HHS Public Access

Author manuscript

J Complex Netw. Author manuscript; available in PMC 2015 December 01.

Published in final edited form as:

J Complex Netw. 2014 December ; 2(4): 356–372. doi:10.1093/comnet/cnu037.

Using the network reliability polynomial to characterize and design networks

STEPHEN EUBANK[*,†], **MINA YOUSSEF**[*], and **YASAMIN KHORRAMZADEH**[*,‡]

[*]Network Dynamics and Simulation Science Laboratory, Virginia Bioinformatics Institute

[†]Department of Population Health Sciences, Virginia-Maryland Regional College of Veterinary Medicine

[‡]Department of Physics Virginia Tech, Blacksburg, Virginia 24061

Abstract

We consider methods for solving certain network characterization and design problems that arise in network epidemiology. We argue that the network reliability polynomial introduced by Moore and Shannon is a useful framework in which to reason about these problems. Specifically, we show how efficient estimation of the polynomial permits characterizing and distinguishing very large networks in ways that are are dynamically relevant. Furthermore, a generalization of flows and cuts to structures that determine the reliability suggests a new measure of edge or vertex centrality that we call *criticality*. We describe how criticality is related to the more common notion of betweenness and illustrate its application to targeting interventions to control outbreaks of infectious disease. Although our applications are to infectious disease outbreaks, the methods we develop are applicable to many other diffusive dynamical systems over complex networks.

Keywords

complex networks; network topology; network reliability; network theory; graph theory; graphical models

1. Introduction

1.1 Important problems in infectious disease epidemiology

The spread of infectious disease through a population is well-represented as a diffusion process on a contact network whose vertices represent hosts and whose edges represent opportunities for transmission [3]. For example, the network version of the commonly-used *Susceptible – In f ectious – Recovered*, or $S - I - R$, model is equivalent to bond percolation[6]. We can view network structure as a set of model parameters alongside the usual biological parameters of the host-pathogen interaction such as incubation period or susceptibility. This perspective raises the possibility of applying new tools to infectious

eubank@vt.edu.

disease epidemiology. Two questions in particular can be viewed as specializations of network characterization and design problems:

- **Q1 Characterization:** How can we parameterize aspects of network structure that have important dynamical consequences?
- **Q2 Design:** What structural changes – i.e. what changes to these structural parameters – most cost-effectively control the consequences of an outbreak?

These questions have, of course, been raised many times in many domains besides epidemiology. Proposed parameterizations include most graph statistics, such as distributions of degree, clustering, shortest-path lengths, and eigenvalue spectra of the adjacency and related matrices. Note, however, that answers to these questions depend on a cost function that defines the "consequences", whereas graph statistics do not. We develop and illustrate a theoretical framework and practical methodology for answering these questions when the costs are properties of dynamical processes on the network. We propose using Moore and Shannon's concept of network reliability [12] to characterize the network, and provide a general algorithm for finding a set of edge or vertex deletions that achieves maximal change in reliability.

For model results to inform policy, the limitations of the models must be well-understood. In the case of networked epidemiology models, that requires understanding the sensitivity of the model to uncertainty in network specification. Moreover, since the biological parameters are largely beyond our control, the only "control surface" for epidemiology is the structure of the contact network. For example, isolating or vaccinating an individual with a perfect transmission-blocking vaccine removes the corresponding vertex from the network; closing a location where people come into contact, such as a school, removes edges corresponding to all the contacts that would have occurred there. Answers to the characterization and design questions will permit a better understanding of sensitivity and control in network epidemiology.

1.2 Network characterization and design

A network can be characterized by assigning it to an equivalence class. Two networks are deemed equivalent if and only if an observable has the same (or similar) value on both. Clearly, if two networks are isomorphic, they are equivalent, but our notion of equivalence will be much weaker than isomorphism. Characterizations are usually based on observables that are simple graph statistics not directly related to any cost function. For example, so-called "scale-free" networks form an equivalence class defined by degree distributions, "small-world" networks form an equivalence class defined by the distribution of shortest paths, etc.

A general approach to designing improvements to a given network under a budget has three steps, illustrated in Figure 1:

1. Characterize the original graph, i.e. evaluate the mapping E from graphs to equivalence classes.

2. Characterize the desired graphs in terms of a "target" equivalence class, i.e. evaluate the mapping O from an observable to an equivalence class.

3. Find a minimal set of changes to the original graph that transform it to one in the target equivalence class.

Unfortunately, the relationship between the topology of a network and values of a dynamical observable on the network is extremely complicated in general. Hence, either E or O will be complicated, and both are required. On one hand, when simple graph statistics define equivalence classes, E is simple but O is not. In this case, the distribution of observables across an equivalence class (which was defined without regard to the observable) is not necessarily concentrated, as illustrated in Figure 1. It is possible that a change in the network that *decreases* the cost *on average* over the equivalence class, will actually *increase* the cost when applied to a *particular* network. On the other hand, when equivalence classes are induced by values of the observable, O is trivial but E is not. Without an easy way to determine membership, it is hard to generate instances of graphs in the target equivalence class. Even though there is no free lunch, we claim that this second approach is worth pursuing. The most expensive step in designing networks is step 3, and the second approach allows us to establish provable reductions in the cost function itself, rather than a more or less related function. As Tukey said, "Far better an approximate answer to the right question … than an exact answer to the wrong question."

1.3 Network reliability

We describe here the application of Moore and Shannon's concept of network reliability [12] to provide a practical, efficiently computable organizing principle for characterizing and designing networks. Since its introduction in the 1950's, the network reliability polynomial has remained more of an interesting theoretical construct than a practical tool for working with large networks. In large part, this is due to well-established complexity results for both its evaluation and approximation. However, as the authors have recently observed, estimation of the polynomial to within practically useful confidence intervals is easy, even without taking into consideration any properties of the graph [4, 17]. Estimation is also embarrassingly parallel, and we have extended this previous work by developing a distributed implementation, available to researchers as a web service, that scales to graphs with tens of millions of edges, limited only by the memory available to each computing element. We demonstrate this here by estimating the reliability polynomial for a contact graph representing the New River Valley with more than 4 million edges. Furthermore, we have introduced an interpretation for the reliability polynomial's coefficients in terms of minimal subgraphs which we refer to as *structural* motifs [4, 8]. Structural motifs support analytical reasoning about the consequences of changes in network structure.

Ranking edges by betweenness and removing the top-ranked ones is often suggested as a heuristic solution to the network design problem. Network reliability can be used to generalize the notion of betweenness to include the specific dynamical phenomena and cost functions of interest. Furthermore, the usual Ford and Fulkerson Max Flow / Min Cut theorem [5] can be extended to structures that are not normally considered "cuts" or "flows", specifically the structural motifs that determine the reliability polynomial. By relating

reliability to flows and cuts on a network, we demonstrate that the generalized betweenness can in principle be used to solve the network design problem. We evaluate the feasibility of approximating this solution on large networks using our distributed reliability estimation tool.

Section 2 provides a brief, self-contained introduction to network reliability, including an extension to general damage models. We provide very general definitions to emphasize the broad applicability of the formalism and the methods we will develop. For ease of exposition, we immediately introduce simplifications tailored to the applications in this manuscript. In particular, Section 2.2 develops an extended analogy to cuts and flows for structural motifs, which motivates our heuristic algorithm for ranking edges. Section 3 suggests methods for answering the questions **Q1** and **Q2,** characterizing and designing networks. Section 3.1.1 describes an efficient way of estimating the reliability polynomial for graphs with tens of millions of edges. Section 3.1.2 describes the use of reliability estimates to characterize networks. Related methods were proposed in [4], but here they are placed on firmer theoretical ground. In particular, Section 3.2 extends the notion of betweenness centrality in the context of minimal cuts to structural motifs. Section 3.3 describes the networks to which we apply these methods in Section 4.

2. Theory

2.1 Network Reliability for Characterization

2.1.1 Definition—To address **Q1,** we rely on *Moore-Shannon reliability*. For a general introduction to network reliability, see Colbourn [1]. The Moore-Shannon reliability for a network is the probability that it functions correctly after sustaining damage [12]. Network reliability depends on three things:

1. the network itself, here represented as a labeled graph G with E edges and V vertices;
2. a criterion that defines what it means to function correctly, here represented by a *rule r* that is a binary function of graphs $r(g) \in \{0, 1\}$. We say that a graph is "accepted" if $r(g) = 1$;
3. a damage model, i.e. a parameterized measure over subgraphs $g \subset G$, denoted $p_{\vec{x}}(g)$, where $\vec{x}$ are the parameters of the damage model.

The reliability is the expected value of the rule r over all possible subgraphs weighted by the probability of the subgraph under the damage model:

$$R_G(\vec{x}) \equiv \sum_{g \subset G} r(g)\, p_{\vec{x}}(g) \quad (2.1)$$

It is often the case that many subgraphs have the same probability of occurrence under the damage model. We can rewrite the reliability in terms of the set of equivalence classes induced by the damage model. Thus, if there are C such classes $\{c_1, \ldots, c_C\}$ and the ith class contains $|c_i|$ subgraphs, each appearing with probability $p_{\vec{x}}(c_i)$, then

$$R_G(\vec{x}) = \sum_{k=1}^{C} \sum_{g \in c_k} r(g)\, p_{\vec{x}}(g) \quad (2.2)$$

$$= \sum_{k=1}^{C} R_k p_{\vec{x}}(c_k) = \sum_{k=1}^{C} P_k |c_i| p_{\vec{x}}(c_k). \quad (2.3)$$

This form for the reliability applies to labeled, directed, multigraphs under arbitrary damage models and arbitrary reliability rules. For ease of exposition and simplicity of notation, we will restrict our attention here to unlabeled, undirected, simple graphs under a single damage model for a single reliability rule. Recovering the fully general theory and methods is not difficult. We will use Moore and Shannon's original damage model, in which each edge is chosen independently with probability x from the *original* graph G. If the original graph is a complete graph on V vertices, our damage model is equivalent to Erdős-Rényi measure on the space of graphs with V vertices; in general, the original graph strongly biases the structure of subgraphs selected under the damage model [2]. This bias is the reason the reliability polynomial characterizes structure in the original graph. This damage model corresponds to bond percolation and thus to networked models of infectious disease spread, with x representing the conditional probability of transmission across a link [6]. Specifically, the probability that an $S - I - R$ outbreak seeded in a set of index vertices infects exactly a set T of vertices is given by the total probability under the damage model that the union of all the connected components including at least one index vertex is exactly T.

Equivalence classes under this damage model are sets of subgraphs that have the same number of edges. There are $C = E + 1$ such sets. The number of subgraphs in the equivalence class with k edges is $|c_k| = \binom{E}{k}$. The probability with which any of these subgraphs occurs is $p(g|x) = x^k (1 - x)^{E-k}$. Summarizing, we have

$$R_G(x) = \sum_{k=0}^{E} R_k x^k (1-x)^{E-k} = \sum_{k=0}^{E} P_k \binom{E}{k} x^k (1-x)^{E-k}. \quad (2.4)$$

We use two reliability rules here: "*AR*-0.2" accepts graph g if and only if the mean square size of connected components in $g \succcurlyeq 0.2V$; *ST*-reliability accepts graph g if and only if it contains a path between two specified vertices S and T. These two rules are examples of *coherent* rules, for which adding an edge to an accepted graph cannot make it unacceptable. *AR*-0.2 has an important interpretation as the expected probability that an outbreak seeded in a single vertex chosen uniformly at random will eventually infect 20% or more of the vertices. *ST*-reliability, also known as "two-terminal" reliability, is useful for making the analogy to betweenness.

For a coherent rule, P_k is monotonic nondecreasing in k. For nontrivial original graphs, we have $R(0) = 0$ and $R(1) = 1$, and thus $P_0 = 0$ and $P_E = 1$. Hence we can define two special

values of k: k_- is the smallest value of k such that $P_k > 0$; k_+ is the largest value of k such that $P_k < 1$. To leading order in x, $R(x) \approx R_{k_-} x^{k-}$; to leading order in $1 - x$, $R(x) \approx 1 - R_{k_+} (1 - x)^{k+}$.

2.1.2 Interpretation—As shown in [8], we can expand the binomial factor $(1 - x)^{E-k}$ in Equation 2.4 to rewrite $R(x)$ as a sum of monomials:

$$R(x) = \sum_{k=0}^{E} M_k \begin{pmatrix} E \\ k \end{pmatrix} x^k, \quad (2.5)$$

where

$$M_k \equiv (-1)^k \sum_{l=0}^{k} (-1)^l \begin{pmatrix} k \\ l \end{pmatrix} P_l. \quad (2.6)$$

We have described a simple physical interpretation of M_k in terms of special subgraphs of G that we call *structural* motifs [8]. A structural motif of the network G is a minimal accepted subnetwork, i.e. a subnetwork $g \subset G$ for which $r(g) = 1$ that would not be accepted if any of its edges were removed. A motif is a specific subgraph that occurs in multiple places in the original graph [11]. It is in this sense that structural motifs are *motifs*. Structural motifs are motifs that fully determine the reliability polynomial. Our usage of the term "motif" differs slightly from Alon and others in that structural motifs can be very large; our usage of the structural motifs themselves differs from theirs in that the motifs are not pre-defined by an analyst, but instead emerge from the dynamics and the rule. For example, for *AR*-0.2, trees that include exactly 20% of the vertices are structural motifs; for *ST*-reliability, non-self-intersecting paths from S to T are structural motifs. Importantly, the structural motifs for *ST*-reliability need not be *shortest* paths – any path will do as long as it does not contain extraneous edges.

If we define $n_k^{(l)}$ as the number of unions of l structural motifs that contain exactly k edges, then it can be shown that [8]

$$M_k \begin{pmatrix} E \\ k \end{pmatrix} = \sum_{l=1}^{E} (-1)^{l-1} n_k^{(l)} \quad (2.7)$$

Thus, the sizes of the structural motifs and their unions completely determine the reliability polynomial. It is in this sense that these motifs are the *structural* motifs.

2.2 Criticality

To address question **Q2**, we extend the intuitive notion of being on a critical path to a notion of criticality for arbitrary properties of dynamics. See Page and Perry for a related approach [14]. Colloquially, an edge is critical if it is on the critical path between S and T , i.e. if its removal ensures there is no path from S to T. If there are multiple paths from S to T , no single path is critical, and the binary notion of criticality must be extended to reflect the fraction of the paths that contain the edge. The notion of criticality must be further extended

to account for the fact that different paths contribute differently to the dynamics. For example, if there are two paths of different length between S and T, the shorter path is often more important than the longer one. Betweenness is the concept that captures these extensions.

In our more general context, structural motifs play the role of critical paths. We correctly account for the possibility of multiple structural motifs with different contributions to the dynamics with this definition: the *criticality* of a set of edges is the difference in reliability between the graph G in which they appear and the graph $G' \subset G$ in which they do not.[1] Since reliability depends on the rule, the damage model, and its parameter values $\vec{x}$, criticality also depends on these things. The reliability polynomial weights each structural motif in precisely the way it contributes to dynamical phenomena of interest, as specified by the reliability rule, in the parameter range of interest, as specified by $\vec{x}$.

In general, the criticality of an edge is a very complicated function of the overlaps among the structural motifs that contain it. However, we illustrate the concept with a simple example in which the criticality can be expressed easily. Suppose we add a structural motif of size k_0 to a graph G, and that it is edge-disjoint from any existing structural motif in the graph. Then, using Equations 2.5 and 2.7, it can be shown that the reliability of the new graph, $R'(x)$ is:

$$R'(x) = R(x)\left(1 - x^{k_0}\right) + x^{k_0}. \quad (2.8)$$

Thus the criticality of any edge in the new structural motif is $R'(x) - R(x) = x^{k0}(1 - R(x))$.

To apply the concept of criticality to answering question $Q2$, we define a generalized notion of capacity in such a way that a generalized Min Cut / Max Flow theorem will hold. Specifically, we define the generalized *capacity* of an edge to be the number of structural motifs that include it. For ST-reliability, an edge's capacity under this definition is the number of times it appears in a non-self- intersecting path from S to T; for AR-0.2, it is the number of trees with exactly $0.2V$ vertices in which it appears. Clearly, generalized capacity can also be thought of as a generalized notion of betweenness.

We define a generalized *edge cut* in a network under a given reliability rule as a set of edges whose removal reduces the reliability to 0. A minimal cut is one that has no proper subgraphs that form a cut. We define a generalized *flow* with respect to a given reliability rule as the number of structural motifs that appear in the graph. Removing the edges that comprise a cut reduces the reliability to 0 by definition. Remembering that a structural motif is a *minimal* accepted subgraph, we note that any structural motif can be broken by removing any one of its edges. Hence a cut contains at least one edge from every structural motif. Therefore the total capacity of the edges in a cut must be at least as large as the flow. If structural motifs are not edge-disjoint, removing an edge in their overlap breaks more than one motif. Our definition of capacity properly accounts for the case of non-disjoint motifs: if

[1] A similar definition for vertex criticality can be made, with obvious changes in the following remarks.

a single edge appears in c motifs, then removing that edge breaks all c and removes c units of flow.

This analogy between cut, flows, and betweenness and their generalized versions suggests the existence of a greedy algorithm for finding a minimum cut, i.e. a minimal cut using the smallest possible number of edges. We do not pursue this here, but use the analogy to motivate a heuristic approach to ranking edges.

3. Methods

3.1 *A1*: Using reliability to characterize graphs

3.1.1 Estimating reliability efficiently—Reliability provides a natural way to characterize graphs and thus to determine important differences between them. However, exact determination – and even approximation – of coefficients in the reliability polynomial for many rules and many classes of networks is known to be hard, often #–P hard [1]. Much of the work on reliability has focused on ways to take advantage of properties of particular rules or classes of graphs, or on efficient ways to organize a recursive computation. In contrast, our estimation procedure is simply to evaluate the reliability rule for each of a sample of s subgraphs with k edges drawn from G according to the damage model. The fraction of subgraphs in the sample that are accepted yields an estimate of $\hat{P}_k$. We expect the number of accepted subgraphs in our sample to be distributed binomially with parameters sP_k and s. If we make the common approximation that the parameter P_k in this binomial distribution is approximately given by its sample mean $\hat{P}_k$ then we can bound the probability that the true P_k is outside any desired interval around $\hat{P}_k$. We can also take advantage of constraints including monotonicity and the finite set of possible values for P_k. We find that the entire set of coefficients can be estimated to a useful uniform, absolute precision on a laptop for graphs with millions of edges [17]. Furthermore, the estimation procedure is an embarrassingly parallel computation, since the sampling and rule evaluation can be performed independently and asynchronously, with very little inter-processor communication.

We have written software for estimating reliability that implements a variety of rules under either the independent edge or independent vertex damage models and can handle large, labeled graphs. The largest graph it handles is constrained by available memory. It has been tested on graphs with up to 50 million edges, which required roughly 5 hours (edge damage) or 15 hours (vertex damage) with 240 processes, using about 4 GB per process. The reliability for more modest graphs, such as those with 1000 edges, can be evaluated on a laptop in a few seconds. As noted above, running time is independent of graph structure. Instead, it is dominated by the time required to evaluate the rule on a graph and the number of samples required to reach the desired precision. It depends weakly on the values k_- and k_+, as most samples will be drawn from this interval and evaluating the rule generally scales with the size of the subgraph. This tool has been made available to researchers via the Cyber-Infrastructure for Network Science (CINET) web site http://ndssl.vbi.vt.edu/cinet.

3.1.2 Identifying dynamically important differences between networks—

Reliability reorganizes all the information about a graph's structure, both local and global, into a form that allows us to determine the differences between graphs that are relevant to our specific question (the reliability rule) by inspection. Given two graphs with the same number of edges E and with reliability polynomials $R_1(x)$ and $R_2(x)$, we first find the value of x which maximizes their difference, $x_m \equiv \arg\max_x |R_1(x) - R_2(x)|$. The difference in reliability between these graphs is mostly due to subgraphs of size $k_m = x_m E$ because of the strong windowing created by the binomial factor $\binom{E}{k} x^k (1-x)^{E-k}$ in Equation 2.4. By evaluating the reliability rule on samples of subgraphs with k_m edges, we can find accepted subgraphs in graph 1 that do not appear in graph 2 and identify the edges missing from graph 2 that are responsible for the difference. These are exactly the differences that are most important dynamically.

If, in addition, we know the graph *model*, that is, how the graphs were generated, we can build a distribution of reliability polynomials under that graph model. This distribution is the null distribution for the hypothesis that any given graph has the same dynamical properties as those of graphs drawn from the graph model. In other words, this places the problem of distinguishing two graphs in a traditional statistical hypothesis testing framework. For example, in the left panel of Figure 3 the "curve" on the left is actually one hundred *different* curves generated by one hundred *different* random graphs with the same number of edges and vertices. There is no need for a formal test of significance to appreciate that the curve on the right is extremely unlikely under the distribution of curves on the left. The novelty here is that the test is based directly on dynamical properties – it does not require first arguing that the value of a statistic is significantly different from what would be expected under the null and then separately arguing that this difference is sufficient to induce a difference in a dynamical observable.

3.2 *A2*: Ranking edges by importance

The budget for controlling an outbreak of infectious disease is rarely large enough to reduce the probability that it will spread to 20% of the population to 0, corresponding to finding a cut for the *AR*-0.2 rule. Instead, we try to prioritize changes to the network structure, for example ranking edges to target for removal. Our heuristic, based on the greedy algorithm referred to in Section 2.2, is to rank edges in order of their criticality. Like betweenness, the criticality must be re-evaluated after any change to the graph's structure.

A straightforward implementation of the greedy algorithm identifies structural motifs and removes an edge from each. We have found through experimentation that this is not a particularly good strategy for several reasons:

1. a great deal of computation is required to ensure that an accepted subgraph is minimal;
2. concentrating on individual structural motifs does not identify edges that are in the overlap of many structural motifs; i.e. all edges in any single structural motif appear to be equally important;

3. although every motif contributes equally to a *cut*, motifs contribute differently to a *ranking*.

The last point is related to a ranking's dependence on the damage model's parameter x: at $x = 1$, every structural motif is equally important because the existence of any one guarantees that the reliability will be 1; at $x = 0$, every structural motif is equally unimportant because none of them has any chance of appearing in a subgraph with 0 edges. We have designed a heuristic that takes this behavior into account.

We first find the value k for which $R(k/E) = 0.5$. Next, using the 2×2 contingency table described in [4], we evaluate for each edge (the fraction of accepted graphs when the edge is present) - (the fraction of accepted graphs when the edge is absent). If the edge is not part of a motif, both terms will be approximately P_k, and their difference will be close to 0. If the edge is part of a motif of size k_0, the first term will be approximately $((k-1)/E)^{k_0-1}$, the probability that all the other edges in the motif were selected for the subgraph; the second term will be less than P_k, depending on how many other structural motifs there are and how they overlap. A more careful argument could derive the sampling distribution for the difference in each of these cases, but for ranking edges we do not need this extra complexity. The larger the difference, the more important the edge is. Hence we use Algorithm 1 to rank edges.

3.3 Example networks

For experiments in a previous paper [17], we generated a large set of graphs with 992 edges, 341 vertices, and carefully controlled degree distributions, assortativity-by-degree, and number of triangles. Each graph was created by swapping edges in one of two original graphs, a connected Erdős-Rényi graph ("GNM") drawn by choosing edges independently at random and rejecting any graphs that were not connected, and a hand-designed connected, scale-free-like ("SFL") graph. The degree distribution of all graphs based on the GNM graph is (1, 9), (2, 7), (3, 33), (4, 58), (5, 54), (6, 53), (7, 57), (8, 31), (918), (10, 8), (11, 7), (12, 3), (13, 2), (14, 1)); and the degree distribution of all graphs based on the SFL graph is (4, 256), (8, 64), (16, 16), (32, 4), (64, 1). Figure 2 shows constrained edge-swapping operations that adjust the assortativity-by-degree and number of triangles while maintaining the degree distribution unchanged. See [17] for more details on the ranges of assortativity and triangles in these graphs.

Algorithm 1 Ranking edges by dynamical importance

```
Initialize edge cut set ∅ → {s}
Evaluate k : R_G(k/E) = 0.5
while R_G(k/E) ≠ 0 do
  repeat
    Select a subgraph g with k edges
    Evaluate r(g)
    for each edge do
      Increment counters present, absent, presentAndAccepted, and/or absentAndAccepted as
      appropriate
    end for
  until desired precision achieved
  Rank edges by value of presentAndAccepted/present − absentAndAccepted/absent
  Remove the most important edge e, i.e. G = G\e
  Update the edge cut set, i.e. e ∪ {s} → {s}
  Evaluate reliability R_G(k/E)
end while
```

We also use friendship networks obtained from the National Longitudinal Study of Adolescent Health ("Add Health") [7]. Add Health is a longitudinal study of a sample of

adolescents who were in grades 7-12 in the United States during the 1994-95 school year. The study collects information about the respondents' social, economic, psychological and physical well-being with contextual data on the family, neighborhood, community, school, friendships, peer groups, and romantic relationships.

Finally, to demonstrate that these techniques are feasible for large graphs, we use an estimated social contact for the New River Valley region near Blacksburg, Virginia. This network was generated in the Network Dynamics and Simulation Sciences Laboratory according to methods described elsewhere, and has been made publicly available [13, 15]. It contains more than 4.1 million edges and 150 thousand vertices.

4. Results

4.1 Characterizing graphs using reliability

Figure 3 shows the reliability polynomial under *AR*-0.2 for the New River Valley social network. We also evaluated the reliability polynomial for 100 Erdős-Rényi graphs with the same number of edges and vertices as the NRV network. Clearly, the NRV network's reliability is significantly different from an Erdős-Rényi network's. Characterizing these networks as in the right panel of Figure 1 would place the NRV network in a different equivalence class from all the others. Of course, the NRV network is placed in a different equivalence class from the Erdős-Rényi graphs under many graph statistics, including degree distribution. The utility of the current approach is that the difference can be detected whether or not the analytic relationship between the statistics and the reliability is understood. For example, one could use constrained edge-swapping to develop an ensemble of random graphs that share many statistical properties with the NRV network and conduct this same test. The right panel of Figure 3 illustrates a linear transformation of transmissibility that makes the reliability on the NRV network identical to the reliability on an Erdős-Rényi network. We remark further on the implications of this renormalization in the Discussion section.

4.2 Identifying structural differences using reliability

We exhibit the results of the methods in Section 3.1.2 on two of the SFL graphs described in Section 3.3 shown in Figure 4 (left and middle panels). They have the same number of vertices (341) and edges (992), the same assortativity-by-degree (0.25), and the same degree distribution. We have used the degree- and assortativity-preserving edge swapping technique shown in Figure 2 to change the number of triangles. The graph in the center panel contains 1251 triangles, while the one in the left panel contains 910 triangles. Although they look very similar to the eye, not surprisingly, their reliability under many rules differs.

The first step in the comparison is to determine the value of k for which $R(k/E)$ has the largest difference between the two graphs. Figure 5a (left) shows the reliability polynomials $R(x)$ for each graph and their difference as a function of edge failure probability for the *AR*-0.2 rule. A peak in the difference in reliability for these graphs is observed at $k \approx 428$. Structural motifs yield sets of edges found only in A or only in B that dock with sets of edges in the intersection of A and B to form reliable networks. In this case, we note that the

smallest structural motif in graph A must be much smaller than in graph B. One example of such a structural motif is displayed in the right panel of Figure 4.

4.3 Ranking edges

Using algorithm 1, we found a cut in 230 GNM graphs and 93 SFL graphs. To verify our results, we compared them with those obtained using the matrix tree theorem. Kirchhoff's matrix tree theorem [9] states that the total number of spanning trees in a graph equals any cofactor of the Laplacian matrix of that graph. The Laplacian matrix is the diagonal matrix of vertex degrees minus the adjacency matrix. To rank the edges using Kirchhoff's theorem, we first computed the total number of spanning trees in the graph. An edge's criticality is the reduction in number of minimum spanning trees when that edge is removed from the graph. Note that for this rule, all structural motifs have exactly $V - 1$ edges, so there is no complication arising from motifs with different sizes. We found that the most critical edge determined through Kirchhoff's theorem always belongs to the edges in the cut set obtained using algorithm 1, although it is not always the highest ranked edge.

We also found cuts under AR-0.2 for the AddHealth graphs. Table 1 shows the characteristics of a subset of Add Health graphs and the number of edges in the cut produced by algorithm 1. The cuts require removing from 70% to 74% of all edges. This is large, but smaller than would be expected (87%) if the networks were degree-regular with the observed degree.

We ranked edges for the SFL graphs in Figure 4 and compared the reliability polynomials as we removed either 25 or 50 top-ranked edges with those obtained by removing the same number of randomly selected edges. Results are shown in the right panel of Figure 5b. The difference is barely noticeable for 25 edges, but clearly significant for 50 edges.

We ranked edges for the NRV network under AR-0.2. We found the top 4152 edges (approximately 0.1% of all edges) and examined the effect on reliability of removing these edges from the network. The optimal ranking for this case is not known. Instead, we compare our results with the effect of removing the same number of edges chosen uniformly at random. As before, we created an ensemble of networks with random edges deleted for generating a distribution of changes in reliability under the null hypothesis that our algorithm's selection was no better than random. In this case we used an ensemble of size 10. We expect that the effect of removing 0.1% of the edges on the dynamics over a large graph will be very small. We also expect any effect for our algorithm to be most evident near x for which $R(x) = 0.5$, because the algorithm concentrates its effort at that point. For the NRV network under this rule, this corresponds to $x \sim 0.0224$. Figure 6 confirms our expectations. Moreover, it demonstrates that the edge ranks depend on x. Our choice of evaluating the difference in reliability for x such that $R(x) = 0.5$ seems justified by this figure, because the average reduction over the interval is clearly larger for edges selected by algorithm 1 than for randomly selected edges.

5. Discussion

Network reliability depends on dynamics and, for a given dynamical process, on the parameters of the process and the observed features. A network cannot be characterized sufficiently without taking the dynamics and observations into account. We argue that the reliability polynomial itself is a natural tool for characterizing networks that takes both dynamics and observations into account. The reliability polynomial depends on the dynamics through the damage model; it depends on the observed features through the reliability rule; and its value varies from 0 to 1 across the domain of dynamical parameters.

The primary reason to characterize networks is to understand how changes in a network affect dynamical outcomes. Such an understanding is crucial for both model sensitivity analysis and solving network design problems. We argue that the characterizations provided by the reliability polynomial are useful for understanding the effect of changes in network structure. They can be used both to identify network structures responsible for changes in outcomes, as in Section 3.1.2, and to guide attempts to control dynamics by changing the network, as in Section 3.2.

The results displayed in Figure 3 raise an important issue of model identifiability in network epidemiology. It is very difficult to estimate the person-person transmissibility of a newly emerging infectious disease; likewise, it is very difficult to estimate the contact network structure. The possibility of renormalizing transmissibility illustrated here means that only the *combination* of network structure and transmissibility can be estimated from population level data, not either separately. This would not be a problem except that there is no guarantee that the same renormalization applies when these networks are perturbed, e.g. when outbreak controls are applied. Thus the fact that a combination of network and transmissibility fits observed data does not necessarily imply that the model will correctly predict the outcome of interventions.

The ability to rank edges in order of their contribution to dynamical phenomena supports quantitative analysis of targeted interventions in an infectious disease outbreak. We can compare the reduction in reliability achieved by the targeted intervention with both the reduction produced by an ensemble of random interventions and the optimal reduction, as shown in Figure 6. Moreover, the reduction can be evaluated either for a specific value of transmissibility, or in expectation across a range of possible transmissibilites.

5.1 Future directions

We note that the restrictions imposed on the analyses we have performed here – to an independent edge damage model for unlabeled, undirected graphs under a single reliability rule – are in no way required by the theoretical framework. The results presented here are just a few examples of the analytical power the Moore-Shannon approach brings to network analysis. There are many opportunities for further research into theory, methodology, and applications, including:

- proof that a greedy algorithm is appropriate for generalized cuts and flows;
- tight bounds on the reliability polynomial;

- efficient approximation methods for criticality;
- extension to generalized contagion dynamics;
- extensions to other damage models, especially models that mix vertex and edge failures;
- definition of coherent reliability rules useful for studying dynamics on directed, labeled graphs;
- comparisons to graph spectral methods;
- application to the community detection problem.

Moreover, the results obtained here are not yet applicable to the problem of controlling an outbreak of disease in a real population. There is no practical way to determine the criticality of a contact between two people, for example. It remains to identify observable properties of the edges that correlate with the ranking determined here. For example, one might correlate rank with the demographic labels (such as age, gender, household size) associated with vertex endpoints or the activity labels (such as work, school home) associated with the edges themselves.

We hope that future network analyses will not restrict themselves to characterizing a network using only statistics that do not take dynamics into account, or evaluating the performance of a network design strategy for only a single set of dynamical parameters, or ignoring label and direction constraints.

Acknowledgment

We thank the organizers of the SITIS 2013 workshop and members of the Network Dynamics and Simulation Science Laboratory (NDSSL), especially M. Marathe, for their suggestions and comments.

6. Funding

This work has been partially supported by the Defense Threat Reduction Agency (DTRA) [award number HDTRA1-11-1-0016]; the National Institute of General Medical Sciences of the National Institutes of Health (NIH) [Models of Infectious Disease Agent Study (MIDAS) award number 2U01GM070694- 09] and by the National Science Foundation (NSF) [Network Science and Engineering Grant CNS- 1011769]. The content is solely the responsibility of the authors and does not necessarily represent the official views of DTRA, the NSF, or the NIH.

This research uses data from Add Health, a program project directed by Kathleen Mullan Harris and designed by J. Richard Udry, Peter S. Bearman, and Kathleen Mullan Harris at the University of North Carolina at Chapel Hill, and funded by grant P01-HD31921 from the Eunice Kennedy Shriver National Institute of Child Health and Human Development, with cooperative funding from 23 other federal agencies and foundations. Special acknowledgment is due Ronald R. Rindfuss and Barbara Entwisle for assistance in the original design. Information on how to obtain the Add Health data files is available on the Add Health website (http://www.cpc.unc.edu/addhealth). No direct support was received from grant P01-HD31921 for this analysis.

References

1. Colbourn, CJ. The Combinatorics of Network Reliability. Oxford University Press; 1987.
2. DuBois T, Eubank S, Srinivasan A. The Effect of Random Edge Removal on Network Degree Sequence. Electronic Journal of Combinatorics. 2012; 19(1):P51.
3. Eubank S, Guclu H, Kumar VSA, Marathe M, Srinivasan A, Toroczkai Z, Wang N. Modelling disease outbreaks in realistic urban social networks. Nature. 2004; 429(6988):180–184. [PubMed: 15141212]

4. Eubank S, Youssef M, Khorramzadeh Y. Determining and Understanding Dynamically Important Differences between Complex Networks Using Reliability-Induced Structural Motifs. 2013 International Conference on Signal-Image Technology & Internet-Based Systems (SITIS). 2013:641–648. IEEE.
5. Ford L, Fulkerson D. Maximal Flow through a Network. Canadian Journal of Mathematics. 1956; 8:399–404.
6. Grassberger P. On the critical behavior of the general epidemic process and dynamical percolation. Mathematical Biosciences. 1983:157–172.
7. Harris K, Halpern C, Whitsel E, Hussey J, Tabor J, Entzel P, Udry J. The National Longitudinal Study of Adolescent Health. 2009
8. Khorramzadeh Y, Youssef M, Eubank S. Analyzing Network Reliability Using Structural Motifs. arXiv: [physics.soc-ph], submitted to Phys. Rev. E. 2014
9. Kirchhoff G. Über die Auflösung der Gleichungen, auf welche man bei der Untersuchung der linearen Verteilung galvanischer Ströme gefuhrt wird. Ann. Phys. Chem. 1847; 72:497–508.
10. Mieghem PV, Wang H, Ge X, Tang S, Kuipers FA. Influence of Assortativity and Degree-preserving Rewiring on the Spectra of Networks. The European Physical Journal B. 2010; 76(4): 643–652.
11. Milo R, Shen-Orr S, Itzkovitz S, Kashtan N, Chklovskii D, Alon U. Network motifs: simple building blocks of complex networks. Science. 2002; 298(5594):824–827. [PubMed: 12399590]
12. Moore E, Shannon C. Reliable circuits using less reliable relays. Journal of the Franklin Institute. 1956; 262(3):191–208.
13. Network Dynamics and Simulation Sciences Laboratory. 2013. Data set release 4, New River Valley estimated contact network
14. Page L, Perry J. Reliability polynomials and link importance in networks. IEEE Transactions on Reliability. 1994:51–58.
15. Swarup S, Eubank SG, Marathe MV. Computational Epidemiology as a Challenge Domain for Multiagent Systems. The Twelfth International Conference on Autonomous Agents and Multiagent Systems (AAMAS), Paris, France. May.2014 2014 :5–9.
16. Winterbach W, de Ridder D, Wang H, Reinders M, Mieghem PV. Do greedy assortativity optimization algorithms produce good results? The European Physical Journal B. 2012; 85(5)
17. Youssef M, Khorramzadeh Y, Eubank S. Network reliability: The effect of local network structure on diffusive processes. Phys. Rev. E. 2013; 88:052810.

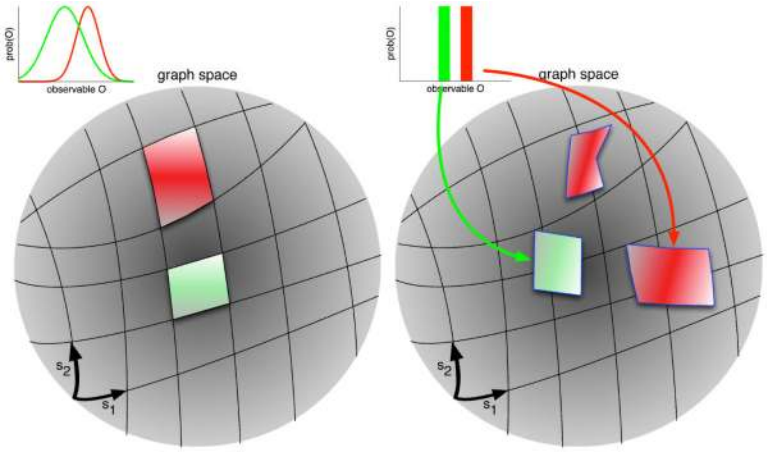

FIG. 1.

(Left:) A coordinate system on graph space defined by the values of two graph statistics s_1 and s_2, for example assortativity-by-degree and clustering coefficient. The red and green areas are two different sets of equivalent graphs, where equivalence is defined by the values of s_1 and s_2. The distributions of an observable, for example, the infection attack rate, for each equivalence class are caricatured in the plot. In general, there is no guarantee that these distributions are unimodal or non-overlapping. (Right:) An alternative pair of equivalence classes under a definition of equivalence induced by the observable. By definition, the distribution of observables for each equivalence class is concentrated and non-overlapping; however, the support of any equivalence class is not necessarily convex or even contiguous in the $s_1 - s_2$ coordinate system, as suggested by the red regions.

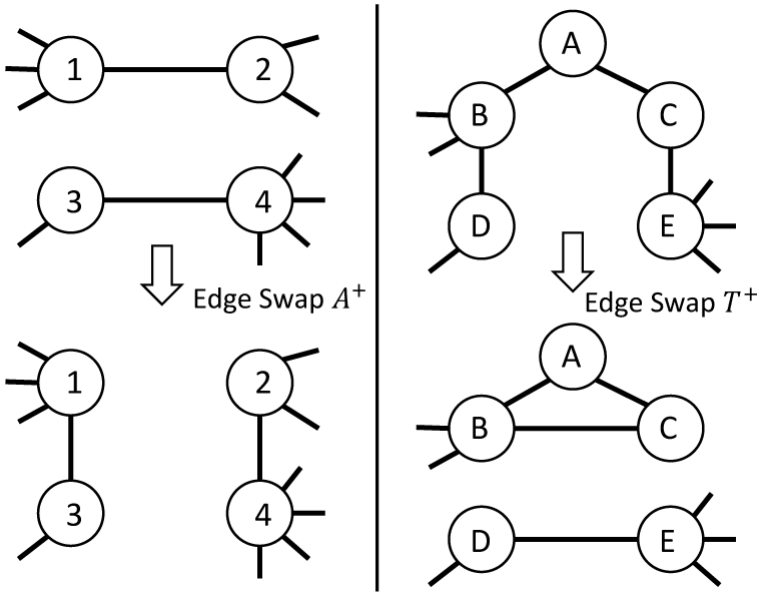

Fig. 2.

(left panel) Assortativity-changing edge swap: vertex degrees are $d_1 = 4$, $d_2 = 3$, $d_3 = 2$, and $d_4 = 5$. The contributions of these vertices to assortativity are $d_1d_2 + d_3d_4 = 22$ and $d_1d_3 + d_2d_4 = 23$ so the network at the bottom has a higher assortativity than the one at the top [10, 16]. If the network at the top is connected, the network at the bottom will also be connected if there is a path from vertex 1 to vertex 2. (right panel) Assortativity-preserving, triangle-changing edge swap: *B* and *D* have no neighbors in common, nor do *C* and *E*. The vertex degrees are $d_B = d_E = 4$ and $d_C = d_D = 2$. Their contributions to assortativity are $d_Bd_D + d_Cd_E = 40 = d_Bd_C + d_Dd_E$ so the network at the top has the same assortativity as the one at the bottom. If the network at the top is connected, the network at the bottom will also be connected if there is a path from *B* to *D*. This swap changes the number of triangles in the network by at least one – more, if *B* and *C* have any common neighbors besides *A*.

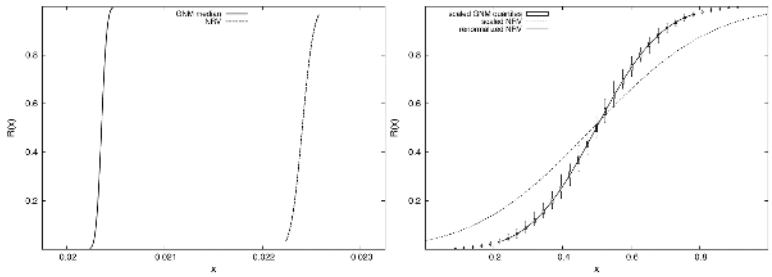

Fig. 3.

Characterizing epidemic dynamics on an estimated contact network for the New River Valley Here, $R(x)$ is the probability that an outbreak seeded in a single randomly selected individual will spread to at least 20% of the population if the transmission probability across every edge is x. *Left:*The median reliability for 100 Erdős-Rényi random graphs with the same number of edges and vertices as the NRV network is on the left; the reliability for the NRV network is on the right. Note the expanded x scale – this is a very sharp epidemic transition and the difference between the curves, though statistically and practically significant, is small. However, the distribution of reliability across the Erdős-Rényi ensemble is too tight to be discernible even at this scale. *Right:* After scaling both reliability curves linearly by $x \to (x - x_-)/(x_+ - x_-)$, the threshold behavior is still noticeably different. The dotted curve sows the reliability of the NRV network under this scaling; the boxes represent 0, 25, 50, 75, and 100% quantiles of the ensembles under this scaling. A further renormalization of the transmissibility for the NRV network, $x \to 0.56x + 0.225$, determined by eye, produces a "scaling form" for the reliability, the solid curve. That is, the reliability of the NRV network at a scaled value of x is indistinguishable from the reliability of an Erdős-Rényi random graph.

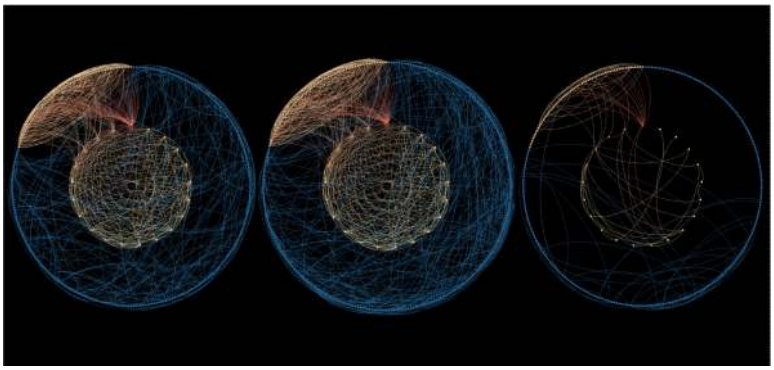

Fig. 4.

Two graphs with 992 edges each, the same scale-free-like degree distribution, and the same assortativity-by-degree (0.25), but with different numbers of triangles (1251 on the left, 900 in the center). Vertices and edges are colored, sized, and arranged by degree. Right: a 241-edge structural motif for this rule in the 900-triangle graph that does not occur in the 1251-triangle graph.

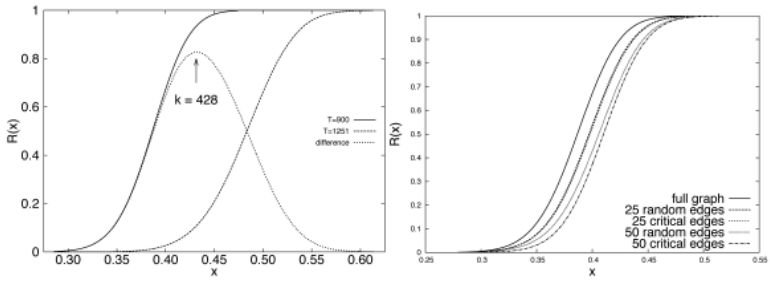

Fig. 5.

Left: $R(x)$ for the two graphs shown in Figures 4 (left and middle panels) along with the difference. The difference peaks around $k = xE = 428$, indicating that one graph has many more structures with 428 edges that are accepted by AR-0.2 than the other. This is most likely due to the difference in k_{-} – 241 vs. 295 edges – between the two graphs. Right: The change in reliability for the graph in Figure 4 (center panel) as edges are removed either at random or according to their criticality as defined in the text.

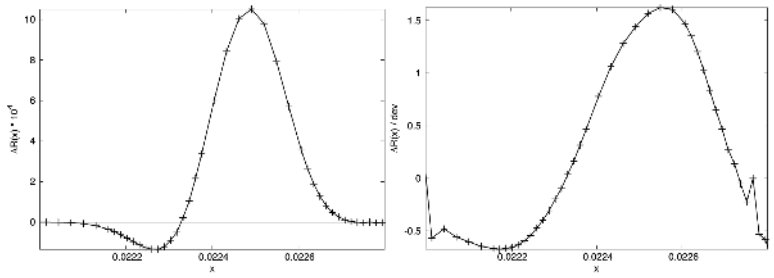

Fig. 6.

We evaluate the quality of the edge ranking strategy in algorithm 1 by comparing the effects on reliability for the NRV network of removing the edges selected with a randomly chosen set of edges. We remove a set of 4152 edges (approximately 0.1%) from the network and evaluate the *AR*-0.2 reliability of the remaining graph. For the random edge selection, we repeat this 10 times to estimate the mean and the standard deviation in reliability. The range of x values plotted here spans the entire transition range, over which $R(x)$ for the original graph rises from 10^{-3} to $1 - 10^{-3}$. (Left) The difference between the mean reliability of edges selected randomly and edges selected according to algorithm 1. Positive values indicate that our algorithm selects edges that reduce the reliability more than a random selection. The absolute difference is very small because we have removed such a small fraction of the edges. (Right) The difference between reliabilities relative to the standard deviation in the 10 sets of randomly selected edges. Values greater than 1 indicate that our algorithm selects edges that reduce the reliability by more than one standard deviation more than the randomly selected edges. The spikes at the left and right sides of the plot arise from small-sample statistics in our estimates of the standard deviation.

Table 1

The fraction of edges whose removal is required to cut Add Health graphs for the *AR*-0.2 reliability rule. For uniform mixing *S* –*I*–*R* model when the mean degree is *d*, the threshold transmissibility for herd immunity is 1/*d*. Below this threshold, outbreaks do not spread very far. To control an outbreak in such a system, the mean degree must be reduced to at most 1. For each of the AddHealth graphs, this corresponds to removing 87% of the edges. The cuts we find remove fewer edges, due to the non-uniformity of mixing represented by network topology.

Vertices	Mean degree	% of edges in cut
291	7.81	0.74
457	7.44	0.70
205	7.89	0.71
255	7.87	0.74
685	8.16	0.70
426	7.46	0.77