Fast Moving Sampling Designs in Temporal Networks
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Abstract

Introduction
In a study related to this one [1] I set up a temporal network simulation environment for evaluating network intervention strategies. A network intervention strategy consists of a sampling design to select nodes in the network. An intervention is applied to nodes in the sample for the purpose of changing the wider network in some desired way. The network intervention strategies can represent natural agents such as viruses that spread in the network, programs to prevent or reduce the virus spread, and the agency of individual nodes, such as people, in forming and dissolving the links that create, maintain or change the network. The present paper examines idealized versions of the sampling designs used to that study. The purpose is to better understand the natural and human network designs in real situations and to provide a simple inference of design-based properties that in turn measure properties of the time-changing network. The designs use link tracing and sometimes other probabilistic procedures to add units to the sample and have an ongoing attrition process by which units are removed from the sample.

Properties of with-replacement random walks in graphs and their Markov chain Monte Carlo modifications are described [2]. Eigenvector values of random walk designs have been used as measures of centrality in social networks since [3], [4]. Limiting selection probabilities of random walk in a network were proposed as a ranking measure for web pages returned by a search engine were proposed in [5]. The difficulties of obtaining a random sample of web pages is discussed in [6]. Use of random walk design to reach all nodes in a network as fast as possible is taken up in [7]. A “forest fire” sampling design in [8], based on a network creation procedure in [9], traces a random number of links out and adds nodes without replacement. Links in are back-traced with a lower probability. The purpose is to obtain a sample that, somewhat like a large random sample, captures characteristics of the complete network.

The designs of this paper offer an increased flexibility, have both an acquisition and a attrition process, giving properties of stochastic stationarity where desired. In temporarily changing networks the moving average and exponential smoothing measures allow the with-replacement versions of the designs to continuously approximate their own inclusion properties, which in turn can be used to highlight temporally high-interest areas of the network. Thes measures are much more concentrated than are the eigenvector values of
random walks. Without-replacement versions of these designs, or modifications allowing
with-replacement with lower probability or only when stuck can be used to reach new
areas of the changing network over time.

Methods

Fast moving designs for design-based inference

Since the purpose of the simulations is to assess the effectiveness of intervention designs
and since the virus in the simulations has a tendency to explode unexpectedly into new
areas, it is some interest to try to anticipate where it might potentially explode into next.
One possibility is to keep a running tabulation on connected components and note when
the virus spread has intersected with a component. However, components are continually
changing and a component might be technically connected but thinly so from one part
to another. That is there may be few paths from one part of a component to another.
Another possibility is to look at the population graph as if frozen in time and calculate the
expected increase of virus prevalence at the next step using the number and configuration
of links our from the current virus sample. At the same time the expected decrease is
calculated using the stage specific node mortality rates for the virus-infected nodes. Birth,
death, immigration, and emigration rates can be weighed in also. The difference between
the rates of increase and decrease gives a partial measure of the expected net change.
Such a calculation is conditional on the network configuration at the given time \( t \). What
is missing from the calculation is the social movement of individuals, the drift of social
groups with respect to each other, and the potentials for new formations of links after
those movements, as well as deletions of current links.

A different type of measure uses idealized designs that are similar to the designs by
which the virus spreads but faster moving and faster mixing. There are many possible
variations on such designs. Among the simplest traces links out with independent
Bernoulli probabilities \( p \) per link. The value of \( p \) here tends to be much higher than the
transmission rates of HIV and higher than the realistic tracing rates of seek and treat
intervention designs. The simplest of these designs uses equal tracing rates. We consider
several of these idealized types.

**Design 1.** At time \( t \) links out from the current sample are traced with equal prob-
ability \( p_t \), independently. The target sample size is \( \nu \). Sample size just before additions
and removals at time \( t \) is \( n_{t-1} \). The rate at which nodes in the sample are removed from
the sample is denoted \( r_t \), that is, for any node in the sample, \( r_t \) is the probability it is
removed at that time step. To maintain a sample size stochastically around \( \nu \) either \( p_t \)
or \( r_t \) or both are adjusted based on current sample size, that is, on \( n_{t-1} \). With “back
control”, let \( p_t \) be constant and \( r_t = (n_t - \nu) / n_t \) if \( n_t - \nu > 0 \) and \( r_t = 0 \) otherwise.

With “front control”, let removal rate \( r_t \) be constant and adjust tracing rate \( p_t \) based
on \( n_{t-1} \) to add stochastically any shortfall from target sample size \( \nu \). Since some nodes
not in the sample may be linked from more than one node in the sample, the expected number of nodes added for a fixed rate $p_t$ is

$$\sum_{\{i : i \notin s_{t-1}\}} \left[ 1 - \prod_{j \in s_{t-1}, e(j,i) \in E_{t-1}} (1 - p_t) \right]$$

As an approximation to stochastically maintain the sample size around the target size, set the tracing rate to be $p_t = (\nu - n_{t-1})/#E_{s+}$ if $\nu - n_{t-1} > 0$ and $p_t = 0$ otherwise, where $#E_{s+}$ is the number of links out from the sample. That is, $#E_{s+} = \#\{e(i,j) \in E_{t-1} : i \in s_{t-1}, j \notin s_{t-1}\}$.

It is sometimes of interest to have fixed rates $p$ and $r$ of link-tracing and node removal. In such a case the stochastic sample size $n_t$ stochastically reflects the density of nodes in the network. For some types of dynamic networks, such as those with preferential attachment depensation in link formation, the fluctuations in sample size under fixed rates can be very pronounced.

In addition, at time $t$ nodes not in the sample may be added independently at random to the sample with some small probability $d_t$, so that the expected number of nodes added this way is $d_t(N_t - n_t)$.

This design is without-replacement in that a node currently in the sample just before time $t$ is not re-selected at time $t$. It is with-replacement, however, in the sense that a node previously in the sample that has been removed can be re-selected at any time.

A design of this type can be modified so that probabilities of selection and removal depend on node or link values.

**Design 2.** This design is much like the first but is with-replacement even of units currently in the sample. At time $t$ a unit $i$ can be selected even though it is already in $s_{t-1}$, which is the sample as sampling first starts at time $t$. Any unit in $s_{t-1}$ can be re-selected only once at time $t$. This design is similar in its properties to Design 1, but concentrates farther into the most link dense, connected parts of the population.

**Design 3.** This design concentrates still farther by letting the sampling at time $t$ be completely with-replacement. With each unit $i$ we tabulate $m_t(i)$, the number of times it has been selected at time $t$.

**Design 4.** Here we let Design 1 be completely without-replacement, so that any unit that is currently or has ever been previously in the sample is not eligible for re-selection. In contrast to the first three designs which tend to concentrate their effort in highly connected parts of the population, the without-replacement design, even though it is tracing links, tends to spread farther and farther out, reminiscent of a random sample, as time goes on. The design can get stuck, with no links out to units that have not been already sampled at some time. A small random selection probability will let it eventually jump to new nodes. A variation of this design allows with-replacement sampling only when link tracing is stuck. It is also possible to have a steady, small probability of with-replacement sampling.
Design 5. This design is specifically for use with an epidemic such as HIV. In this design link-tracing continually begins with nodes infected with the virus. At time $t$ independent Bernoulli sampling selects infected nodes with probability $p_0$. Link tracing of nodes already in the sample (from time $t-1$) independently with probability $p_l$. There is a constant attrition rate $r$ removing nodes from the sample. In this way selection and attrition come into dynamic, fluctuating balance. No set limit is placed on the number of steps links are followed out from infected nodes, but attrition stochastically limits that number to a few. The sample thus highlights uninfected nodes at most immediate risk for infection. An uninfected node with more network links or paths from the current virus sample tends to be in the sample more often than a node that is connected to the virus sample by fewer links or paths. Variations on this design have set rules on number of steps out, for example fixed limit one step or two steps of tracing from an infected node.

Design 6. In each of the above designs the sampling is limited to a single round, that is, a single wave of selections at time $t$. Design 6 takes any of those designs and lets it run for some number $k$ of waves at time $t$. Thus, for designs having stable limiting distribution properties, including limiting inclusion probabilities for each node, that limit can be approached at each time step. As the network itself changes, the limits change at each time step.

All of these designs can alternatively be considered a single type of network design with different parameter values corresponding to acquisition and removal rates, existence of sample size targets, with-replacement and without-replacement types and rates, recruiting activeness depending on factors such as time in sample, coupons held, numbers of waves at a time step, and similar characteristics. Natural designs such as used by a virus to spread in a population, and practical designs such as seek and treat designs for spreading tests and interventions and respondent-driven designs for assessing risk behaviors in a population, are modeled as designs of these types having special characteristics. One design may interact with another through competition or mutual enhancement, one design may modify its parameter values to adapt to another, and the effect of intervention designs can include changing the network structure of the population.

Design 0. Random walk designs in the dynamic network are collectively called Design 0. At time $t-1$ the random walk sits on some node, say node $i$, so that the indicator variable $Z_{t-1}(i) = 1$ and for all other nodes $j \neq i$, $Z_{t-1}(j) = 0$. Let $d_t(i)$ be the number of nodes to which node $i$ connects. That is, $d_t(i)$ is the out-degree of node $i$. The random walk selects one of these links at random, with probability $1/d_t(i)$, and traces that to its destination node, say node $j$. The random walk now sits on node $j$, so that $Z_t(j) = 1$ and $Z_t(i) = 0$. Sampling is with-replacement, so that the walk can move back to node $i$ at any time that is is connected to the current walk node. If the random walk has a positive probability of staying at the node where it is at a time step, it is called a “lazy” random walk. The random walk design can be modified to allow weights on links with probability of following a link depending on its weight relative to the other links out.

When a random walk design is run in a network that changes with time, some behaviors
are seen that do not occur with a random walk in a static network. In a static network, a random walk is stuck in the single connected component in which it starts, unless it is allowed to make a jump at from time to time to a randomly selected unit. In the dynamic graph setting, a random walk might be stuck for some time in an isolated component. But over time that component might connect with another and a new component formed, so the random walk moves in the new component. The random walk might move to a node whose links are subsequently deleted, so that it is stuck on that single node until a new link forms, unless it is allowed to make a random jump at that point. Further, the node on which the walk sits might be deleted from the graph at time \( t \), in which case the walk ends. The design might be modified to start a new walk at each such event.

When \( \nu \) random walks are run independently in the same graph, we can view it as a single design of our general type as follows. At any time \( t - 1 \) any node \( i \) in the population has associated with it a value \( M_{t-1}(i) \) representing the number of walks that sit on that node at that time; \( 0 \leq M_{t-1}(i) \leq \nu \) and \( \sum_{i \in U_t} M_{t-1}(i) = \nu \). At time \( t \) for node \( i \), \( M_{t-1}(i) \) independent multinomial selections are made, the result of each selection being a transfer of one count transferred from node \( i \) to one of its linked nodes or else remaining at node \( i \). When a count is transferred to a linked node \( j \), \( M_t(j) \) is incremented by 1 and \( M_t(i) \) is decremented by 1. Typically, random jumps are allowed, and are automatic when a node having one or more walks on it is deleted. A random jump means that a node \( j \) is selected at random from the population and 1 is added to \( M_t(j) \).

**Flame rank**

Any of the fast mixing designs of this section can be averaged or smoothed to estimate design or network properties. Let \( Z_t(i) = 1 \) if node \( i \) is in the sample at time \( t \) and \( Z_t(i) = 0 \) otherwise, so that the random collection \( \{ Z_t(i), i \in U_t \} \) are the sample inclusion indicators for the nodes in the current population.

With a static graph, for which \( G = \{ U, E \} \) does not change with time but the sampling process \( \{ S_t \} \) progresses indefinitely in time with a stationary distribution, the cumulative means \( 1/T \sum_{t=0}^{T-1} Z_t(i) \) converge in probability to fixed sample inclusion probabilities \( \pi_i \) as \( T \to \infty \), for \( i = 1, ..., N \).

The limiting inclusion probabilities and associated stationary distribution are particularly well understood for the random walk design in a static graph, where the \( (\pi_1, ..., \pi_n) \) is the first eigenvector for the adjacency matrix of the graph, associated with eigenvector \( \lambda = 1 \), and the second eigenvector is a measure of how fast the design mixes to that stationary distribution.

The dynamic graph case has had much less study and is less well understood, even for the random walk.

In the dynamic case each node has a sample inclusion indicator variable \( Z_t \) providing a time series of values 0 and 1 for each time step while the node exists.

Let \( t_{ci} \) be the time that node \( i \) came into existence or entered the population. At time
the cumulative mean $(1/t - t_0) \sum_{s=t_0}^{t} Z_s(i)$ represents the proportion of time the node has been in the sample. Because of changes in the network structure during that time, the cumulative mean might not be a good approximation for the current probability that node $i$ is included in the sample.

For the dynamic setting we calculate for each node a moving average value, which averages the indicator variables for the most recent values, back to some lag $L$. That is, $v_t(i) = \sum_{j=0}^{L} \theta_j Z_{t-j}(i)$, with $\sum_{j=0}^{L} \theta_j = 1$; for instance with equal weights $\theta_j = 1/L$ or half-normal weights $\theta_j = e^{-(j^2)/2\sigma^2}/\sum_{k=0}^{L} e^{-(k^2)/2\sigma^2}$. For simplicity and computational efficiency we are using most often an exponentially weighted moving average

$$v_t(i) = \lambda v_{t-1}(i) + (1 - \lambda) Z_t(i)$$

which corresponds to decreasing weights $\theta_j = \lambda^j$ for lag $j$ going indefinitely into the past, with $|\lambda| < 1$.

On one level we are using the fast moving design for a simple design-based inference telling us only about the design itself. That is, the design is estimating its own unit inclusion probabilities in a current interval of time. But in doing so, current dynamic properties of the network are also being estimated. By its nature the design produces a sample process that spends a lot of its time with units that are well connected. A unit spending a lot of recent time in the sample is likely to be reachable by many sample paths from other units, including direct links and paths of length more than one. Conversely, that unit has a lot of paths out to other units. A unit with a high current value of the moving average $v_t(i)$ is a unit that, if it is sparked by an infection of a virus, is likely to result in a flame spreading to other units with the initial high transmission rate of early infection stage. Visually, in the dynamic network simulations one sees areas of high $v_t$ value, colored in shades of red, that are areas of above average probability of seeing a virus spread explosion. For this reason we refer to measures such as $v_t$ with the free-style link tracing set designs as “flame rank.”

## Results and Discussion

This study uses fast-moving idealized temporal network sampling designs to understand and anticipate the natural of natural network designs, such as those of infectious agents, and intervention designs used by human organizations and individuals to counteract those. The virus HIV adapts to an uneven, time-varying human sexual network by having a high transmission rate in the short early stage of infection and a low rate in the long chronic stage. The high early rate enables explosive spread in dense network clusters and, because of the trade-off between transmission rate and mortality rate of host, allows long survival between temporal clusters allowing some strains of virus to persist until another cluster is reached.
The flexible designs such as designs 1-3 in this paper spend much of their time in the areas of the network in which such explosions can occur. By averaging the inclusion indicators of these designs using moving average or exponential smoothing techniques, the designs provide a measure that highlights areas in which virus would spread fast if ignited by one or more initial infections. This useful in visual interpretation of simulation studies on intervention strategies, and suggests that designs of similar types could prove useful in distribution real-world interventions through temporally changing networks.

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