion of what a community represents. For example is it based on some common but unobserved traits of nodes? Is it defined by some factors that influence nodes' behaviors? Is it defined by some affinity that agents feel for each other? Is it meant to capture some natural complementarity in association that is not directly observed but which favors link formation? As we vary what a community represents, the optimal method for identifying communities will correspondingly change. In particular, it is important to have an idea of how community structure will affect network formation. As if we do not have an idea of how community structure influences the observed network, then it is difficult to know how to recover the community structure from the observed network. Unfortunately, much of the literature by taking a "I will know a community when I see it" approach. That is, the literature has generally started with a simple algorithm for partitioning nodes of a network, based on some heuristic, without a firm foundation in terms of defining what communities are, how they influence network formation, or why this algorithm is a natural way for uncovering them. Thus, communities have tended to be defined to be whatever the algorithms find rather than deriving the algorithms as a technique for identifying a well-defined notion of community. That is not to say that we could not develop a well-defined notion of community corresponding to each technique, but rather that the literature has generally failed to be careful about this

[11] Wasserman and Faust [615], Snijders and Nowicki [574], and Newman [**?**], [**?**] provide additional background on various parts of this literature.

point and has not proceeded in as scientific a manner as one might like. At the end of this chapter I return to discuss some approaches that are built from the ground up. Hopefully, such techniques will be proliferate, and there will be a re-examination of the many techniques for identifying community structures with more attention paid to what communities represent and how they relate to network structure.[12]

CONCOR

An early and widely used method for partitioning nodes into communities is called CONCOR (for "convergence of iterated correlations"), as developed by Breiger, Boorman, and Arabie [87].[13] The idea is as follows.

Start with an observed social network described by an adjacency matrix g, which can be either directed or undirected. Two nodes are thought of as being similar if they have a similar pattern of relationships with other nodes. One way to gauge how similar node i is to node j in terms of the network of relationships is to examine how similar row $(g_{i1}, \ldots, g_{in})$ is to row $(g_{j1}, \ldots, g_{jn})$.[14] A measure of how similar these rows are to each other is to examine the correlation between row i and row j.[15]

The CONCOR algorithm does not stop here. This first step leads to a correlation matrix C, where c_{ij} is the correlation between row g_i and row g_j of the adjacency matrix. Next, let us measure how similar row i of the correlation matrix C is to row j, via the same method. If nodes i and j are similar, then they should have similar rows of correlations with other nodes. So, the algorithm then measures the correlation between rows c_i and c_j of the correlation matrix. In this way, we form a new correlation matrix $C^{(2)}$. Iterating, the algorithm generates a matrix of correlations of correlations

[12] To varying extents, the same criticism can be made of many measures in social network analysis. For example, there is much still to be learned about what different measures of centrality, prestige, clustering, ..., really capture, beyond some of the heuristics discussed in Chapter **??**.

[13] Breiger, Boorman, and Arabie provide references to earlier versions of CONCOR that were used in some specific studies, and CONCOR was further elaborated upon by White, Boorman and Breiger [628] and Boorman and White [86].

[14] In the case of directed networks, this misses some of the action as it focuses on relationships that are directed outward, while in the undirected case it captures all of a node's relationships. One can also perform the described algorithm on columns. Using columns would not change the analysis in undirected networks, but could lead to a very different analysis in the case of a directed network as it focuses on inward relationships, which can differ dramatically from outward ones.

[15] That is, view the row g_i as a random variable that takes on value g_{ik} if state k is realized. Placing equal likelihood on the n states, the correlation described above is simply the correlation between g_i and g_j.

Figure 13.2.2. *The community structure found via CONCOR on the network in Figure 13.2.1 when looking for four communities.*

of..., denoted $C^{(t)}$, after t iterations. Generally, this converges as t grows, so that the entries of $C^{(t)}$ approach some limit. In fact, except in exceptional cases, this process converges to a matrix of (at most) two blocks where the entries are 1 and -1.[16] That is, two blocks (which partition the nodes into two groups) emerge such that $C_{ij}^{(t)}$ converges to 1 when i and j are in the same block and $C_{ij}^{(t)}$ converges to -1 when i and j are in separate blocks.

As this only produces two blocks, one can repeat the procedure on the network starting with each block separately to further subdivide the blocks. By choosing when to stop subdividing, one ends up with a community structure. To see how this works, let us pre-specify that we wish to find a community structure with four communities. Then we operate CONCOR once to find two communities. Then we operate it again on the resulting communities to find four communities. For example, in this way CONCOR finds the structure in Figure 13.2.2.

While CONCOR and its variations are included in many programs for network

[16] See Schwartz [**?**] for background on convergence properties of CONCOR and related methods of iterated covariance.

analysis, what one actually obtains through iterating on the correlation is not so obvious.[17] That is, what does it really mean for two nodes to be in the same block under this procedure? Why is this a reasonable way to group nodes? Another difficulty is that it is not obvious how many times to split the blocks.

Repeated Bisection

CONCOR is a method that repeatedly bisects the set of nodes based on a specific technique of grouping nodes. There are other methods, which developed out of the computer science literature, that also work by repeated bisection. For example, a quite simple principle is to simply start by bisecting the set of nodes into two groups such that there is a minimal number of links between the two groups, with some rule based on what to do in the case where more than one bisection leads to the same minimum. Then one can repeat the procedure on the emergent groups. Again, using some stopping rule, one ends up with a community structure.

There are many variations on this basic idea. Instead of minimizing the number of links between the two groups, one might try to maximize some measure of how many links exist within each group, less how many go across the groups (e.g., see Kernighan and Lin [368]). Or, one might rely on more sophisticated methods where one examines the eigenvectors of the adjacency matrix or an associated Laplacian matrix (e.g., see Fiedler [230] and Pothen, Simon and Liou [520]).[18]

Beyond the question of the how one measures how good a bisection is, there is also a question of whether one searches over all possible bisections or limits attention to certain types of bisections. For example one can pre-specify the sizes of the two sets of nodes. For example, one might only consider bisections into equal (or nearly equal) sized sets of nodes. This is not a minor technicality, as it can lead to a sizeable difference in the number of potential bisections that one needs to consider. Also, many of these methods would tend to bisect the network very asymmetrically if no constraints are imposed, since, for instance, minimizing the links between groups might be found by identifying a single node with low degree and separating that from the rest of the network, and it is not clear that this would be sensible. This relates back to the earlier criticism that we are not quite sure what we are looking for, and so the answer to this question is not tied down.

In addition to measuring the optimality of a bisection, and which bisections to

[17] See Schwartz [552] for a criticism along these lines.

[18] See Newman [483] for an overview of some of those techniques.

consider, there is the stopping decision which we saw can be somewhat arbitrary. Finally, one can also move beyond bisections. For example, one can start with the problem of splitting the set of nodes into some number of (nearly) equal sized groups in a way that minimizes the links across groups and/or maximizes the number of links within groups.

Edge Removal

One method that avoids the issue of predetermining the sizes of the groups to bisect a network into, instead works by repeatedly removing edges of the network and keeping track of the component structure of the resulting graph to determine a community structure. Such a method, developed by Girvan and Newman [271], iteratively removes edges by calculating the betweenness of each link and then removing the link that has maximum betweenness. The logic is that if a link has a very high betweenness score, then it is connecting (at least) two groups of nodes that otherwise are quite separate. These groups would then be natural candidates to be separate communities of nodes. This process can be done in various ways, depending on the notion of betweenness used.

Let us demonstrate this technique on the example from Figure 13.2.1, using the easy-to-calculate measure of the betweenness of a link that Girvan and Newman use (a variation on Freeman's notion discussed in Section [**?**]), which is the number shortest paths between pairs of nodes in the network that involve the link in question. That is, for each link we count the total number of geodesics in the network that include that link. The link with the highest count is the one we remove. (It could be that a pair of nodes has more than one shortest path that involves the same link. For example, nodes 8 and 5 have two shortest paths between them that involve the link 56.) Once a link is removed, one repeats the process on the resulting subgraph, calculating new betweenness scores at each step.

Figure 13.2.2 shows the resulting community structure under this algorithm if one stops when the betweenness of an edge reaches 2 (so that the highest betweenness measure of any link remaining in the network is 2; see Exercise 13.3 for the precise steps).

The calculations involved in order to run the Girvan and Newman algorithm can become extensive as the number of nodes grows, as the betweenness measures involve finding all shortest paths through a given link. In view of this, there are various alternative measures and algorithms that have been developed (see Newman [483] for

Figure 13.2.2. *The community structure found via the Girvan-Newman Algorithm on the network in Figure 13.2.1.*

discussion and references).

This algorithm runs into the same issue that we saw with bisection methods: when to stop. Newman and Girvan [484] propose a method for determining when to stop this (or another) algorithm. For any community structure Π, one can calculate the following measure that Newman and Girvan call *modularity*. For two communities $\pi \in \Pi$ and $\pi' \in \Pi$ let $e_{\pi\pi'}(g)$ denote the fraction of all edges in the network that connect nodes in π to nodes in π'. Then the modularity of the community structure Π is

$$M(\Pi, g) = \sum_{\pi \in \Pi} e_{\pi\pi}(g) - \sum_{\pi \in \Pi, \pi' \in \Pi \pi'' \in \Pi} e_{\pi\pi'}(g) e_{\pi'\pi''}(g).$$

Modularity measures the proportion of edges that lie within communities minus the expected value of the same quantity in a graph such that all nodes have the same degrees but links are generated uniformly at random (ignoring community structure). When this measure is 0, then the communities are not capturing much of anything. If the measure is positive, then the communities are capturing more of a fraction of links internally than one would expect at random. When the measure is negative, then the community structure is cutting against the link pattern in that there are more links

across communities and fewer within than one would see at random. So, the idea is to maximize this modularity measure, and a rule for stopping an algorithm is that one stops if the modularity decreases by further edge removal. One has to be careful, as there can be local maximizers that are not global maximizers, and so one technique is to continue operating the algorithm in question to exhaustion, and then to go back and pick the community structure which leads to the highest modularity measure.

Hierarchical Clustering

A approach that differs from CONCOR, repeated bisection techniques, and edge removal builds up communities by adding new nodes to groups successively by examining how similar pairs of nodes are, rather than starting from one large community and breaking it apart. This methodology underlies a whole class of algorithms, called "hierarchical clustering" methods.

The ideas are as follows. The foundation is to have some measure of how similar two nodes are based on a given network. There are many such measures. One could use the correlation coefficients between the rows of the adjacency matrix, $C^{(1)}$, which was the first step of the CONCOR process above. Instead, we could calculate the distance between the vectors g_i and g_j (using Euclidean distance; or city-block distance - the number of entries that differ across the two vectors). We could also use various measures built on path distances or other indications of how the roles of two nodes within the network compare. The important point is that there is some measure that the analyst believes captures the appropriate notion of how similar two nodes are in the given application.

For the purpose of illustration, let us measure similarity between nodes i and j, via a slight variation[19] on the city block distance between rows, or in particular set the distance between nodes i and j to be

$$b_{ij}(g) = \#\{k | g_{ik} \neq g_{jk}, k \neq i, k \neq j\}.$$

Thus, if $b_{ij}(g) = 0$, then i and j are structurally equivalent. More generally, $b_{ij}(g)$ indicates the number of other nodes k with whom i and j differ in their relationships. So it directly counts the differences between the neighborhoods of nodes i and j.

In order to use the distance information to construct a community structure, let us start with a threshold of 0. We form a graph (that is purely for algorithmic purposes

[19] The variation is that we do not examine the cases where $k = i$ or $k = j$, as those are not relevant for our purposes.

and might look quite different from the original g), denoted $g^{(0)}$, as follows. Link any two nodes together that have $b_{ij}(g) = 0$. Thus, a link between two nodes indicates that we think they are "similar" in that they are at a low distance from each other. If we stop here, then we end up with a community structure that is the partition induced by the components of this network, $g^{(0)}$.[20] As there may not be many pairs of nodes that are structurally equivalent, $g^(0)$ will tend to have very few links, and so we usually end up with a very sparse community structure with many small communities if we stop with a threshold of 0. This suggests raising the threshold for how distant nodes can be from each other and be linked - or considered "similar". If we set a threshold t, then we end up with a graph

$$g^{(t)} = \{ij | b_{ij}(g) \leq t\}.$$

As we raise the threshold, the components of the induced graph continue to grow as more edges are added. The community structure at some threshold t, denoted $\Pi^{(t)}$, is the partition of nodes induced by the components of the network $g^{(t)}$ at some threshold t, so it is $\Pi(N, g^(t))$ (recalling notation from Section **??**). Eventually, as we raise t to $n-1$, we end up with a completely connected graph and just one community.

To get a feeling for how this works, let us apply it to the network in Figure 13.2.1. First, note that nodes 2 and 3 are structurally equivalent, as are nodes 7 and 9, so that $b_{23}(g) = 0 = b_{79}$. As these are the only such pairs, if we set the threshold to be 0 then the resulting community structure is

$$\Pi^{(0)} = \{\{1\}, \{2,3\}, \{4\}, \{5\}, \{6\}, \{7,9\}, \{8\}, \{10\}\}.$$

If we raise the threshold to 1, then we find new pairs of nodes that are "similar" to each other: nodes 7 and 8 only differ by one relationship, and in fact $1 = b_{78}(g) = b_{89}(g) = b_{12}(g) = b_{13}(g)$. We end up with

$$\Pi^{(1)} = \{\{1,2,3\}, \{4\}, \{5\}, \{6\}, \{7,8,9\}, \{10\}\}.$$

Next, given that $b_{3,10}(g) = 2$, $b_{4,10}(g) = 2$, $b_{5,10}(g) = 2$, $b_{8,10}(g) = 2$, $b_{6,7}(g) = 2$, we end up with just a single component under $g^{(2)}$ and so the resulting community structure at a threshold of 2 is already

$$\Pi^{(2)} = \{\{1,2,3,4,5,6,7,8,9,10\}\}.$$

[20] Note that structural equivalence is not a transitive relationship. That is, it is possible to have $b_{ij}(g) = 0 = b_{jk}(g)$, while $b_{ik}(g) = 1$. This happens when $g_{ij} \neq g_{kj}$. Thus, it is possible to have components of $g^{(0)}$ that are not cliques.

Figure 13.2.2. *The dendrogram or hierarchical tree generated by running a hierarchical clustering algorithm based on a simple (dis)similarity measure on the example from Figure 13.2.1.*

The term hierarchical clustering refers to the fact that as we raise the distance threshold (or lower the similarity threshold) for when we consider two nodes to be similar, groups of nodes continue to merge and we end up with a sort of hierarchy. The hierarchical tree, known as a *dendrogram*, generated for this example is pictured in Figure 13.2.2.

There are several challenges with such methods. First, we need to know when it is reasonable to stop the process. This can often be more of an art than a science, and so researchers will report the full hierarchy indicating at which thresholds different components coalesce. This report is often in the form of a hierarchical tree like the one pictured in Figure 13.2.2. One can also use modularity, or some other method, to choose among potential community structures. Second, the way in which communities coalesce is a bit questionable. For example, once we set the threshold distance to be 2 in the above example, the similarities between node 10 and several other nodes is largely responsible for bringing all of the nodes together into one community. However, "similarity" in measured in this way is not necessarily transitive. For example, nodes in the group $\{1, 2, 3\}$ are now in the same community with the nodes in the group

$\{7, 8, 9\}$ because they are each sufficienty "similar" to node 10, and yet any node from the first group is at a distance of at least 4 from any node in the second group, and in some cases are at a distance of 6 (e.g, $b_{1,7}(g) = 6$). This is generally a challenge with such methods, as a single node can cause many nodes to be grouped together that are not very similar to each other.

13.2.3 Stochastic Block Models and Communities

As mentioned at the outset of this section, a central difficulty behind all of the algorithmic methods discussed above is that we are not sure what "communities" they are designed to uncover. If we iteratively remove edges from a network, what are we uncovering and why is that a sensible way to proceed? What sorts of communities do we end up with when we examine a similarity measure and identify communities via hierarchical clustering? The problem is that the methods described above are defined by the algorithms and not by having a theory or model of what a community structure is. Communities simply happen to be what we end up with. This is not to say that such methods cannot be built up from some foundation, but rather that such foundations do not yet exist.

A different approach is to start with an explicit idea of what a community is and how networks are generated as a function of the underlying community structure. Then we can work from the foundation: given the network structure, we can try to deduce which community structure is most likely to be present, as we know the likelihood with which different community structures lead to various networks. This is a standard statistical approach to the problem - one presumes a model of how data (here a network of relationships) are generated from underlying parameters (here a community structure) and then one examines the data to statistically infer the parameters of the model. When applied to social networks this is sometimes referred to as *a posteriori block modeling*.

A natural version of this is a variation of a model of Holland, Laskey, and Leinhardt [316], as analyzed by Snijders and Nowicki [574].[21] Each node belongs to a group, which can be thought of as a block or community. To stick with the definitions above, let us call it a community and work with community structures, so that each node belongs to exactly one community.

[21] This is also related to other models, such as those of Holland and Leinhardt [**?**] and Fienberg and Wasserman [231]. It has experienced a recent resurgence (e.g., see Newman and Leicht [**?**]) in a portion of the literature unaware of its origin in the older literature.

The model is that the probability of a link between two nodes depends on which communities the given nodes lie in. The probability, for instance, could be higher within a community than across communities. There might also be some pattern of link probabilities depending on specific communities. In particular, the general form of the model is to have the probability of a link between a node in community π and a node in community π' be designated by a parameter $\eta_{\pi\pi'}$. The formation of each link is independent of the formation of every other link. The restriction of the model is that any two nodes in a given community are "equivalent" in the sense that the probability that either of them forms a link with any other node is the same. So, one can think of this as a form of probabilistic structural equivalence.

If we work with undirected networks, then $\eta_{\pi\pi'} = \eta_{\pi'\pi}$, while we can allow the probabilities to differ in a directed network.

A community structure with m communities, together with a list of the m^2 parameters $\eta_{\pi\pi'}$, leads to a well-defined probability that any given network will form. The probability that link ij forms is $\eta\pi_i\pi_j$ where π_i is the community to which i belongs. So, the probability (or "likelihood") of a network g is

$$L(g|\pi,\eta) = \left(\prod_{ij\in g} \eta_{\pi_i\pi_j}\right)\left(\prod_{ij\notin g}(1-\eta_{\pi_i\pi_j})\right). \tag{13.12}$$

One of the difficulties with the model in its fullest generality is that it allows for many parameters and might not really tie much down. For example, by setting the community structure to have each node in its own community, and then setting link probabilities across communities to be 1 when a link exists and 0 otherwise, we would end up predicting that our observed network should have been the one that formed. There are so many free parameters that we can explain any possible network exactly. So, in order for this approach to be meaningful, we need to place additional restrictions on the parameters of the model. These will generally be governed by the specific application and thus some additional information of what communities represent.

A special case of this (studied by Copic, Jackson, and Kirman [164][22]) is one where there is one probability for links within a community and another probability for links across communities. That is, there are just two probabilities, $1 \geq p_{in} > p_{out} \geq 0$, such that $\eta_{\pi\pi} = p_{in}$ for any $\pi \in \Pi$, and $\eta_{\pi\pi'} = p_{out}$ when $\pi \neq \pi'$. So, here communities are

[22] They consider a more general variant which is special in the η's but also allow for multiple links and varying capacities across links.

groups of nodes that are more likely to interact with each other, and interaction across communities is less likely.

To see how this model can be used to uncover a community structure given network data, let us explore this two-probability case in more detail. As mentioned above, specifying Π, p_{in}, and p_{out} leads to a well-defined probability of observing any particular network g for the unweighted and undirected version of the model (and for a weighted and directed version, see Exercise [**?**]).

Given a community structure Π, let $In(\Pi)$ be the set of all pairs of nodes that lie within the same community under Π and $Out(\Pi)$ is the set of all pairs of nodes that are in different communities under Π. That is,

$$In(\Pi) = \{ij \mid \text{ there exists } \pi \in \Pi \text{ such that } \{i, j\} \subset \pi\},$$

and $Out(\Pi)$ is the set of all pairs of nodes that are not in $In(\Pi)$. Let

$$T_{in}(g, \Pi) = |g \cap In(\Pi)|$$

be the number of links that are in the network g and that lie within communities under Π. Similarly, let $T_{out}(g, \Pi) = |g \cap Out(\Pi)|$ be the number of links that are in the network g and that lie across communities under Π.

The probability of observing network g if Π is the community structure is described by the likelihood $L(g|\Pi, p_{in}, p_{out})$, where

$$L(g|\Pi, p_{in}, p_{out}) = p_{in}^{T_{in}(g,\Pi)} (1 - p_{in})^{|In(\Pi)| - T_{in}(g,\Pi)} p_{out}^{T_{out}(g,\Pi)} (1 - p_{out})^{|Out(\Pi)| - T_{out}(g,\Pi)}. \tag{13.13}$$

Thus, given a community structure Π, we have a well-defined probability of each possible network.

13.2.4 Maximum-Likelihood Estimation of Communities

Given the probabilities of seeing each possible network as a function of the community structure, we can then invert the problem and ask which community structure leads to a highest likelihood of generating the network that we have actually observed. Maximizing this likelihood is equivalent to maximizing the log of this likelihood, which is often easier to work with. By taking the log of the likelihood function, $\ell(g|\Pi, p_{in}, p_{out}) = log\,(L(g|\Pi, p_{in}, p_{out}))$, we end up with a very manageable expression for the relative likelihood of observing a particular network g if the community

structure is Π:

$$\ell(g|\Pi, p_{in}, p_{out}) = \log(L(g|\Pi, p_{in}, p_{out})) = k_1|In(\Pi)| + k_2 T_{in}(g, \Pi) + k_3|Out(\Pi)| + k_4 T_{out}(g, \Pi), \tag{13.14}$$

where the k's depend only on p_{in} and p_{out}.[23]

Noting that $|Out(\Pi)| = \frac{n(n-1)}{2} - |In(\Pi)|$ and $T_{out}(\Pi) = |g| - T_{in}(\Pi)$, we can rewrite (13.14) as

$$\ell(g|\Pi, p_{in}, p_{out}) = (k_1 - k_3)\,|In(\Pi)| + (k_2 - k_4)\,T_{in}(g, \Pi) + r, \tag{13.15}$$

for a r that depends only on $|g|$, p_{in} and p_{out}, and not on Π.

So, the community structure that is identified via this method is the Π that maximizes $(k_1 - k_3)\,|In(\Pi)| + (k_2 - k_4)\,T_{in}(g, \Pi)$. We have boiled down the problem of finding a community structure to a calculation that just involves examining a weighted difference of the number of pairs of nodes lie within the same communities and the number of links lie within communities. Noting that $k_1 - k_3 < 0$ and $k_2 - k_4 > 0$, as we group more nodes together we see two competing effects in terms of how the likelihood changes: the second expression in (13.15) increases, while the first one decreases. The relative rates at which this occurs depends on the *relative* density of how many links are within a community compared to how many pairs of nodes lie within communities.

Algorithms for Maximum Likelihood Estimation

There are two challenges to implementing this method. One is that p_{in} and p_{out} need to be estimated along with the community structure, as they determine the k parameters. Dealing with this is relatively straightforward and involves an iterative procedure: one begins with an initial estimate of these parameters, which then leads to a initial estimate of a community structure. Next, based on a the first estimation of the community structure one can estimate p_{in} and p_{out} directly by examining the fraction of links within communities compared to the potential number, and similarly for across-community links. One can then iterate on this process.[24]

The second challenge is a bit more difficult to deal with. It is that the number of potential community structures grows exponentially in the number of nodes. With

[23] In particular, $k_1 = \log(1 - p_{in})$, $k_2 = \log\left(\frac{p_{in}}{1-p_{in}}\right)$, $k_3 = \log(1 - p_{out})$, and $k_4 = \log\left(\frac{p_{out}}{1-p_{out}}\right)$.

[24] As Copic, Jackson and Kirman [164] show, as the number of potential relationships is increased, there is a unique consistent pair of a community structure Π and p_{in} and p_{out} which lead to estimates of each other.

Figure 13.2.4. *The community structure found via the Maximum Likelihood algorithm on the network in Figure 13.2.1.*

even moderate numbers of nodes, this makes it impossible to calculate the likelihoods of the given network for all possible partitions. With a small number of nodes, one can do the calculations directly, as for the network in Figure 13.2.1, where one ends up with the community structure pictured in Figure 13.2.4.

However, for larger numbers of nodes, one has to employ some sort of approximation technique. Various techniques can be found in Snijders and Nowicki [574], Copic, Jackson, and Kirman [164], and Newman and Leicht [**?**].

13.2.5 Latent Space Estimation

The model of community structures in Section 13.2.3 is relatively simple in that it simply posits that link probabilities are completely governed by community membership. In some settings, there are more complex relationships that underlie the relationships between nodes. There might be many attributes, including socio-economic, geographic, and a variety of status attributes like profession, religion, gender, race, membership in organizations, and so forth that influence the relationships. There might also be hierarchies of nodes according to various measures, and these all might come together

in different ways to influence the chance that two nodes are linked to each other. A community structure is an extreme model of this. More generally, one can model richer underlying structures that help determine relationships.

A straightforward generalization of the maximum likelihood approach outlined above for community structures is to posit some model of structures and attributes and how a given network is to emerge under various parameters of the model. Take some general structure S to be the primitive, which might include all sorts of information about nodes and layers of groupings. Each S then leads to a likelihood of observing a given network g, denoted $L(g|S)$. Given that we observe g, we can look across potential S's to find the one which maximizes the likelihood of having seen g – that is the S that maximizes $L(g|S)$.[25]

An example of this, beyond the basic community membership model, is known as "latent space estimation." The idea is that nodes are located in a space and the probability that they are linked is dependent on their spatial locations (e.g., see Hoff, Raftery, and Handcock [**?**] and Hoff [312]), generally with the probability of a link increasing as nodes are closer together.[26] The space can take many forms, but provides an explicit model of how networks emerge and what we wish to uncover. The critical element in such estimation is to ensure that the model has some limits in terms of the number of parameters to be estimated, so that one does "overfit" the data.

13.3 Exercises

EXERCISE **13.1** *Identification with Contextual Effects.*

Consider the following generalization from Manski [424] of the model in (13.6).

$$Y_i = a + b_1 E[Y_i|x_i] + b_2 x_i + b_3 z_i + b_4 E[z_i|x_i] + \varepsilon_i. \tag{13.16}$$

Here z_i is a contextual effect, and i's expectation of z_i can matter too. Show that the parameters a, b_1, b_2, and b_4 are not identified.

[25] One can alternatively do a Bayesian analysis, where one has a prior probability distribution, P, over possible S's, and then given the likelihoods $L(g|S)$, one applies Bayes' rule to derive a posterior probability that S is actually in place. One chooses S to maximize $\frac{L(g|S)P(S)}{\sum_{S'} L(g|S')P(S')}$. This is equivalent to maximizing $L(g|S)P(S)$ and is the same as maximum likelihood estimation if we set the prior, $P(S)$, to be equal across structures.

[26] One can think of the community structure model as a special case where the space is a hypercube with n vertices, all nodes in the same community are located at the same vertex.

EXERCISE **13.2** *Identification Problems with Nonlinear Models.**

Consider the following two alternative models of behavior.

The first model is as follows. In each period a parent is replaced by its child, who then becomes a parent in the next period. The child makes a 0 or 1 decision (e.g., to attend university) and dependent upon the parent's choice. If the parent took decision 1, then the child takes decision 1 with probability q_1, while if the parent took decision 0, then the child takes decision 1 with probability q_0, where $1 \geq q_1 \geq q_0 \geq 0$.

In the second model, there are two such "families". In each period, one of the two families is selected by the toss of a fair coin. That family (and only that family) has its member ("the parent") die and be replaced by a child. In this model, the child then makes a decision. The child looks to the other family (its neighbor), and if that neighbor has taken decision 1, then the child takes decision 1 with probability p_1, while if the neighbor took decision 0, then the child takes decision 1 with probability p_0, where $1 \geq p_1 \geq p_0 \geq 0$.

Show the following result from Calvo-Armengol and Jackson [**?**]. For any such specification of $1 \geq q_1 \geq q_0 \geq 0$ in the first model, there is a specification of $1 \geq p_1 \geq p_0 \geq 0$ in the second model that leads to an observed probability of a child taking action 1 conditional on the parent's choice which is exactly the same as that of the first model. Do this by calculating these conditional probabilities for any given p_1 and p_0, and show that the range is the set of (q_1, q_0) such that $1 \geq q_1 \geq q_0 \geq 0$.

EXERCISE **13.3** *Applying the Girvan-Newman Algorithm to the Network in Figure 13.2.1.*

Which link has the highest betweenness score at the first step in the Girvan-Newman algorithm applied to the network in Figure 13.2.1 and what is that score? Indicate the next two edges to be removed. Which edges would be removed next if we continued?

EXERCISE **13.4** *Multiple Community Memberships.*

Consider the following variation on a model of community structures. There are a set of "clubs" that agents can be members of.[27] In the special case where each agent must be in one club and only one club, then this reduces to a community structure (ignoring any empty clubs), but more generally we might allow agents to belong to

[27] One can also think of these as activities that an agent can undertake, such as a sport; or as an attribute that an agent might have, such as their ethnicity, profession, etc.

more than one club, or even no clubs. An agent's likelihood to be linked to another agent depends on the number of clubs they are in together. The probability that two agents are linked is p_k, where k is the number of clubs that they are both members of and p_k is increasing in k.

Describe a likelihood method for recovering club membership for a fixed number of clubs.

EXERCISE **13.5** *Hierarchies and Communities.*

Consider augmenting a community structure by a hierarchy. That is, starting with a community structure Π, let h be a "hierarchy" function such that $h(\pi) \in \{1, 2, \ldots, K\}$ indicates which level of the hierarchy pi lies in. Let the probability that a node links to another node in the same community be p_{in} and the probability that a node in a community in level k links to a node in a different community in level k' be $p_{kk'}$.

Describe a likelihood method for recovering the community structure and hierarchy function given a presumption that there are at most K levels to the hierarchy and fixing some starting estimates of the $p_{kk'}$'s.

Allowing for a directed network, describe a method for recovering the community structure, hierarchy function, and the $p_{kk'}$'s; under a constraint that $p_{kk'} > p_{k'k}$ when $k > k'$.

Chapter 14

Afterword

This book is intended to provide researchers with an overview of models of social and economic networks and the many techniques for analyzing them, while including empirical perspective. By drawing from the multitude of disciplines that contribute to network analysis and the variety of perspectives underlying them, I have sacrificed being comprehensive with respect to any particular viewpoint. I have tried to provide a coherent view of the overall landscape, while still giving a good sense of the richness that emerges from the underlying mosaic.

There is much that is exciting about the study of social and economic networks. The tool box of powerful models and methods is poised to lead to new discoveries. The emergence of increasingly large and extensive data sets, and the awakening of more areas of study to the importance of social structure, provide for a growing reach of network analysis. Agent-based modeling and large-scale experiments are becoming more efficient and should also lead to new insights. Beyond the existing tools, network science is also exciting in that it calls out for further development of methods and models. We have seen many examples of this. We need more models that incorporate both the randomness that governs the opportunity for people to form relationships, as well as the incentives underlying the choices of which relationships appear and endure. We need more models that capture how networks influence behavior. There is much still to be learned about how the social networked aspect of many economic and social interactions influence employment patterns, wage distributions, the pursuit of education, social mobility, conflict, learning, and various other behaviors. Moreover, we still know next to nothing about the co-evolution of networks and behavior, and clearly behavior and network structure influence each other. There are important open questions regarding how network structure impacts a distribution of the benefits that

accrue to different actors in a network, as well as how this feeds back to network formation. There are also many fundamental methodological questions concerning what summary statistics of networks (clustering and centrality measures, community structures, and so forth) really capture. This partial list already presents a formidable but enticing agenda for the future.

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