Dynamic spatial and network sampling
Steven K. Thompson
1 Department of Statistics and Actuarial Science, Simon Fraser University, Burnaby, BC, Canada
* E-mail: thompson@sfu.ca

This paper considers some designs for sampling and interventions in dynamic networks and spatial temporal settings. The sample spreads through the population largely by tracing network links, although random sampling or spatial designs may be used in addition. To investigate the effectiveness of different designs for finding units on which to make observations and introduce interventions is investigated through simulations. For this purpose a dynamic spatial network model is developed based on simple stochastic processes. The sampling processes considered have both acquisition processes and attrition process by which units are added and removed from the sample. The effect of an intervention introduced with a given sampling design is assessed by the change in the resulting equilibrium distribution or, in more detail, by the distribution of sample paths resulting from the intervention strategy.

Introduction

Sampling of populations that change in time involves a number of challenges. For populations having spatial structure, network relations, or both, additional challenges arise, along with features that a sampling design can take advantage of. Many of the hard-to-reach human populations are unevenly distributed in geographic or social space and at least partially hidden from view.

Dynamic network sampling refers to sampling designs for obtaining samples in dynamic networks as well as to dynamic designs for obtaining samples in static networks.

This paper describes an approach to evaluating the effects of interventions in epidemics and obtaining effective intervention strategies using network modeling and a sampling design approach to introducing potential interventions. Local intervention strategies to alleviate the HIV epidemic serve as the focus. For the purpose of evaluating combinations of strategies, a dynamic network model in constructed and simulations with interacting designs are analyzed. While relatively simple the modeling approach is powerful for the purpose. It includes variable factors of interest such as clustering, mixing, rates of change in relationships, social drift and change, stage-specific transmission rates, and changes in degree distributions. Interventions are introduced into this population through link-tracing and combination sampling designs, so that different ways of introducing them can be compared. The types of interventions to be compared individually and in combinations include ones that exist, such as access to condoms, promotion of reduced change rates in relationships or in numbers of concurrent relationships, access to combination antiretroviral treatments and adherence programs, and seeking earlier testing and treatments, and distribution programs for potential treatments that are not yet available, such as vaccines and treatments to clear the virus.

Flexible sampling designs termed generically dynamic network sampling are used for introducing the interventions into the population. The designs, which use a combination of link-tracing and other designs such as random sampling are described first in idealized form. These designs also serve as models for what happens in the real situations of contact-tracing, seek and treat, and various respondent-driven sampling procedures in which the actual procedures used are not completely controlled. Finally, but significantly, the class of designs serves as the model for how a virus such as HIV spreads in the population. In the statistical sampling literature a sampling design is generally characterized by a selection process for bringing units into the sample. These designs have in addition an attrition process by which units are removed from the sample. The stochastic balance between the selection and removal processes determine whether the sample is increasing, decreasing, or fluctuating in an equilibrium distribution. With a controlled sampling design this sample size distribution is determined by the investigators. In a design
such as seek and treat the largest possible sample size might be desired, but reaches natural limits based on increasing difficulties of contact tracing or participants dropping out of a program. In the case of a virus network sampling design, we can seek to intervene with our own design to decrease the rate of spread and drive the equilibrium distribution to the lowest possible level.

Static network models have been extended to the dynamic situation fairly recently by a number of approaches. [1–4] and [5] developed an interesting class of network evolution models based on behavioral characteristics of actors/nodes such as tendencies toward reciprocity, transitivity, homophily, and assortative matching. At the same time he developed inference methods to estimate model parameters from incomplete longitudinal data. A summary of this work together with a review of other approaches to dynamic network modeling is contained in [6]. [7] present a dynamic network model based on exponential random graph models. A recent summary of statistical network models is provided by [8].

The social space approach to network modeling is introduced in [9], using latent space models for (static) networks, and a simple dynamic extension of this approach is described by [10]. Spatial point processes with clustering tendencies have been used as the basis for simulations of stochastic graph models (static rather than dynamic) with which to evaluate sampling designs and inference methods by [11].

Design-based inference methods for link-tracing designs in networks have been developed in [12]. The current approach to likelihood-based inference with link-tracing designs was introduced in [13], developed for Bayes inference in [14], with Markov chain Monte Carlo computational Bayes inference used for adaptive web sampling designs in Kwanisai, M. (2005) [Estimation in Link-Tracing Designs with Subsampling. Ph.D. thesis. The Pennsylvania State University, University Park, PA, USA] and [15]. This approach was further developed used with additional models in [16]. Issues of inference in network epidemic models are additionally discussed in [17].

[18] describe empirical likelihood based confidence intervals for adaptive cluster sampling. [19] analyze weighting systems for estimation in indirect sampling, a class of adaptive network designs.

Approaches combining design and model based methods include the random walk asymptotics based estimators used with respondent driven sampling [20, 21, 22, 23, 24], and [12]. A different approach is used in [25] and [26]. A different approach still combining design and model based methods is developed in [27].

An approach bring network effects to epidemic compartment models by having different groups with different network degrees is described in [28]. Properties of networks in which relationships shift preferentially that are missed by static network epidemic models are examined in [29]. The stability of casual contact and close contact patterns over time was studied using diary based methods with 49 volunteers, finding that the close contacts tended to be more stable than casual contacts. Epidemic threshold properties of simple dynamic network models in which degree says constant but neighbors exchange, that is, identity of partners change instantaneously at random times are described in [30].

Compartmental models are modified to add some network effects in [31]. Network structure and change patterns in relation to individual behaviors were investigated in [32] for syphilis among young people and HIV among drug users, finding in both studies that spread of disease was associated with network cohesion, in the form of separation of components or local density of connections. [33] examine network effects in compartmental models by including a contact or mixing matrix into the model, comparing assortative mixing patterns, in which individual’s contacts tend to be within their own group and dissortative patterns, in which contacts tend to be between groups. Early work in modeling the dynamics of the HIV epidemic includes [34, 35, 36] and [37]. The importance of concurrent relationships in the spread of the HIV epidemic is investigated in [38] and [39].

The models for dynamic spatial network populations and interacting designs developed in work also have some relationship to the literature on evolutionary dynamics. [40] provides a summary of models of species interactions, epidemics, and selection based on systems of partial differential equations. [41] describe recent work on stochastic point process models built on top of that approach. Among the many cases of ecological systems exhibiting the sort of spatial, temporal, and network patchiness addressed by
the models and designs of this paper, a good example is described by [42].

[43] (Supplement 1) modeled the individual variability of adherence over time for an individual as well as the variability between individuals. Their model, used for the purpose of estimating parameters, is individual based but not network based except to the extent of having assumed degree distributions. [44] describes a modeling approach based on a set of partial differential equations with the addition of some temporal network aspects such as degree distributions in which contacts change, describing mean behavior for infinite network size and approximate behavior for moderate size. [45] presents opposing views of different authors on the relative importance of early stage transmission. [46]. [47] describe a network of 50,185 sexual contacts between 6,642 escorts and 10,106 sex buyers as reported on a Web discussion forum. Dynamic epidemic models showing selective advantage of virulent strains in early stage of an epidemic and advantage shifting to less virulent strains, which allow their host to survive longer, as the epidemic matures were compared to laboratory studies with colonies two competing strains of bacteria [48], finding agreement with the model predictions.

Methods

Dynamic network model

To investigate the effectiveness of different sampling and intervention strategies, a model producing a dynamic population network is required. For this purpose, the model does not necessarily need to include every possible detail of a population, but should include any relevant factor that affects the effectiveness of a design or strategy. We model the population as fluctuating yet stable, that is, existing in a stochastically fluctuating equilibrium, so that it provides a base for trying different intervention strategies and following the results through time, comparing those outcomes with those without the intervention. We want to model to be rich enough so that we can investigate the effects of different amounts of clustering, rates of change, mixing between groups, degree distributions, and other relevant parameters. The model is constructed in layers, each layer a simple stochastic process. First there is a time changing spatial process. This is a spatial point cluster process, in which the clusters or social groups drift in a social space and nodes within groups change position relative to each other over time. This approach is in the spirit of the the social space models of [9] and [10] but with the additional attributes such as clustering, mixing, social change, sex, degree dynamics, and population dynamics involving birth and death processes needed for the sampling strategy investigations. The motion of the points is based on small increments of diffusion yet is stable in the sense of maintaining the clustering over time. Links form and dissolve probabilistically over time based on distance between nodes and other factors including sex of node, current degree of node. The stochastic duration of nodes, or conversely the rate of change in relationships, is governed by a renewal process. In addition, an insertion and deletion process accounts for births, deaths, immigration, and emigrations of nodes from the study region and includes a population dynamics to keep the population size and even group sizes in an equilibrium distribution. This is the base population to which the interacting sampling strategies are applied.

Sampling designs

The type sampling designs we consider for obtaining an ongoing sample of units from the ever-changing population includes both a selection process and an attrition process. The selecting process is dominated by link-tracing, but to a lesser extent, and also at the initiation of sampling, units may be selected at random or by some other standard design such as a spatially distributed one. At time $t$ in the sampling process we have a sample $s_t$ of units or nodes. We trace a set of links out from that sample and add the linked nodes to the sample. Additional nodes may be selected by simple random sampling or some type of time-location sampling, though the probability of this may be small relative to the link-tracing
A simple but versatile class of designs in this type uses conditional Bernoulli link tracing. In these designs a link \((i, j)\) from node \(i\) to node \(j\) is traced with probability \(p_{ij}\), independently, given current values at that time step, of the tracing of other links. The tracing probabilities can depend on values of the origin and destination node or of the relationship between them and can change over time. The number of links followed at any time step is random and at many times may be zero. In addition to depending on individual nodes and links, the probabilities of tracing can depend on characteristics of the entire sample including current sample size.

Other designs in the class include tracing at most one link out from the sample at a given time step, or selecting a random sample without replacement of a target number of the nodes, tracing all of the links out if there are fewer of them than the target.

The attrition process by which nodes are removed from the sample includes, unavoidably in the dynamic setting, any deletions of nodes from the population due to deaths or emigrations. In addition, the attrition procedure may include removal of nodes from the sample without their deletion from the population.

Active sample units are those from which links, if available, can be traced. The sample may also include inactive units, such as people who are retained in the sample for treatment or follow-up interviews but from whom links will no longer be traced. The sample may be with-replacement or without-replacement. The concepts active and with-replacement are generalized to continuous variables between 0 and 1, where a value less than 1.0 represents dampening of the probability of tracing a link from that node or of selecting it again after its removal from the sample.

Sample size and its increase or decrease is controlled by the balance between the selection and attrition processes. In a seek and treat design it may be desired to have sample size as large as possible and to retain members in treatment. In a monitoring design for surveillance it may be desired to maintain a sample size near a target value, even as the individuals making up the sample change over time. This can be accomplished by adjusting the selection probability downward if the sample size is above target and adjusting it upward if sample size is below target. Similarly, rates of removal from the sample can be adjusted based on current sample size. With the seek and treat designs sample sizes tend to come into a stochastic equilibrium distribution over time as it becomes harder to find new cases or trace from them, as participants drop out of the sample, or budget constraints impose limits.

To understand what controls the equilibrium distribution of sample size over time it is useful to view some aspects of the network geometry of a link-tracing sample in a dynamic network. At any time point the sample has a node volume, which is the number of nodes in it, and a link surface, which is the number of links from nodes in the sample to nodes outside the sample. As sample size increases the ratio of surface to volume tends to decrease, with most designs of the type we consider. Partly this is because as sample size increases in a finite population and links are followed at some point there will be fewer links to follow. But the decrease in ratio typically occurs much earlier. One reason is that link-tracing design of the types considered here generally select units having high degree (many links) with high probability. As those units and their contacts come into the sample many of the links become contained in the sample and there become over time fewer links pointing out of the sample. Second, a node with degree \(d\) coming in to the sample through tracing of a link from a sample node, will have up to \(d - 1\) of its links pointing out of the sample. Units selected into the sample at a given time tend to have higher degree than is average for units in the sample and higher degree out of the sample than the average for sample units at that time. The more time it spends in the sample, the smaller the proportion becomes of its links that point out of the sample. For the sample as a whole, as the sampling progresses and sample size becomes larger, a higher proportion of links from sample nodes are internal to the sample, leaving a smaller proportion on the surface. Clustering of links in the population also affects the pattern of surface in relation to volume during the course of the sampling. The speed of growth of the sample depends on the number of links on its surface and the tracing rates of these surface links. The rate of attrition from the
sample, on the other hand, is related to the volume of the sample and the deletion and removal rates associated with those units. Thus as surface to volume ratio increases, the rate of acquisition relative to attrition decreases and the sample size comes into a stochastic equilibrium distribution. These effects are striking in simulation of various types of sampling designs, both human-designed ones and natural ones.

With link-tracing designs, the probability that a node is selected into the sample is usually higher for nodes having more links, or more or more links pointing in to them in the case of directed links. While there are exceptions to this, such as the uniform walk designs in Thompson (2006b), in almost all cases higher selection probabilities for nodes with higher degrees result naturally from the way the sample is selected.

With a dynamic population such as modeled here, in which nodes drift over time in an underlying social space, links form in relation to social distance and change over time, and nodes and links have some clustering tendencies, the speed of sampling in relation to this change has an effect on the type of sample that results. If the rate of link-tracing is very fast, then selection of the next \( k \) nodes, for \( k \) some fixed number, might tend to be all or most in the same cluster or highly connected. If the rate of link-tracing is very slow, the next \( k \) nodes are more likely to be spread out in social space and less highly connected with each other and include selections from different clusters.

**Example - HIV Epidemic**

A local population or community through which an epidemic of HIV spreads conceived as a dynamic network, with nodes representing people and links representing the types of relationships between people through which the virus can transmit. We think of the virus as having a dynamic network sampling design that selects a sample of people by following links, so that the current sample of the virus is the set of individuals in the population who are infected. By infecting a person the virus makes an intervention that affects not only the state of the person’s health but affects the temporal network structure of the population by affecting survival rates and with them, network connections over time. Per-act transmission rates, while generally low, are variable depending on stage of infection, specific nature of the contact act, and other factors. Since there is at present no treatment to consistently clear the virus from a person’s body the attrition process of the sampling design occurs with mortality or, from the perspective of the local modeling, when an individual moves out of the study community. In addition to link-tracing, nodes can come into the virus’ sample through immigration of an infected person into the study region or through “random” events such as a resident individual traveling outside the region and returning with an infection.

In terms of the sample design parameters used by the virus in spreading the epidemic, the design is without-replacement if we are considering only the increase in sample size as the measure of prevalence of the disease in the population. On the other hand, multiple infections do occur and can be modeled as with-replacement selection, which may of practical importance in terms of recombination events between different strains of virus. The transmission rate at reinfection may be lower than at an initial infection. Highest transmission rate occurs with early stage of infection, having a variable duration of several weeks. This is followed by a lower rate for a long period during chronic stage and possibly a higher rate later. In terms of design parameters this corresponds to the most active units in the sample, in terms of tracing rate, being those recently selected, with “active” being a continuous variable that changes over time. Membership in the sample and stage affect deletion rate through mortality and possibly affect emigration out of a study population also. Further, an increase in tracing rate is associated with an increase in deletion rate, when comparing different strains and different stages. Tracing/transmission rate from one node to another is affected by values of the origin node, the destination node, and the link or relationship between them. Finally, attrition from the sample occurs only with deletion from the population, so long as there is no practical cure for HIV available. With development and distribution of a functional cure, however, direct removal of a person from the sample would become a possibility.
Interventions to counter the spread of the virus are similarly conceived as being distributed to individuals in the community with a dynamic network sampling design that uses random or time-location sampling or a combination of procedures. Widely used procedures for bringing interventions, such as seek and treat designs using contact tracing and respondent driven sampling methods using coupons can be evaluated in this way. The ideal is to bring interventions in such a way that they benefit not only the sample individuals to which they are applied but the wider community by decreasing further spread. A seek and treat design might for example start with cases that are tested. If the test is positive, the links from that node are with some probability traced. When a link is traced, the node to which it leads is if possible tested. If the test is positive, interventions including combination antiretroviral drugs to improve health and decrease the rate of transmission onward can be prescribed along with counseling. If the test result is negative, interventions could include counseling and provision of barrier methods to decrease the probability of transmission in. When a vaccine becomes available that is even partially effective this is where it could be offered.

In terms of the sample geometry, tracing rates, and temporal speed of sampling described in the previous section for dynamic network sampling designs, the virus HIV appears to have a dual strategy. At times it can spread very fast, appearing in the simulations as a local explosion. And it can persist for long periods with low rates of transmission, while the sample over time spreads out socially and relationships change, until it encounters favorable conditions and ignites a new local explosion. One factor that makes this pattern possible is the high rate of transmissibility in the brief early stage of infection compared to the much longer lasting but lower transmission rate of the chronic stage. In an expansion in a cluster of high average degree, when a new node is infected, it enters the first stage. With the high transmission rate and locally high number of links around there is the possibility of one or more additional transmissions while the newly incident node is still in early stage. The result is that some, though not all, of the transmissions during the period of rapid expansion are from nodes in early stage, and the higher transmission rate of early stage catalyzes the local expansion. If early stage transmission rate is no higher than the chronic stage rate, local expansions still occur but require a higher density of links in a local cluster to have an effect. A local expansion cluster can also be catalyzed by a high latent transmission rate over its links. This could happen for example in a local concentration of a contributing infection such as a genital ulcer disease.

The most prevalent contributing factor to local explosive expansion is perhaps somewhat surprising and results from the dynamic network sampling design characteristics. At incidence, the person newly infected with HIV has on average a higher degree than is average for people in the population. This is a design property of link-tracing designs of this type. This is especially pronounced in early stages of the epidemic but persists even at equilibrium levels. More notably, in terms of surface and volume properties of the sample, the newly incident person tends to have a higher proportion of his or her links pointing to partners outside of the sample, that is to uninfected partners, compared to the average degree out for all infected cases. The degree-out at incidence tends to be higher even compared to the degree-out that the same individual will have after being in the sample for some time. This is because over time more of the persons contacts come to be infected, either from that individual or another since those contacts are in a high-risk area of social/network space. With the high degree-out of an incident node coinciding with the high transmission rate of early stage, the effects of the two factors multiply to increase the rate of spread of the virus and contribute to the pattern of local explosions. Once a local explosion has run its course there tends to be a period of low surface to volume ratio, and what links there are on the surface tend to be mainly from nodes in chronic stage, having low transmission rate but relatively long survival time. Those are the conditions under which a dynamic network sample tends to spread out the subsequent new selections in social/network space.
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