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**The Dissertation Committee for Figaro L. Loresto Jr. Certifies that this is the  
approved version of the following dissertation:**

**EXPLORING THE USE OF SOCIAL NETWORK ANALYSIS ON  
PHYSICIAN NETWORKS CREATED FROM MEDICARE DATA  
THROUGH STUDYING THE USE OF MINIMALLY INVASIVE  
BREAST BIOPSY AMONG PHYSICIANS: DESCRIPTIONS,  
REGRESSIONS, AND NETWORK MODELS**

**Committee:**



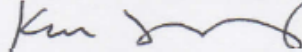
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Dr. Daniel Jupiter, PhD  
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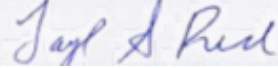
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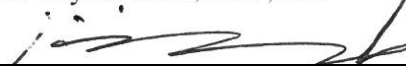
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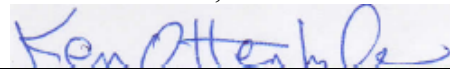
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**by**

**Figaro L. Loresto Jr., BSN, RN**

**Dissertation**

Presented to the Faculty of the Graduate School of  
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## **Dedication**

To my parents, exemplars of sacrificial love

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This dissertation has been an arduous journey...a journey that would have been left unfinished if not for the guidance, support, and love of those around me. To them, much gratitude and acknowledgements are deserved and expressed.

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Finally, to my Heavenly Father who named me, provided for me, and given me a passion to live life, loving Him and those around me. You are my all.

**Exploring the use of social network analysis on physician networks  
created from Medicare data through studying the use of minimally  
invasive breast biopsy among physicians: Descriptions, regressions, and  
network models**

Publication No. \_\_\_\_\_

Figaro L. Loresto Jr., PhD

The University of Texas Medical Branch, 2018

Supervisor: Daniel Jupiter

Social Network Analysis (SNA) has been applied in a variety of scientific fields. In particular, SNA has been utilized with Medicare data to study the structure of physician networks. We utilized SNA to elucidate the structure of physician networks derived from Medicare data, to gain a better understanding of variation in treatment patterns ascertained from Medicare data. This was in service of a fuller exploration of utility of SNA use on networks derived from Medicare data. With the main context being the use of minimally invasive breast biopsy among physicians in Texas, our aims were to assess whether network structure, as identified by SNA, and measures derived from these networks, are useful as supplements to standard statistical models such as hierarchical regression. Further, we aimed to build social network models, specifically exponential random graph models and network autocorrelation models, in exploring the structure of physician networks and in determining if social relationships affect the outcome of interest. Our results reveal that network analysis has potential in not only controlling for variation in regression models but in also highlighting the importance of physician

relationships and network positions in health outcomes and health outcomes research. However, a better understanding of the interpretation of these physician networks derived from Medicare data is needed in order to fully tap into the potential of network analysis in health services research.

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## List of Abbreviations

ACO	Accountable Care Organization
ACSA	Ambulatory Care-Sensitive Hospital Admission
CPT	Current Procedural Terminology
ERGM	Exponential Random Graph Models
HLRM	Hierarchical Logistic Regression Model
ICC	Intraclass Correlation Coefficient
ICD	Implantable Defibrillation
MCMC	Markov Chain Monte Carlo
MEDPAR	Medicare Provider Analytic and Review File
NCCN	National Comprehensive Cancer Network
NPI	National Provider Identification
OUTSAF	Outpatient Standard Analytic File
PCP	Primary Care Physician
RGV	Rio Grande Valley
SNA	Social Network Analysis



## **SECTION 1: BACKGROUND**

### **Section 1.1: Introduction and Brief History of Social Network Analysis**

People are “embedded in thick webs of social relations and interactions” (Borgatti, Mehra, Brass, & Labianca, 2009). This idea has garnered much attention in social science and has led to the formal study of social relations in networks. Such a web of social relations, or a social network, can be described as a “specific set of linkages between a defined set of social actors” (Walker, 1969). Social Network Analysis (SNA) provides a formal framework within which to study these social relations. Formally, social networks are represented as graphs of nodes (actors) and edges (relationships) that mathematically represent the social relations, linkages, or interactions between these nodes.

This mathematical representation allows the tools of graph theory to be used to formalize and analyze these networks, and the social relations they represent (Hollstein, 2014). Specifically, network measures such as degree, centrality, and transitivity provide numerical values that represent social structure and social phenomena. For example, degree, a basic network measure describing the number of connections a node has to other nodes within a network, can be used to describe the potential for social activity for that node (Robins, 2015).

Some believe that SNA traces its beginnings at least to Jacob Moreno and his work in the 1930s. Moreno was a developmental psychologist studying role assignment of elementary school students. In the course of his work, he developed a methodology for collecting data that has become widely used in SNA (Carrington, 2014; T.W. Valente,

2010). His methodology involved the collection of names of students deemed to be fit for certain roles, such as leader, friend, etc. These names were given by students, who would “nominate” their peers for the roles listed above (T.W. Valente, 2010). The data produced from this methodology provided insight into the social structure of the groups of students studied by Moreno. From this information, he identified students who were likely to be more socially popular and mentally healthy, as defined by receiving more nominations for friends and leaders (T.W. Valente, 2010). He was then able to target therapeutic activities to students who were less mentally healthy (Carrington, 2014). Further, Moreno is credited with having coined the term “sociometry”, the methodology described above, and with developing the “sociogram”, a visual representation of his data (Carrington, 2014).

By the 1950s, the relationship and similarity between the sociogram and graph theory had become widely understood. Various research groups began exploring and applying graph theoretic concepts to their work on social structure within communities. Two prominent groups became centers for development of this methodology: the Manchester Anthropologists and the Harvard Structuralists (Carrington, 2014; T.W. Valente, 2010). The Manchester Anthropologists applied sociometric methodologies and ethnographic methods to study urban life in Britain and Africa (Carrington, 2014; T.W. Valente, 2010). Aware of Moreno’s work, they applied his methods to visualizing and to analyzing sociometric data (Carrington, 2014). Work emerged from this group suggesting that structured interactions between individuals within a specific urban community affect everyday life (T.W. Valente, 2010). The second group, the Harvard Structuralists, used sociograms to visualize and analyze social structures of various communities, specifically

communities in the Deep South (Carrington, 2014). These structuralists, so called because of their emphasis on network structure, became foundational in the development of a social network research paradigm within the United States (T.W. Valente, 2010).

From the 1960s to the present, SNA has seen an increase in scope, not only in the fields to which it has been applied, and in which work has been published, but also in terms of the mathematical methodologies developed for its application (Carrington, 2014; T.W. Valente, 2010). Presently, SNA sees utility in multiple disciplines such as economics, epidemiology, and physics (Carrington, 2014). This increase in scope is related to the increasing and continued development and sophistication of statistical and mathematical models utilized to analyze networks (Carrington, 2014). As Carrington states, “the use of mathematical models in social networks analysis supports incredible cross-fertilization across substantive areas” (2014).

## **Section 1.2: Social Network Analysis in Health Care**

Research in healthcare utilizes SNA methodology in various ways. Valente divides the use of SNA in health care into five categories: the study of social support and its impact on health; the study of HIV/STDs transmission; examination of community health interventions; research on inter-organization collaborations to improve health service provision; and understanding health provider performance (2010). As an example of these applications, network methodology allows identification of key players and opinion leaders within a network. One study identified physicians who were such key players in their network, and used these key players to promote vaginal birth after a first cesarean (VBAC) birth (Lomas et al., 1991). Hospitals that utilized these identified key

players as change agents had higher VBAC rates as compared to hospitals that did not utilize these key players.

Another example of SNA utilization in health care involved understanding how physicians adopt new innovations. Health care is an evolving field, with new innovations and treatments constantly being developed and introduced. In a classic study of diffusion of innovation (the process whereby new ideas spread within networks), prescription patterns of a new drug, tetracycline, among physicians in private medical practices in Illinois were studied (Coleman, Katz, & Menzel, 1957). The authors concluded that early adopters of tetracycline tended to be physicians who were more integrated into their networks: i.e., the networks in which these adopters practiced were cohesive (Coleman et al., 1957). Multiple re-analyses have been conducted of the same data set, resulting in a variety of apparently contradictory findings (M Kilduff & H. Oh, 2006). One study found that it was not cohesion but rather structural equivalence, or similarity “in patterns of relations with other individuals”, that impacted early adoption (Burt, 1987; M Kilduff & H. Oh, 2006). Subsequent analyses have found that neither cohesion nor structural equivalence affected adoption, or alternatively that both cohesion and structural equivalence affected adoption (P.V. Marsden & J. Podolny, 1990; Strang & Tuma, 1993; van den Bulte & Lilien, 2001). The authors of these papers used different approaches and perspectives, which lead to their differing results. However, the majority of the authors alluded to physician relationships affecting the adoption of the new drug, in one way or another.

### **Section 1.3: Social Network Analysis and Medicare Data**

### **SECTION 1.3.1: BACKGROUND**

SNA has been used in studies utilizing administrative databases such as Medicare. One particular study has validated a method using Medicare data in the identification of collaborative relationships (Barnett, Landon, O'Malley, Keating, & Christakis, 2011). In this study, Barnett et al. utilized Medicare data from a Boston Hospital referral region (2011). They created a physician network where nodes are physicians and two physicians are said to have a tie, or share a patient, if both physicians submit a claim for that same patient (Barnett et al., 2011). This Medicare derived network was compared to a network derived from a web-based questionnaire asking about a physician's collaborative relationships. Barnett et al. found that the greater the number of shared patients, the more likely it is that the two physicians have a collaborative relationship (82% with nine shared patients) (2011).

The above method has been applied in a variety of studies using administrative databases to create and to study networks. One study utilized this method to identify professional physician collaborative networks within hospital referral regions (HRR) (Landon et al., 2012). Network characteristics, such as degree, were compared and found to vary between physician collaborative networks (Landon et al., 2012). Another study utilized the Barnett et al. SNA methodology to help identify potential accountable care organizations (ACOs), suggesting that the networks discovered using SNA methodology and Medicare data were suitable candidates for ACOs (Landon et al., 2013). Another study examined how hospital-based physician networks and their structure affect spending and utilization of hospital services (Barnett et al., 2012). Barnett et al. found that physicians with higher normalized degree (number of physicians whom they share

patients, divided by the total number of patients shared with other physicians) are more likely to have higher spending and health care utilization (2012).

One study sought to explore how network communities, or tightly connected sub-networks within a physician network, impact the treatment of prostate cancer (Pollack, Weissman, Bekelman, Liao, & Armstrong, 2012). The authors found that prostatectomy rates differed between communities within a physician network (Pollack et al., 2012). Using a similar methodology, another study expanded this work to determine if urologist network characteristics such as community assignment and degree affected rates of complication after radical prostatectomy (Pollack, Wang, et al., 2014). Using a generalized linear mixed-effects model with patients nested within urologists and urologists nested within network communities, this study suggested variation of complication rates across urologist communities. Furthermore, urologist's average degree significantly affected complication rates (Pollack, Wang, et al., 2014).

Another study utilized SNA methodology to determine whether providers who have more shared patients with other providers provide higher quality of care at lower cost (Pollack, Frick, et al., 2014). Using network methodology, the authors created a metric called "care density", a patient-level measure describing "the amount of patient-sharing among his or her outpatient providers" (Pollack, Frick, et al., 2014). The authors suggested that those providers with higher "care density" tend to have aspects of higher quality of care and lower cost of care (Pollack, Frick, et al., 2014).

Utilizing SNA methodology to create networks using Medicare data, Casalino et al. attempted to determine if physician network characteristics affected ambulatory care-sensitive hospital admissions (ACSAs) (2015). ACSA's are admissions for disease

processes, such as congestive heart failure, that are preventable with appropriate primary care (Casalino et al., 2015). Physician networks were built using the methodology described in Barnett et al., resulting in 417 physician networks across five states (Casalino et al., 2015). The authors found that ACSA rates varied significantly between networks, with a 46% difference in rates of admission between the communities at the 25<sup>th</sup> percentile and 75<sup>th</sup> percentiles of admission performance (Casalino et al., 2015). Conducting a multivariate analysis, they found that network structure characteristics, such as number of primary care physicians, affected ACSA rate, suggesting that networks with larger number of primary care physicians have higher ACSA rates (Casalino et al., 2015). Within the same model, they found that a physician's degree significantly and positively affected ACSA rate; however, this effect was small (0.003) (Casalino et al., 2015).

A further study utilized SNA methodology to explore physician collaboration networks, and also utilized exponential random graph models (ERGMs, see Section 5) to understand underlying structures of these physician collaboration networks (Uddin, Hossain, Hamra, & Alam, 2013). Further, Uddin et al. related network measures, such as density (proportion of observed edges over total possible number of edges), to total hospitalization costs and to readmission rates. The purpose was to explore correlations between physician collaboration and patient outcomes (2013). This study concluded that density of physician collaboration networks is positively correlated with hospitalization costs and readmission rates (Uddin et al., 2013). The ERGMs used in this study revealed that the 2-star parameter (see Section 5) has significant impact on hospitalization costs (Uddin et al., 2013). Furthermore, Uddin et al. assessed the variation in healthcare

spending and readmission rates between community networks (Uddin, Kelaher, & Piraveenan, 2015). This study suggests that spending and readmission rates vary across physician communities, and that average number of nodes per community is positively correlated with readmission rates (Uddin et al., 2015).

Moen and colleagues studied hospital specific networks derived from Medicare data, using SNA methodologies, to understand physician adherence to use of implantable defibrillators (ICDs) (Moen, Austin, Bynum, Skinner, & O'Malley, 2016). The authors found that centrality measures such as degree do not have an effect on ICD adherence (Moen et al., 2016). Moen et al. utilized ERGMs to examine homophily (the tendency for similar individuals to form ties) within their physician networks (2016). Results varied between hospitals. As an example, at one hospital, St. Mary Medical Center, pairs of cardiologists and emergency physicians were more likely to form ties as compared to other specialties (Moen et al., 2016).

### **SECTION 1.3.2: LIMITATIONS AND OPPORTUNITIES**

Many of the studies mentioned above utilized basic bivariate statistics to study SNA metrics. Several employed logistic regression or multi-level models with SNA metrics as main effects. However, opportunities still exist in this area, as most studies focus on one level of analysis (network level, community level, or physician level, see Section 2), or one network metric (degree or density), to the exclusion of others. For example, in the study of Pollack et al. on prostatectomy rates, the density of a community could have been used as an additional explanatory variable in the logistic regression, to understand whether cohesive communities have higher or lower prostatectomy rates (2012).

Further, to the best of our knowledge, there is a lack of research as to whether network communities can be used to supplement standard statistical analysis such as hierarchical regressions. In hierarchical regression using Medicare data, hospitals, referral regions, or service areas are often utilized as levels within which physicians are nested. Network communities are another level within which physicians could be nested, but the impact of using this level has not been systematically evaluated. Nor has there been formal comparison of the explanatory power from using different types of levels.

Another aspect of SNA that many current studies utilizing Medicare data do not address, by nature of their analysis plans, is the dependency structure of social networks. Network measures on individual actors have inherent interdependency, as the data is itself relational (Kolaczyk, 2009). To understand and to leverage these dependencies in examining network structure requires modeling tools such as ERGMs. Furthermore, network autocorrelation models could also be utilized in such a setting to model how network structures can affect outcomes, while accounting for network dependencies.

## **Section 1.4: Overview of Minimally Invasive Breast Biopsy Context**

In this work, we wish to address the limitations and opportunities outlined in Section 1.3.2. The context in which we examine the extension of the use of SNA in Medicare data is the rate of use of minimally invasive breast biopsy (MIBB), as recorded in Medicare data.

In 2009, the National Comprehensive Cancer Network (NCCN) set recommendations that at least 90% of initial diagnostic biopsies for breast or mammographic abnormalities be minimally invasive (Bevers et al., 2009). Compared

with open (operative) biopsy, MIBB offers several advantages such as lower cost and lower complication rates (Verkooijen et al., 2002). However, recent studies have demonstrated that MIBB rates for initial biopsies are well below the 90% recommended in the NCCN guidelines (Breslin et al., 2011; Clarke-Pearson et al., 2009; Holloway, Saskin, Brackstone, & Paszat, 2007; Williams et al., 2011; Zimmermann et al., 2013). Zimmerman et al. characterized regional variation in the use of MIBB (2013). Another study demonstrated that significant variation in the use of MIBB exists within and between facilities and between physicians (Tamirisa et al., 2015). After adjusting for surgeon factors, the use of MIBB ranged between facilities from 7.5% to 96.0% (median = 49.2%). After adjusting for hospital factors and surgeon characteristics, the use of MIBB ranged between surgeons from 8.0% to 87% (median = 50.9%) (Tamirisa et al., 2015).

It is known that physician relationships affect the diffusion of new ideas, such as the use of MIBB, as well as medical decision-making (Burt, 1987; Coleman et al., 1957; M Kilduff & H. Oh, 2006; P.V. Marsden & J. Podolny, 1990; Strang & Tuma, 1993; van den Bulte & Lilien, 2001). Thus, studying these physician relationships adds a new perspective in explaining the variation in MIBB utilization. SNA applied to examining a physician's network of relationships provides a methodology for exploring how these physician relationships affect the use of MIBB. A full exploration of this perspective requires more than simply looking at the network measures; rather it needs an in depth look at the way in which networks of physicians are formed, and how their structures impact behavior.

## **Section 1.5: Specific Aims**

The overall goal of this work is to explore the utility of SNA in examining Medicare data within the context of studying MIBB rate. To this end, this work has the following specific aims.

- Aim One: Determine whether regression utilizing SNA characteristics of physician networks explains more variation in treatment patterns than standard hierarchical analyses with hospitals as a third level.
- Aim Two: Model physician networks using ERGMs and network autocorrelation models to gain further insight into network structure, and how network structure impacts patterns of treatment.

This work will be organized as follows:

- Section 2 provides details about the methods of network creation utilized, and the network measures considered.
- Sections 3 and 4 provide details about the methods used in Aim One, specifically the regression methods used in this study, and also present relevant results. Section 3 focuses on a global perspective, considering measures and methodologies for network-level analysis. Section 4 focuses on a local perspective, considering measures and methodologies for nodal-level analysis.
- Sections 5 and 6 details ERGMs and network autocorrelation methodologies and relevant results.
- Section 7 discusses the results described in the previous Sections.

## **SECTION 2: GENERAL METHODS: A DESCRIPTION OF DATA, NETWORK CREATION, AND NETWORK MEASURES**

### **Section 2.1: Cohort Selection**

This study utilizes the 100% Texas Medicare data, a data set that contains the total enrollment and claims files for Medicare beneficiaries within Texas. As in Tamirisa et al., the patient cohort was obtained from the following files: Denominator File, Outpatient Standard Analytic File (OUTSAF), Carrier Standard Analytic File, and Medicare Provider Analysis and Review File (MEDPAR) (Tamirisa et al., 2015). The Denominator File contains demographic and enrollment data for each beneficiary; claims for outpatient facility services and physician services were obtained from the OUTSAF and Carrier Standard Analytic Files; and MEDPAR was used for any inpatient hospital claims data. Census data was used to provide ZIP code-level education and income estimates.

We selected patients from seven metropolitan regions in Texas. These regions were chosen to incorporate geographic diversity within Texas. Using the Office of Management and Budget delineations of metropolitan regions, we defined our regions by counties (Budget, 2013). The regions selected are as follows: Austin, Dallas, El Paso, Houston, Lubbock, San Antonio, and Rio Grande Valley. We focused on four years: 2009 to 2012. For each year from 2009 to 2012, we conducted cohort selection and network creation, as described in what follows.

### **Section 2.2: Physician Identification**

To identify our physicians, those who treat breast cancer patients, we first needed to identify breast cancer patients. We identified these patients based on the following inclusion and exclusion criteria from Tamirisa et al.: women with age greater than or equal to 66; who had a breast biopsy within the year of interest; with continuous enrollment in Medicare Part A & B in the year of interest, and with no health maintenance organization coverage in the twelve months prior to and after diagnosis; and who received breast cancer diagnosis as confirmed by the resection of the tumor after biopsy. Restricting our cohort to patients with cancer diagnosis ensures that the MIBB procedure is specific to breast mass (2015). As in Tamirisa et al., we utilized the following Current Procedural Terminology (CPT) codes for the identification of biopsies and mastectomies: 19100, 19101, 19102, 19103, 10021, 10022, 19110, 19120, 19125, 19126, 19160, 19162, 19301, 19302, 19303, 19304, 19305, 19306, 19307, 19180, 19182, 19200, 19220, and 19240 (2015). We used the following ICD-9 codes for the identification of breast cancer: 174.0 and 233.0 (Tamirisa et al., 2015).

We restricted our attention to physicians involved in the care of breast cancer patients. This allowed the study of important relations that impact physicians', and specifically surgeons', use of MIBB, while excluding relationships that might pertain to other aspects of care. We examined four types of physicians: primary care physicians, biopsy physicians, surgeons, and radiologists. Primary care physicians (PCPs) are physicians of selected specialties (family practice, general practice, or internal medicine) involved in the primary care of a patient. PCPs were identified from Medicare data using an algorithm developed by the Dartmouth Institute (Goodman et al., 2003). Surgeons are the physicians who did the breast surgery, and radiologists are those who read the

mammograms. Biopsy physicians are the physicians who did the breast biopsy of the patients, and were either radiologists or surgeons. Physicians were identified using their National Provider Identification (NPI) number to obtain specialties and demographic information. Patients were assigned to physicians based on plurality of visits (PCPs) or of procedure claims (biopsy physicians, surgeons, or radiologists). Furthermore, each physician was assigned a metropolitan region and hospital for each year based on the plurality of patient visits (PCPs) or procedure claims (for biopsy physicians, surgeons, and radiologists) for breast cancer patients for that year.

### **Section 2.3: Network Creation**

To create the physician networks, where physicians are nodes and edges are shared patients, we utilized the shared patient model validated by Barnett et al. (Barnett et al., 2011). Each edge is valued, or weighted, based on the number of patients shared by the two physicians connected by the edge. Two physicians share a patient if both physicians submit a claim for that same patient within a specified period of time, for us, the year of study. According to Barnett et al., the more patients that two physicians share, the more likely they are to be collaborators (2011). In their study, among physician pairs who shared nine or more patients, 82% of these physician relationships were verified by survey as being real collaborative relationships (Barnett et al., 2011). Following Barnett et al., we say that two physicians have a collaborative relationship if they share nine or more patients, and no collaborative relationship if they share eight or fewer patients (2011). Since our interest is in the presence of collaboration, we did not use weighted ties

beyond network construction, and in the calculation of the network measure of strength (see Section 2.4.2).

To build our physician collaboration network we began with a bipartite network. A bipartite network is one in which nodes are divided into two disjoint groups, and in which all connections are between and not within those groups: e.g., people and their memberships in organizations, or patients and their relationships to physicians (Moen et al., 2016). We are ultimately interested in studying physician-to-physician networks; thus, we next transformed the bipartite network into a unipartite network, where physicians are connected to physicians. Specifically, we created an incidence matrix consisting of patient-physician relationships, with each row representing a patient and each column representing a physician. The entry for each row and column represents whether a claim was submitted by that physician for that patient. Using matrix multiplication, we built the physician-physician adjacency matrix, a matrix where the rows and columns are physicians, and the entry in a given row and column represents the total number of shared patients for that pair of physicians. This procedure creates a unipartite network of physicians with weighted edges (Barnett et al., 2011; Landon et al., 2012). Then, as we are only interested in whether a collaborative relationship exists, those edges with weight nine or greater were kept, and given a value of 1, and those edges with weight less than or equal to eight were given a value of 0. Further, we deleted any nodes that were not connected to any other nodes.

The original cohort only contained claims from breast cancer patients, and the physicians involved in the care of these patients. It did not include any other claims from those physicians. This exclusion could have led to us missing other shared patient

interactions between these physicians, for those patients who were not breast cancer patients. To capture these interactions, we expanded our cohort: for the year of interest, we obtained all claims for all patients submitted by the physicians in our original physician cohort, not just those with breast cancer. It is this fuller data set that we used to create our collaboration network above.

## Section 2.4: Network Measures

### SECTION 2.4.1: NETWORK MEASURES AND CONNECTIVITY

Network measures are values calculated within networks describing relationships between nodes, and positions of nodes within networks. These measures can supplement information usually derived from claims data, allowing the introduction of these relational and positional measures into studies of claims data. The measures can be examined locally, studying characteristics of individual physicians; or globally, studying average measures over regions, communities, or entire networks; or by using network-wide versions of local measures. Table 2.1 summarizes the local and global measures of interest in this study. We explicitly note that the calculation of these network measures is based on an undirected network, a network where the edges have no direction, and based on unweighted edges (with the exception of strength, see below).

Before defining network measures, it is useful to discuss movement and connectivity within networks. We define a *walk* on graph  $G$  from node  $i$  to  $j$  as a sequence of nodes and edges, where each edge is a connection between the node prior to and the node subsequent to it, on the walk. Within this sequence, nodes  $i$  and  $j$  are the endpoints of the sequence (i.e., node  $i$  to edge  $ik$  to node  $k$ , ..., node  $k'$ , edge  $k'j$ , node  $j$ )

(Kolaczyk, 2009). *Walks* are further differentiated into *trails*, which are walks without repeated edges; and *trails* are further differentiated into *paths*, which are trails without repeated nodes (Kolaczyk, 2009). Two nodes in a network are said to be *reachable* from each other if there is a walk between them. A *connected* network is defined as a network  $G$  where every node is reachable from every other node (Kolaczyk, 2009). A *subnetwork*  $G'$  of a network  $G$  is a network consisting of a subset of the nodes in  $G$ , and a subset of those edges in  $G$ , connecting the nodes in  $G'$ . A *triangle* is a complete sub-network of three nodes and three edges. A *connected triple* is a sub-network with three nodes and exactly two edges.

The *length* of a path is defined as the number of edges in the path (Kolaczyk, 2009; Moen et al., 2016). The shortest path (there may be more than one), or *geodesic* path, between a pair of nodes is an important ingredient of many network measures. Its length, or the *geodesic distance*, is calculated as the number of edges in the geodesic path (Kolaczyk, 2009; Moen et al., 2016).

**Table 2.1: Network Measures of Interest**

Variable	Formula	Interpretation
<b>Local (Nodal) Level</b>		
<i>Degree</i>	$Deg_i = \sum_{j \in N_i} e_{ij}$	--Larger values indicates greater potential for social activity (Freeman, 1976)
	where $e_{ij} = 1$ if and only if nodes $i$ and $j$ are connected by a tie	--Can be used to describe the whole network by plotting the distribution of all degrees in a network
<i>Strength</i>	$Str_i = \sum_{j \in N_i} w_{ij}$	--A weighted extension of the degree measure
	where $w_{ij}$ is the weight of the edge connecting nodes $i$ and $j$	--In our context, an approximation of the physician's patient load

**Betweenness Centrality**

$$C_{Bij} = \sum_{j < k} \frac{g_{ijk}}{g_{jk}}$$

where  $g_{ijk}$  is the number of geodesic paths between  $j$  and  $k$  that include  $i$ , and  $g_{jk}$  is the total number of geodesics between  $j$  and  $k$

--Can be interpreted as a given node's "control" of communication within a network (Robins, 2015; Freeman, 1979)

**Closeness Centrality**

$$C_{cij} = \frac{1}{\sum_j d_{ij}}$$

where  $d_{ij}$  is the geodesic distance between node  $i$  and all other nodes within the network  $j$

--A small value of closeness centrality indicates lesser importance, as compared with a large value

--Often interpreted as a measure of diffusion of flow within networks, or the influence of a given node on such flow (Robins, 2015)

**Transitivity (Local)**

$$C_i = \frac{\tau_{\Delta}(i)}{\tau_3(i)}$$

where  $\tau_{\Delta}(i)$  is the number of triangles (closed triples) containing node  $i$  in the network, and  $\tau_3(i)$  is the number of connected triples containing node  $i$

--Indicates the level of closure, or the extent to which "friends of friends are friends", around the given node (Robins, 2015)

**Global (Network) Level****Density**

$$Dens(G) = \frac{2E}{n(n-1)}$$

where  $E$  is the total number of edges within the network, and  $n$  is the number of nodes within the network

--Interpreted as the potential for social activity within the network

--A denser network may provide the opportunity for more social activity (Robins, 2015; Valente, 2007)

**Betweenness Centralization**

$$C_B(G) = \frac{2 \sum (\max(C_{Bij}(G)) - C_{Bij})}{n^2 - 3n + 2}$$

where

$$C_{Bij} = \sum_{i < k} \frac{g_{ijk}}{g_{ik}}$$

$g_{jik}$  = the number of geodesic paths connecting  $i$  and  $k$  including  $j$ ,

$g_{ik}$  = the total number of geodesic paths connecting  $i$  and  $k$ ,

$\max(C_{Bij}(G))$  = the maximum value of  $C_{Bij}$  in the network,

$n$  = number of nodes of in the network

--Measures the tendency of a network to focus on a few individuals as points of collaboration (Freeman, 1978)

--A high value may indicate a highly centralized network and the potential presence of hubs that can control communication, information, or collaboration (Valente, 2007)

**Transitivity (Clustering Coefficient)**

$$C_i(G) = \frac{1}{n} \sum_{i=1}^n C_i$$

--A higher value indicates that the nodes within the network tend to cluster into smaller groups (Robins, 2015)

where  $C_i = \frac{\tau_{\Delta}(i)}{\tau_3(i)}$ ,  $\tau_{\Delta}(i)$  is the number of triangles (closed triples) that include node  $i$ , and  $\tau_3(i)$  is the number of connected triples that include node  $i$

**Characteristic Path Length**

$$c = \frac{1}{m} \sum_{i=1}^m d_i$$

--Small values indicate the ease of spread of information or resources through the network (Telesford et al., 2011)

where  $d_i$  is the geodesic path length and  $m$  is the number of geodesic paths

## SECTION 2.4.2: LOCAL MEASURES

*Degree* is a basic network measure defined as the number of direct connections a node has to the other nodes within the network, or the number of edges adjacent to the node. It is formally defined as:

$$Deg_i = \sum_{j \in N_i} e_{ij},$$

where  $e_{ij} = 1$  if and only if  $i$  and  $j$  are connected by an edge. A larger value indicates more potential for social activity, as the node has more connections to other nodes, as compared to nodes with smaller degree (Freeman, 1979).

Furthermore, while the degree of each node is a local property, the totality of degrees in a network can be used to describe the whole network. Plotting the distribution of all degrees within a network is an example of this type of description. This distribution of all degrees in a network is a basic topological feature.

*Strength* is an extension of degree to weighted networks, given by the following formula:

$$Str_i = \sum_{j \in N_i} w_{ij},$$

where  $w_{ij}$  is the weight of the edge connecting nodes  $i$  and  $j$ . While our main interest is unweighted collaboration networks, we included this measure in our analysis as a measure to approximate a physician's patient load.

*Betweenness centrality* of the node  $i$  is defined as:

$$c_{bij} = \sum_{j \neq k} \frac{g_{ijk}}{g_{jk}},$$

where  $g_{ijk}$  is the number of geodesics between  $j$  and  $k$  that include  $i$ , and  $g_{jk}$  is the total number of geodesics between  $j$  and  $k$  (Freeman, 1979; Robins, 2015). In our context, it is a measure of how frequently physician  $i$  appears on the geodesic paths between all other physician pairs. This measure describes the relative importance of a node, interpreted as a given node's 'control' of communication within a network (Freeman, 1979; Robins, 2015).

*Closeness centrality* of a given node is the inverse of the sum of all geodesic distances from that node to all others (Freeman, 1979; Robins, 2015). Closeness is given by the formula:

$$c_{cij} = \frac{1}{\sum_j d_{ij}},$$

where  $d_{ij}$  is the geodesic distance between  $i$  and  $j$  (Freeman, 1979). A small value of closeness centrality indicates that a node is less important or central, as compared to a node with a larger value of closeness centrality. Closeness centrality is often interpreted as a measure of diffusion or flow within networks (Robins, 2015).

*Transitivity* of node  $i$  is formulated as follows:

$$c_i = \frac{\tau_{\Delta}(i)}{\tau_3(i)},$$

where  $\tau_{\Delta}(i)$  is the number of triangles in the network that contain node  $i$ , and  $\tau_3(i)$  is the number of connected triples containing node  $i$  (Kolaczyk, 2009). Nodal transitivity describes the local density of a given node, and indicates the level of closure around that given node; whether “friends of friends are friends” (Robins, 2015). As an example, high transitivity would indicate that the physician is included in more closed sub-networks of physicians. Low transitivity would indicate the opposite.

### SECTION 2.4.3: GLOBAL MEASURES

The global network statistics we considered for this study are as follows: density, betweenness centralization, transitivity (clustering coefficient), and characteristic path length. These measures describe the whole network, rather than just individual nodes.

The *density* is the number of ties in a network relative to the number of total possible ties within a network. It is defined as follows:

$$Dens(G) = \frac{2E}{n(n-1)}$$

where  $E$  is the total number of edges within the network and  $n$  is the number of nodes within the network. This measure is sometimes interpreted as the potential for social activity, as with higher density there are more pathways for collaboration or interaction (Robins, 2015; T.W. Valente, 2010). Density is affected by network size (A. Smith, Calder, & Browning, 2016); as we are comparing density between regions with varying network sizes, we *normalize* density by dividing the measure by the number of nodes in the network.

*Betweenness centralization* is a network level measure of betweenness centrality (see Section 2.4.2). This measure tests the tendency of a network to focus on a few

individuals as points of collaboration or information flow (Freeman, 1979). It is calculated as follows:

$$C_B(G) = \frac{2 \sum (\max(C_B(G)) - C_{Bij})}{n^2 - 3n + 2},$$

where

$C_{Bij}$  is the betweenness centrality (see Section 2.4.2),  $\max(C_B(G))$  is the maximum  $C_{Bij}$  in the network, and  $n$  is the number of nodes in the network.

A high betweenness centralization value may indicate a highly centralized network. According to Valente, highly centralized networks have the potential presence of hubs that can control communication, information, or collaboration (T.W. Valente, 2010).

*Transitivity* is the tendency within a network that “the friend of my friend is my friend” (Robins, 2015; Salter-Townshend, White, Gollini, & Murphy, 2012). It is defined as:

$$C_t(G) = \frac{1}{n} \sum_{i=1}^n C_i,$$

where  $C_i$  is the local transitivity (see section 2.3.2). A higher value of transitivity indicates that the nodes within the network tend to cluster together into smaller groups (Robins, 2015).

*Characteristic path length* is the mean of all geodesic distances within a network. Formally, it is defined as follows:

$$c = \frac{1}{k} \sum_{l=1}^k d_l,$$

where  $d_l$  is the geodesic distance of geodesic  $l$ , and  $k$  is the number of geodesic paths. Small characteristic path lengths allow for the easy spread of information or

resources through the network (Telesford, Joyce, Hayasak, Burdette, & Laurienti, 2011).

## **Section 2.5: Network Communities**

Communities are tightly connected sub-networks within a network. There is much interest in the study of communities in network science, as many networks of scientific interest can be naturally divided into these sub-networks (Karrer, Levina, & Newman, 2008). Per Karrer et al., through the exploration of these communities, an investigator can gain further insight into the functionality of complex networks (2008).

Communities have been studied in social network studies utilizing Medicare data. Within physician networks created from Medicare data, Pollack et al. created communities using the Girvan-Newman algorithm described below, and compared the prostatectomy rates between these communities (Pollack et al., 2012). This study concluded that within a physician network in a given city, communities varied in prostatectomy rates (Pollack et al., 2012). This illustrated variation in treatment patterns within cities that may not have been seen without looking at communities. Landon et al. utilized communities as a potential method for identifying groups of physicians suitable for becoming Accountable Care Organizations (ACOs), which are groups of physicians who “work within the current framework of current fee-for-service that also guarantees beneficiaries the flexibility to go to any participating provider they choose” (Landon et al., 2013).

Many algorithms exist to detect communities in networks. Girvan and Newman developed an algorithm to detect these sub-networks by maximizing betweenness

centrality of edges, also known as edge betweenness, within each derived community (Girvan & Newman, 2002). Edges that possibly separate communities are sequentially removed. A goodness-of-fit test known as modularity is used to determine the optimal number of communities (Pollack et al., 2012). Modularity refers to “the difference between the number of edges within communities and the expected number of edges under a null model” (Karrer et al., 2008). However, this algorithm is computationally demanding and is not suitable for larger networks. Clauset et al. introduced a fast-greedy algorithm for larger networks that optimizes modularity “by exploiting shortcuts in the optimization problem and using more sophisticated data structures” (Clauset, Newman, & Moore, 2004). This algorithm produces communities that are mutually exclusive, meaning that each node can only belong to one community (Clauset et al., 2004). We utilized this fast-greedy algorithm for detecting communities within our physician networks.

## **SECTION 3: REGIONAL NETWORKS AND COMMUNITIES**

### **Section 3.1: Purpose and Overview of Section**

The purpose of this section is to provide a descriptive and exploratory view of the regional networks at the global level. The goal of this descriptive and exploratory analysis of the regional networks is to inform the regression analyses that we will carry out in Section 4, in service of Aim One. Further, this section contributes to the overall goal of exploring whether network analysis methodology applied to Medicare data has utility in the setting of understanding utilization of MIBB.

In this section, regional networks are described using network measures such as density, and network structures such as number of physicians. These measures are examined for each year from 2009 to 2012. The degree distribution, as described below, is assessed for each regional network for each year from 2009 to 2012.

Next, communities for each region are computed through the use of the fast-greedy algorithm described in Section 2. With communities as the unit of analysis, a simple linear regression will be conducted to assess the effect of selected network measures and structures on community level rates of MIBB. For this analysis, we focus only two years: 2009 and 2012. We restrict to these years because we had a small number of communities, so incorporating years in a multi-level framework is not possible. Further, we in restricting to these years, we are able to compare results from the year the guidelines were established to those a few years later.

Table 3.1 describes the variables we examined in this section, for both the regional and community level analyses. We focus on the following global measures:

degree distribution, density, betweenness centralization, transitivity (clustering coefficient), and characteristic path length. These measures were described and defined in Section 2.

**Table 3.1: Variables Considered in this Section**

Measures	Definition/Operationalization
<i>Network Characteristics</i>	
Number of Breast Cancer Patients	The number of patients within a given region or community.
Ratio of Biopsy Surgeons to Biopsy Physicians	Calculated by dividing the number of surgeons who conducted a breast biopsy within a region or community by the total number of physicians who conducted a breast biopsy within that region or community.
Minimally Invasive Breast Biopsy Rate (MIBB)	Calculated by dividing the number of patients who received MIBB within a region or community by the total number of patients in that region or community.
Nodes	Number of physicians within a given region or community.
Edges	Number of edges between physicians within a given region or community.
<i>Network Measures</i>	
Centralization	Measures the extent to which the edges in the network tend to be concentrated at a small number of central nodes. Defined as in Table 2.1.
Density (Normalized)	The number of edges in the network divided by the number of edges possible in the network.
Transitivity	Quantifies the tendency that if node A is connected to node B and to node C, that node B and node C will be connected. Defined as in Table 2.1.
Characteristic Path Length	Measures the average of all shortest paths connecting two nodes. Defined as in Table 2.1.

### Section 3.2: The Small-world Phenomenon and the Scale-free Property

The small world phenomenon is that a network is highly clustered (has high transitivity) and has small characteristic path length. This results in a network having the property of “regional specialization with efficient information transfer” (Telesford et al., 2011; Watts & Strogatz, 1998). To assess this property, we compare the observed transitivity and characteristic path length in the network of interest to the transitivity and

characteristic path length calculated from simulated random networks, with the exact same numbers of nodes and numbers of edges as the original. Specifically, we use a measure,  $\sigma$ , introduced by Humphries et al. (Humphries, Gurney, & Prescott, 2006). In their approach, ratios of observed transitivity and the mean of the simulated transivities ( $t_\sigma$ ), and of observed characteristics path lengths and the mean of the simulated characteristic path lengths ( $c_\sigma$ ) are computed (Humphries et al., 2006; Telesford et al., 2011). These two ratios yield  $\sigma$ , through the formula  $\sigma = \frac{t_\sigma}{c_\sigma}$ . If  $\sigma > 1$ , then the network is considered small-world.

The scale-free property is directly tied to the degree distribution (Barabasi & Albert, 1999). If the degree distribution of a network follows a power-law, it is generally viewed as being scale-free (Barabasi & Albert, 1999). A power-law distribution is defined by  $p(x) \propto x^{-\alpha}$ , where  $\alpha$  is the exponent or scaling factor (Clauset, Shalizi, & Newman, 2009). The scaling factor  $\alpha$  is typically between 2 and 3 for the power-law distributions most often observed in real world networks (Barabasi & Albert, 1999; Clauset et al., 2009). Per Barabasi and Albert, preferential attachment (tendency of new nodes introduced into the network to connect to nodes with higher degree) can lead to a network having a scale-free degree distribution (1999).

Historically, simple scatter plots of the degree distribution were used to assess the power-law. The scatter is plotted on axes in the logarithmic scale. If the distribution falls in a straight line in this plot, then it is considered to follow a power-law (Clauset et al., 2009). Furthermore, one can calculate the slope of this line to estimate  $\alpha$ . However, Clauset et al. discuss several problems with this approach, such as generation of systematic errors in estimating  $\alpha$ , and difficulty in objectively assessing the power-law by

viewing a line (2009). Thus, Clauset et al. developed a more rigorous methodology to assess whether a distribution follows a power-law. Their approach utilizes both maximum-likelihood fitting methods and goodness-of-fit tests (through the Kolmogorov-Smirnov statistic and likelihood ratios) (2009). A p-value that is significant indicates that the distribution does not follow a power-law.

### **Section 3.3: Analysis Plan**

For each regional network, we described each variable in Table 3.1 through plots showing the variables' trends over time (2009 to 2012). Using transitivity and characteristic path length, we assessed the small-world property as outlined above. For each region and for each year, degree distributions were plotted and the scale-free property assessed through the methods outlined above.

Physician communities were created using the fast-greedy algorithm, separately for each region for each year (see Section 2.4). With these communities as the unit of analysis, we examined patterns of MIBB use. For this analysis we restricted to large communities, defined as communities with ten or more breast cancer patients. Further, we compared these communities between regions for each of the variables, including MIBB rate, described above, utilizing the chi-squared test or ANOVA, as appropriate, separately within each year. We further created scatterplots to display, as an exploration, the relationship between normalized density and betweenness centralization, and the MIBB rate.

Restricting to the years 2009 and 2012 separately, we ran multivariate regression models for rate of MIBB, including all communities in all regions. In this analysis, our

units of analysis are the network communities derived from each network and our outcome is the rate of MIBB per community. The main effects in these models are normalized density and betweenness centralization. These variables are chosen as they are known to impact the dissemination of new ideas within a network (T.W. Valente, 2010). As control variables, we included only the ratio of number of biopsy surgeons to number of biopsy physicians, and transitivity.

Below is the summary of the linear regression model:

$$y_i = \beta_0 + \beta_1 X_i + \beta_2 Z_i + e_i,$$

where

$y_i$  = rate of MIBB for community  $i$ ,

$X_i$  = main effects (density and/or betweenness centralization),

$Z_i$  = community level ratio of biopsy surgeons to biopsy physicians, or transitivity,

$\beta_1$  = regression coefficient associated with degree centralization or density,

$\beta_2$  = regression coefficient associated with ratio of biopsy surgeon to biopsy physician, or transitivity,

$\beta_0$  = intercept,

$e_i \sim N(0, \sigma^2)$ .

As we have a small number of communities, we limited the number of variables in each of the models. Specifically, we proceeded as follows:

- Model 1a-1d: We regressed MIBB rate on each of the main effects and control variables separately.
- Model 2a-2b: We regressed MIBB rate on normalized density, together with each individual control variable.

- Model 3a-3b: We regressed MIBB rate on betweenness centralization, together with each individual control variable.
- Model 4: We regressed MIBB rate on normalized density and betweenness centralization.
- Model 5a-5b: We regressed MIBB rate on both main effects, together with each individual control variable.

Furthermore, we repeat this analysis within regions with five or more large communities.

## **Section 3.4: Results**

### **SECTION 3.4.1: REGIONAL NETWORKS TRENDS**

For this section, we note that our unit of analysis is at the regional network level. Networks are displayed in Appendix A. Trend plots for the network variables of interest are displayed in Appendix B. Dallas had the highest number of physicians, across all years (754 in 2009 and 682 in 2012). Lubbock had the lowest number of physicians across all years (65 in 2009 and 48 in 2012). Generally, over time, the number of physicians was stable in most regions. Dallas and Houston had the largest decrease from 2009 to 2012 (9.5% in Houston and 15.7% in Dallas). Dallas had the highest number of edges across all years (8017 in 2009 and 6860 in 2012). El Paso and Lubbock had the lowest number of edges. Austin had the highest rate of change, with the number of edges decreasing by 35% from 2009 to 2012.

Dallas had the highest number of breast cancer patients across all years (890 in 2009 and 811 in 2012). El Paso and Lubbock had the lowest number of breast cancer patients. The number of breast cancer patients largely remained stable over the years, in

most regions, with the exception of Houston and Dallas, which both experienced decreases (13.8% and 19.8% decrease, respectively). Rio Grande Valley (RGV) had the highest ratio of biopsy surgeons to biopsy physicians, at 60% in 2009 and 51% in 2012. El Paso had the lowest ratio of biopsy surgeons to biopsy physicians at 33% in 2009 and 22% in 2012. There is a trend of a decrease in this ratio, with Lubbock experiencing the highest rate of decrease at 35%.

Lubbock had the highest normalized density at 0.00929 in 2009 and 0.01403 in 2012. Dallas and Houston had the lowest normalized density across all years. Further, Lubbock experienced the greatest increase of normalized density compared to the other regions. There was a 51% increase of normalized density in Lubbock from 2009 to 2012. Betweenness centralization varied across regions from 2009 to 2012. Dallas, Houston, and RGV had an overall decrease in betweenness centralization from 2009 to 2012. Dallas, in particular, had an increase of 57.9% from 2009 to 2012, only to decrease 50% from 2011 to 2012. Austin had a 440% increase in centralization from 2011 to 2012.

Across all years and within all regions, transitivity remained largely stable. In 2009, Lubbock and Austin both had the highest transitivity (0.85). Dallas and Houston had the lowest transitivity (0.77). In 2012, Lubbock had the highest transitivity (0.87), and Houston had the lowest transitivity (0.74). Characteristic path length was mostly stable across all years within all regions. Typically, larger networks had higher characteristic path lengths as compared to smaller networks. This measure ranged from 1 to 3.

Across all years within all regions, MIBB rate was increasing. RGV had the lowest MIBB rate across all years. However, RGV did experience the highest increase (18%) in MIBB rate.

### SECTION 3.4.2: SMALL-WORLD AND SCALE-FREE PROPERTIES

Tables 3.2 and 3.3 display transitivity (observed and simulated), characteristic path length (observed and simulated), and  $\sigma$  measure for all networks. For 2009 and 2012, all regions had  $\sigma$  measures greater than 1. Interpreting this absolutely, all networks display the small world property.

Plots, separately for each region, of the degree distribution across all years are found in Appendix A. Large networks such as Houston and Dallas display unimodal degree distributions; whereas smaller networks such as Lubbock and RGV display bimodal degree distributions. Table 3.4 displays the p-value from the goodness-of-fit tests for the power law described in Clauset et al. (2009). Only RGV (2009 and 2010) and El Paso (2011 and 2012) seem to display a power-law distribution for degree.

**Table 3.2: Small-world Property (2009)**

	Transitivity (Observed)	Transitivity (Simulated)	Characteristic Path Length (Observed)	Characteristic Path Length (Simulated)	$\sigma$
<b>Austin</b>	0.85	0.19	1.88	1.81	4.31
<b>Dallas</b>	0.77	0.03	2.82	2.51	22.8
<b>El Paso</b>	0.83	0.40	1.61	1.60	2.06
<b>Houston</b>	0.77	0.04	2.65	2.29	16.6
<b>Lubbock</b>	0.85	0.59	1.41	1.41	1.44
<b>Rio Grande Valley</b>	0.82	0.20	2.00	1.79	3.67
<b>San Antonio</b>	0.83	0.17	2.01	1.83	4.45

**Table 3.3: Small-world Property (2012)**

	Transitivity (Observed)	Transitivity (Simulated)	Characteristic Path Length	Characteristic Path Length	$\sigma$
--	----------------------------	-----------------------------	-------------------------------	-------------------------------	----------

			(Observed)	(Simulated)	
<b>Austin</b>	0.86	0.17	1.83	1.89	5.22
<b>Dallas</b>	0.77	0.03	2.84	2.51	22.7
<b>El Paso</b>	0.83	0.36	1.63	1.64	2.32
<b>Houston</b>	0.74	0.05	2.66	2.29	12.7
<b>Lubbock</b>	0.87	0.66	1.35	1.34	1.31
<b>Rio Grande Valley</b>	0.81	0.24	1.85	1.76	3.21
<b>San Antonio</b>	0.84	0.15	2.04	1.85	5.08

**Table 3.4: Power Law p-values for all Years and all Regions**

	2009	2010	2011	2012
<b>Austin</b>	<0.001	<0.001	<0.001	<0.001
<b>Dallas</b>	<0.001	<0.001	0.001	<0.001
<b>El Paso</b>	<0.001	0.031	0.084	0.103
<b>Houston</b>	<0.001	<0.001	<0.001	<0.001
<b>Lubbock</b>	<0.001	<0.001	0.001	<0.001
<b>Rio Grande Valley</b>	0.072	0.173	0.016	0.017
<b>San Antonio</b>	<0.001	<0.001	<0.001	<0.001

### SECTION 3.4.3: COMMUNITY LEVEL RESULTS

In this section, we report results only for 2009 and 2012, and we note that our unit of analysis is at the network community level. The fast-greedy algorithm (see Section 2), employed in each region separately, detected 25 large communities in 2009 and 22 large communities in 2012. With communities as units of analysis, there is a significant difference between regions in terms of the mean MIBB rate, with Houston having the highest MIBB rate in 2009 (mean = 0.9, SD = 0.07) and both Dallas and Houston having the highest MIBB rate in 2012 (0.93, 0.2). These results are similar to the MIBB rate results from the analysis of regional networks described in the trend plots above.

**Table 3.5: Community Level Means of Specified Variables, For Community Networks by Region (2009)**

Variables (n = number of large	Austin (n = 4)	Dallas (n = 5)	El Paso (n = 3)	Houston (n = 5)	Lubbock (n = 3)	Rio Grande Valley	San Antonio (n = 3)	<i>p-value</i>
--------------------------------------	-------------------	-------------------	--------------------	--------------------	--------------------	-------------------	------------------------	----------------

communities)					(n = 2)			
Network Characteristics								
MIBB Rate (Mean (SD))	0.86 (0.08)	0.90 (0.03)	0.84 (0.09)	0.91 (0.07)	0.78 (0.13)	0.50 (0.04)	0.71 (0.19)	0.0012
Breast Cancer Patients (Mean (SD))	63.3 (52.9)	178 (126.7)	20 (13.9)	170.3 (100.4)	33 (28.3)	63.5 (26.2)	91.7 (69.8)	0.12
Ratio of Biopsy Surgeons to Biopsy Physicians (Mean(SD))	0.52 (0.19)	0.38 (0.10)	0.43 (0.12)	0.27 (0.14)	0.41 (0.03)	0.61 (0.06)	0.53 (0.21)	0.15
Network Measures								
Number of Nodes (Mean (SD))	61.5 (34.8)	150.8 (97.5)	26.0 (8.2)	138.0 (99.8)	30 (9.9)	71.5 (14.8)	90.0 (53.3)	0.17
Number of Edges (Mean (SD))	635.3 (647.1)	1392.8 (1288.3)	184 (96.6)	1286 (1014.8)	308 (205.1)	943 (227.7)	1368 (1024.4)	0.46
Normalized Density (Mean (SD))	0.01 (0.01)	0.005 (0.009)	0.02 (0.009)	0.005 (0.007)	0.02 (0.007)	0.006 (0.002)	0.007 (0.009)	0.06
Characteristic Path Length (Mean (SD))	1.69 (0.24)	2.21 (0.43)	1.45 (0.05)	2.05 (0.45)	1.34 (0.02)	1.62 (0.07)	1.70 (0.16)	0.03
Centralization Betweenness (Mean (SD))	0.17 (0.04)	0.22 (0.12)	0.09 (0.02)	0.11 (0.01)	0.03 (0.02)	0.06 (0)	0.08 (0.01)	0.01
Transitivity (Mean (SD))	0.86 (0.02)	0.80 (0.04)	0.83 (0.01)	0.81 (0.05)	0.86 (0.007)	0.84 (0)	0.83 (0.03)	0.09
*Bolded variables differ significantly between regions								

In terms of other network characteristics such as the mean number of breast cancer patients and mean ratio of biopsy surgeons to biopsy physicians, there is no significant difference between regions in the years 2009 and 2012. Characteristic path length and betweenness centralization differed significantly between regions in 2009, with Dallas having the highest characteristic path length (2.21, 0.12) and betweenness centralization (0.22, 0.12). Tables 3.5 and 3.6 summarize the above results.

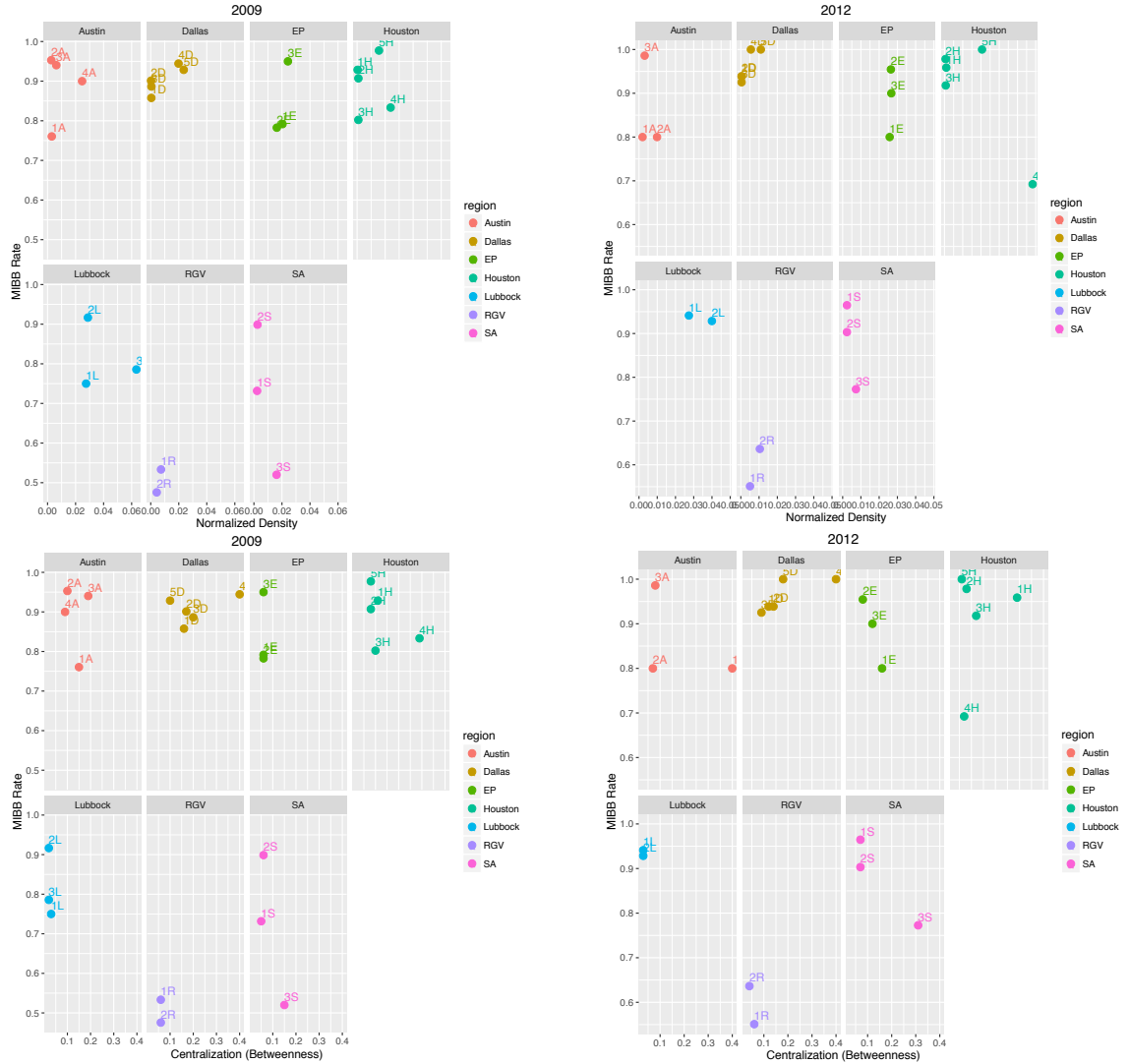
**Table 3.6: Community Level Means of Specified Variables, For Community Networks by Region (2012)**

<b>Variables (n = number of large communities)</b>	<b>Austin (n = 3)</b>	<b>Dallas (n = 5)</b>	<b>El Paso (n = 2)</b>	<b>Houston (n = 5)</b>	<b>Lubbock (n = 2)</b>	<b>Rio Grande Valley (n = 2)</b>	<b>San Antonio (n = 2)</b>	<b>p-value</b>
<i>Network Characteristics</i>								
<b>MIBB Rate (Mean(SD))</b>	<b>0.91 (0.2)</b>	<b>0.93 (0.2)</b>	<b>0.91 (0.2)</b>	<b>0.93 (0.2)</b>	<b>0.90 (0.3)</b>	<b>0.63 (0.4)</b>	<b>0.89 (0.3)</b>	<b>&lt;0.0001</b>
Breast Cancer Patients (Mean/(SD))	63.3 (23.5)	178.6 (147.8)	22.3 (2.1)	139.4 (100.1)	22 (12.2)	63.5 (26.2)	91.7 (72.0)	0.16
Ratio of Biopsy	0.51	0.19	0.48	0.23	0.24	0.49	0.41	0.08

Surgeons to Biopsy Physicians (Mean/(SD))	(0.12)	(0.17)	(0.13)	(0.16)	(0.06)	(0.22)	(0.18)	
<i>Network Measures</i>								
Number of Nodes (Mean/(SD))	74.7 (12.6)	175.8 (126.0)	32 (7.1)	135.5 (117.5)	34 (4.2)	63 (11.3)	90.3 (55.2)	0.39
Number of Edges (Mean/(SD))	595 (23.5)	1151 (985.5)	118.5 (65.8)	841.6 (670.1)	223 (175.4)	779.5 (337.3)	1126.7 (920.3)	0.53
Normalized Density (Mean/(SD))	0.004 (0.0003)	0.10 (0.02)	0.016 (0.005)	0.005 (0.006)	0.018 (0.002)	0.007 (0.001)	0.007 (0.007)	0.65
<b>Characteristic Path Length (Mean/(SD))</b>	<b>1.74 (0.045)</b>	<b>2.10 (0.33)</b>	<b>1.53 (0.04)</b>	<b>2.12 (0.38)</b>	<b>1.41 (0.02)</b>	<b>1.6 (0.0)</b>	<b>1.77 (0.081)</b>	<b>0.024</b>
Centralization Betweenness (Mean/(SD))	0.12 (0.03)	0.19 (0.11)	0.095 (0.05)	0.15 (0.07)	0.04 (0.03)	0.06 (0.007)	0.093 (0.04)	0.19
<b>Transitivity (Mean/(SD))</b>	<b>0.53 (0.07)</b>	<b>0.39 (0.04)</b>	<b>0.62 (0.09)</b>	<b>0.57 (0.16)</b>	<b>0.71 (0.03)</b>	<b>0.56 (0.01)</b>	<b>0.57 (0.07)</b>	<b>0.03</b>

\*Bolded variables differ significantly between regions

Figures 3.1 displays scatterplots of the MIBB rate vs. the main effects for 2009 and 2012, respectively. Recall that these plots were created to display, as an exploration, the relationship between normalized density and betweenness centralization, and rate of MIBB. These plots were further examined by region, displaying how for each region the main effects related to rate of MIBB. For normalized density, there were no discernable patterns in the relationship with the MIBB rate, in looking at all communities in all regions together. However, if we focus our attention within regions, in Dallas and Houston the normalized density appears to have a positive effect on the rate of MIBB for both 2009 and 2012. This is similar to the behavior seen with betweenness centralization. In Dallas, betweenness centralization appears to have a positive effect on the rate of MIBB.



**Figure 3.1: Correlation Plots of Main Effects vs Rate of MIBB by Region for 2009 and 2012.**

Table 3.7 summarizes the linear regression results for 2012. In the Model 1 regression, including all communities in all regions for 2012, normalized density had a negative but non-significant effect on MIBB rate, while betweenness centralization had a positive but non-significant effect on MIBB rate. For the covariates in the same analysis (Model 1), transitivity had a negative non-significant effect, while the ratio of the number of biopsy surgeons to biopsy physicians had a negative significant effect on MIBB rate. Including this ratio in Model 2b, the effects of normalized density intensified. Including

this ratio in the models that include both main effects (Model 5b), the effects of normalized density intensified while the effects of betweenness centralization decreased. Adding transitivity decreased the effects of normalized density (Model 2a and Model 5a).

**Table 3.7: Linear Regression Estimates (2012)**

Variables	Normalized Density	Centralization Betweenness	Ratio	Transitivity
<b>All (n = 22)</b>				
<b>Model 1a</b> (Coef/p-value/R <sup>2</sup> )	-1.90/0.4/0.04	--	--	--
<b>Model 1b</b> (Coef/p-value/R <sup>2</sup> )	--	0.21/0.4/0.04	--	--
<b>Model 1c</b> (Coef/p-value/R <sup>2</sup> )	--	--	<b>-0.38/0.004/0.34</b>	--
<b>Model 1d</b> (Coef/p-value/R <sup>2</sup> )	--	--	--	-0.62/0.3/0.04
<b>Model 2a</b> (Coef/p-value/R <sup>2</sup> )	-1.19/0.6/0.06	--	--	-0.44/0.5/0.06
<b>Model 2b</b> (Coef/p-value/R <sup>2</sup> )	-2.13/0.2/0.39	--	<b>-0.38/0.003/0.39</b>	--
<b>Model 3a</b> (Coef/p-value/R <sup>2</sup> )	--	0.21/0.4/0.09	--	-0.60/0.3/0.09
<b>Model 3b</b> (Coef/p-value/R <sup>2</sup> )	--	0.22/0.25/0.39	<b>-0.38/0.004/0.39</b>	--
<b>Model 4</b> (Coef/p-value/R <sup>2</sup> )	-1.41/0.5/0.06	0.16/0.5/0.06	--	--
<b>Model 5a</b> (Coef/p-value/R <sup>2</sup> )	-0.46/0.9/0.09	0.19/0.5/0.09	--	-0.53/0.5/0.09
<b>Model 5b</b> (Coef/p-value/R <sup>2</sup> )	-1.65/0.4/0.41	0.15/0.5/0.41	<b>-0.38/0.004/0.41</b>	--
<b>Dallas (n = 5)</b>				
<b>Model 1a</b> (Coef/p-value/R <sup>2</sup> )	<b>7.93/0.02/0.83</b>	--	--	--
<b>Model 1b</b> (Coef/p-value/R <sup>2</sup> )	--	0.19/0.1/0.55	--	--
<b>Model 1c</b> (Coef/p-value/R <sup>2</sup> )	--	--	<b>-0.20/0.01/0.92</b>	--
<b>Model 1d</b> (Coef/p-value/R <sup>2</sup> )	--	--	--	-0.10/0.8/0.02
<b>Model 2a</b> (Coef/p-value/R <sup>2</sup> )	<b>9.65/0.02/0.95</b>	--	--	0.26/0.15/0.95
<b>Model 2b</b> (Coef/p-value/R <sup>2</sup> )	2.58/0.47/0.95	--	-0.14/0.2/0.95	--
<b>Model 3a</b> (Coef/p-value/R <sup>2</sup> )	--	<b>0.31/0.01/0.97</b>	--	<b>-0.51/0.03/0.97</b>
<b>Model 3b</b> (Coef/p-value/R <sup>2</sup> )	--	0.05/0.5/0.94	-0.17/0.06/0.94	--
<b>Model 4</b> (Coef/p-value/R <sup>2</sup> )	<b>6.31/0.02/0.98</b>	0.11/0.05/0.98	--	--
<b>Model 5a</b> (Coef/p-value/R <sup>2</sup> )	3.85/0.4/0.99	0.19/0.3/0.99	--	-0.21/0.6/0.99
<b>Model 5b</b> (Coef/p-value/R <sup>2</sup> )	-14.5/0.8/0.98	0.77/0.7/0.98	-0.08/0.8/0.98	--
<b>Houston (n = 5)</b>				
<b>Model 1a</b> (Coef/p-value/R <sup>2</sup> )	-4.43/0.1/0.60	--	--	--

<b>Model 1b</b> (Coef/p-value/R <sup>2</sup> )	--	1.72/0.2/0.44	--	--
<b>Model 1c</b> (Coef/p-value/R <sup>2</sup> )	--	--	<b>-0.60/0.01/0.93</b>	
<b>Model 1d</b> (Coef/p-value/R <sup>2</sup> )	--	--	--	-1.04/0.4/0.24
<b>Model 2a</b> (Coef/p-value/R <sup>2</sup> )	-11.6/0.07/0.90	--	--	2.89/0.1/0.90
<b>Model 2b</b> (Coef/p-value/R <sup>2</sup> )	<b>-3.31/0.03/0.98</b>	--	<b>-0.47/0.03/0.98</b>	--
<b>Model 3a</b> (Coef/p-value/R <sup>2</sup> )	--	2.17/0.5/0.45	--	0.44/0.8/0.45
<b>Model 3b</b> (Coef/p-value/R <sup>2</sup> )	--	1.35/0.1/0.93	-0.52/0.13/0.93	--
<b>Model 4</b> (Coef/p-value/R <sup>2</sup> )	<b>-7.89/0.01/0.98</b>	<b>0.61/0.03/0.98</b>	--	--
<b>Model 5a</b> (Coef/p-value/R <sup>2</sup> )	-10.7/0.3/0.92	0.73/0.7/0.92	--	3.07/0.3/0.92
<b>Model 5b</b> (Coef/p-value/R <sup>2</sup> )	-2.55/0.3/0.98	0.39/0.6/0.98	-0.48/0.1/0.98	--

\*Bolted results indicate significance.

Model 1a-1d: main effects and control variables (separately)

Model 2a-2b: density with control variables

Model 3a-3b: centralization with control variables

Model 4: density and centralization

Model 5a-5b: density and centralization with control variables

For the separate regional analysis for 2012 (n=5 for both Dallas and Houston), normalized density and betweenness centralization differed in their effects on MIBB rate, as compared with the all communities in all regions analysis. Across all models, normalized density had a mostly positive effect on MIBB rate in Dallas and a mostly negative effect on MIBB rate in Houston. Some of these effects were significant (see Table 3.7).

## **SECTION 4: REGRESSION ANALYSIS**

### **Section 4.1: Purpose and Overview of Section**

Our first aim seeks to determine whether regression including social network analysis characteristics and/or measures of physician networks explains additional variation in patterns of MIBB use beyond that explained by standard regression techniques. In Section 3, we explored network analysis of Medicare data at a high level, describing global network measures such as density and centralization betweenness of both the regional networks and community networks (derived from the regional networks). Further, with community networks as units of analysis, we explored the effects of these network measures on MIBB rate. In this section, we focus on the nodal perspectives of social network analysis, specifically looking at how a physician's degree or betweenness affects their use of MIBB. Further, we explore whether or not the addition of these measures adds substantively to our regression models.

In this section, we first explored the relationship between nodal network characteristics and/or measures and MIBB use. The main purpose is to determine which network characteristics and measures significantly impact the use of MIBB. Two different models were considered: a linear regression (regressing a biopsy physician's rate of MIBB on a physician's network characteristics/measures), and a logistic regression (regressing a patient's receipt of MIBB on their biopsy physician's network characteristics/measures). It is important to note that the unit of analysis for the linear regression is the physician while the unit of analysis for the logistic regression is the patient.

Second, in a hierarchical model framework, we explored the relationships between network characteristics or measures and the use of MIBB, modeling patients as nested within biopsy physicians nested within communities. This is a different approach from standard hierarchical models in clinical observational studies, where health referral regions or hospitals are often used as the third, or highest, level. Following this pattern we also examined such models, with hospital as the third level. As this is a new concept, we first compared the clustering mechanisms of community and hospital, assessing whether or not these clusters are similar to each other. Then, we ran the two hierarchical models and compared the models, to explore which better explains outcomes.

## **Section 4.2: Methods**

### **SECTION 4.2.1: VARIABLES, OUTCOMES, AND VARIABLE SELECTION**

For this section, we utilized the networks described in Section 2 (see Section 2.3), focusing on the same regions (Austin, Dallas, El Paso, Houston, Lubbock, Rio Grande Valley, San Antonio) and years (2009 and 2012). Communities were created as described in Section 2 (see Section 2.5). For the purposes of the hierarchical models, patients were assigned to physicians, and physicians were assigned to communities and to hospitals (see Section 2.2).

A number of network characteristics and measures were considered for this analysis. Each of these characteristics and measures was calculated separately within each region or community, as appropriate, in each year. Table 4.1 includes the list of all variables considered in this chapter.

#### **Table 4.1: List of Variables Considered for Regression Analyses**

---

<b>Global Network Measures</b>	Density (Normalized)
	Characteristic Path Length
	Transitivity
	Centralization (Betweenness)
	Centralization (Degree)
	Centralization (Closeness)
	Number of Triangles
	Number of Nodes
	Number of Edges
	Average Degree (Normalized)
	Diameter
	Average Strength (Normalized)
	MIBB Rate
	Number of Patients
<b>Global Network Characteristics</b>	Number of Biopsy Physicians
	Number of Biopsy Surgeons
	Number of Biopsy Radiologists
	Ratio of the Number of Biopsy Surgeons to the Number of Biopsy Physicians
	Mean Physician Years of Practice
	Mean Biopsy Physician Years of Practice
	Mean Biopsy Surgeon Years of Practice
	Mean Physician Age
	Mean Biopsy Physician Age
	Mean Biopsy Surgeon Age
	Number of non-US Trained Physicians
	Number of non-US Trained Biopsy Physicians
	Number of non-US Trained Biopsy Surgeons
	Number of Female Physicians
	Number of Female Biopsy Physicians
	Number of Female Biopsy Surgeons
	Number of White Patients
	Number of Non-white Patients
	Ratio of White Patients to All Patients
	Number of Patients Living in Metropolitan Areas
	Number of Patients Living in Non-Metropolitan Areas
	Number of Patients Living in Rural Areas

	Ratio of Patients Living in Metropolitan Areas to All Patients
	Average Education Quartile
	Average Income Quartile
	Number of Patients 66-74 Years
	Number of Patients > 75 Years
	Ratio of Patients 66-74 to All Patients
<b>Local Network Measures</b>	Degree
	Betweenness Centrality
	Closeness Centrality
	Eigenvector Centrality
	Strength
	Transitivity
	Triangles

---

For regression of physician MIBB rates, we restricted our attention to biopsy surgeons. We recall from Section 2 (see Section 2.2) that the biopsy surgeon is the physician who performed the patient's biopsy, but classified him or herself as a surgeon. Rate of MIBB was calculated as the number of MIBBs that the biopsy surgeon performed, divided by the number of biopsies they performed.

Considering the individual patient's receipt of MIBB allows us to determine if the networks characteristics of their biopsy physician's networks affected the patient's receipt of MIBB. Our outcome is whether or not a patient received MIBB. We only consider MIBBs done by biopsy surgeons.

We first examined our list of variables (Table 4.1), and selected those to include in the regression models, using the following algorithm. Regression models (linear or logistic) were built to regress outcome on each Table 4.1 variable separately. This was done separately for each region as well as within the entire network, and was repeated for each year. Variables that were significant in these regression models were noted as

important. We calculated the rate of importance for each variable: the number of times that variable appeared as significant in the regression models over the total number of regression models including that variable. Some nodal measures such as betweenness centrality were calculated using two methods: calculating the measure considering the whole regional network of the physician, and calculating the measure considering the community network of the physician. We gave priority to the measures calculated within the community network as our interest lies in a physician's influence or position within their local collaboration networks. That is to say, if both variables were considered important enough to include in the models, we only included the measures calculated within the community network. Appendix C lists the variables in Table 4.1 in descending order of rate of importance. We prioritized our variable selection to include in the full linear, logistic, and hierarchical model based not only on the rate of importance, but also what previous literature states affecting outcomes.

We chose the following network measures based on their rate of importance: degree, betweenness centrality, closeness centrality, transitivity, and strength (See Section 2.4.2). As these measures were calculated on networks and communities of various sizes, we normalized the following measures: degree, strength, betweenness centrality, and closeness centrality. Degree and closeness centrality were divided by  $n - 1$ , where  $n$  is the number of nodes in the network (community) used to calculate the measures. Strength was divided by the maximal strength within the network (community). Betweenness centrality was normalized according to the following formula:

$$\frac{2 * (C_{Bij}(G))}{(n * n - 3 * n + 2)}$$

where  $C_{Bij}(G)$  is the betweenness centrality, and  $n$  is the number of nodes in the network (community) used to calculate betweenness (Freeman, 1979).

We included other non-network covariates, based on importance and what is cited as influential in the literature, for both the physician regressions and patient regressions. For the linear regressions, we included the following physician covariates: age, years of practice, non-US trained, gender, and biopsy surgeon specialty (surgeon or some other specialty). For the logistic regressions, we did not include the biopsy physician specialty as we restricted the logistic analysis to include only biopsy surgeons (see Section 4.2.2). Furthermore, for the logistic regressions, we also included patient level covariates: non-Metropolitan residence, non-White ethnicity, age 75+, education (quartile), and income (quartile). For education and income, lower quartile represents fewer years of education and lower yearly income.

#### **SECTION 4.2.2: REGRESSION METHODS: LINEAR AND LOGISTIC**

For the linear regression, we considered several models. Multivariate regression models were used (see model outline in Section 3.3). The unit of analysis for these models was biopsy surgeons, with outcome being the biopsy surgeon's rate of MIBB. Model 1 only included physician covariates listed above. Model 2 included only the network measures described above. Model 3 included both the physician covariates and network measures. For these analyses, we focused on biopsy surgeons. We do this to explore the effect of network measures on the biopsy surgeons' rate of MIBB use, and

including all biopsy physicians would have limited the data, as biopsy radiologists can only do MIBBs. In these regressions, we included all biopsy surgeons in all regions. Similar to Section 3.3, we separately ran the analysis for 2009 and 2012.

For the logistic regressions, we also considered several models. The unit of analysis for these models was patient, with the outcome being whether the patient received MIBB. We first remark that each patient is assigned to multiple physicians of different types, such as their biopsy physician, PCP, surgeon, and radiologist; thus, we focused our analysis on the biopsy physician associated with each patient. This means that we only considered network measures and covariates related to a patient's biopsy surgeon and included these variables in the models. We further restricted the analysis to patients assigned to biopsy surgeons with stated surgeon specialty, for reasons noted above, as our interest is in how these physicians practice. Model 1 included only patient covariates. Model 2 included only biopsy surgeons' covariates as described above (excluding surgeon specialty). Model 3 included the biopsy surgeon network measures, and Model 4 included all patient covariates, biopsy surgeon covariates, and biopsy surgeon network measures. Because of the skewness of betweenness, strength, and closeness, multiple network measures were log transformed (strength, closeness) or scaled (betweenness) to improve parameter estimation. Further, we calculated odds-ratios and 95% confidence intervals.

#### **SECTION 4.2.3: HIERARCHICAL LOGISTIC REGRESSION MODELS**

To fulfill the first aim, we conducted hierarchical logistic regression models (HLRMs). We considered two types of three-level hierarchical logistic regression models: one model where patients are nested within biopsy surgeons, nested within hospitals, and one model where patients are nested within biopsy surgeons nested within communities. Before running the models, we compared the clustering mechanisms of

community and hospital for each region, assessing whether or not these clusters are similar to each other. To assess this similarity, we utilized a cluster validation measure known as purity. In defining purity, we have two given cluster mechanisms, one giving clusters  $Cluster_i^1, i=1, 2, \dots, r$ , and the second giving clusters  $Cluster_j^2, j=1, 2, \dots, k$ . We further define the following:

$$n_{ij} = |Cluster_i^1 \cap Cluster_j^2|,$$

which denotes the number of physicians in both  $Cluster_i^1$  and  $Cluster_j^2$  (Zaki & Meira, 2014).

Purity for a specific region is calculated as follows:

$$purity = \frac{1}{n} \sum_{i=1}^r \max_{j=1}^k \{n_{ij}\}$$

where

$r$  = the total number of  $Cluster_i^1$ ,

$k$  = the total number of  $Cluster_j^2$  (Zaki & Meira, 2014).

As an exploratory analysis, we examined this purity measure for the cluster mechanisms of community and hospital, for all regions, for the year 2012. Further, as the purity measure is not symmetrical, examined these measures with each of hospital and community playing the role of  $Cluster_i^1$  and  $Cluster_j^2$ .

Within these models types, multiple models were run, differentiated by what covariates were included in the models. It is important to note that we restricted these analyses to patients who had surgeons conduct their biopsy, for the reasons outlined in Section 4.2.2. This allows interpretation of the results within the context of biopsy

surgeons, that is, e.g., whether or not a biopsy surgeon's degree will affect their patient receiving MIBB.

The following formulizes the null model utilized in this study:

$$y_{ijk} = \gamma_{000} + V_{00k} + U_{0jk} + e_{ijk}$$

where

$y_{ijk}$  = receipt of MIBB (Y/N), for patient  $i$  of biopsy surgeon  $j$  in hospital or community  $k$ ,

$\gamma_{000}$  = overall intercept of the model,

$V_{00k}$  = random effect for hospital or community  $k$ ,

$U_{0jk}$  = random effect for biopsy physician  $j$  in hospital or community  $k$ ,

$e_{ijk}$  = residual.

We assume that  $V_{00k}$ ,  $U_{0jk}$ , and  $e_{ijk}$  are distributed normally.

For these models, we calculated the intraclass correlation coefficient (ICC). ICC enables us to assess the variance contribution of the group level to the outcome (Finch, Bolin, & Kelley, 2014; Snijders & Bosker, 2012). For a three level hierarchical linear model, ICC is formally described by the following formulas:

for assessing the contribution of the level-two cluster:  $\frac{\tau^2 + \varphi^2}{\sigma^2 + \tau^2 + \varphi^2}$ ,

for assessing the contribution of the level-three cluster:  $\frac{\varphi^2}{\sigma^2 + \tau^2 + \varphi^2}$ ,

where

$\sigma^2$  is the between patient variance,

$\tau^2$  is the between biopsy surgeon variance,

$\varphi^2$  is the between hospital or community variance.

Because we are utilizing HLRMs, we replace  $\sigma^2$  with the value 3.29. This is the implied variance of the level-one residuals in a logistic distribution (Snijders & Bosker, 2012).

We first built null models for both the hospital and the community models, with random effects for the second level (biopsy physician) and for the third level (hospital or community). Then we built further models: Model 1 controlled for patient characteristics and biopsy surgeon characteristics (excluding surgeon specialty). Model 2 controlled for patient characteristics, biopsy surgeon characteristics, and biopsy surgeon network characteristics. These covariates are described previously (see Section 4.2.2). To improve model convergence, we centered and scaled each continuous covariate. ICCs at the biopsy surgeon level and the hospital or community level were calculated to assess the levels' contribution to the variance of the outcome. We restricted our model building to the years 2009 and 2012 (see Section 3.1 for rationale).

## Section 4.3: Results

### SECTION 4.3.1: LINEAR REGRESSION

In this section, we note that our unit of analysis is at the physician level and the outcome of our models is the biopsy surgeon's rate of MIBB. Table 4.2 summarizes the results for the physician linear regressions. For Model 1 in 2009, there was a significant negative effect of non-US trained biopsy on a surgeon's rate of MIBB (-0.27, p-value < 0.001), and a significant positive effect for a biopsy surgeon being female on a surgeon's rate of MIBB (0.11, p-value < 0.05). For 2012, a biopsy surgeon being female also had a significant positive effect on a biopsy surgeon's rate of MIBB (0.18, p-value < 0.05).

**Table 4.2: Linear Regression Coefficient Estimates**

	Model 1		Model 2		Model 3	
	2009	2012	2009	2012	2009	2012
<i>Biopsy Surgeon Characteristics</i>						

Age	-0.011	-0.011	-	-	-0.014	-0.014
Years of Practice	0.011	0.011	-	-	0.013	0.015
Non-US Trained	<b>-0.27**</b>	-0.07	-	-	<b>-0.24**</b>	-0.06
Female	<b>0.11*</b>	<b>0.18*</b>	-	-	<b>0.11*</b>	<b>0.17*</b>
Surgeon Specialty	-0.08	-0.02	-	-	-0.01	-0.01
<b><i>Biopsy Surgeon Network Measures</i></b>						
Degree	-	-	<b>-1.05**</b>	-0.30	<b>-0.91*</b>	-0.26
Transitivity	-	-	-0.10	-0.38	-0.14	-0.36
Closeness	-	-	<b>1.25*</b>	0.19	<b>1.28*</b>	0.25
Betweenness	-	-	-2.26	3.72	-2.84	2.90
Strength	-	-	<b>0.93*</b>	0.02	<b>0.83*</b>	0.17

\*p-value < 0.05

\*\*p-value < 0.001

Model 1: physician characteristics only

Model 2: physician network characteristics only

Model 3: all covariates

In Model 2, degree, closeness, and strength had significant effects on a biopsy surgeon's MIBB rate for 2009. A biopsy surgeon's degree (the number of a surgeon's direct collaborators) had a significant negative effect on the rate of MIBB (-1.05, p-value < 0.001). Closeness (a surgeon's "influence" within his network) and strength (potential number of patients a surgeon treats) both had a significant positive effect on the rate of MIBB (1.25, p-value < 0.05; 0.93, p-value < 0.05, respectively). For Model 3 in 2009, these effects were maintained, with only slight changes in the parameter estimates (see Table 4.2). For Model 3 in 2012, being female maintained its significance with minimal change in the estimate from Model 1.

#### SECTION 4.3.2: LOGISTIC REGRESSION

In this section, we note that our unit of analysis is at the patient level. Table 4.3 summarizes the results of the logistic regressions. For patient characteristics, area of residence (OR: 2.10, CI: 1.07-4.27, Year: 2012), patient age (1.40, 1.04 – 1.87, 2009), patient education (1.24, 1.01-1.53, 2009), and patient income (1.81, 1.34-2.55, 2012) all

had significant positive effect on whether a patient received MIBB (Model 1).

Controlling for all other factors in Model 4, only area of residence remained significant (3.12, 1.40-7.07, 2012). In terms of biopsy surgeon characteristics (Model 2), surgeon age (1.07, 1.01-1.14, 2009), years of practice (0.91, 0.86-0.97, 2009; 0.90, 0.81-0.98, 2012), non-US trained (0.54, 0.33-0.85, 2009), and male gender (0.62, 0.40-0.97, 2012) significantly affected patients receiving MIBB. Controlling for all other factors (Model 4), surgeon male gender (0.54, 0.31-0.92, 2009) and non-US trained surgeons (0.67, 0.46-0.95, 2009) significantly affected whether patients received MIBB.

**Table 4.3: Logistic Regression Odds Ratios Estimates**

	Model 1		Model 2		Model 3		Model 4	
	2009 OR (CI)	2012 OR (CI)	2009 OR (CI)	2012 OR (CI)	2009 OR (CI)	2012 OR (CI)	2009 OR (CI)	2012 OR (CI)
<b>Patient Characteristics</b>								
Non-Metropolitan Residence	1.22 (0.67 2.26)	2.10 <b>(1.07 4.27)</b>	-	-	-	-	1.22 (0.62 2.40)	3.12 <b>(1.4 7.09)</b>
Non-White Ethnicity	1.14 (0.75 1.74)	0.98 (0.54 1.81)	-	-	-	-	1.32 (0.84 2.09)	1.10 (0.55 2.23)
Age 75+	1.40 <b>(1.04 1.87)</b>	1.04 (0.69 1.58)	-	-	-	-	1.33 (0.97 1.83)	1.25 (0.78 2.01)
Education (Quartile)	1.24 <b>(1.01 1.53)</b>	0.84 (0.61 1.15)	-	-	-	-	1.17 (0.97 1.48)	0.94 (0.64 1.37)
Income (Quartile)	1.04 (0.84 1.29)	1.81 <b>(1.31 2.55)</b>	-	-	-	-	1.10 (0.85 1.41)	1.91 (1.28 2.88)
<b>Biopsy Surgeon Characteristics</b>								
Age	-	-	1.07 <b>(1.01 1.14)</b>	1.08 (0.98 1.18)	-	-	1.02 (0.96 1.09)	0.99 (0.89 1.11)
Years of Practice	-	-	0.91 (0.86 0.97)	0.90 <b>(0.81 0.98)</b>	-	-	0.97 (0.91 1.03)	0.99 (0.89 1.11)
Non-US Trained	-	-	0.54 (0.33 0.85)	0.98 (0.53 1.88)	-	-	0.54 <b>(0.32 0.92)</b>	1.47 (0.65 3.29)
Male	-	-	0.99 (0.72 1.36)	0.62 <b>(0.40 0.97)</b>	-	-	0.67 <b>(0.46 0.95)</b>	0.51 (0.29 0.86)
<b>Biopsy Surgeon Network Measures</b>								
Degree (Normalized, log)	-	-	-	-	0.74 (0.42 1.28)	1.45 (0.73 2.95)	0.88 (0.46 1.66)	1.52 (0.70 3.29)
Transitivity	-	-	-	-	1.27 (0.30 5.36)	0.02 <b>(0.002 0.2)</b>	1.64 (0.36 7.65)	0.02 <b>(0.001 0.2)</b>
Closeness (log)	-	-	-	-	2.38 (0.21 2.81)	0.12 (0.004 2.7)	3.26 (0.21 51.1)	2.58 (0.007 8.7)
Betweenness (scaled)	-	-	-	-	456 <b>(40.6 9E3)</b>	91 <b>(2.8 2E4)</b>	491 <b>(36.1 1E4)</b>	82 <b>(2.5 2E4)</b>
Strength (log)	-	-	-	-	1.04 (0.74 1.46)	0.52 <b>(0.4 0.7)</b>	1.05 (0.73 1.53)	0.52 <b>(0.34 0.79)</b>

\*Bolded results indicate significance

Model 1: patient characteristics

Model 2: biopsy surgeon characteristics

Model 3: biopsy surgeon network measures

Model 4: all covariates

For network measures, a biopsy surgeon's betweenness centrality (a surgeon's "control" of information within his network) significantly and positively affected a patient receiving MIBB in both 2009 and 2012 (456, 40.6-9E3, 2009; 91, 2.8-2E4, 2012). Further, a biopsy surgeon's transitivity (a surgeon's tendency to work in closed clusters) (0.02, 0.002-0.2, 2012) and strength (potential number of patient a surgeon treats) (0.52, 0.4-0.7, 2012) significantly and negatively affected a patient receiving MIBB.

Controlling for all other factors (Model 4), the above network measures remained significant for their respective years with very little change in the odds ratio.

### SECTION 4.3.3: HIERARCHICAL LOGISTIC REGRESSION MODELS

In this section, we note that our unit of analysis is at the patient level and the outcome of the models is the patient's receipt of MIBB. Table 4.4 summarizes the purity results. When comparing clusters where  $Cluster_i^1$  is the community and  $Cluster_j^2$  is the hospital, purity measures range from 0.2543 to 0.6942, with Austin having the lowest purity measure, and Lubbock having the highest purity measure (0.6942). When comparing clusters where  $Cluster_i^1$  is the hospital and  $Cluster_j^2$  is the community, purity measures range from 0.8108 and 0.9922, with El Paso having the lowest purity measure, and Lubbock having the highest purity measure.

**Table 4.4: Purity Results for All Regions (2012)**

Region	$Cluster_i^1 =$ Community $Cluster_j^2 =$ Hospital	$Cluster_i^1 =$ Hospital $Cluster_j^2 =$ Community
Austin	0.2543	0.9069
Dallas	0.3179	0.9782
El Paso	0.5952	0.8108
Houston	0.4475	0.9430
Lubbock	0.6942	0.9862
RGV	0.4153	0.9922
San Antonio	0.6035	0.8939

Table 4.5 summarizes the ICC results from the HLRMs. For the hospital model type, surgeon level ICC in the null models changed from 2009 to 2012; doubling: from 15.4% in 2009 to 32.4% in 2012. For the community model type, surgeon level ICC in the null models changed minimally over time. Introducing patient characteristics and biopsy surgeon characteristics minimally changed the ICCs for the surgeon level for both

model types for both years. However, controlling for network characteristics (Model 2) reduced the ICCs for the surgeon level for both model types and both years; an almost 50% reduction in ICCs was seen for the surgeon level for both model types and both years. Comparing between model types, surgeon level ICC was lower in the hospital model type as compared with the community model type.

**Table 4.5: Summary of ICC by Model Type from 2009 and 2012**

	Hospital Model Type				Community Model Type			
	Biopsy Physician (Level Two) ICC		Hospital (Level Three) ICC		Biopsy Physician (Level Two) ICC		Community (Level Three) ICC	
	2009	2012	2009	2012	2009	2012	2009	2012
<b>Null</b>	0.302	0.542	0.231	0.059	0.416	0.482	0.105	0.124
<b>Model 1</b>	0.305	0.474	0.217	0.064	0.418	0.420	0.085	0.154
<b>Model 2</b>	0.171	0.324	0.270	0.126	0.284	0.258	0.118	0.264

Null Models: three level models with surgeons as the second level and hospital/community as the third level

Model 1: three level models controlling for patient characteristics and physician characteristics

Model 2: three level models controlling for patient characteristics, physician characteristics, and network measures.

For the hospital model type, hospital level ICC in the null model decreased from 2009 to 2012 (0.231 vs. 0.059). Introducing network characteristics increased the hospital level ICC in 2012 (0.059 vs. 0.126). For the community model type, community level ICC in the null model had a minimal increase from 2009 to 2012 (0.105 vs. 0.124). Similar to the hospital model type, introducing network characteristics increased the community level ICC in 2012 (0.124 vs. 0.264). Comparing between model types for the null model, hospital level ICC was larger than the community level ICC for 2009 (0.231 vs. 0.105). However, in 2012, this pattern reversed, with community ICC higher than hospital level ICC (0.124 vs. 0.059, respectively).

Table 4.5 summarizes the odds-ratio from the HLRMs. Significant results were seen only in 2012. For both Model 1 and Model 2 and in both model types, patient income had a significant positive association with patient receipt of MIBB (OR ranges:

1.99 – 2.20, LCI: 1.04-1.12, UCI: 3.83-4.24). For Model 2, the biopsy surgeon's transitivity (a surgeon's tendency to work in clusters) had a significant positive association with patients receiving MIBB, in both model types (OR: 1.99-2.13, LCI: 1.04-1.10, UCI: 3.83-4.12). Further, for the community model type, male biopsy surgeon gender significantly negatively affected the patient's receipt of MIBB for both Model 1 and Model 2 (OR: 0.28-0.34, LCI: 0.10-0.11, UCI: 0.74-0.96).

**Table 4.6: Hierarchical Logistic Regression Estimates**

	Hospital				Community			
	Model 1		Model 2		Model 1		Model 2	
	2009	2012	2009	2012	2009	2012	2009	2012
<b>Patient Covariates</b>								
Non-Metropolitan Residence	0.76 (0.30 1.96)	1.94 (0.64 5.85)	0.72 (0.30 1.79)	2.65 (0.87 8.06)	0.82 (0.33 2.02)	1.63 (0.54 4.91)	0.79 (0.32 1.92)	1.99 (0.65 6.05)
Non-White Ethnicity	1.15 (0.63 2.11)	1.10 (0.41 2.93)	1.17 (0.65 2.11)	1.13 (0.43 2.97)	1.14 (0.63 2.03)	0.95 (0.36 2.53)	1.16 (0.65 2.08)	1.41 (0.53 3.74)
Age 75+	1.47 (0.96 2.23)	1.30 (0.69 2.46)	1.36 (0.91 2.05)	1.42 (0.76 2.66)	1.42 (0.96 2.11)	1.12 (0.60 2.09)	1.35 (0.90 2.02)	1.33 (0.72 2.46)
Education (Quartile)	1.07 (0.73 1.56)	0.71 (0.38 1.34)	1.12 (0.77 1.61)	0.72 (0.38 1.36)	1.08 (0.75 1.56)	0.65 (0.34 1.23)	1.13 (0.78 1.63)	0.58 (0.30 1.09)
Income (Quartile)	1.14 (0.77 1.70)	2.18 (1.12 4.24)	1.09 (0.74 1.60)	2.20 (1.12 4.30)	1.12 (0.77 1.63)	1.99 (1.04 3.83)	1.06 (0.72 1.56)	2.13 (1.10 4.12)
<b>Biopsy Surgeon Covariates</b>								
Age (scaled)	1.15 (0.32 4.11)	1.13 (0.11 11.3)	0.83 (0.27 2.55)	0.57 (0.06 5.27)	1.29 (0.37 4.44)	0.73 (0.09 5.58)	0.98 (0.33 2.99)	0.46 (0.07 2.96)
Years of Practice (scaled)	0.74 (0.20 2.72)	0.53 (0.05 5.15)	1.01 (0.32 3.19)	0.99 (0.11 9.0)	0.68 (0.19 2.39)	0.84 (0.11 6.37)	0.88 (0.28 2.72)	1.25 (0.19 8.08)
Non-US Trained	0.81 (0.29 2.28)	2.12 (0.53 8.46)	0.91 (0.36 2.29)	1.68 (0.46 6.2)	0.85 (0.31 2.37)	2.52 (0.61 10.4)	1.00 (0.40 2.48)	2.28 (0.62 8.43)
Male	0.73 (0.35 1.54)	0.37 (0.13 1.05)	0.62 (0.32 1.20)	0.38 (0.14 1.01)	0.67 (0.33 1.37)	0.34 (0.11 0.96)	0.61 (0.32 1.15)	0.28 (0.10 0.74)
<b>Network Measures of Biopsy Surgeon</b>								
Degree	--	--	0.72 (0.34 1.53)	1.35 (0.58 3.15)	--	--	0.72 (0.33 1.59)	1.87 (0.61 5.72)
Transitivity	--	--	0.90 (0.45 1.81)	0.37 (0.15 0.93)	--	--	0.95 (0.64 1.89)	0.36 (0.14 0.92)
Closeness	--	--	1.23 (0.70 2.32)	0.80 (0.40 1.60)	--	--	1.38 (0.73 2.59)	0.60 (0.26 1.40)
Betweenness	--	--	60.6 (0.23 2E4)	3.09 (0.30 31.4)	--	--	239 (0.99 6E4)	3.41 (0.22 52.0)
Strength	--	--	2.21 (0.94 5.19)	0.95 (0.47 1.93)	--	--	1.97 (0.98 3.93)	0.94 (0.39 2.24)

\*Bolted results indicate significance

Model 1: three level models controlling for patient characteristics and physician characteristics

Model 2: three level models controlling for patient characteristics, physician characteristics, and network measures

## **SECTION 5: NETWORK MODELS: EXPONENTIAL RANDOM GRAPH MODELS**

### **Section 5.1: General Overview of Exponential Random Graph Models and Purpose of Section**

#### **SECTION 5.1.1: GENERAL OVERVIEW**

Exponential random graph models (ERGMs) are statistical models that, for an observed network, allow for inferences about how given network configurations, such as the number of triangles, influence the presence of edges within the network. In other words, ERGMs are statistical models of network structure allowing for inferences regarding the presence of patterns within the network (Goodreau, Kitts, & Morris, 2009; Robins & Lusher, 2013). An ERGM builds a probability distribution on the set of all possible networks on a set of fixed nodes—those in the observed network—based on the configurations of interest. In this distribution of networks, the observed network is the “average network” (Robins & Lusher, 2013).

Each configuration of interest is a pattern of nodes and a subset of edges among them (Robins, Pattison, Kalish, & Lusher, 2007). For example, an edge configuration is a pair of nodes with a connection between them; a 2-star configuration is a set of three nodes where one node is connected to the other two nodes; a 3-star configuration is a set of four nodes where one node is connected to the other three nodes; a triangle configuration is a set of three nodes where all three nodes are connected to each other (Koskinen & Daragnova, 2013). Parameter estimates are calculated for those configurations included in the exponential model. The value of the parameter can be interpreted as the tendency of a network in the possible population of networks to contain

that configuration (Robins et al., 2007). For example, a network with a higher parameter value of the triangles configuration exhibits a tendency for clustering in population of random networks centered at the given network.

### **SECTION 5.1.2: ERGMS BACKGROUND**

ERGMs are used to answer questions about network structure; specifically, in exploring processes that are involved in the creation of networks. These models have been used to study such processes in multiple fields, and we provide a few examples of their use in the literature.

Goodreau et al. utilized ERGMs to examine processes that generated friendship networks (2009). ERGMs were used to analyze adolescent friendship networks in 59 schools studied in the National Longitudinal Survey of Adolescent Health. The desire was to examine the effects of an adolescent's sociality (ability to make friends), homophily (propensity to establish friendships within the same grade, sex, or race), and triadic closure (friends of a friend will be friends) on generating friendship networks (Goodreau et al., 2009). Modeling friendship networks in an ERGM framework allowed understanding of the generative patterns of friendship networks. Goodreau et al. found that networks within grade levels tend to be more cohesive, and that females are more likely to form triadic closures than males (2009). In terms of homophily and depending on the composition of the schools, blacks tend to have higher homophily compared to other races, meaning that the propensity for blacks to form friendships with other blacks is greater than that, as an example, of whites forming friendships with other whites (Goodreau et al., 2009). Further, Goodreau et al. found that homophily and triadic closure interact with sociodemographic conditions in structuring the process of friendship

formation (2009). For example, white, black, and Asian students show high propensity for homophily and within-category triadic closure, representing cohesion within their groups, whereas Hispanic students do not exhibit such network structures (Goodreau et al., 2009).

Another example involves the use of ERGMs in exploring structural differences between networks derived from observed behavior and networks derived from subject recall. This study defined the behavior network using the frequency of dyadic interactions between two individuals, and the recall network using each individual's recollection of these interactions (Quintane, 2013). ERGMs for this study included the following structural parameters: edge (parameter controlling for density), alternating star (parameter controlling for the degree distribution), isolates (parameter controlling for non-connected nodes), path closure (parameter controlling for the presences of closed triangles in the network), and multiple connectivity (parameter controlling the number of unclosed triangles in the network) (Quintane, 2013). The study found that the behavior and recall networks are structurally different, specifically in the closure of transitivity process (Quintane, 2013). Quintane found that nodes in the behavior networks tend to cluster more, as evidenced by positive and significant path closure parameters, as compared with nodes in recall networks (2013).

Another study utilized ERGMs to study physician collaboration networks derived from an Australian insurance claims dataset, with the aim of comparing network structures of physician collaboration networks that have high hospitalization cost and readmission rates, to physician collaboration networks that have low hospitalization cost and readmission rates (Uddin et al., 2013). In this study, hospitalization cost is defined as

all payments made by the health insurance company and readmission rate is defined as the percent of patients who were admitted more than once (Uddin et al., 2013). This study specified ERGMs using structural characteristics that were assumed to be driving forces of the formation of the networks (Uddin et al., 2013). Uddin et al. found that the 2-star parameter, a parameter interpreted as the tendency for physicians within a network to work with multiple partners, was significantly different between the high cost network and low cost networks, with high cost networks having higher values ( $p < 0.05$ ) (2015). This suggests that physicians in high cost networks tended to have multiple relationships with other physicians as compared with physicians in low cost networks. Furthermore, there was a significant difference in the alternating k-star parameter, a more robust network parameter than the k-star parameter for assessing centralization, between high readmission networks and low readmission networks, with low readmission networks less likely to be centralized (Uddin et al., 2013).

Another study utilized ERGMs to examine physician networks derived from Medicare data (Moen et al., 2016). Their study compared the network structure of physician and hospital networks within two adjacent hospital referral regions (HRRs), each network with a different level of adherence to clinical guidelines regarding implantable cardioverter defibrillator (ICD) therapy (Moen et al., 2016). Adherence was operationalized as the ratio of ICDs being used as the primary prevention modality for heart failure patients to the total number of ICDs used for heart failure. In this study, the authors explored the effects of physician specialty homophily (e.g., family practice physicians connected to other family practice physicians) and alternating k-stars (Moen et al., 2016). The log-odds transformed physician practice homophily coefficient is

interpreted as the change in the log-odds of the presence of a tie if the nodes have the same physician specialty, as compared to if they do not have the same physician specialty, while holding the rest of the network constant (Moen et al., 2016). Moen et al. found that cardiology physicians are more likely to form ties with other cardiology physicians, rather than ties with physicians in other specialties (Moen et al., 2016). Furthermore, Moen et al. found that physicians in family practice were less likely to form ties with other family practice physicians than with physicians in other specialties (2016).

### **SECTION 5.1.3: SECTION PURPOSE**

In this section, we utilize ERGMs to examine our regional networks of physicians. Our goal is to expand the literature using ERGMs in the analysis of networks derived from Medicare data. Utilizing ERGMs enables the exploration of the role of specific network measures such as degree, centrality, clustering, and homophily in the formation of these physician collaboration networks. We explore whether the network configurations and network development processes play a significant part in the formation and the structure of our regional networks of physicians, derived from Medicare data.

This section is divided into the following parts: We first describe mathematical considerations of ERGMs. We then describe model specifications of ERGMs in general, and describe the models built specifically for this study. Finally, we describe the results.

## **Section 5.2: Methods**

### **SECTION 5.2.1: MATHEMATICAL CONSIDERATIONS OF ERGMS**

ERGMs have the following form, specifying the probability of a set of ties  $Y$  given a set of nodes and their attributes:

$$P(Y = y \mid n \text{ actors}) = \frac{\exp(\sum_{k=1}^k \theta_k z_k(y))}{c}$$

where the  $z_k(y)$  terms represent model covariates (e.g., alternating k-stars, edges, nodal attributes),  $\theta_k$  are the parameters to be estimated, and  $c$  is a quantity that ensures that the formula above is a proper probability distribution (Goodreau et al., 2009; Koskinen & Daragnova, 2013; Moen et al., 2016; Robins et al., 2007). It is theorized that tie formation is an actor dependent process; that is, actors and their attributes affect the formation of social structure and ties (Goodreau et al., 2009; Lusher & Robins, 2013). Taking the logit of this formula allows one to examine the conditional log-odds of individual ties, expressed as:

$$\text{logit}(P(Y_{ij} = 1 \mid n \text{ actors}, Y_{ij}^c)) = \sum_{k=1}^k \theta_k \delta z_k(y)$$

where " $Y_{ij}^c$  denotes all pairs other than  $Y_{ij}$ , and  $\delta z_k(y)$  is the amount by which  $z_k(y)$  changes when  $Y_{ij}$  is toggled from 0 to 1" (Goodreau et al., 2009).

An important consideration in examining ERGMs is the assumption of dyadic dependence (dependence structure), that ties are not independent of each other in tie formation, as well as the particular description of this dependency used in modeling (Koskinen & Daragnova, 2013). Dyadic dependence concerns the endogenous tie-formation process; that is, tie formation is dependent on the pairs of nodes within a network, rather than on individual nodes. Dependence can be modeled in many ways. Examples include the triad closure model (friends of friends will be friends) as used by Goodreau et al., and the Markov dependence model (ties sharing a node will be

dependent) as used by Moen et al. and Uddin et al. (2009; 2016; 2013). Dependence assumptions and considerations, which are mostly scientific and content concerns, determine network specifications in an ERGM (Koskinen & Daragnova, 2013). We note that, absent any dyadic dependence, the model above will only include terms that represent nodal attributes. This is a dyadic independence model, and is simply a logistic regression (Goodreau et al., 2009; Koskinen & Daragnova, 2013).

The goal of ERGMs is the estimation of  $\theta_k$ . Some models of ERGMs, such as models with the Markov dependence assumption, utilize a pseudo-maximum likelihood estimation method with logistic regression as the computational device (Goodreau et al., 2009; Handcock, 2003; Koskinen & Snijders, 2013; Wimmer & Lewis, 2010). However, pseudo-maximum likelihood estimations are limited in their utility, as the estimation technique often produces infinite coefficient values, despite convergence of the model (Handcock, 2003). Markov Chain Monte Carlo (MCMC) methods were implemented to address these issues with pseudo-maximum likelihood estimation (Handcock, 2003; Koskinen & Snijders, 2013; Wimmer & Lewis, 2010). With MCMC estimation, parameters are first estimated using pseudo-maximum likelihood, and then updated, from a simulated distribution of random graphs explored using MCMC (Wimmer & Lewis, 2010).

While MCMC improves estimation, the derived models often suffer from model degeneracy. Degeneracy here refers to the problem that parameters obtained using this technique are implausible; yielding a graph that has all connections in place or a graph that has no connections at all (Handcock, 2003; Wimmer & Lewis, 2010). Per Handcock, model degeneracy occurs for two reasons: there is no maximum likelihood for the

parameters of interest – in other words, the network specifications are not important for the structure or formation of the network; or the model is not specified correctly – in other words, the network specifications are not all accounted for within the model (2003).

## **SECTION 5.2.2: DESCRIPTION OF THE DATA AND ERGM MODEL SPECIFICATIONS**

For this section, we utilized the data set and the networks created in Section 2. As our interest is in exploration of these tools, we do not utilize our full range of available networks, in order to ease the computational and time burden of the models we run. We restrict our analysis to the year 2012 and to the following regions: Houston, El Paso, and RGV. These regions were considered because of the differences in the rate of MIBB (Houston and El Paso are much higher rates than RGV) and the sizes of their networks (Houston is large, El Paso is of moderate size, and RGV is small). We built ERGMs for each metropolitan region.

We built ERGMs of a class called social selection models, models that examine whether nodal attributes, such as gender or age, affect the formation of ties within a network (Robins & Daragnova, 2013). In social selection models, a binary categorical or continuous nodal attribute can be included as a covariate. Positive parameter estimates for binary categorical variables carry the interpretation that nodes with that attribute tend to have more network ties than nodes without that attribute (Robins & Daragnova, 2013). Positive parameter estimates for a continuous variable suggests that those with higher values of the variable tend to have more network ties compared to those with lower values of the variable (Robins & Daragnova, 2013). Furthermore, social selection models may also include homophily effects for both categorical and continuous variables. For our models, we consider uniform homophily for categorical variables: whether two nodes

have the same value, or different values, for each of the given categorical variables of interest. We examine this type of homophily, as our interest lies in whether having similar values of these covariates impacts the structure of the network differently as compared to having connections between nodes that are not similar to each other. In the context of physician practice homophily, we explore whether, for example, two physicians being of the same defined specialty increases the likelihood of formation of a tie as compared with two physicians of different specialties. For these homophily terms, it is useful to examine the conditional log-odds transformation of the parameter estimates. These transformed parameter estimates are interpreted as the odds of an edge appearing, given the presence of homophily in the variable in question (Goodreau et al., 2009). For our continuous homophily terms, we considered the absolute difference of the continuous variables.

For our specific models, we included the following nodal attributes (covariates) as binary variables (yes or no): female, non-US trained, PCP physician type, biopsy physician type, surgeon physician type, and dual physician type. Dual physician type indicates a surgeon who both did the biopsy and the surgery to treat the cancer. We further examined uniform homophily for each of the above variables. We included the following continuous nodal attributes, both as nodal attributes and as absolute difference: age and years of practice (YOP).

We considered the following network configurations: GWDEGREE and GWESP. GWDEGREE and GWESP refer to the geometrically weighted degree and geometrically weighted edgewise shared parameter, respectively (Goodreau et al., 2009; Levy, Lubell, Leifeld, & Cranmer, 2016; Wimmer & Lewis, 2010). Including GWDEGREE is

equivalent to including a term for degree distribution (alternating k-star), but with the interpretation of preferential attachment (new nodes in the network form ties with nodes of high degree). A negative GWDEGREE parameter indicates a network creation process under which nodes are more likely to form relationships with nodes of higher degree (i.e., nodes that are more popular) (Levy et al., 2016). GWESP is equivalent to modeling triangles, with a positive estimate indicating higher likelihood of formation of clusters. GWESP further accounts for higher order triangles. Geometrically weighted terms are formulated differently than the equivalent alternating k-stars and triangles for the purpose of reducing the problem of degeneracy (Goodreau et al., 2009; Wimmer & Lewis, 2010).

In our analysis, we first computed descriptive statistics such as number of physicians, number of edges, number of PCPs, etc. for each of the regional networks (Houston, El Paso, and RGV). To test differences between regions, we carried out chi-squared tests for the categorical variables and ANOVAs for the continuous variables (age, years of practice, and MIBB rate). Second, we ran the following ERGMs: a model with nodal attribute, uniform homophily, and absolute difference terms (Model 1); a model with nodal attribute terms, uniform homophily terms, the absolute difference terms, and GWDEGREE (Model 2); a model with nodal attribute terms, the uniform homophily terms, absolute difference terms, and GWESP (Model 3); and a model with the nodal attribute terms, uniform homophily terms, absolute difference terms, GWDEGREE, and GWESP (Model 4). The R package, “statnet”, was utilized for computing the models (Handcock et al., 2017).

## **Section 5.3: Results**

Table 5.1 summarizes network attributes across the networks (Houston, El Paso, and RGV); there were significant differences between networks in terms of network attributes. Specifically, the proportions of non-US Trained physicians, Dual physicians (surgeons who did both the biopsy and the surgery to treat the cancer), females, and MIBB rates were different between regions.

**Table 5.1: Descriptive Statistics for Regional Networks (2009 & 2012)**

	Houston N (%)	Rio Grande Valley N (%)	El Paso N (%)	p-value
<b>Nodes</b>	513	124	62	--
<b>Edges</b>	5918	1845	678	--
<b>Biopsy Physicians</b>	139 (27%)	37 (29%)	22 (35%)	0.3522
<b>Surgeons</b>	91 (17%)	28 (23%)	15 (24%)	0.27
<b>PCPs</b>	271 (52%)	69 (56%)	29 (47%)	0.43
<b>Radiologists</b>	141 (27%)	27 (22%)	17 (27%)	0.52
<b>Non-US Trained</b>	<b>122 (24%)</b>	<b>51 (41%)</b>	<b>30 (48%)</b>	<0.0001
<b>Dual</b>	<b>32 (6%)</b>	<b>21 (17%)</b>	<b>8 (13%)</b>	0.0004
<b>Female</b>	<b>176 (34%)</b>	<b>19 (15%)</b>	<b>12 (19%)</b>	<0.0001
<b>Age (Mean/SD)</b>	48.7 (14.5)	48.9 (14.1)	49.0 (18.2)	0.982
<b>Years of Practice (Mean/SD)</b>	22.8 (11.4)	23.0 (10.4)	24.3 (13.2)	0.608
<b>MIBB Rate</b>	<b>96%</b>	<b>59%</b>	<b>90%</b>	<0.0001

\*Bolded indicates significance

For the Houston network, Model 4 did not converge. In Model 1, the following nodal attributes were significant: age, YOP, female, PCP, surgeon, and biopsy physician (coefficient estimates = 0.006, -0.017, -0.43, -1.96, -2.25, -0.15, respectively, all p-values < 0.05). Those who are older are actively forming ties compared to those who are younger, and those who have higher YOP are less actively forming ties as compared to those who have lower YOP. Further, females, PCPs, surgeons, and biopsy physicians are less likely form ties as compared to males, non-PCPs, non-surgeons, and non-biopsy physicians. In the same model, the following homophily terms were significant: female, PCP, surgeon, and biopsy physician (0.19, -0.28, -0.25, -0.096, respectively, all p-values < 0.05). These homophily terms were negative (except for female), indicating lower likelihood of forming ties between nodes with the same attribute value, holding all else

constant (e.g., there is less likelihood for PCPs to be connected to other PCPs, as compared to PCPs being connected to non-PCPs). For gender, the opposite effect held. The absolute difference of age was significant, with a negative coefficient, indicating that physicians in these networks tend to form ties to those closer to themselves in age (-0.019, p-value < 0.05). For Model 2, GWDEGREE was negative and significant, indicating that physicians in these networks have a higher likelihood of forming ties with physicians of higher degree (-3.92, p-value < 0.05). Adding the GWDEGREE term did not change the other terms significantly, but did remove the significance of the surgeon homophily term. For Model 3, GWESP was positive and significant, indicating an increased likelihood of triadic closures in this network (8.63, p-value < 0.05). Adding this GWESP term changed some of the estimates and ablated significance of some parameters; specifically, the covariates of PCP and Surgeon. Table 5.2 summarizes these results.

**Table 5.2: Houston ERGM Coefficients**

	<b>Model 1</b>	<b>Model 2</b>	<b>Model 3</b>
	Estimate (SE)	Estimate (SE)	Estimate (SE)
<b>Edges</b>	-0.075 (.29)	0.025 (.31)	<b>-12.60* (.58)</b>
<b>Nodal Attributes</b>			
Age (nodecov)	<b>0.006* (.002)</b>	0.005 (.00)	-0.002 (.00)
Years of Practice (nodecov)	<b>-0.017* (.003)</b>	<b>-0.017* (.00)</b>	-0.004 (.00)
Female (nodefactor)	<b>-0.43* (.03)</b>	<b>-0.39* (.04)</b>	<b>-0.15* (.02)</b>
Non-US Trained (nodefactor)	0.004 (.04)	-0.025 (.05)	0.05 (.05)
PCP (nodefactor)	<b>-1.96* (.04)</b>	<b>-1.96* (.05)</b>	<b>-1.01* (.04)</b>
Surgeon (nodefactor)	<b>-2.25* (.12)</b>	<b>-2.18* (.13)</b>	<b>-1.16* (.09)</b>
Biopsy Physician (nodefactor)	<b>-0.15* (.03)</b>	<b>-0.16* (.03)</b>	<b>-0.06* (.22)</b>
Dual (nodefactor)	0.53 (.28)	0.50 (.27)	0.53 (.22)
<b>Homophily</b>			
Age (absdiff)	<b>-0.019* (.00)</b>	<b>-0.017* (.00)</b>	<b>-0.009* (.00)</b>
Years of Practice (absdiff)	0.006 (.00)	0.005 (.00)	-0.002 (.00)
Female (nodematch)	<b>0.19* (.03)</b>	<b>0.21* (.05)</b>	<b>0.23* (.04)</b>
Non-US Trained (nodematch)	0.03 (.05)	-0.008 (.06)	0.06 (.05)

PCP (nodematch)	<b>-0.28* (.04)</b>	<b>-0.28* (.05)</b>	0.04 (.06)
Surgeon (nodematch)	<b>-0.25* (.12)</b>	-0.22 (.14)	-0.001 (.10)
Biopsy Physician (nodematch)	<b>-0.096* (.03)</b>	<b>-0.11* (.04)</b>	<b>-0.101* (.05)</b>
Dual (nodematch)	-0.002 (.28)	0.028 (.27)	0.18 (.21)
<b>Network Structure</b>			
GWDEGREE	--	<b>-3.92* (.51)</b>	--
GWESP	--	--	<b>8.63* (.37)</b>
<b>AIC</b>	39841	39809	36991

\*Bolted indicates significance

\*\*nodefactor: categorical nodal attribute inserted in ERGMs in R; nodecov: continuous nodal attribute inserted in ERGMs in R; nodematch: homophily categorical variable inserted in ERGMs in R; absdiff: homophily continuous variable inserted in ERGMs in R

Model 1: Nodal Attributes and Homophily Terms

Model 2: Nodal Attributes, Homophily Terms, GWDEGREE

Model 3: Nodal Attributes, Homophily Terms, GWESP

For the RGV network, Model 2 and Model 4 did not converge. In Model 1, the following covariate terms were significant: non-US trained, PCP, surgeon, and biopsy physician (0.152, -2.135, -1.801, 0.617, respectively, all p-values < 0.05). Non-US trained physicians and biopsy physicians were actively forming ties as compared to US trained physicians and non-biopsy physicians. Further, PCPs and surgeons were less active in forming ties as compared to non-PCPs and non-surgeons. In terms of homophily, the following terms were significant: non-US trained and PCP (0.191, -0.402, respectively, all p-values < 0.05). The non-US trained term was positive, indicating increased likelihood of homophilous ties on this attribute. The PCP term was negative, indicating decreased likelihood of homophilous ties on this attribute. The absolute difference of years of practice was significant and negative (-0.018, p-value < 0.05), indicating physicians forming ties to other physicians closer in years of practice. Adding the GWESP term in Model 3 did not change the parameter estimates significantly. The GWESP term was significant and positive (169, p-value < 0.05) for this network, indicating an increased likelihood of triadic closures. Table 5.3 summarizes these results.

**Table 5.3: RGV ERGM Coefficients**

	<b>Model 1</b>	<b>Model 2</b>	<b>Model 3</b>
	Estimate (SE)	Estimate (SE)	Estimate (SE)
<b>Edges</b>	<b>0.928* (.38)</b>	--	-217 (1.1)
<b>Nodal Attributes</b>			
Age (nodecov)	0.002 (.01)	--	0.003 (.01)
Years of Practice (nodecov)	0.002 (.01)	--	0.001 (.01)
Female (nodefactor)	-0.051 (.12)	--	-0.032 (.01)
Non-US Trained (nodefactor)	<b>0.152* (.05)</b>	--	<b>0.142* (.05)</b>
PCP (nodefactor)	<b>-2.135* (.09)</b>	--	<b>-1.947* (.08)</b>
Surgeon (nodefactor)	<b>-1.801* (.15)</b>	--	<b>-1.696* (.16)</b>
Biopsy Physician (nodefactor)	<b>0.617* (.09)</b>	--	<b>0.516* (.09)</b>
Dual (nodefactor)	-0.176 (.19)	--	-0.088 (.19)
<b>Homophily</b>			
Age (absdiff)	0.010 (.01)	--	0.010 (.01)
Years of Practice (absdiff)	<b>-0.018* (.01)</b>	--	<b>-0.018* (.01)</b>
Female (nodematch)	0.062 (.13)	--	0.093 (.14)
Non-US Trained (nodematch)	<b>0.191* (.07)</b>	--	<b>0.190* (.07)</b>
PCP (nodematch)	<b>-0.402* (.08)</b>	--	<b>-0.277* (.10)</b>
Surgeon (nodematch)	0.003 (.14)	--	0.000 (.15)
Biopsy Physician (nodematch)	0.001 (.08)	--	0.011 (.09)
Dual (nodematch)	0.092 (.01)	--	0.058 (.18)
<b>Network Structure</b>			
GWDEGREE	--	--	--
GWESP	--	--	<b>169* (.91)</b>
<b>AIC</b>	6309	--	6259

\*Bolded indicates significance

\*\*nodefactor: categorical nodal attribute inserted in ERGMs in R; nodecov: continuous nodal attribute inserted in ERGMs in R; nodematch: homophily categorical variable inserted in ERGMs in R; absdiff: homophily continuous variable inserted in ERGMs in R

Model 1: Nodal Attributes and Homophily Terms

Model 2: Nodal Attributes, Homophily Terms, GWDEGREE

Model 3: Nodal Attributes, Homophily Terms, GWESP

For the El Paso network, Model 3 and 4 did not converge. In Model 1, the YOP, female, PCP, and surgeon nodal attributes were negative and significant (-0.027, -1.964, -1.573, -2.448, -0.297, respectively, p-value < 0.05). In terms of homophily, the PCP term was significant and negative (-0.297, p-value < 0.05). The absolute difference term for YOP was significant and negative (-0.032, p-value < 0.05). In Model 2, the addition of the GWDEGREE did not change the parameter estimates of the other terms. The

GWDEGREE term was negative and significant (-5.62, p-value < 0.05). Table 5.4 summarizes these results.

**Table 5.4: El Paso ERGM Coefficients**

	<b>Model 1</b>	<b>Model 2</b>	<b>Model 3</b>
	Estimate (SE)	Estimate (SE)	Estimate (SE)
<b>Edges</b>	<b>3.147* (.85)</b>	<b>3.160* (.86)</b>	--
<b>Nodal Attributes</b>			
Age (nodecov)	0.013 (.01)	0.015 (.01)	--
Years of Practice (nodecov)	<b>-0.027* (.01)</b>	<b>-0.029* (.01)</b>	--
Female (nodefactor)	<b>-1.964* (.51)</b>	<b>-1.925* (.54)</b>	--
Non-US Trained (nodefactor)	-0.020 (.09)	-0.032 (.09)	--
PCP (nodefactor)	<b>-1.573* (.18)</b>	<b>-1.589* (.19)</b>	--
Surgeon (nodefactor)	<b>-2.448* (.41)</b>	<b>-2.451* (.41)</b>	--
Biopsy Physician (nodefactor)	0.119 (.20)	0.111 (.20)	--
Dual (nodefactor)	0.249 (.56)	0.285 (.57)	--
<b>Homophily</b>			
Age (absdiff)	0.012 (.01)	0.012 (.01)	--
Years of Practice (absdiff)	<b>-0.032* (.01)</b>	<b>-0.032* (.01)</b>	--
Female (nodematch)	-0.758 (.53)	-0.776 (.55)	--
Non-US Trained (nodematch)	-0.055 (.12)	-0.053 (.12)	--
PCP (nodematch)	<b>-0.297* (.14)</b>	<b>-0.284* (.14)</b>	--
Surgeon (nodematch)	-0.494 (.38)	-0.503 (.38)	--
Biopsy Physician (nodematch)	-0.247 (.15)	-0.249 (.15)	--
Dual (nodematch)	0.830 (.53)	0.815 (.54)	--
<b>Network Structure</b>			
GWDEGREE	--	<b>-5.62* (1.4)</b>	--
GWESP	--	--	--
<b>AIC</b>	1779	1774	

\*Bolted indicates significance

\*\*nodefactor: categorical nodal attribute inserted in ERGMs in R; nodecov: continuous nodal attribute inserted in ERGMs in R; nodematch: homophily categorical variable inserted in ERGMs in R; absdiff: homophily continuous variable inserted in ERGMs in R

Model 1: Nodal Attributes and Homophily Terms

Model 2: Nodal Attributes, Homophily Terms, GWDEGREE

Model 3: Nodal Attributes, Homophily Terms, GWESP

Comparing Model 1 across regions, we see that the PCP nodal attribute term and the homophily term were consistently negative and significant. RGV had a significant and positive non-US Trained nodal attribute and homophily terms, while in the other networks this term was not significant. Table 5.5 summarizes these results.

**Table 5.5: ERGM Model 1 Coefficients Compared Between Regional Networks**

	Houston Estimate (SE)	Rio Grande Valley Estimate (SE)	El Paso Estimate (SE)
<b>Edges</b>	-0.075 (.29)	<b>0.928* (.38)</b>	<b>3.147* (.85)</b>
<b>Nodal Attributes</b>			
Age (nodecov)	<b>0.006* (.002)</b>	0.002 (.01)	0.013 (.01)
Years of Practice (nodecov)	<b>-0.017* (.003)</b>	0.002 (.01)	<b>-0.027* (.01)</b>
Female (nodefactor)	<b>-0.43* (.03)</b>	-0.051 (.12)	<b>-1.964* (.51)</b>
Non-US Trained (nodefactor)	0.004 (.04)	<b>0.152* (.05)</b>	-0.020 (.09)
PCP (nodefactor)	<b>-1.96* (.04)</b>	<b>-2.135* (.09)</b>	<b>-1.573* (.18)</b>
Surgeon (nodefactor)	<b>-2.25* (.12)</b>	-1.801* (.15)	<b>-2.448* (.41)</b>
Biopsy Physician (nodefactor)	<b>-0.15* (.03)</b>	<b>0.617* (.09)</b>	0.119 (.20)
Dual (nodefactor)	0.53 (.28)	-0.176 (.19)	0.249 (.56)
<b>Homophily</b>			
Age (absdiff)	<b>-0.019* (.00)</b>	0.010 (.01)	0.012 (.01)
Years of Practice (absdiff)	0.006 (.00)	<b>-0.018* (.01)</b>	<b>-0.032* (.01)</b>
Female (nodematch)	<b>0.19* (.03)</b>	0.062 (.13)	-0.758 (.53)
Non-US Trained (nodematch)	0.03 (.05)	<b>0.191* (.07)</b>	-0.055 (.12)
PCP (nodematch)	<b>-0.28* (.04)</b>	<b>-0.402* (.08)</b>	<b>-0.297* (.14)</b>
Surgeon (nodematch)	<b>-0.25* (.12)</b>	0.003 (.14)	-0.494 (.38)
Biopsy Physician (nodematch)	<b>-0.096* (.03)</b>	0.001 (.08)	-0.247 (.15)
Dual (nodematch)	-0.002 (.28)	0.092 (.01)	0.830 (.53)

\*Bolded indicates significance

\*\*nodefactor: categorical nodal attribute inserted in ERGMs in R; nodecov: continuous nodal attribute inserted in ERGMs in R; nodematch: homophily categorical variable inserted in ERGMs in R; absdiff: homophily continuous variable inserted in ERGMs in R

Model 1: Nodal Attributes and Homophily Terms

Model 2: Nodal Attributes, Homophily Terms, GWDEGREE

Model 3: Nodal Attributes, Homophily Terms, GWESP

## **SECTION 6: NETWORK MODELS – NETWORK AUTOCORRELATION MODELS**

### **Section 6.1: General Overview of Network Autocorrelation Models and**

#### **Purpose of Section**

Social behaviors often occur within the context of social networks; thus, a node's social behavior within a network is dependent on the relationships between it and other nodes, and those between other nodes (Leenders, 2002). Network autocorrelation models are models of nodal behavior that consider these nodal interdependencies. Specifically, they study how a node's social behavior may be influenced by a node's position within the network, and the behavior and the characteristics of neighboring nodes (Leenders, 2002; M. Smith, Gorgoni, & Cronin, 2016). These models utilize one or more of several possible weight matrices that describe effects of nodes on each other, and relationships between nodal attributes. It is through these weight matrices that interdependencies between nodes are incorporated into the model estimation procedures (Leenders, 2002; M. Smith et al., 2016).

These models have been utilized in multiple settings, such as studying academic performance, political science, and social influence studies (Chun, Kim, & Kim, 2012; Fujimoto & Valente, 2012; Hays, Kachi, & Franzese, 2010). They have also been utilized in studying transit networks, communication networks, and trade networks (Chun et al., 2012; Hays et al., 2010; M. Smith et al., 2016). In an example of a social influence study, Fujimoto and Valente utilized these models to study smoking behavior among adolescents, within their friendship networks, examining how friendships affect smoking behavior (2012). The weight matrix that these authors specified incorporated the

influence of mutual or reciprocated friendship nominations, as well as the influence of one-sided friendship or non-reciprocated friendship nominations (Fujimoto & Valente, 2012). They found that reciprocated friendships had a greater impact on smoking behavior than non-reciprocated friendships (OR: 4.44, CI: 3.27-6.01 vs. OR: 2.07, CI: 1.64-2.61) (Fujimoto & Valente, 2012).

To our knowledge, there have not been any studies utilizing these models in networks created from Medicare data. The purpose of this section is to describe the use of network autocorrelation models in exploring factors that contribute to the use of MIBB. This section comprises the following parts: a brief overview of the mathematical considerations of network autocorrelation models, including model specification of network autocorrelation models; a brief description of the data we utilized in our analyses; a description of the outcome variable and covariates used in our analysis; a specification of the weight matrices we utilized in the analysis; descriptive results, and model results.

## **Section 6.2: Methods**

### **SECTION 6.2.1: NETWORK AUTOCORRELATION – MATHEMATICAL CONSIDERATIONS AND MODEL SPECIFICATIONS**

Leenders describes the mathematics of network autocorrelation models; what follows is an overview of these considerations (2002). We let  $y$  be a vector corresponding to the nodes in a network, where each entry in the vector records for the corresponding node the social behavior or outcome of interest. The entries of the vector can be continuous, or binary. We let  $X$  be a matrix of covariates for the nodes in the network,

just as in a regression model (e.g., age, gender, etc.). Network autocorrelation models take the influence of the nodes on each other into account through a weight matrix,  $W_y$ .

Weight matrices describe specific network effects and spatial effects. Multiple weight matrices, each of them representing a specific type of influence of nodes on other nodes within the network, can be included in the model. We considered the following types of weight matrices: attribute similarity, structural similarity, and netlag. Attribute similarity calculates a similarity matrix based on nodal attributes such as gender (Leifeld & Cranmer, 2017). This matrix captures whether two nodes connected to each other are similar in some specified nodal attribute. Structural similarity captures the extent to which two nodes are connected to the same neighboring nodes (Leifeld & Cranmer, 2017). Netlag calculates a partial network lag matrix to capture how the outcome of a node's neighbors affect the node's outcome; specifically it allows the inclusion of those values in  $y$  corresponding to a node's neighbors, and other nodes in the network, as covariates in our regression model (Leifeld & Cranmer, 2017). Table 6.1 provides more specific details of the weight matrices used in our study.

**Table 6.1: Summary of Weight Matrix Effects**

Variables	Description/Interpretation
<i><b>Weight Matrices Effects</b></i>	
Attribute Similarity	This term is based on a nodal attribute (Leifeld & Cranmer, 2017). In our context, it captures whether two physicians connected to each other are similar in terms of being biopsy physicians, non-US trained, or female.
Structural Similarity	Two nodes are structurally similar if they share the same neighboring nodes. (Leifeld & Cranmer, 2017). In our context, a physician may be affected by the high performance of another physician who is connected to the same group of physicians.
Netlag	This term is a spatial network term, capturing the autocorrelation in networks. In other words, it captures whether a node being connected to a high performing node (in terms of outcome) will affect the node's performance (Leifeld, 2017). In our context, it is asking whether a physician being connected to a physician whose rate of MIBB met recommendations will affect whether their rate of MIBB meets recommendations.

Formally, a simple network autocorrelation model has the following notation (Leenders, 2002):

$$y = \rho W_y + \varepsilon,$$

where  $\varepsilon \sim N(0, \sigma^2)$ . This model can be extended to include a matrix of covariates,  $X$ :

$$y = \rho W_y + X\beta + \varepsilon,$$

where  $\varepsilon \sim N(0, \sigma^2)$ .

The above model is used to estimate  $\rho$  and  $\beta$ , and thus infer how influence (i.e., a node being connected to a higher performing node, operationalized through netlag), interdependencies (i.e., mutual friendships; structural similarity), or covariates (i.e., attribute similarity) affect  $y$ , each while controlling for each other, and possibly for underlying covariates.

#### **SECTION 6.2.2: DATA, OUTCOMES, COVARIATES, WEIGHT MATRIX SPECIFICATIONS, AND MODELS**

As we did in studying ERGMs, we focused on only a few networks, here only for the year 2012. Houston and Rio Grande Valley were chosen because they are different sized networks, and have very different rates of MIBB. Section 2.3 describes the derivation of these networks.

As our outcome variable for each physician we chose to utilize whether or not the rate of MIBB for that physician met NCCN guidelines. The MIBB rate for a given physician was calculated by looking at all patients within our breast cancer cohort, who claimed service from that physician, and computing the percentage of the patients thus defined who received MIBB. If the MIBB rate of a physician was greater than 0.90, we said that the physician had a rate of MIBB meeting recommendations. Thus, we are

modeling whether or not physician attributes, network position, etc. affects a physician's rate of MIBB meeting recommendations.

We included the following network measures as controls, as previous analyses suggested the influence of these measures on MIBB: betweenness centrality and local transitivity (see Section 2.4.2 for definitions). The following nodal attributes were included as covariates: physician's age, physician years of practice, whether or not the physician is a PCP, whether or not the physician is a surgeon, and whether or not a physician is a Radiologist.

We included weight matrices of the types specified and introduced above. For the attribute similarity matrices, the following attributes were considered: biopsy physician, non-US trained, and female. We note that there is an attribute similarity matrix for each listed attribute. The interest is in whether a physician with a given attribute value connected to another with the same attribute value is more likely to have a rate of MIBB meeting recommendations. For netlag, we included a lag of 1 and a lag of 2. A lag of 1 captures immediate neighbor effects while a lag of 2 capture effects of nodes at a distance of 2 from a given node.

Descriptive statistics were obtained for covariates and outcome: frequencies with percentages for categorical variables, and means with standard deviations for continuous variables. We considered three network autocorrelation models for each network; for all three models the outcome is whether a physician's rate of MIBB meets recommendations. Model 1a considers the effect of attribute similarity, for the three attributes mentioned above, on the outcome. Model 1b considers the effect of structural similarity, and Model 1c considers the effect of netlag, including lag 1 and lag 2. Model 2

includes all the weight specification matrices and network measures, thus exploring the effects of the weight specification matrices on the outcome, while controlling for network measures. Model 3 controls for weight specification matrices, network measures, and nodal attributes (those mentioned specifically in the above as covariates of interest).

## Section 6.3: Results

Houston had 513 physicians within the 2012 network. RGV had 124 physicians. For Houston, 428 (89.3%) physicians had rates of MIBB meeting NCCN recommendations. For RGV, only 62 (50%) physicians had rates of MIBB meeting NCCN recommendations. Houston had 122 (23.8%) physicians who were non-US trained, while RGV had 51 (41.1%) physicians who were non-US trained. RGV had only 19 (15.3%) physicians who were female while Houston had 176 female physicians (34.3%). Table 6.2 summarizes these and other descriptive statistics for the Houston and RGV networks.

**Table 6.2: Descriptive Statistics for the Houston and RGV Networks**

	Houston	Rio Grande Valley (RGV)
<b>Number of Physicians</b>	513	124
<b>Biopsy Physicians (n (%))</b>	139 (27.1%)	37 (29.8%)
<b>Surgeons (n (%))</b>	91 (17.7%)	28 (22.6%)
<b>PCP (n (%))</b>	271 (52.8%)	69 (55.6%)
<b>Non-US Trained (n (%))</b>	122 (23.8%)	51 (41.1%)
<b>Female (n (%))</b>	176 (34.3%)	19 (15.3%)
<b>Age (mean (SD))</b>	48.7 (14.5)	48.9 (14.1)
<b>YOP (mean (SD))</b>	22.8 (11.4)	23.0 (10.4)
<b>Betweenness Centrality (mean (SD))</b>	425.7 (1165)	52.0 (116.7)
<b>Transitivity (mean (SD))</b>	0.71 (0.29)	0.81 (0.22)
<b>Outcome (n (%))</b>	458 (89.3%)	62 (50%)

For Houston, attribute similarity of biopsy physician was significant in all three models. A biopsy physician connection to another biopsy physician, as compared to a biopsy physician connection to a non-biopsy physician, negatively affected that biopsy

physician having a rate of MIBB meeting NCCN requirements (parameters ranging from -0.0035 and -0.0042, all p-values < 0.05). Further, in Model 2, a non-US trained physician connection to another non-US trained physician, as compared with a non-US trained physician connection to a US-trained physician, significantly and positively affected that non-US trained physician having a rate of MIBB meeting NCCN requirements (0.0038, p-value < 0.05). Structural similarity had a significant positive effect on a physician having a rate of MIBB meeting NCCN recommendations in Models 2 and 3 (0.039, p-value < 0.05 and 0.044, p-value < 0.05, respectively). Similarly, netlag of 1, i.e. a physician being directly connected to a physician with a rate of MIBB meeting NCCN guidelines, had a significant positive effect on a physician having a rate of MIBB meeting NCCN recommendations, in Models 2 and 3 (0.888, p-value < 0.05 and 0.089, p-value < 0.05, respectively). Furthermore, in Model 3, a physician being a surgeon significantly and negatively affected whether a physician had a rate of MIBB meeting NCCN recommendations (-2.673, p-value < 0.05). Table 6.3 summarizes these results.

**Table 6.3: Network Model Parameter Estimates for Houston, 2012**

	<b>Model 1a</b>	<b>Model 1b</b>	<b>Model 1c</b>	<b>Model 2</b>	<b>Model 3</b>
<b>Intercept</b>	<b>1.568*</b>	1.080	<b>2.182*</b>	-8.491	-7.397
<b>Network Structure</b>					
Attribute Similarity: Biopsy Physician	<b>-0.0042*</b>	--	--	<b>-0.0047*</b>	<b>-0.0035*</b>
Attribute Similarity: Non-US Physician	0.0033	--	--	<b>0.0038*</b>	0.0036
Attribute Similarity: Female Physician	0.0042	--	--	0.0039	0.0033
Structural Similarity	--	0.02084	--	<b>0.0390*</b>	<b>0.0439*</b>
Netlag (1)	--	--	-0.0054	<b>0.0878*</b>	<b>0.0891*</b>
Netlag (2)	--	--	0.0007	0.0013	0.0015
<b>Network Measures</b>					
Betweenness Centrality	--	--	--	-0.0001	-0.000
Local Transitivity	--	--	--	<b>-2.0011*</b>	-1.710
<b>Covariates</b>					
Age	--	--	--	--	-0.0101
Years of Practice	--	--	--	--	-0.0046
PCP	--	--	--	--	-1.8707
Surgeon	--	--	--	--	<b>-2.6731*</b>
Radiologist	--	--	--	--	-1.8868

\*p-value < 0.05

\*\*Bolded results indicate significance

Model 1: only including weight matrices

Model 2: including all weight matrices, controlling for network measures

Model 3: all terms (weight matrices, network measures, covariates)

**Table 6.4: Parameter Estimates of Network Models for RGV, 2012**

	<b>Model 1a</b>	<b>Model 1b</b>	<b>Model 1c</b>	<b>Model 2</b>	<b>Model 3</b>
<b>Intercept</b>	-0.3515	0.1015	2.7755	10.1578	27.63
<b>Weight Matrices Effects</b>					
Attribute Similarity: Biopsy Physician	<b>-0.0363*</b>	--	--	<b>-0.0341*</b>	<b>-0.0613*</b>
Attribute Similarity: Non-US Physician	0.0303	--	--	0.0176	0.0510
Attribute Similarity: Female Physician	0.0122	--	--	0.0129	0.0087
Structural Similarity	--	-0.0344	--	-0.3126	-0.3719
Netlag (1)	--	--	<b>-0.0624*</b>	-0.1101	-0.1300
Netlag (2)	--	--	-0.0936	-0.1252	-0.1607
<b>Network Measures</b>					
Betweenness Centrality	--	--	--	-0.0027	-0.0020
Local Transitivity	--	--	--	3.2715	3.3090
<b>Covariates</b>					
Age	--	--	--	--	0.0503
Years of Practice	--	--	--	--	-0.0657
PCP	--	--	--	--	-16.49
Surgeon	--	--	--	--	-15.10
Radiologist	--	--	--	--	-16.74

\*p-value &lt; 0.05

\*\*Bolded results indicate significance

Model 1: only including weight matrices

Model 2: including all weight matrices, controlling for network measures

Model 3: all terms (weight matrices, network measures, covariates)

For RGV, attribute similarity of biopsy physicians was significant across all three models. A biopsy physician's connection to another biopsy physician, compared with a connection to a non-biopsy physician, negatively affected that biopsy physician having a rate of MIBB meeting NCCN recommendations (parameters ranging from -0.034 and -0.061, all p-values < 0.05). For Model 1, netlag of 1 had a significant negative effect on a physician having a rate of MIBB meeting NCCN recommendations (Model 1c). Table 6.5 summarizes these results.

## **SECTION 7: DISCUSSION, LIMITATIONS, AND CONCLUSIONS**

### **Section 7.1: Discussion and Limitations: Aim One**

#### **SECTION 7.1.1: RESTATING AIMS**

This study sought to examine the utility of social network analysis methodologies in examining and explaining rates of MIBB as recorded in Medicare data. Physician networks were created using Medicare data, with nodes being physicians and edges being shared patients. These networks are considered to be collaboration networks, i.e., networks that broadly describe working relationships between physicians (Barnett et al., 2011). Within the context of exploring possible influences on physicians' use of MIBB, we utilized SNA metrics to capture how physician relationships affect this use. We also examined how physician relationships influence patient receipt of MIBB. However, the overarching goal was to attempt to fully utilize SNA in examining Medicare data, and to assess the usefulness of the methodology, with the above context being a convenient subject area within which to test the tools.

Aim one sought to use SNA metrics to expand on traditional regression methods such as hierarchical linear models, utilized in health care services research. Aim two considered the use of network models, ERGMs and network autocorrelation models, to model the structure of physician networks derived from Medicare data, and to determine whether that network structure affected the use of MIBB. The models in Aim two incorporate network dependencies that traditional regression analyses do not.

#### **SECTION 7.1.2: REGIONAL VARIATION IN MIBB RATES AND NETWORK STRUCTURE**

Recent work has concluded that MIBB rates among surgeons are well below documented guidelines and vary between regions (Tamirisa et al., 2015). These guidelines, established by the NCCN in 2009, recommended that MIBB be used as the gold standard for initial diagnosing of breast cancer, with 90% of first biopsies being MIBB (Bever et al., 2009). Our results suggest that the MIBB rate among all physicians who administer breast biopsies is increasing over time, beginning in 2009. In fact, by 2012, all regions in our study, with the exception of RGV, have MIBB rates above 90%. This suggests that NCCN guidelines are being followed. However, even in 2012 we still see variation of MIBB rates between regions, similar to what has been seen in previous work (Tamirisa et al., 2015; Zimmerman et al., 2012); rates of MIBB vary between regions in Texas: 50% to 90% in 2009 and 59% to 96% in 2012.

This variation in MIBB rates across regions further illustrates the variation in health care systems, service, access, and outcomes between regions, that has been studied by many authors and is well documented (Goodwin, Lin, Singh, & Kuo, 2013; Reistetter et al., 2015; Tamirisa et al., 2015; Zimmermann et al., 2013). A possible reason for some of this regional variation is the variation in regional physician collaboration networks. Previous studies utilizing SNA to examine networks derived from administrative databases have examined the use of physician networks and their characteristics in the explanation of variance in health outcomes. These studies suggest two broad conclusions: physician collaboration networks differ between regions, and adjusting for network measures such as betweenness centrality may explain some of the variance in outcomes (Barnett et al., 2012; Casalino et al., 2015; Landon et al., 2012; Moen et al., 2016;

Pollack, Frick, et al., 2014; Pollack, Wang, et al., 2014; Pollack et al., 2012; Uddin et al., 2015).

Our regional results reveal that regional physician networks within Texas vary in size, network measures such as density, and network characteristics such as ratio of biopsy surgeons to biopsy physicians; this echoes one of the broad conclusions of previous studies utilizing SNA on administrative databases (Barnett et al., 2012; Casalino et al., 2015; Landon et al., 2012; Moen et al., 2016; Pollack, Frick, et al., 2014; Pollack, Wang, et al., 2014; Pollack et al., 2012; Uddin et al., 2015). For example, Landon et al., in studying the variation of patient-sharing networks across HRRs within the United States, concluded that network characteristics such as transitivity differed substantially between these networks (2012). Similarly, in our regional networks, transitivity differed between our networks. Furthermore, it was noted in Landon et al.'s study that transitivity was higher in smaller networks as compared to bigger networks (0.67 vs. 0.48, as an example) (2012). Similarly, transitivity in our relatively smaller networks, such as Lubbock, was higher than in our relatively larger networks, such as Houston (e.g., 0.87 in Lubbock vs. 0.77 in Houston).

As an aside, we provide a possible explanation for the above patterns regarding transitivity. We recall that transitivity has the interpretation that nodes within a network are “connected in dense pockets of interconnectivity”, i.e., two nodes will tend to be connected to each other when each is connected to a third node (T.W. Valente, 2010). Higher transitivity in smaller physician collaboration networks is not surprising, as physicians in these networks have a higher tendency to know each other and thus have a greater chance of collaborating with one another. Further, we note that the transitivity in

our regional networks is higher than the transitivity in Landon et al.'s HRR networks (2012). Landon et al. do not restrict specialties, whereas we do. Our focus is on physicians who work with breast cancer treatment, and this specialization increases the likelihood that physicians already know each other (2012).

### **SECTION 7.1.3: NETWORK MEASURES OVER TIME**

One aspect of physician networks derived from administrative data that has not been thoroughly discussed in the literature is the stability of these physician collaborative networks, in terms of network measures, over time. For other networks, such as personal and research collaboration networks, studies have suggested, or implied, the stability of network measures, such as transitivity (Amat & Perruchas, 2016; Lubbers et al., 2010). To our knowledge, this is the first study that explores the stability of network measures for networks derived from Medicare data. The regional networks for Dallas, Lubbock, and Austin exhibited some instability over time. Lubbock saw a 51% increase in normalized density from 2009 to 2012. Austin showed a 440% increase in betweenness centralization from 2011 to 2012. In terms of betweenness centralization, Dallas had an increase of 57.9% from 2010 to 2011, but then a decrease of 50% from 2011 to 2012.

For Lubbock, an increase in normalized density possibly indicates increased collaboration within the Lubbock physician collaboration network, but as Lubbock is a smaller network, this increased collaboration may only consist of a few more new collaborative ties. The changes in betweenness centralization in Austin and Dallas are more difficult to explain. Betweenness centralization increases indicate that physician collaboration networks are more centralized at a few nodes than they had been previously (see Section 2.4.3). A few possible explanations exist: perhaps there were real structural

changes within the healthcare system in Austin or Dallas; perhaps the results suggest the instability of calculating these measures from networks derived from Medicare data; and perhaps the networks have changed greatly in terms of the particular physicians who are in practice. Further research is needed to fully understand changes in normalized density and betweenness centralization in these regions, and to understand how to capture these changes against a possible background of changing physician roster. One possible further study is to run simulations of networks with structural characteristics similar to those observed in our networks, in order to determine what structural changes are needed to obtain the observed changes. This will yield information such as the number of edges needed to be removed and the number of nodes needed to be removed, to achieve the observed changes; this information may be useful in explaining the phenomenon. Further research would include looking at the healthcare systems, specifically those of the breast cancer systems, of these three regional networks to determine whether there were any changes, such as hospital closures or merging of hospital systems, during the periods of change.

#### **SECTION 7.1.4: SMALL-WORLD AND SCALE-FREE**

Few studies utilizing SNA on Medicare data have formally examined the small world property and the scale-free property of networks derived from Medicare data (Zand et al., 2017). Our results reveal that most of our regional networks were not scale-free networks, with El Paso and RGV as exceptions. According to the  $\sigma$  measure we utilized to assess the small world property, all regional networks met the formal criteria for the small-world property. We must note that individual observed characteristic path lengths for some of our regions, such as Houston and Dallas, are higher than the simulated

characteristics path lengths. This was not an expected result for small world networks, as small world networks have lower observed path lengths than simulated path lengths (Humphries et al., 2006; Telesford et al., 2011). However, an argument can be made that the path lengths are within range (1-3) of networks considered to be small world.

We further note that that fact that our regional networks are small world is in contrast to the study of Zand et al., whose results suggest that networks derived from Medicare data were scale free (2017). This difference could be due to the size of the networks in the two studies. Zand et al.'s networks had upwards of 800,000 nodes, and edges numbers ranging from 40,000,000 to 90,000,000. The largest networks in our study consisted of 754 nodes and 8,346 edges. The difference in size is due to the fact that we were looking at a more specific patient population and a more specific physician population than Zand et al. (2017). It is possible that our restriction of physician types includes in our networks precludes the possibility that networks satisfy the scale-free property.

Barabasi and Albert suggest that the scale-free property is due to the mechanism of preferential attachment in the growth of the networks (1999). Assuming Barabasi and Albert's conclusion, this implies that our regional networks, with the exception of El Paso and Rio Grande Valley, do not grow by preferential attachment. Rather, a different mechanism may be at play in the formation of these networks. The scale-free property results must be viewed cautiously, and this is specifically true of the conclusions of Barabasi and Albert. Though it may be possible that the scale free property gives a glimpse into the mechanisms of network formation, it is also possible that the scale-free property is inherent in all networks of the appropriate size (Keller, 2005). Further, Keller

points out that other network formation mechanisms also lead to the scale-free property. Therefore, future research is needed to examine the absence of the scale-free property in our regional networks, and to determine whether another mechanism of network development is at play. Further utilization of ERGMs with appropriate specifications may assist in further understanding of social mechanisms involved in the creation of these networks (see Section 7.2.1).

Our networks have the small-world property. Studies have acknowledged that network topologies such as the small-world property have a role in social influence processes, specifically diffusion (Peres, 2014). It is suggested that the structure of small-world networks (high clustering and short path lengths) encourages rapid information flow and increased social influence processes (Peres, 2014). In our regional networks, only Houston met the NCCN guidelines in 2009, the year the guidelines were released. By 2010, over half of the regional networks met criteria, and by 2012 all but one of the regional networks met the criteria. This highlights a rapid change in MIBB rates in a short span of time. It is possible that the small-world structure of these networks had some affect on this change.

#### **SECTION 7.1.5: NETWORK COMMUNITIES AND RATE OF MIBB**

Studies conducted by Pollack et al. and Uddin et al. indicate that network communities, identified using community detection algorithms, affect health outcomes such as prostatectomy rates, readmission rates, and hospitalization costs (2012; 2015). This illustrates the second broad conclusion of studies utilizing SNA on Medicare data: network structure and network measures affect outcomes. In the above studies, analyses were conducted at the patient level with communities either compared to each other

through bivariate statistical testing, or utilized as covariates in statistical modeling (Pollack et al., 2012; Uddin et al., 2015). However, this methodology only leads to the conclusion that communities have an effect on outcomes. Results do not speak about the specific network characteristic or structure that leads to or causes the effect on the health outcomes of interest.

We took a different approach for our study. Within a regression framework and with network communities as the unit of analysis, we explored the effects of network community level measures of density, centralization, and transitivity on the rate of MIBB. Considering all communities within all regions, we found that normalized density and betweenness do not significantly affect the community level rate of MIBB. This lack of effect could in part be due to the sample size of the study, with the analyses only encompassing, at most, 22 communities.

Our focus in the above was on exploring the affect of normalized density and centralization on a community's rate of MIBB. In the context of diffusion of innovation, or adoption of new ideas, normalized density and centralization have both been shown to play important roles (T. W. Valente, Chou, & Pentz, 2007). Valente et al. argues that higher values of these measures could either help or hinder the adoption of new ideas, depending on the culture of the networks (T. W. Valente et al., 2007). For instance, denser networks have more pathways by which ideas can travel, if the network's culture is conducive to adoption. As an example, in his study looking at community coalitions and their adoption of an evidenced-based substance abuse program, Valente et al. found that denser network coalitions had increased rates of adoption of evidenced-based substance abuse programs, and concluded that increasing density or centralization within

a network are valid interventions for adopting new ideas (2007). On the other hand, within a culture of resistance, new ideas have a difficult time taking root, and the pathways may become obstacles (T. W. Valente et al., 2007). As an example, Valente et al. comments that highly centralized networks tend to concentrate power, resulting in decreased shared-decision making and fewer opportunities for change (2007).

Considering the parameter estimates and assuming that the lack of significance was due to power, we see that our general results for 2012 suggest that normalized density negatively affected the rate of MIBB. This suggests a culture of resistance toward adoption of new ideas, as the denser networks have lower rates of MIBB. Further research is needed to study this result. Such research should explore notions of cultural predisposition to adoption, and such variables should possibly be included in the analysis as controls.

We briefly discuss our results in the 2012 Dallas networks. In these 2012 networks there was a significant positive association of normalized density with the rate of MIBB. By contrast, in the 2009 results, the normalized density effect was smaller, and was non-significant. Assuming Valente et al.'s conclusions regarding density and diffusion, these results possibly indicate that the healthcare system changed, and that with that change, the culture regarding adoption changed. In this changed situation, the structure of denser networks now allowed for or facilitated the increase in rate of MIBB. It is important to note that the Dallas community networks reveal a pattern contrary to that observed in the full set of communities. As such, these results should be interpreted carefully.

Further, we found in the analysis for all regional communities, that the ratio of biopsy surgeons to biopsy physicians had a significant negative affect on the rate of MIBB. This suggests that as this ratio decreases, the rate of MIBB increases. This is an intuitive result, since a lower ratio implies that biopsy radiologists are more numerous within a given network community relative to biopsy surgeons, leading to more MIBBs. This increase, in turn, may possibly be due to increased referrals to radiologist for biopsies.

In assessing transitivity, we found that transitivity negatively affected the rate of MIBB; that is, the higher the tendency towards clustering within a network community, the lower that network community's rate of MIBB. However, this effect was not significant. Within a diffusion of innovation context, transitivity is known to negatively impact the adoption of new ideas. This is because high transitivity often leads to redundant ties; these ties increase opportunities for diffusion of ideas only within their own cluster, but not to nodes outside of the cluster (Peres, 2014).

We comment on the behavior of normalized density and of betweenness centralization when the ratio of biopsy surgeons to biopsy physicians, and transitivity are included as covariates in our models. We see that the ratio variable and transitivity both affected the normalized density parameter. Specifically, the ratio variable intensified the magnitude of the effect of normalized density (-1.90 vs. -2.13) and transitivity decreased the magnitude of effect of normalized density (-1.90 vs. -1.19). Controlling for the ratio variable could be indicative of the importance of density and agreement to Valente's result. In other words, in keeping this ratio constant, the importance of density is highlighted, implying that a culture of resistance may be at play in the negative effect of

density. Furthermore, controlling for transitivity, the importance of density lessens; this suggests the possibility that culture within clusters may be more important than the culture, or density, of the whole community network.

We comment on some limitations to the analyses mentioned above. First, creation of the community networks was based on the fast greedy algorithm. In general, there is concern as to whether or not this was the correct algorithm to use, and if the community networks derived by this algorithm actually constitute “real-world” networks. Multiple studies have been conducted comparing many community detection algorithms and their validity for accurate detection of communities (Atay, Koc, Bbaoglu & Kodaz, 2017; Pasta & Zaidi, 2017; Wang, Wang, Yu, & Zhang, 2015; Radicchi et al., 2004). Many of these studies created simulated networks with set community structures, and then compared the ability of multiple community algorithms to detect communities. One recent study found that commonly used community algorithms, including the fast greedy, often fail in detecting appropriate communities if the size of the network is large (i.e., > 10,000 nodes), and the size of the community is large (i.e., > 10,000 nodes) (Pasta & Zaidi, 2017). This study indicates the lack of robustness of community algorithms as network size increases. However, we note that the performance of the fast greedy algorithm was mediocre in detecting these communities (Pasta & Zaidi, 2017). We further note that the size of the networks we explore was in the range of where fast greedy performed optimally (Pasta & Zaidi, 2017).

Further sensitivity analyses utilizing different community algorithms are warranted, as are validation studies of these community networks. Sensitivity analyses could be done by utilizing another community detection algorithm and determining if the

communities derived by this community algorithm are similar, in terms of some specified network characteristic(s), to the communities derived by the fast greedy algorithm.

Validation could be done by repeating Barnett's methodology within one or more of these regional networks; that is, surveying the physicians regarding collaboration and creating a network from these collaborations (2011). The fast greedy algorithm could then be run on that created network, to re-derive the network communities. Finally, these communities, and the overall network, could be compared to see if they consist of the same members as the communities and networks derived from the Medicare data.

Second, our analysis consisted of a small number of communities and networks only in Texas. Generalization of results must be done with caution. Finally, our analysis was cross-sectional by nature. Though we did examine two time points to explore diffusion patterns, it would have been better to include year as an effect in our models to fully study the effects of density and centralization on rate of MIBB over time; our small sample size, and the scope of our work, precluded this analysis.

The purpose of this analysis was exploratory. Our goal was to see general patterns in order to gain some understanding of the effects of network structure on rate of MIBB at the global level. To this end, we were able to see some notion of the importance of global network structure on the rate of MIBB, both descriptively and within the context of diffusion of innovation.

#### **SECTION 7.1.6: REGRESSION ANALYSES**

We were interested in looking at whether biopsy surgeons' characteristics and network measures affected the rate of physicians performing or patients receiving MIBB. Below is a concurrent discussion of both the linear model relating network measures to

physicians' rate of MIBB, and the logistic model, relating network measures to patients' receipt of MIBB. Recall that that analyses conducted in these models included only biopsy surgeons.

In both the linear models and logistic models, our results revealed that the surgeon characteristics of gender and training affected both a biopsy surgeon's rate of MIBB, as well as a patient's receipt of MIBB. Being male and having non-US training negatively affected a biopsy surgeon's rate of MIBB, and the likelihood of a patient receiving MIBB. This is consistent with previous results (Tamirisa et al., 2015).

In the linear models, we found that degree negatively affected the rate of MIBB, while closeness and strength positively affected the rate of MIBB. For the year 2009, these results were significant. This suggests that too many collaborators negatively impact a surgeon's practice, while being in a position to control information flow, and/or having a higher patient load, positively impact a surgeon's rate of MIBB. In the logistic models, we found that transitivity, betweenness, and strength affected whether a patient received MIBB. These results are significant in 2012. Strength and transitivity both negatively affected receipt of MIBB, while betweenness positively affected the receipt of MIBB. The negative impact of strength suggests that surgeons who share large volumes of patients opt to do open biopsies, as compared to MIBB. A possible explanation for this is that those surgeons who share high volumes of patients may be unique in their communities in terms of handling the surgical cases. Further research is recommended and could be done by comparing biopsy surgeons who have a high load of patients with biopsy surgeons who do not have a high load of patients in terms of network characteristics and surgeon characteristics. Previous works have explored how a

physician's centrality measures impact outcome. For example, Casalino et al. showed that physicians with higher degree had a higher rate of ambulatory care-sensitive admissions (Casalino et al., 2015). Moen et al. showed that node strength significantly and positively impacted evidence-based ICD therapy (2016).

We note that there were some differences between the effects of network measures on patients' receipt of MIBB, versus biopsy surgeons' rates of MIBB. Specifically, looking at the 2012 adjusted models, the directions of the effects of degree, transitivity, and strength differed in the linear and logistic models. In the linear models, degree and transitivity both negatively affected the rate of MIBB, but in the logistic regression models, they positively affected a patient's receipt of MIBB. Strength positively affected the a surgeon's rate of MIBB, while negatively affecting a patient's receipt of MIBB. This could be due to an "ecological fallacy"; that is, the association of network measures with the aggregated outcome (rate of MIBB by physicians), may not reflect the association of the network measures with the outcome at the individual level (patient receipt of MIBB). As this is an exploratory study of the effect of network measures, we note the importance of seeing this ecological fallacy. Previous works have used network measures within a regression framework on aggregate outcomes (Casalino et al., 2015; Moen et al., 2016). Our work indicates that this may not be the best approach, and that careful consideration must be taken before utilizing network measures within a regression framework. Other possible, and more technical, explanations for the discrepancies between the linear and logistic regressions are the fact that transformations were utilized for some of the network measures, in order to better estimate the logistic

regressions. Further, we only included biopsy surgeons with a documented surgeon specialty in the logistic regressions.

We also remark on the large ORs for betweenness centralization within the logistic model (as well as in the HLRMs discussed below). This is possibly due to the skewed distribution of betweenness centralization. The range of betweenness centralization for biopsy surgeons in 2009 (scaled and normalized) was -0.469 to 7.364. Large regression estimates for betweenness centralization have been noted in previous literature. One study utilizing physician level betweenness centralization as a covariate in their linear models also had a large parameter estimate, calculated as -102698.68 (Uddin et al., 2013).

We further note that these regression results must be viewed cautiously. As an exploratory analysis, we chose to utilize network measures in a regression framework. However, the assumption of independence required in regression does not hold, as the network measures we utilized have inherent dependencies. Our focus was to assess the behavior of these network measures to determine if these measures have some utility; the dependencies would have to be addressed further, if it is found that they have utility.

We now focus on the HLRMs, specifically examining the changes in ICCs over time and between model types (hospital model type vs. community model type). First, we discuss the purity results in comparing cluster mechanisms. Purity results showed that on average, regional communities clustering is not similar to regional hospital clustering. Specifically, communities may not be contained in hospitals; however, hospitals tend to be contained entirely in communities. This suggests that network communities differ from hospitals and therefore worth examination.

For these HLRMs, we sought to examine two primary questions: 1) utility of using community as a third level in hierarchical models for explaining variance, and 2) the effect of network measures on the biopsy surgeons' ICC, and on the hospitals' or communities' ICCs. Our study showed a decrease in hospital ICC, an increase in community ICC, and an increase in biopsy surgeon ICC between 2009 and 2012. An explanation for the decrease in hospital ICC, is an administrative push of practice guidelines at a hospital or practice level. That a hospital has a practice policy of following the recommended NCCN guidelines will greatly impact the practice of surgeons. In our context, we suggest that this hospital level policy possibly controlled for much of the variance in whether or not patients received MIBB, in 2012. We thus surmise that as the practice change becomes more engrained through hospital policies, the hospital level's explanation of variance lessens, as most hospitals become more homogeneous in terms of patients receiving MIBB; this explains hospital level decrease in ICC. This is largely an assumption, however, and further research is needed. Retrospectively examining a hospital whose biopsy policy changed to the NCCN guidelines could be a possible next step. To understand the increase in community level ICC, we first remark that the ICCs were not high to begin with in 2009: an ICC of 0.059 in the null model, and of 0.064 in Model 1 (the model incorporating patient and physician characteristics). However, by 2012, the ICCs more than doubled: 0.124 in the null model, and 0.154 in Model 1. Keeping in mind the increased rate of MIBB by 2012, one explanation is the utility of network communities in sustainable practice change. Assuming that our network communities are collaboration networks, peer support and practice culture possibly contributed more to a patient's receiving MIBB than hospital networks. In other words,

hospitals drive immediate practice change while network communities sustain the change. Any remaining differences in 2012 are due to community level practice differences. We note that we do not directly compare hospital and community impacts, as they are described in separate models: specifically, we don't look at a model that includes effects of both at the same time. An area of future research might be looking at the overlap between communities and hospitals, and determining how that overlap impacts MIBB utilization. The increase in biopsy surgeon ICC between 2009 and 2012 potentially speaks to the fact that some biopsy surgeons are resistant to new procedures or have inadequate resources to implement new procedures. This is further evidenced by the fact that biopsy surgeons ICCs are larger than the hospital and community ICCs for both the null models and Model 1 for 2009 and 2012.

The inclusion of network measures in the above models decreased the ICCs for biopsy surgeons and increased the ICCs for hospitals and communities. These results provide some evidence of the importance of a biopsy surgeon's position within their collaboration network; in other words, these network measures account for some of the variability of the receipt of MIBB. Further, the increased effect of hospital and community on a patient's receipt of MIBB possibly reflects the importance of health systems when network measures are taken into account; that is, individual decisions of physicians may indeed be the determining factor in practice choices, but, when taking their position in the network into account, the decision is often biased by the culture or the policy of their community or hospital. We note that is largely hypothetical, and further research is needed to confirm this possibility. This could be done by introducing into the model a variable that quantitatively measures culture. There is further argument

that community structure matters. When network level structures are taken into account, thereby leveling off differences of surgeons in terms of community, hospital policy matters more. This is because possible impact of the community has been removed as they are being controlled for in the model.

## **Section 7.2: Discussion and Limitations: Aim Two**

### **SECTION 7.2.1: EXPONENTIAL RANDOM GRAPH MODELS DISCUSSION**

We ran ERGMs to address the purpose of Aim Two. We were interested in looking at the network structure of collaborative physician networks derived from Medicare data. To our knowledge, only two other studies have explored ERGMs in networks derived from administrative studies. Uddin et al. focused on network structures such as 2-stars and alternating stars in their ERGMs, while Moen et al. added homophily effects to their ERGMs (2013; 2016). Our work focused both on network structure effects as well as on homophily effects.

We recall that Uddin et al. found differences in network structures, such as the 2-star and alternating star parameters, between their networks (2013). Through the ERGM framework, they concluded that some of their networks, such as the low readmission network, were more centralized than the high readmission networks (Uddin et al., 2013). Though we did not utilize the same network configurations in our ERGMs as Uddin et al., we did a similar comparison of network configurations between networks. We compared three networks: Houston, El Paso, and RGV. As did Uddin et al., we found differences between these networks in terms of network configurations (2013). We found that in the Houston network (the largest and highest MIBB rate network), the

GWDEGREE term and the GWESP term were both significant. This suggests that the formation of the Houston network is affected both by preferential attachment and triad closures: physicians form ties with physicians who are well connected, and physicians tend to cluster. There were differences in comparison of the Houston with the El Paso network and the RGV network. RGV had a significant GWESP term, while El Paso had a significant GWDEGREE term. We note that adding the GWESP term to the ERGM for El Paso resulted in non-convergence of the ERGM, while adding GWDEGREE to the ERGM for RGV resulted in a non-convergent ERGM. This suggests that the RGV's network formation is affected by preferential attachment, while the EL Paso's network formation is affected by triadic closures. Recall that our scale-free results suggested that the RGV and El Paso networks might be influenced by preferential attachment mechanisms in their formation. Now, we also note that Houston network may be affected by the preferential attachment mechanism as well, per the ERGMs, contradicting the scale-free results above. This brings into question the concept of scale-free, and its ties to network formation.

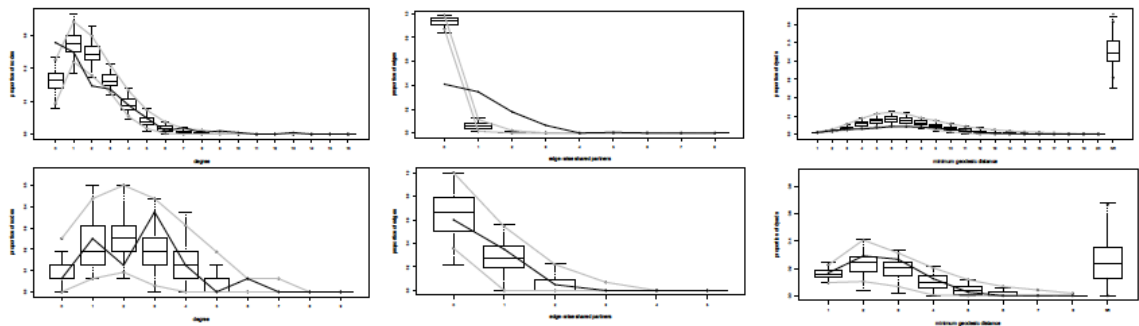
Moen et al. focused the construction of their ERGMs on the inclusion of homophily terms along with the alternating star parameter (2016). Similarly, we included homophily effects. Similar to Moen et al., we found that our PCP homophily term was negative and significant for all three of our networks (2016). This indicates that there is a decreased likelihood for PCPs to form collaborations with other PCPs, as compared with PCPs making connections with non-PCPs. We recall that Barnett et al. validated their Medicare derived networks with name-generator created networks. To derive the latter they specifically asked physicians which physicians they referred to, and from which

physicians they sought advice; they defined these collaborative networks as advice and referral networks (2011). Thus, the Barnett et al. definition of collaboration includes aspects both of advice and referral.

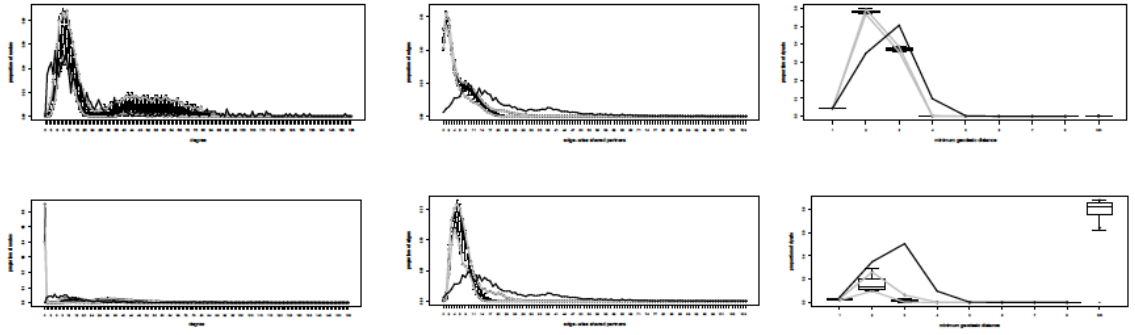
This definition makes it difficult to ascertain the interpretation of the homophily effects. If we define collaboration as “advice seeking”, the pattern observed in our ERGM seems counter-intuitive, suggesting that PCPs do not seek advice from other PCPs, but rather from physicians of other physician types. In our regional networks, PCPs comprised 47% to 52% of the physicians; this highlights the lack of homophily, as the pool of PCPs for other PCPs to connect with is not small. Thus, it is possible that our networks, rather than being “advice” networks, are more akin to “referral” networks. In this context, PCPs are more likely to “refer” to physicians of other types rather than to other PCPs. Further, in the Houston regional network, we see a similar lack of homophily among biopsy physicians, indicating that biopsy physicians (surgeons and radiologists) either do not seek advice from physicians with specialties similar to their own, or that they are likely to refer to other physicians of different specialties.

We comment that the models we ran may have suffered from degeneracy, or poor model fit, according to the goodness-of-fit results. As data from administrative databases like Medicare are being used in ERGMs, discussion of the goodness-of-fit of the ERGMs, and appropriateness of these measures, is needed to further understanding of these physician networks. Unfortunately, previous studies using ERGMs for such networks have not formally discussed the fit of these models. In this discussion, we briefly discuss the goodness-of-fit methodology, then discuss the fit of our ERGMs.

A methodology utilizing observed and simulated networks was developed that allows the assessment of the fit of an ERGM (Hunter, Goodreau, & Handcock, 2008). Hunter et al.'s methodology compares specific structural statistics from the observed network on which the ERGM is built, with those from simulated networks based on the ERGM model derived from the original network (2008). Their procedure utilizes three network structure statistics: geometrically weighted degree, edge-wise shared partners, and the dyadwise shared partner statistic. Hunter et al. suggests that these statistics “appear to capture high-order dependency structure in networks in parsimonious fashion while avoiding the problem of degeneracy” (2008). In other words, these specifications adequately assess network structure without, in most cases, resulting in degenerate models. Using the ERGM based on the original network, many networks are simulated, taking note of the three statistics above. If the original network's statistics are typical of the simulated graphs' statistics then the model has a good fit (Hunter et al., 2008). Figure 7.1 displays a model with a good fit and a model with a bad fit.

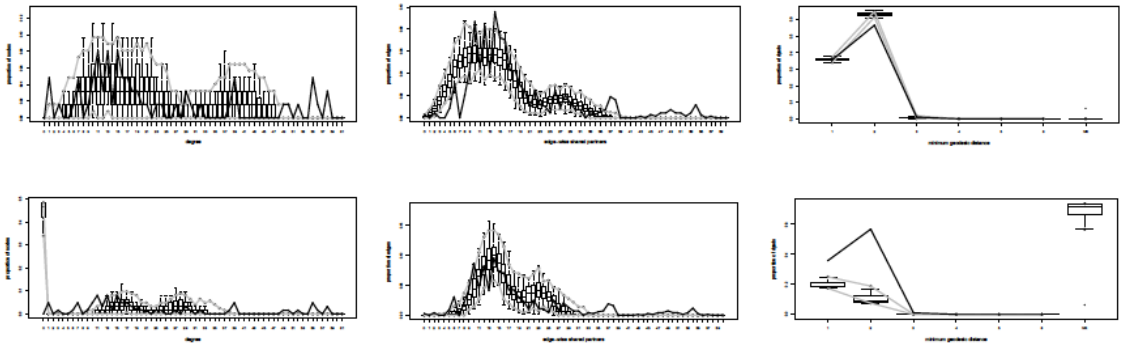


**Figure 7.1: Examples of Goodness of Fit Plots for Three Network Statistics.** The top row represents goodness-of-fit plots of an ERGM that may be misspecified. The bottom row represents goodness-of-fit plots of an ERGM that is considered a good fit.

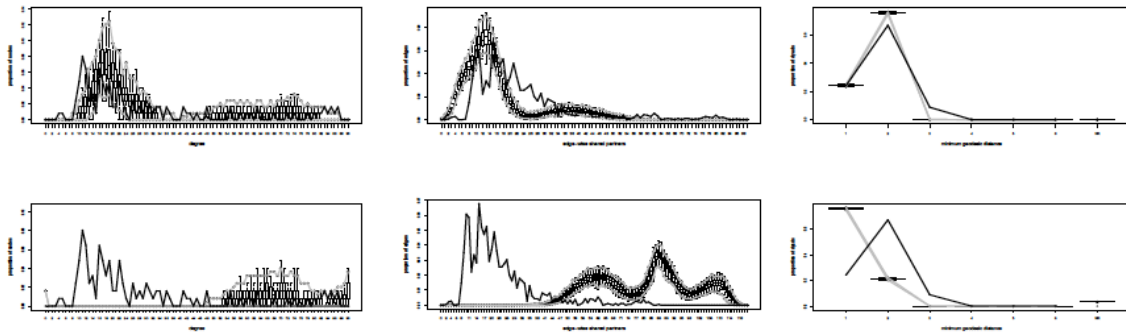


**Figure 7.2: ERGMs Goodness-of-Fit Results for Models 1 and 4 for Houston Regional Networks.** (a) Houston Model 1. (b) Houston Model 4.

We implemented this procedure and generated goodness-of-fit plots for each of our four models. Similar results were noted in Models 1 to 3; thus, we only discuss here the goodness-of-fit for Model 1 and Model 4. Recall that in the three regions we considered, there was convergence for Model 1 and no convergence for Model 4. Goodness-of-fit results are only useful for models that converge; however, we include model 4 as an exploratory example (Hunter et al., 2008; Koskinen & Snijders, 2013). Figures 7.2 to 7.4 display our goodness-of-fit results.



**Figure 7.3: ERGMs Goodness-of-Fit Results for Models 1 and 4 for El Paso Regional Networks.** (a) El Paso Model 1. (b) El Paso Model 4.



**Figure 7.4: ERGMs Goodness-of-Fit Results for Models 1 and 4 for RGV Regional Networks. (a) RGV Model 1. (b) RGV Model 4.**

Our goodness-of-fit results reveal that our ERGM models do not fit well. This implies a misspecification of our models. This means that the network attributes and network structures of GWDEGREE and GWESP do not do a good job in modeling the network structure of these physician networks. This raises the question of properly specifying our models to account for the data. Thus, the exact nature of our Medicare derived networks may need to be reconsidered and restudied. One such study could involve fully exploring the proper specifications of ERGMs for these networks. As this study was exploratory and ERGM application to this data is a relatively new idea, there was little previous knowledge on which to base a proper specification of the ERGMs. Further, we were utilizing models on many different networks, each of which will have a different ERGM specification; thus, the standard practice of introducing network structure and network attribute terms, beginning with homophily terms, one at time was not feasible. The best approach is to re-consider the nature of the network itself, in a theoretical manner, for each individual region, in order to build an ERGM with proper specifications. One way to do so is to re-validate these networks, in the manner of Barnett et al., not as advice but as referral networks. Then, further examination of how referral networks operate based on a theoretical understanding, possibly from a sociological or

organizational perspective, is needed in order to accurately specify the ERGM. We further note that Hunter et al.'s methodology may not entirely appropriate in this setting; Koskinen and Snidjers remarked that goodness-of-fit test should be chosen based on the research question and nature of the network (2008, 2013).

## **SECTION 7.2.2: NETWORK AUTOCORRELATION MODELS DISCUSSION**

Another aspect of Aim Two is the utilization of network autocorrelation models. Recall that network autocorrelation models examine the relationship between nodal dependencies and a specified nodal outcome. Specifically, we examined whether a physician's relationships affected whether or not a physician's rate of MIBB met NCCN standards (see Section 6.2.2). To our knowledge, this is the first application of these types of models to networks derived from administrative databases. Therefore, little is known regarding the behavior of these models in these networks.

Our results revealed that the biopsy physician attribute similarity had a significantly negative effect on the outcome. This was true for all three models and for both the Houston and RGV networks. This negative effect of attribute similarity signifies that biopsy physicians "collaborating" with other biopsy physicians will cause those physicians to be less likely to have rates of MIBB meeting NCCN guidelines. In interpreting these results, we must first make assumptions about the nature of "collaboration" in our network, as above: whether it is "advice" or "referral". If we assume an "advice" framework of collaboration (physicians ask advice from other physicians), a possible interpretation of these results is that biopsy physicians are not a good influence on other biopsy physicians regarding the practice of MIBB. This interpretation has limitations. It is known that the culture of a network influences

behavior. However, we cannot ascertain the culture of our networks. However, if we assume a “referral” framework of collaboration (physicians refer to other physicians), a possible interpretation of these results is that biopsy physicians who are referred patients from PCPs or surgeons and not from other biopsy physicians will likely perform MIBB on those patients. We further see that for the RGV network, the netlag parameter of 1 was negative across all three models (significant for Model 1c) indicating that a physician who was connected to another high performing physician was less likely to have a rate of MIBB meeting NCCN guidelines. In contrast, the Houston network’s netlag parameter of 1 was positive and significant when controlling for network measures and for covariates. This possibly indicates the strong influence of culture within the RGV network.

Our results suggest that structural similarity affects outcome. In the Houston regional network, the structural similarity parameter, after controlling for network measures and/or nodal covariates, has a positive and significant effect on whether a physician has a rate of MIBB meeting NCCN guidelines. Recall that previous diffusion of innovation studies suggested that structural similarity affects adoption (M. Kilduff & H. Oh, 2006; P. V. Marsden & J. Podolny, 1990; Strang & Tuma, 1993; van den Bulte & Lilien, 2001). Our result further supports this claim, with “adoption” meaning having MIBB rates meeting NCCN guidelines. However, we note that our analysis was cross-sectional, and that this fact limits this interpretation. To fully study diffusion of innovations, we must incorporate the changes of networks over time, as this will capture ‘movements’ of the innovation within the networks. Thus, to fully determine the effect of structural similarity on adoption, a longitudinal approach to modeling is recommended.

We further comment on a few limitations on our use of network autocorrelation models on these networks derived from administrative data. Our network itself was limited in that we could not study a network consisting of only biopsy surgeons; we needed to include other physician types, as our physicians of interest were embedded in a larger network including other specialties. As our interest lies with biopsy surgeons, their relationships with each other, and their MIBB practices, this was a major limitation. Specifically, network autocorrelation models examine nodal behavior, but our outcome variable could not be considered as a behavior for all of our physician types, since PCPs who provide primary care do not perform MIBB; and surgeons who conducted the breast resection, and radiologists who read the mammogram may not perform MIBB. However, to create our networks, these physician types needed to be included. It would have been best to consider only biopsy surgeons in our networks. Further study could involve surveying biopsy physicians within a specific regional network regarding whom they seek for advice and utilizing network autocorrelation models on this advice network. Lastly, we only considered a cross-sectional analysis. A strength of these network autocorrelation models is the ability to be able to model in a longitudinal framework to fully study how behavior is affected by network influences over time. Further research in a longitudinal framework is recommended.

### **Section 7.3: Conclusions**

We sought to explore the utility of SNA on networks derived from Medicare data specifically looking at the effect of networks on the use of MIBB. We did this through multiple means: first, through a description of physician collaboration networks at the

regional and community levels, examining the networks' characteristics over time; second, through a regression analysis at the community level, exploring the effect of community level network effects on a network community's rate of MIBB; third, through utilizing both linear and logistic regressions to examine physician level network effects on physician rate of MIBB and on patients' receiving MIBB; lastly, through the utilization of network models: ERGMS to model how network structure affect tie formation, and network autocorrelation models to model how network structure affects whether a physician has a rate of MIBB meeting NCCN standards. We summarize our results below:

- Rate of use of MIBB varied between regional networks and over time. Regional variation of MIBB agreed with previous literature on MIBB and with the larger discussion on regional variation of healthcare.
- From 2009 to 2012, the use of MIBB increased, with most regions meeting NCCN recommendations.
- Formal evaluation of the small world property and scale-free property in our regional networks revealed that all regions are considered small world, but that only a few regional networks display the scale-free property, leading to questions regarding the social mechanism that underlies the formation of these networks, and the larger consideration of the interpretation of these networks.
- Community level density and centralization did not significantly affect a community's rate of MIBB. This may in part be due to the small sample of communities. However, these results, in conjunction with previous literature, illustrate the importance of culture in adoption within network communities.

- A biopsy surgeon's degree, closeness, and strength both had significant effects on a physician's rate of MIBB, while a surgeon's transitivity had a significant effect on whether a patient received MIBB. This may indicate the importance of a biopsy surgeon's position on the specified outcome. In addition, the ecological fallacy was noted when considering these two modeling approaches.
- Within a hierarchical framework, ICC changes were noted on the second level (biopsy physician) and third level (hospital or community) across time. These results highlighted the following: the suggestion that hospital policy may drive the change in practice, but network communities may sustain the change, and the possible importance of network measures in affecting a patient's healthcare.
- ERGMs revealed differing results across regional networks, with a consistent finding that PCPs were likely to form ties with other PCPs. This leads us again to consider whether our networks are "collaboration" networks. Goodness-of-fit results raise questions about the specification of the models and the interpretation of the models.
- Lastly, network autocorrelation models consistently showed that a biopsy physician's connection to another biopsy physician negatively affected their use of MIBB. Primarily, this was an exploratory use of the models and further research is recommended.

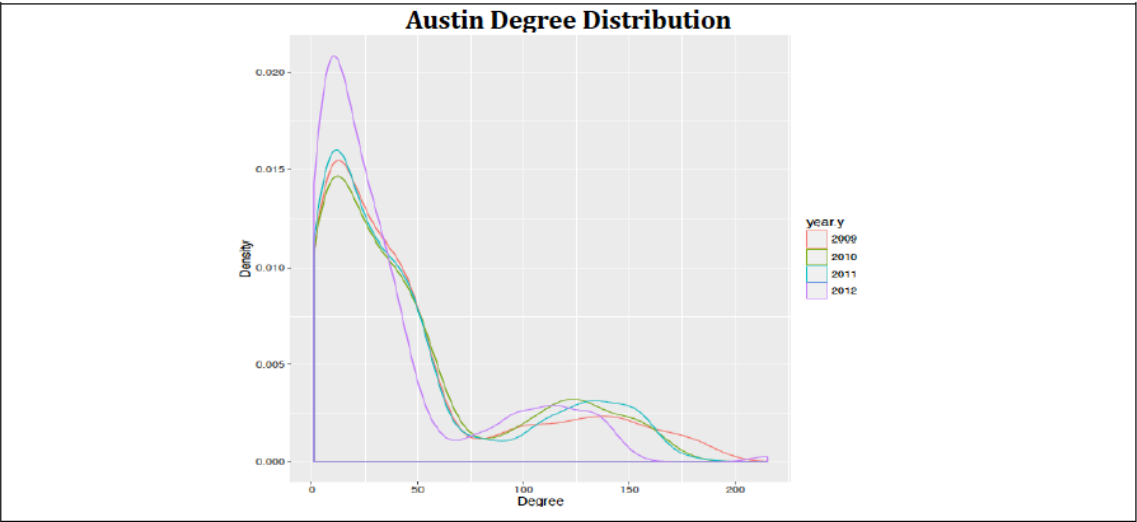
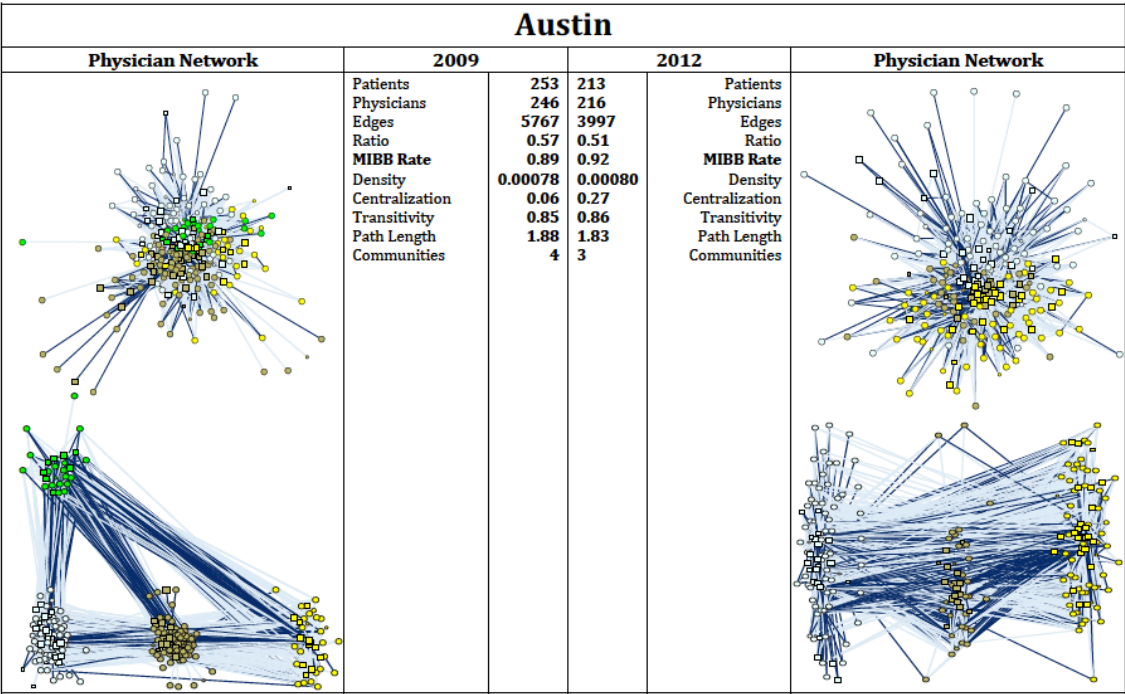
We noted several limitations of this study in the various sections above.

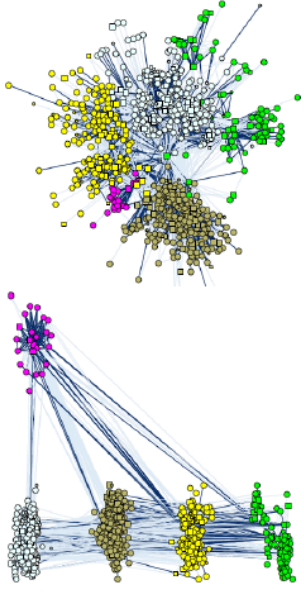
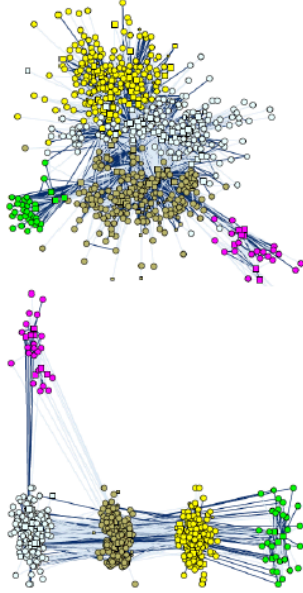
However, one limitation that bears repeating is the nature of these networks; that is, what do these networks really represent? Further research is recommended in validating these networks. This could possibly be through repeating Barnett's study, but with a clearer

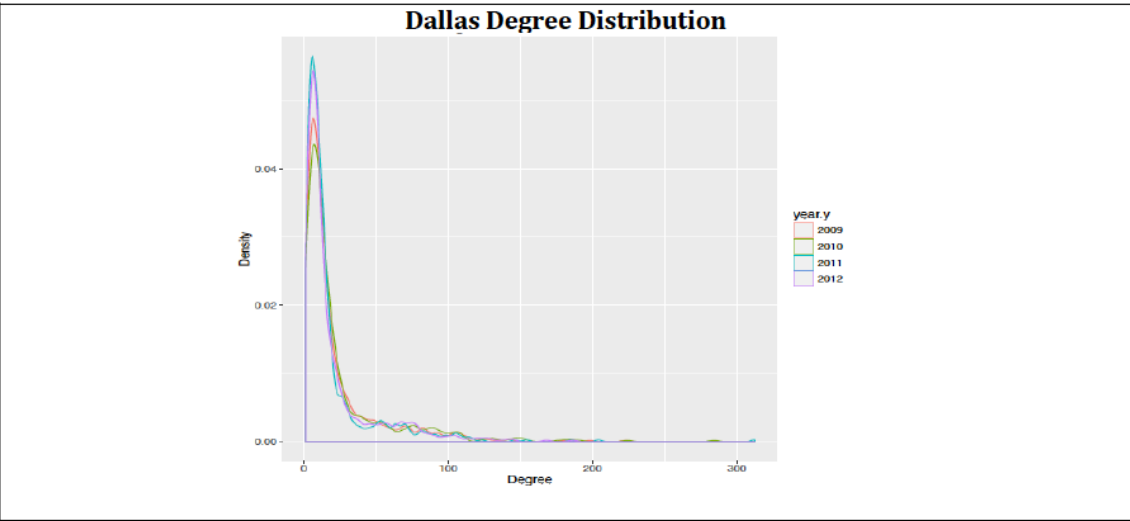
definition of collaboration, and on more diverse sample of physicians. Our results suggest that an “advice” framework or interpretation of collaboration may not be the correct framework or interpretation for these networks derived from Medicare data. Considering a “referral” framework or interpretation may lead to a better understanding of the networks. There is also concern as to whether we utilized appropriate physician types in examining how physician relationships affected MIBB rate. It is possible that not all physician types necessary to answer the question were included to truly answer this question.

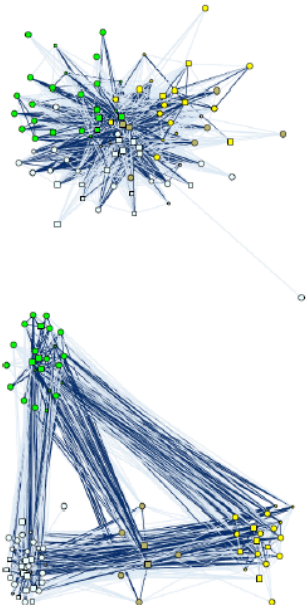
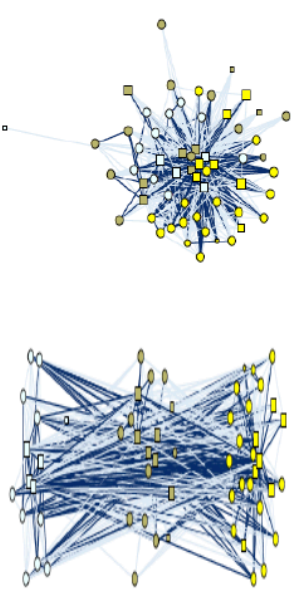
Potential exists within the social network framework. Some examples are as follows: utilizing network measures to control for more variance in regression models; using collaborative communities in hierarchical models; and using network models to fully explore network structure, and to fully explore effects of network structures on outcomes while controlling for relational dependencies. Utilizing the social network framework in studying physician patterns of MIBB provided some interesting insights into health services behavior in Texas, leading to more questions and to more possibilities for future work.

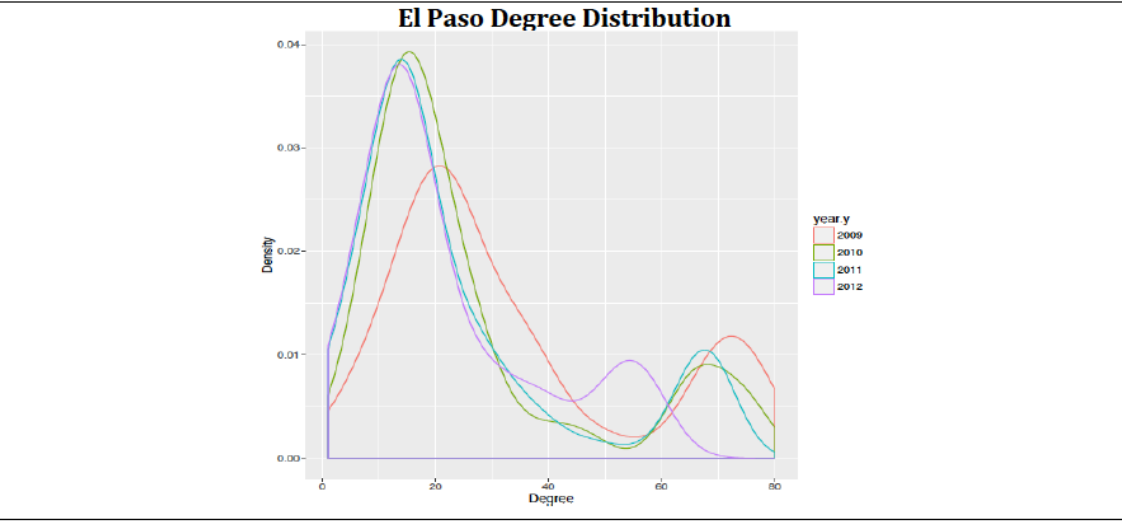
# Appendix A: Texas Regional Networks – Network Graphs and Degree Distributions

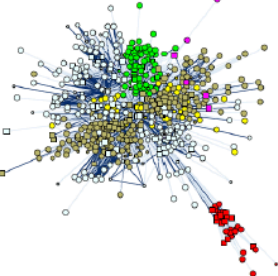
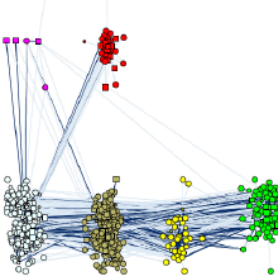
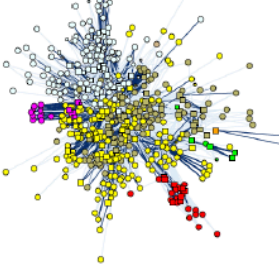
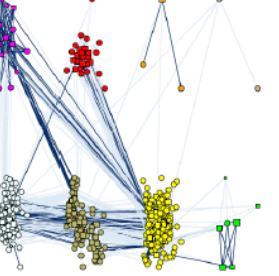


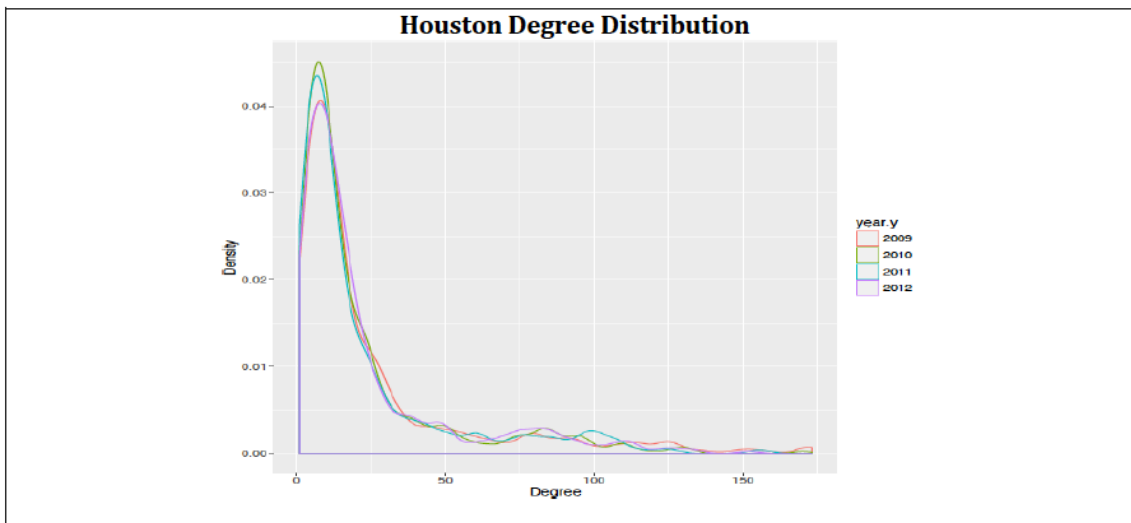
Dallas					
Physician Network	2009		2012		Physician Network
	Patients	890	811	Patients	
	Physicians	754	682	Physicians	
	Edges	8017	6860	Edges	
	Ratio	0.41	0.28	Ratio	
	MIBB Rate	0.89	0.94	MIBB Rate	
	Density (N.)	0.00004	0.00004	Density	
	Centralization (B)	0.18	0.15	Centralization	
	Transitivity (UW)	0.77	0.77	Transitivity	
	Path Length (A)	2.82	2.84	Path Length	
	Communities	5	5	Communities	

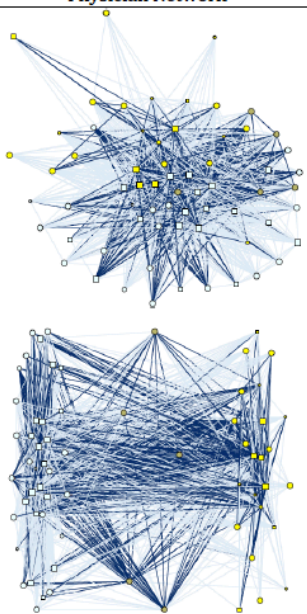
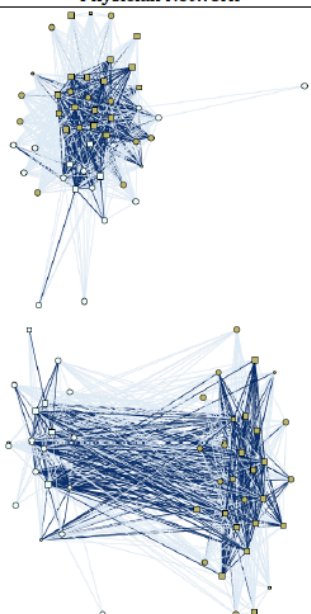


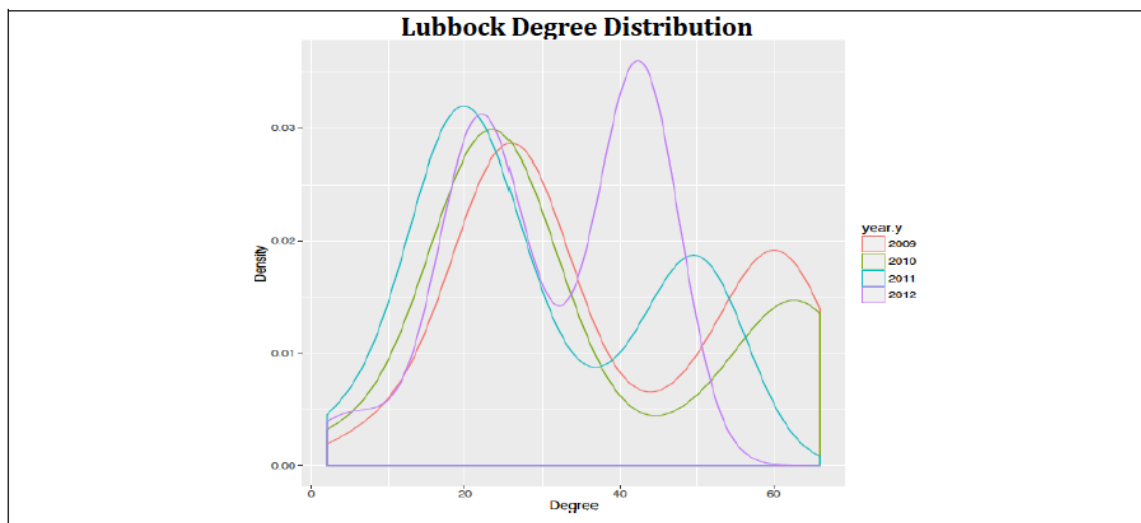
El Paso					
Physician Network	2009		2012		Physician Network
	Patients	67	59	Patients	
	Physicians	85	62	Physicians	
Edges	1424	678	Edges	678	Edges
Ratio	0.44	0.36	Ratio	0.36	Ratio
MIBB Rate	0.84	0.90	MIBB Rate	0.90	MIBB Rate
Density	0.00475	0.00588	Density	0.00588	Density
Centralization	0.05	0.06	Centralization	0.06	Centralization
Transitivity	0.83	0.83	Transitivity	0.83	Transitivity
Path Length	1.61	1.63	Path Length	1.63	Path Length
Communities	4	4	Communities	4	Communities

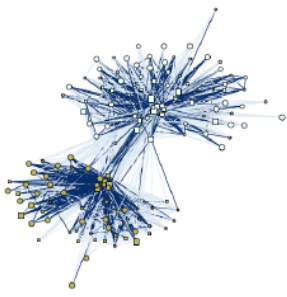
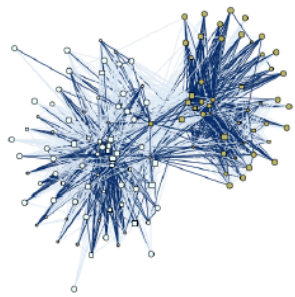
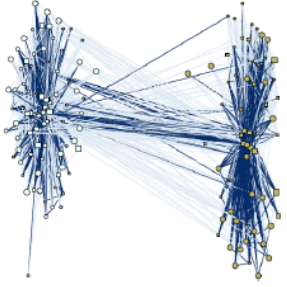
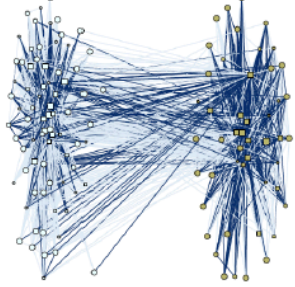


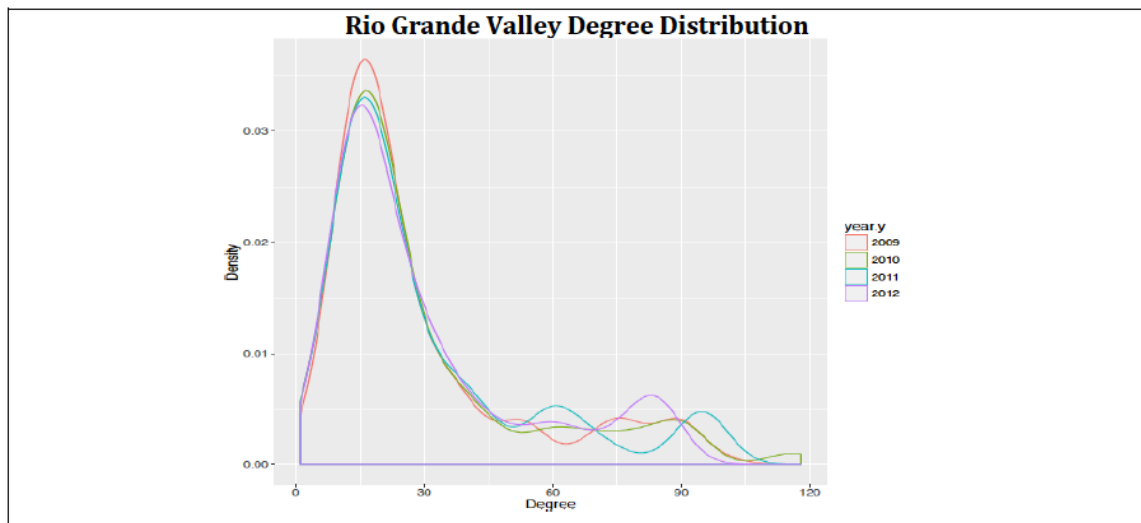
Houston					
Physician Network	2009		2012		Physician Network
 	Patients	607	559	Patients	 
	Physicians	594	513	Physicians	
	Edges	7403	5918	Edges	
	Ratio	0.33	0.22	Ratio	
	MIBB Rate	0.90	0.96	MIBB Rate	
	Density	0.00007	0.00009	Density	
	Centralization	0.10	0.08	Centralization	
	Transitivity	0.77	0.74	Transitivity	
	Path Length	2.65	2.66	Path Length	
	Communities	6	8	Communities	

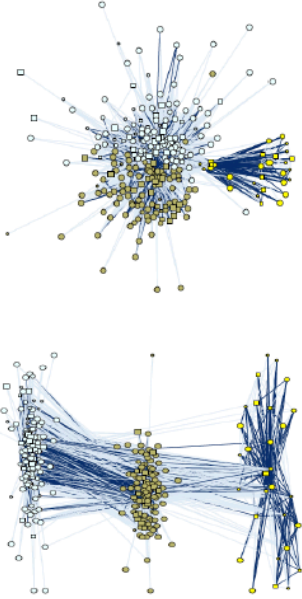
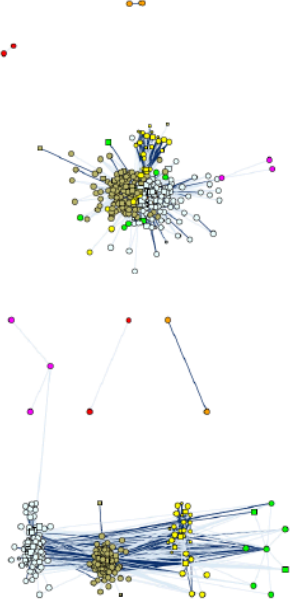


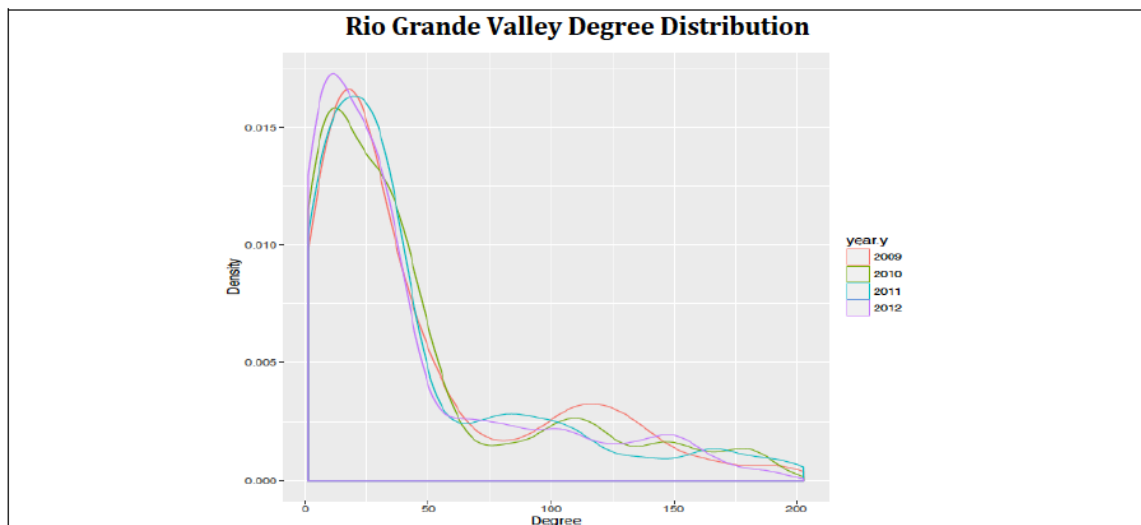
Lubbock					
Physician Network	2009		2012		Physician Network
	Patients	66	48	Patients	
	Physicians	65	48	Physicians	
	Edges	1237	744	Edges	
	Ratio	0.40	0.26	Ratio	
	MIBB Rate	0.85	0.94	MIBB Rate	
	Density	0.00929	0.01403	Density	
	Centralization	0.02	0.03	Centralization	
	Transitivity	0.85	0.87	Transitivity	
	Path Length	1.41	1.35	Path Length	
	Communities	3	2	Communities	



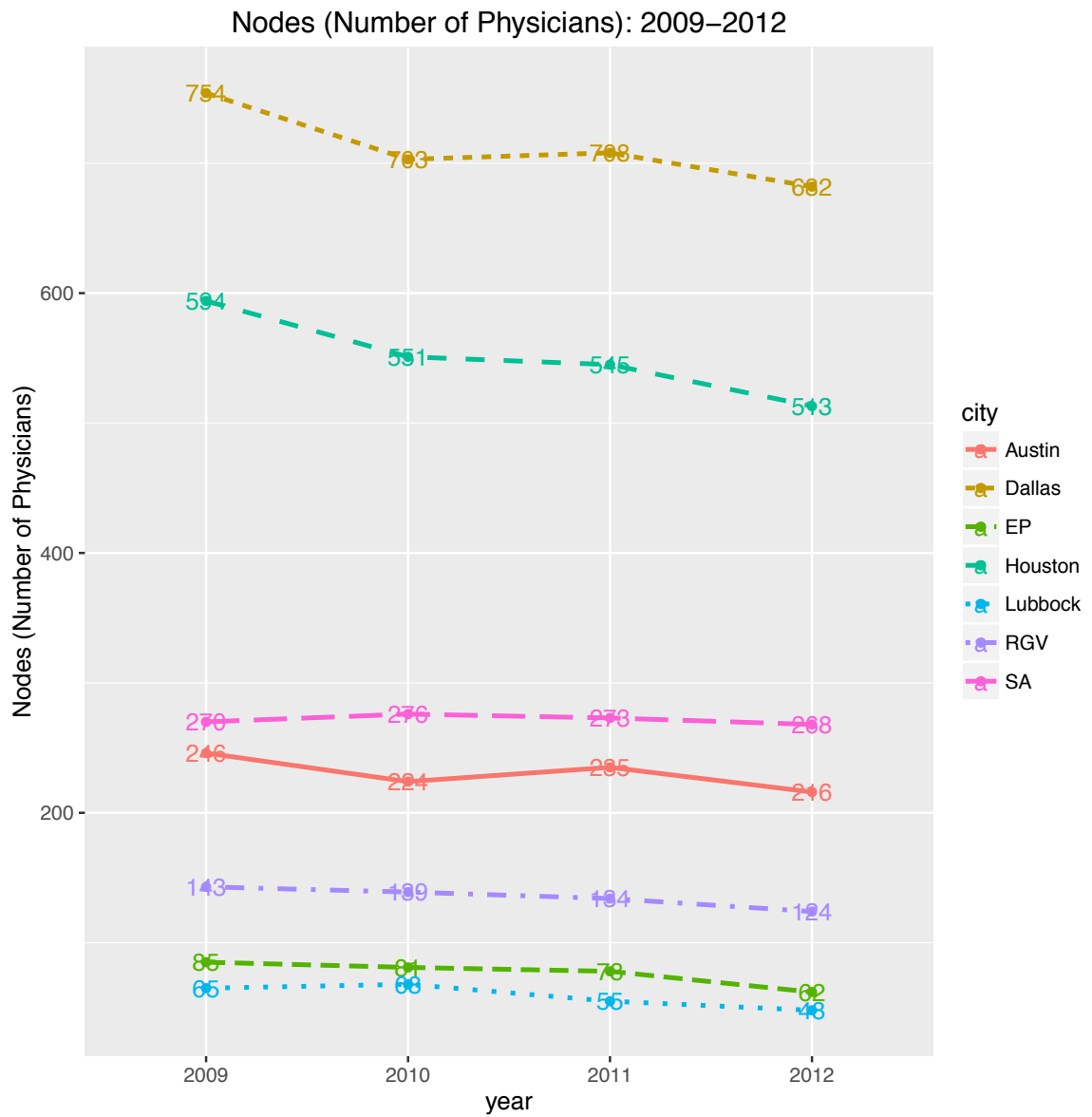
Rio Grande Valley					
Physician Network	2009		2012		Physician Network
	Patients	127	93	Patients	
	Physicians	143	124	Physicians	
	Edges	2070	1845	Edges	
	Ratio	0.60	0.51	Ratio	
	MIBB Rate	0.50	0.59	MIBB Rate	
	Density	0.00082	0.00197	Density	
	Centralization	0.09	0.07	Centralization	
	Transitivity	0.82	0.81	Transitivity	
	Path Length	2.00	1.85	Path Length	
	Communities	2	2	Communities	

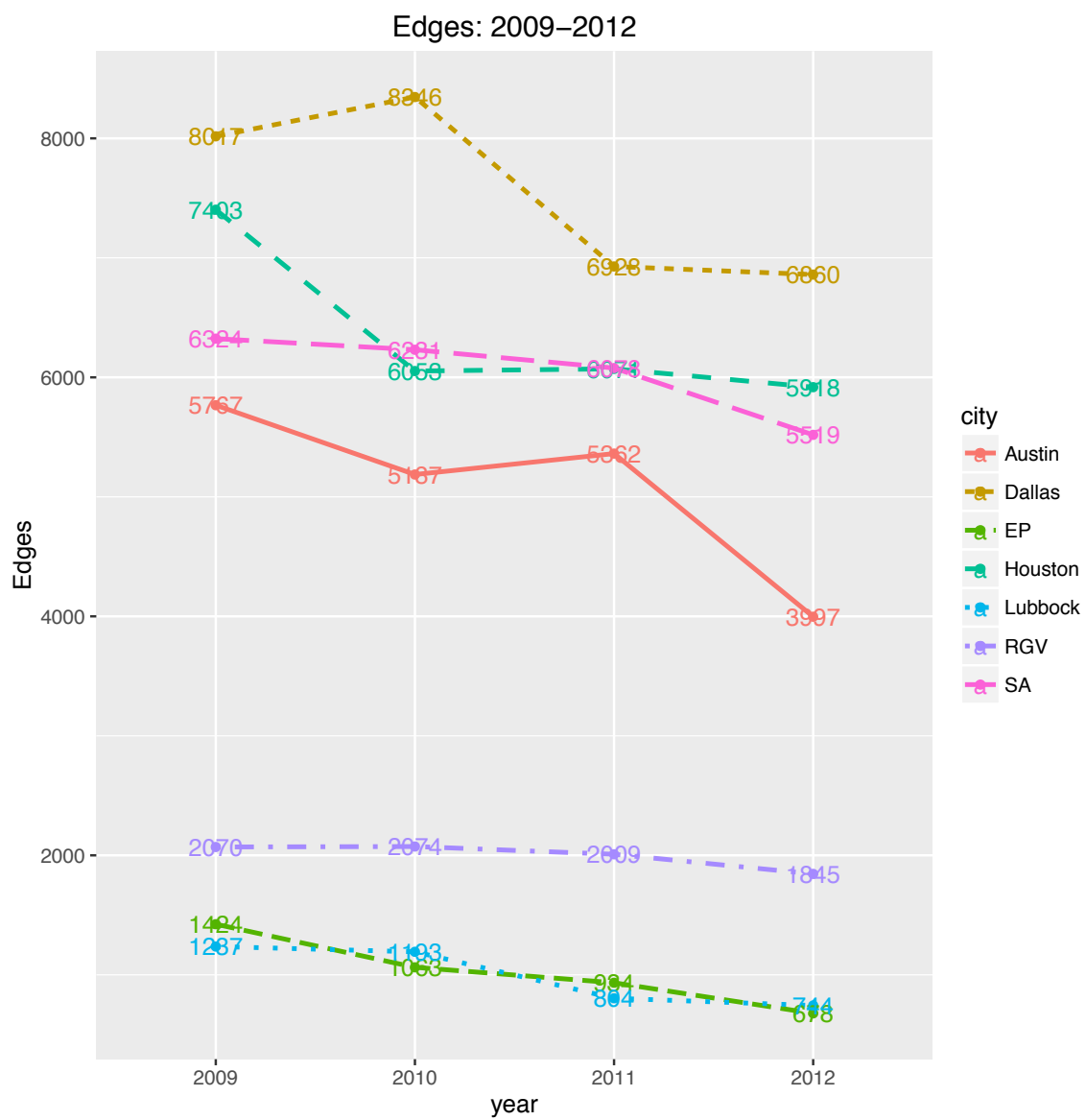


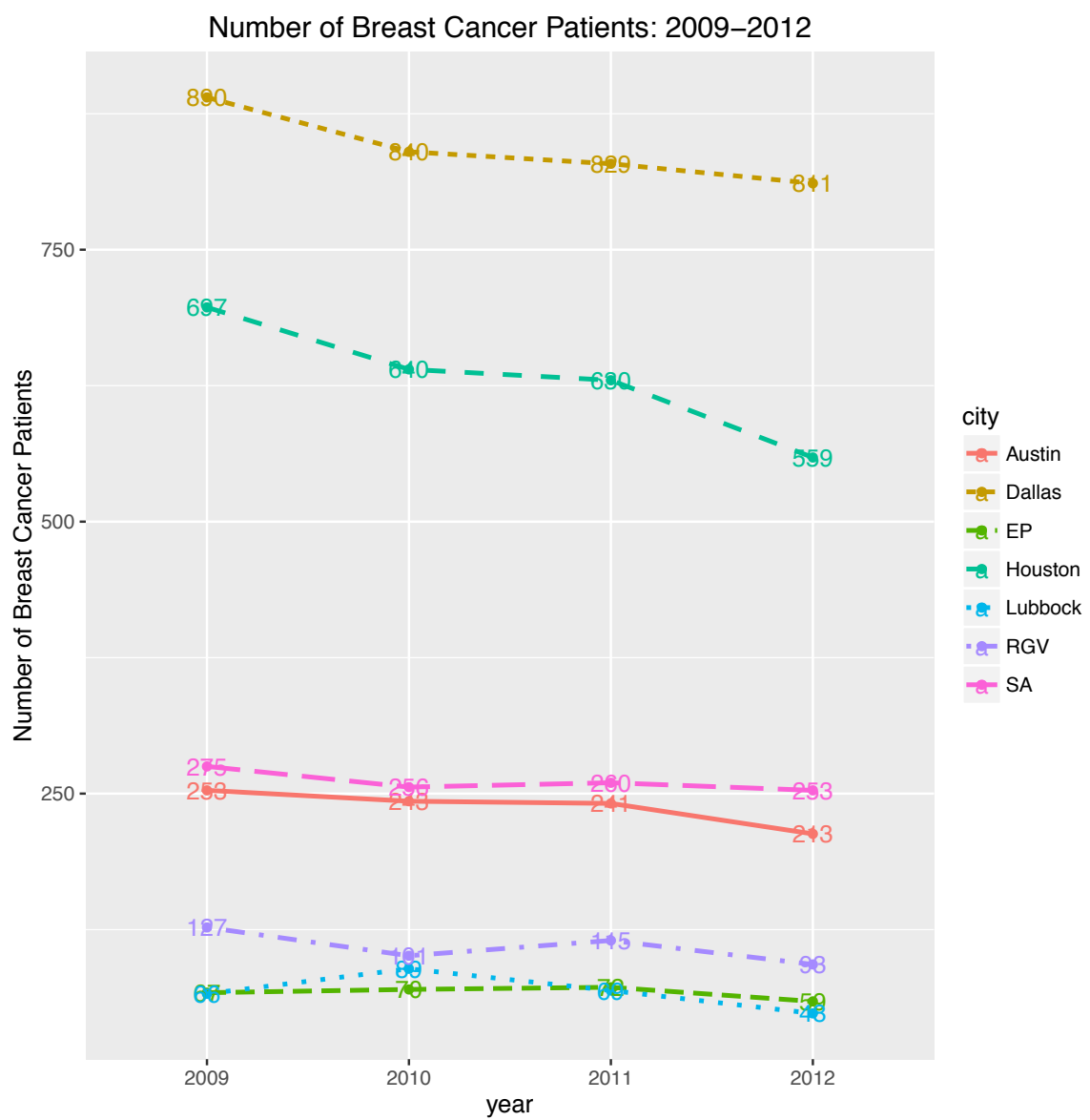
San Antonio					
Physician Network	2009		2012		
	Patients	275	253	Patients	
	Physicians	270	268	Physicians	
	Edges	6324	5519	Edges	
	Ratio	0.44	0.36	Ratio	
	MIBB Rate	0.81	0.90	MIBB Rate	
	Density	0.00064	0.00058	Density	
	Centralization	0.04	0.07	Centralization	
	Transitivity	0.83	0.84	Transitivity	
	Path Length	2.01	2.04	Path Length	
	Communities	3	7	Communities	



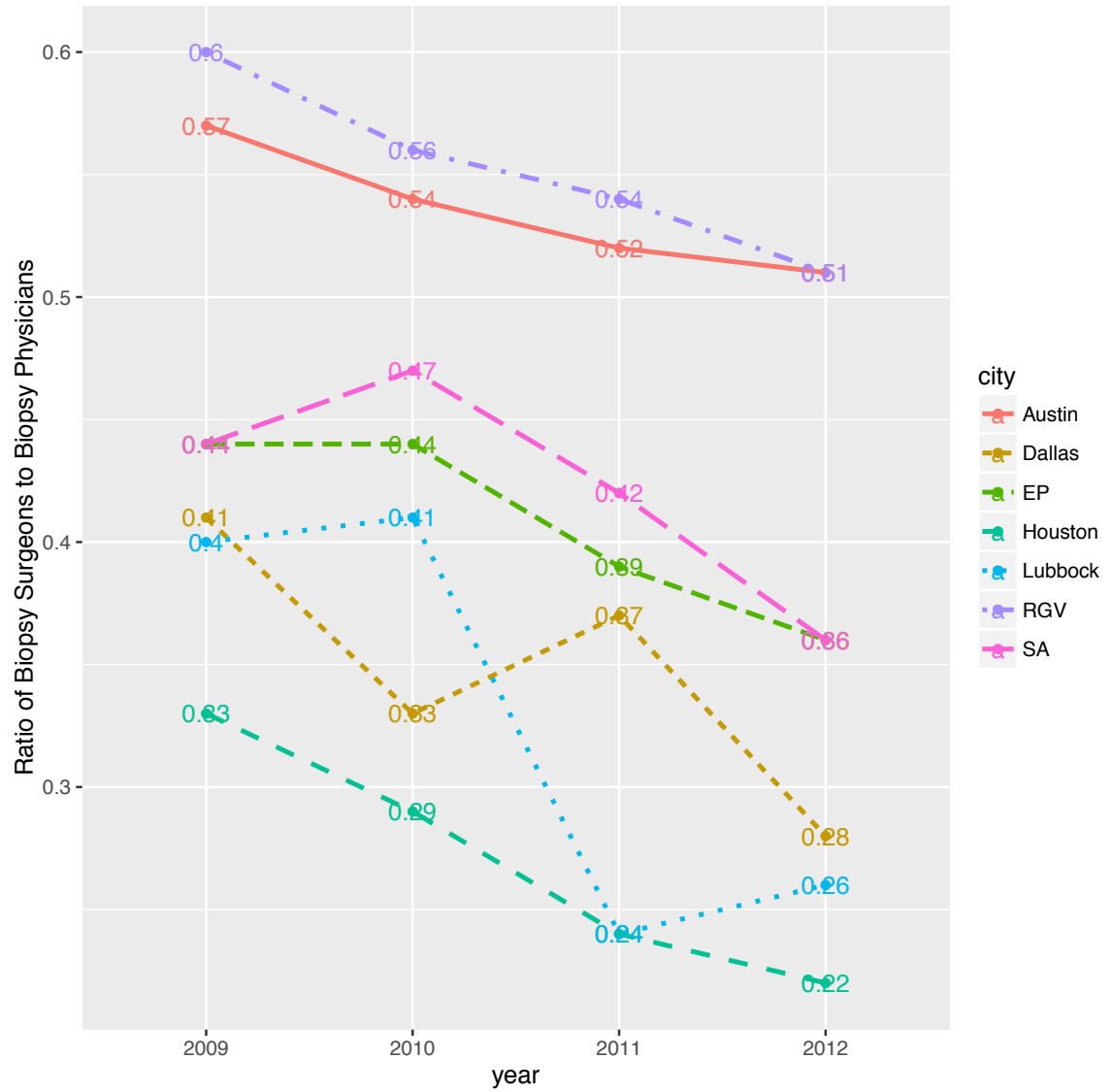
## Appendix B: Network Measures Over Time by Texas Regional Networks

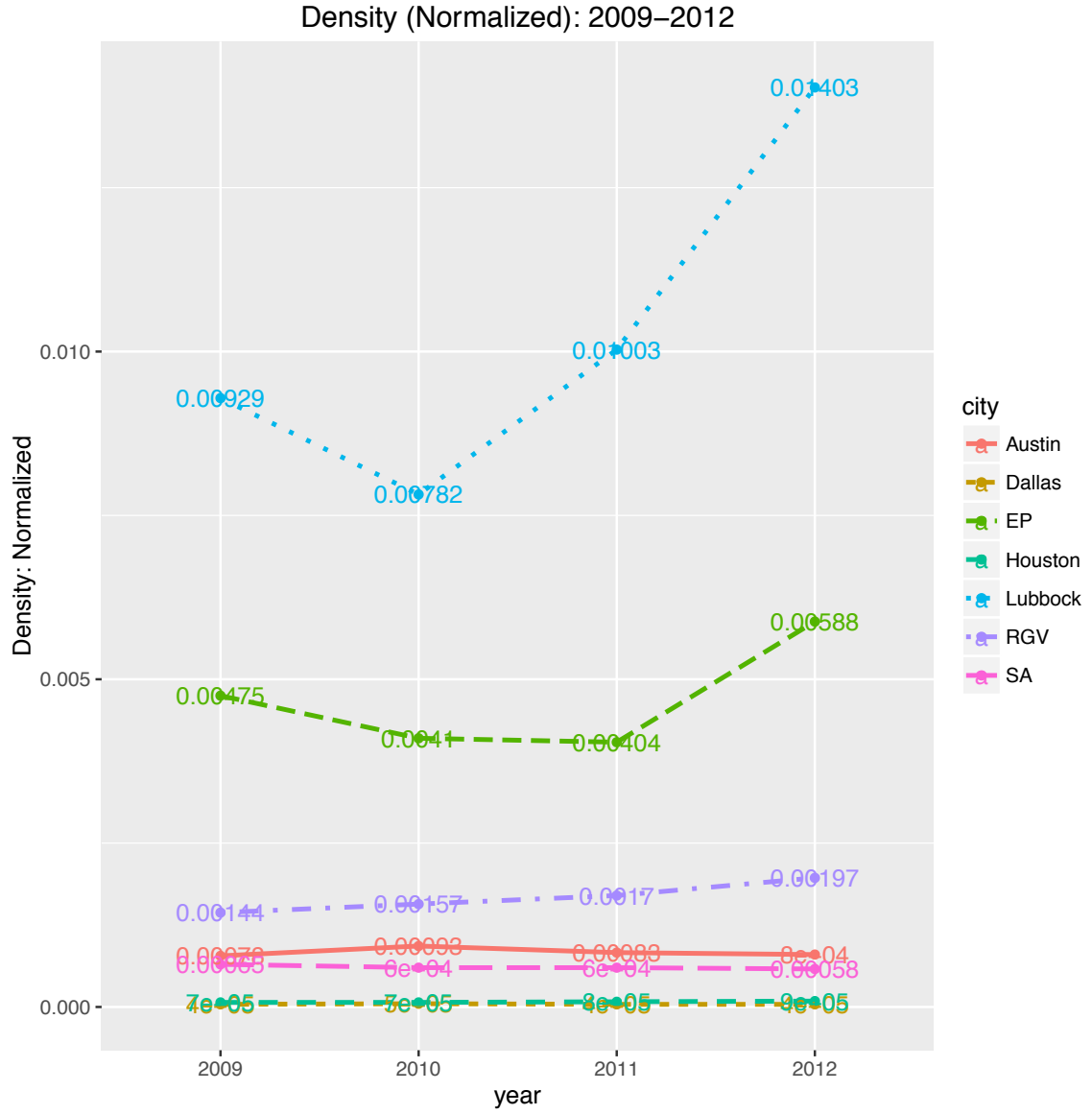


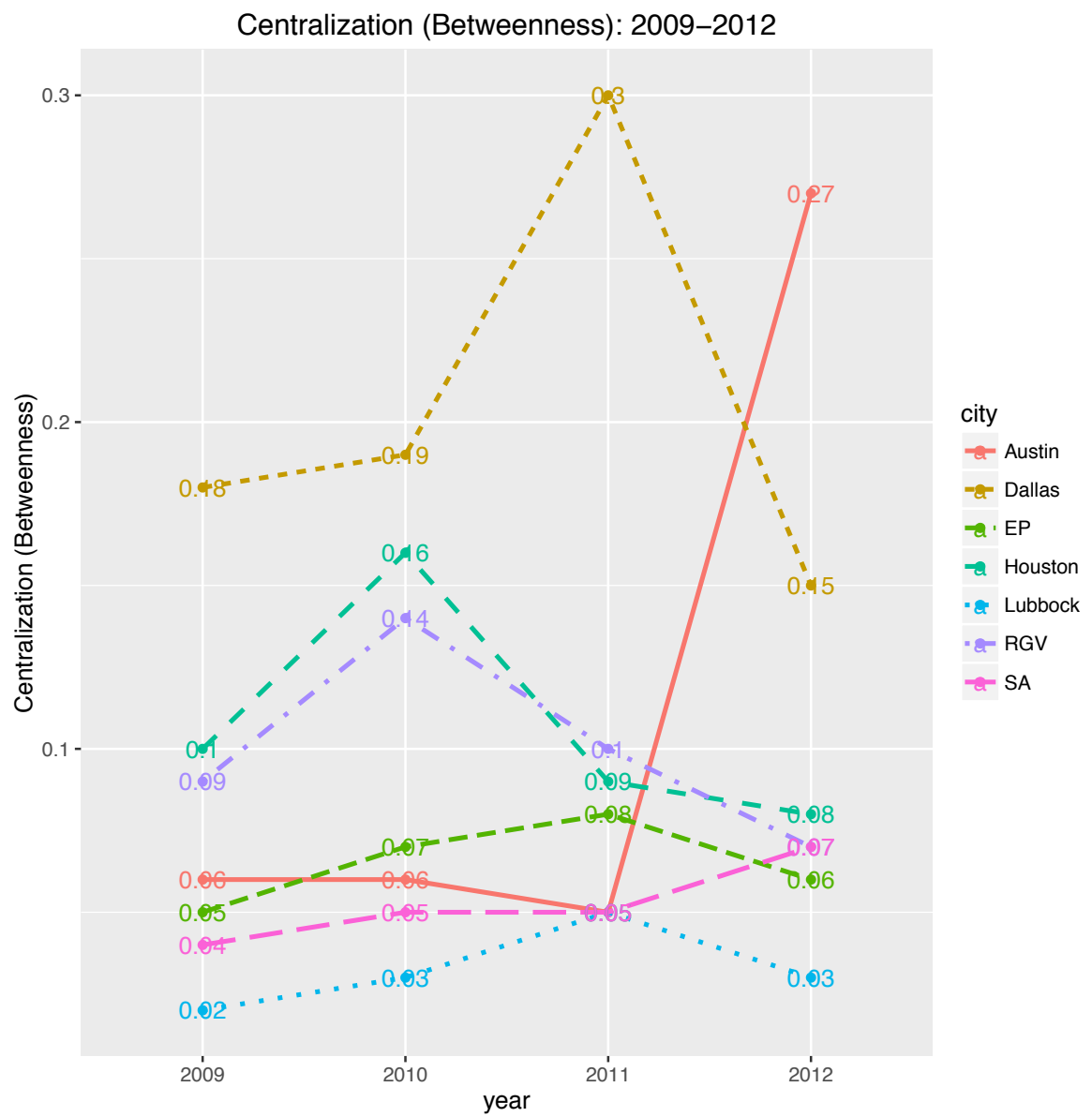




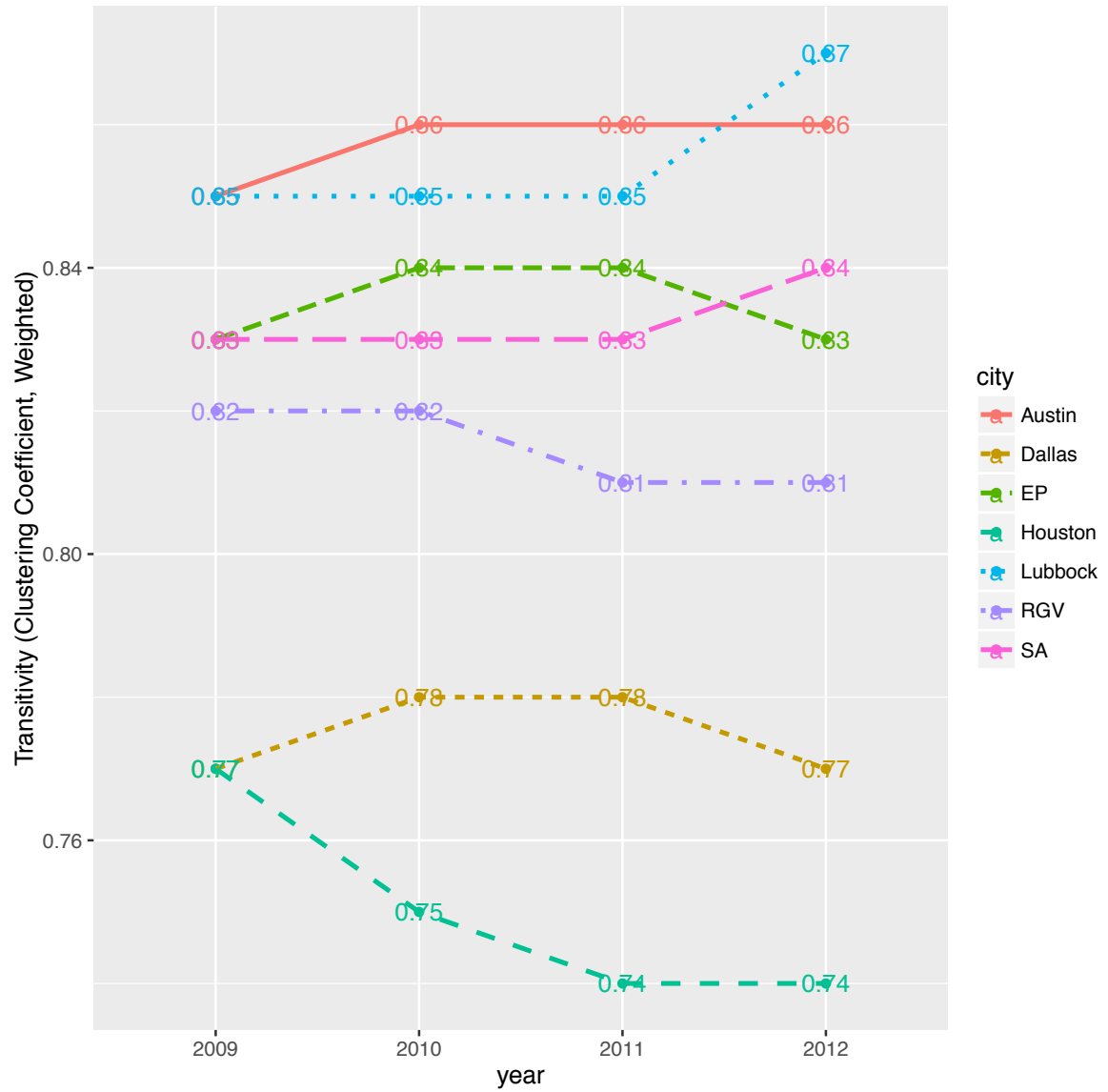
Ratio of Biopsy Surgeons to Biopsy Physicians: 2009–2012

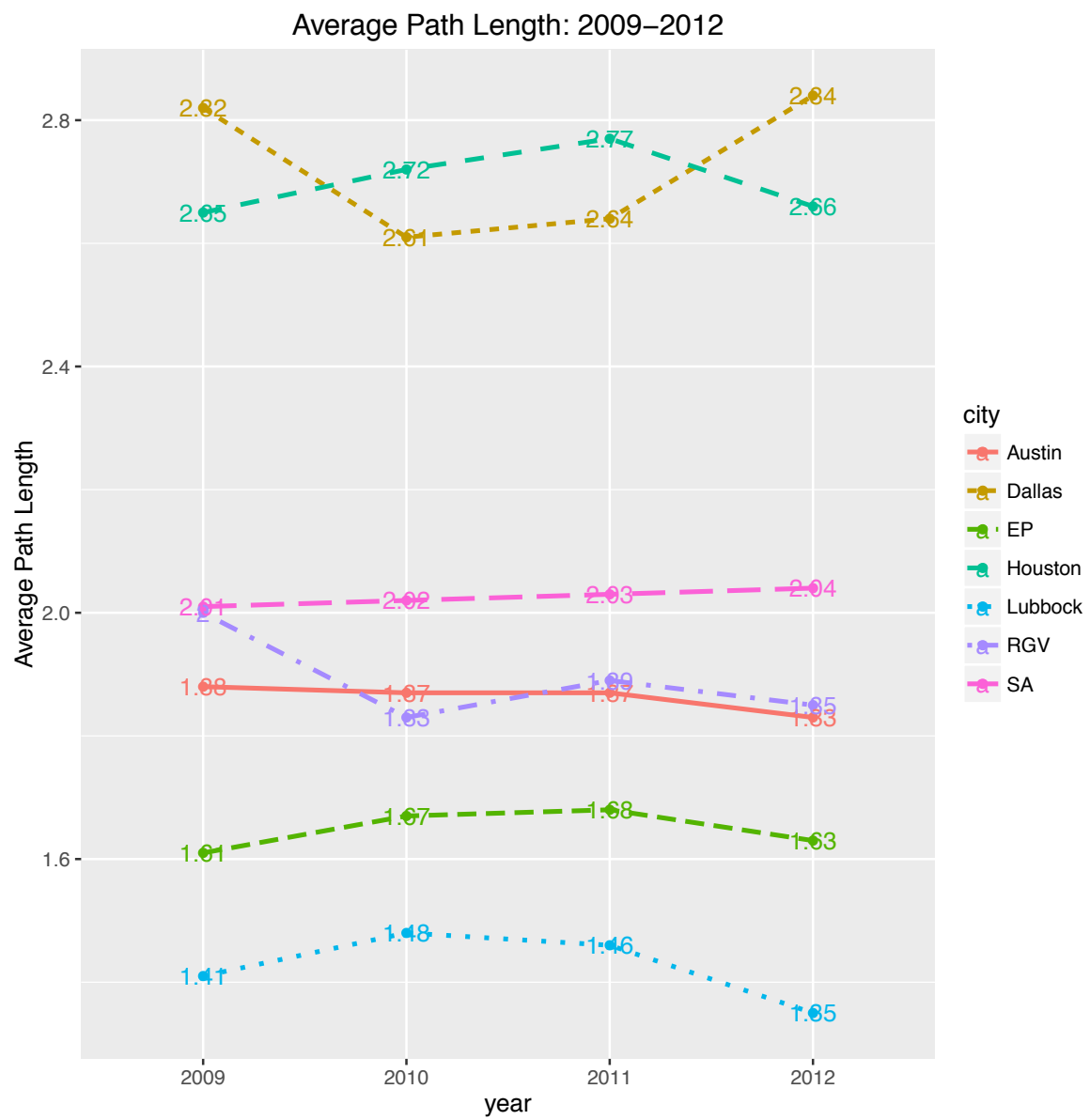


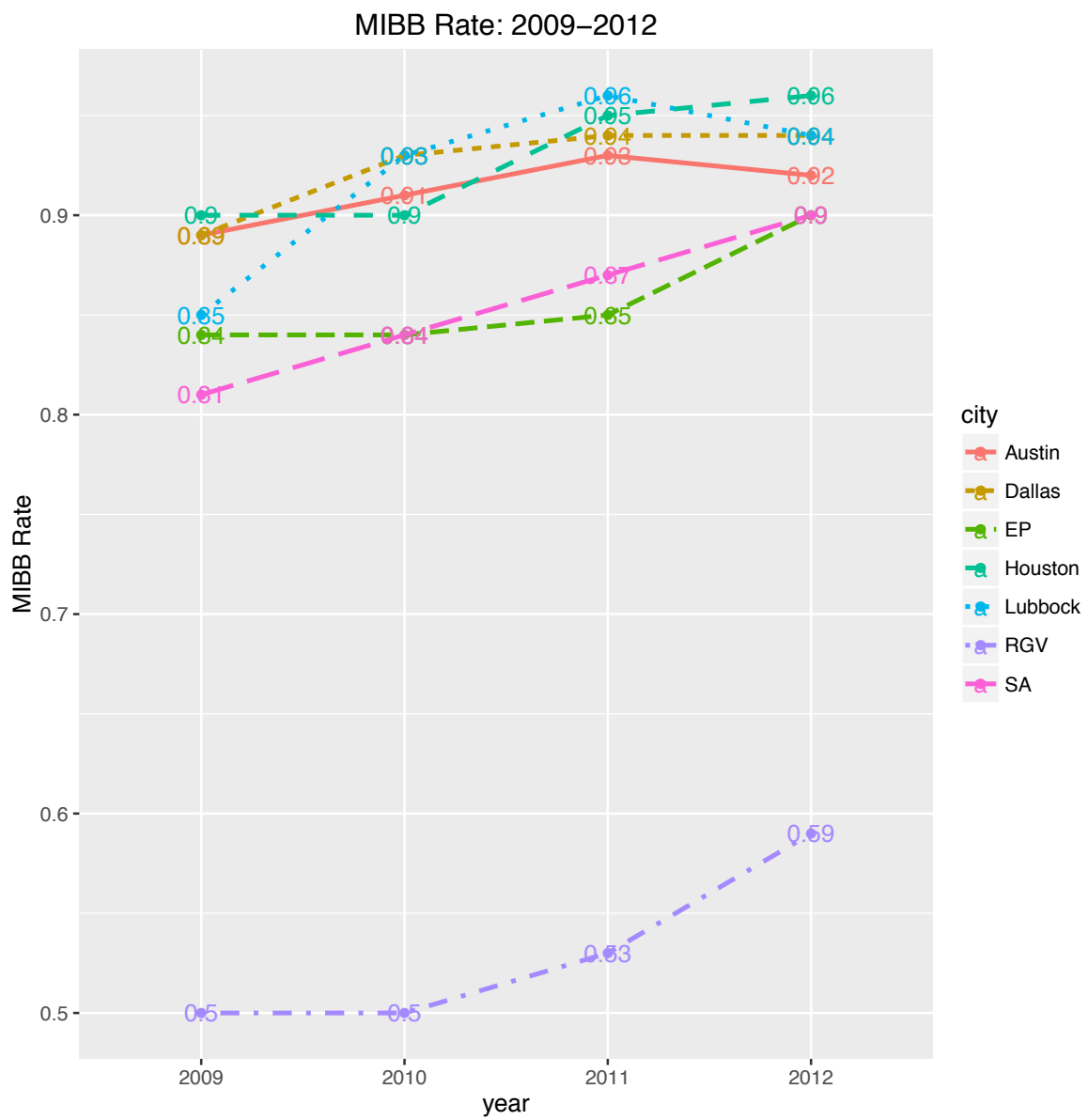




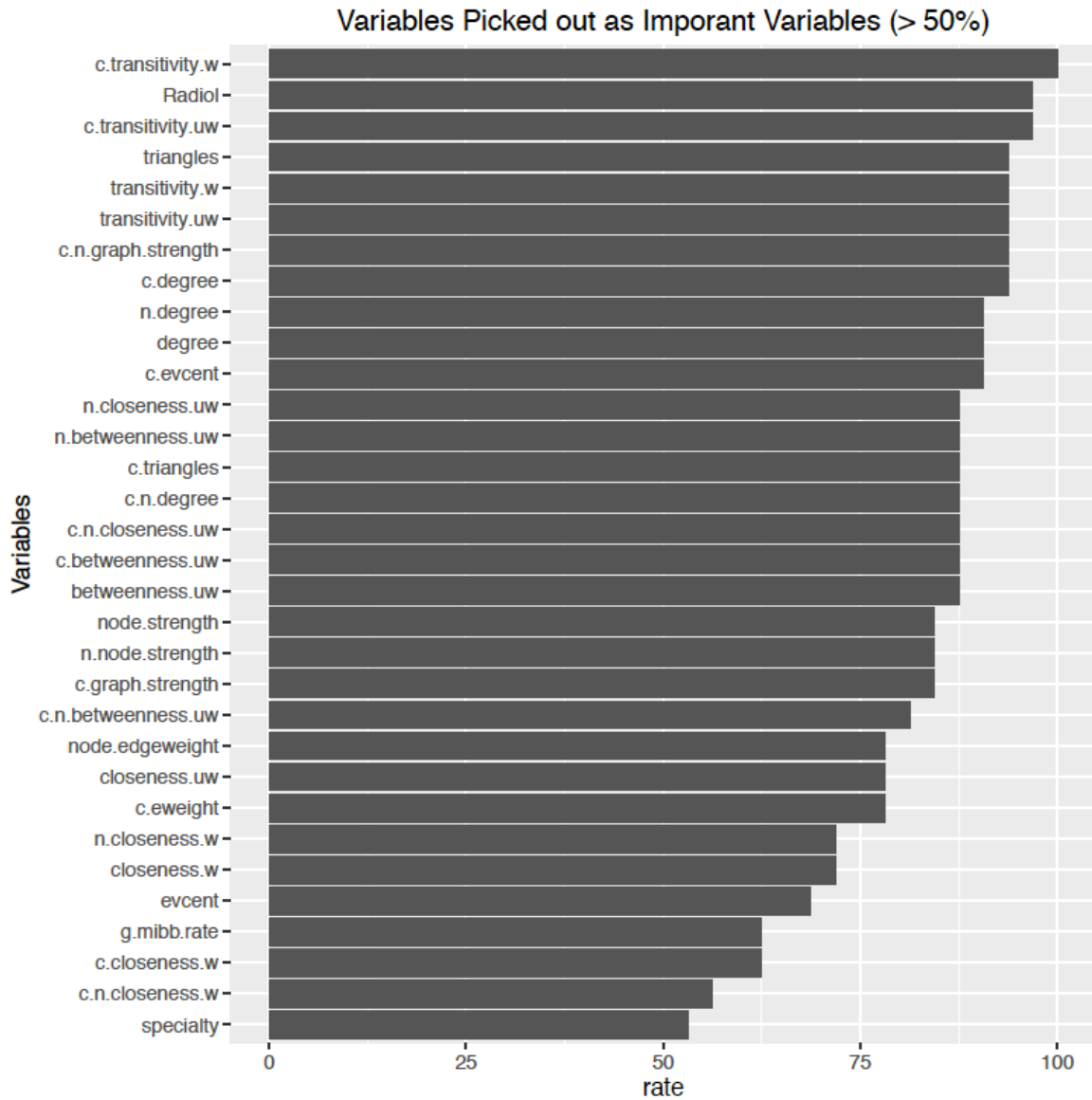
Transitivity (Clustering Coefficient, Unweighted): 2009–2012



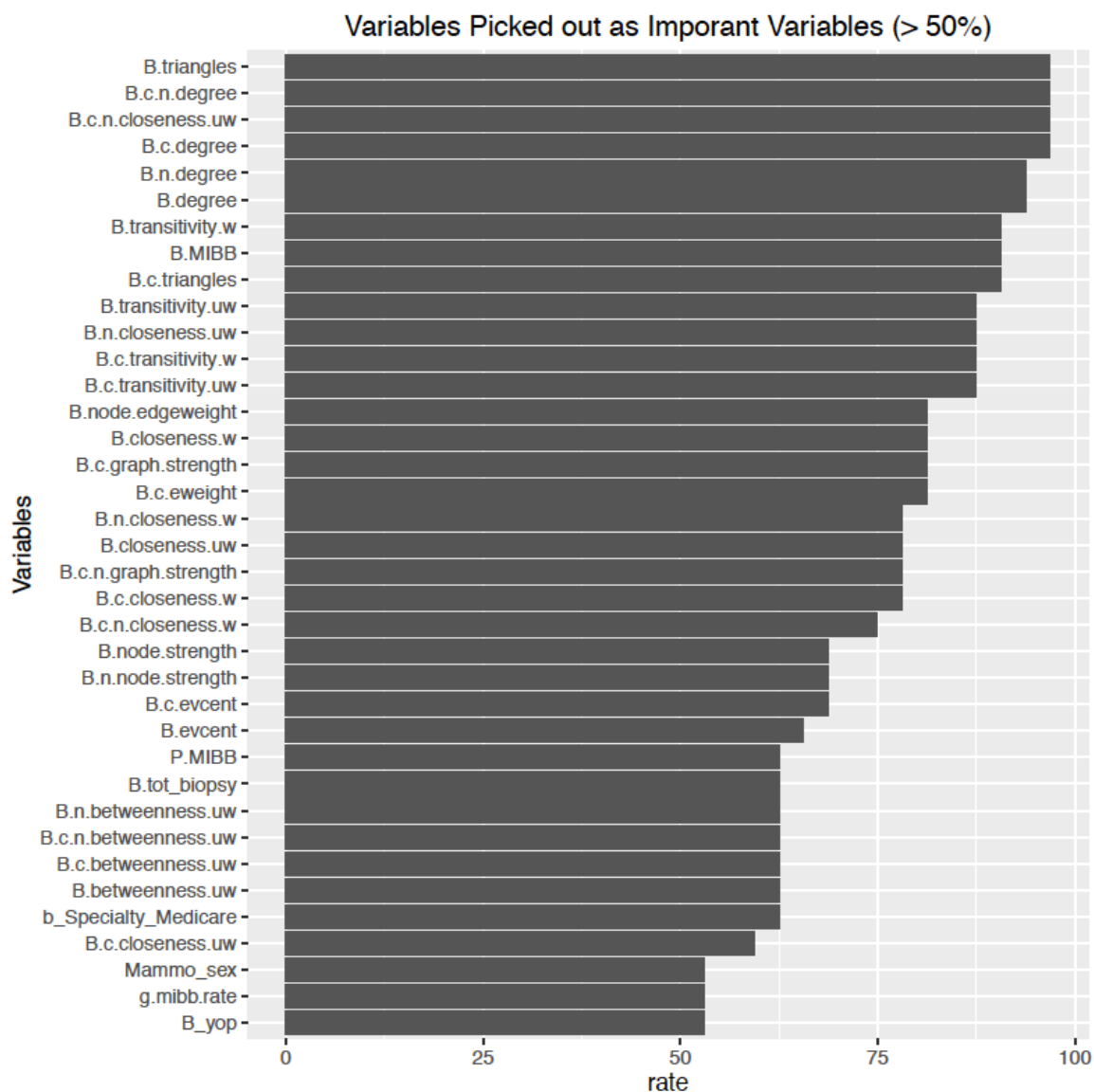




## Appendix C: Important Measure Plots



**Appendix C.1: Important Variable Plot for Physician Level Regression Analysis.** See Section 4.2.1 for methodology description. We prioritized variables included in our models that were normalized, un-weighted, and calculated at the community level.



**Appendix C.2: Important Variable Plot for Patient Level Regressions.** See Section 4.2.1 for methodology. We prioritized variables included in our models that were normalized, un-weighted, and calculated at the community level.

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## **Vita**

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