TemporalPrestige

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Introduction

Epidemiology is a subject of much contemporary relevance. Quarantine and case isolation have been shown to be effective policies to counteract pandemics (Auranen et al. 2023). Moreover, the successful trial of the "Covid-Card", for detecting potential transmission events, suggests that prophylactic identification and isolation of high-risk individuals could be practical in the future. The sociosphere of an individual can be modeled as a series of contact times, each paired with a measure of proximity. We abstractly represent each individual as a node, and each contact event by an undirected edge. This model is called a temporal network. The Susceptible-Infected model, abbreviated as SI, is an epidemiological model in which susceptible individuals can become infected due to a contact with an infectious individual. In the SI paradigm, we assume that infected individuals stay infected indefinitely. Social Network Analysis (SNA) is the study of individuals and their relationships with others. SNA involves constructing a network to model a real-world situation of interest, and calculating metrics related to the network structure. These metrics can be broadly categorized into two types: Population-level measures and Individual-level measures. Centrality is a commonly-used individual-level measure, defined as the influence of a particular individual within a network. Prestige (sometimes called status or rank) is a similar individual-level measure for directional graphs, which only considers incoming dyads.

To date, research on the SI model has largely been focused on computational simulations of many epidemics on a temporal network. In this paper, I propose several measures of prestige in temporal networks, and I apply them to the SI epidemiology framework.

Methods

Data Description

The CovidCard is a bluetooth device developed for detecting close-contact events between carriers. Each card advertises it's presence and detects signals from other cards. Algorithms evaluate the radio signal strength

indicator (RSSI) of close-contacts in real-time, and the signal strength is aggregated over 15 minute time intervals. Each interval was classified as either < 1 meter, < 2 meter and < 4 meter proximity, and the total number of intervals belonging to each class was summed over a two-hour period. The cards can hold up to 128 contact events in short-term cache memory at any given time, of which some are recorded in long-term flash memory. An interaction was recorded in flash memory if it was longer than 2 minutes in duration, and the RSSI exceeded -62dBm (roughly corresponding to a distance of less than 4 meters).

Data Preparation

The last day of the trial period saw an anomalously high number of close-contacts, most likely because participants congregated at a single location to return the cards. For this reason, contact events which occurred on the last day of the trial were omitted. Data which could not be cross-verified by case investigation was removed, and duplicate contact events were omitted.

Temporal Centrality

Generalization of conventional centrality measures to temporal networks requires a high-granularity representation of the network as a graph. Kempe, Kleinberg, and Kumar (2000) proposed a graph where the edge weights are contact times, however this model fails to account for differential rates of transmission. Kim and Anderson (2012) proposed a more general solution. Without loss of generality, consider a set of contact times, $t = (1, 2, 3, \cdots, T)$. We can construct a time-ordered graph, G, with vertices V and edges E, where for all $v_t, u_k \in V$, an edge $e(v_t, u_k) \in E$ can only exist if $k = t + 1$. We can construct this graph for any temporal network without loss of information. Figure 1 illustrates this idea for a simple temporal network. In practice, computational constraints may require aggregation of contact times and thus loss of information. Rocha and Masuda (2014) proposed a centrality measure which considers the stationary distribution of a random walk at time t, however this measure does not generalize well to the Susceptible-Infected (SI) model, where infection is a permanent state.

Define the distance of the temporal shortest path length over time interval [i, j], denoted by $d_{i,j}(v, u)$, as the smallest $d = j - n$, where $i \leq n \leq j$ and there is a path from v_n to u_j. Thus, in Figure 1, the shortest path distance $d_{1,3}(a, b)$ is two, with the temporal shortest path being a_1-b_2-b_3. By representing a temporal network as a high-granularity digraph, we can now generalize conventional measures of prestige and centrality to temporal networks.
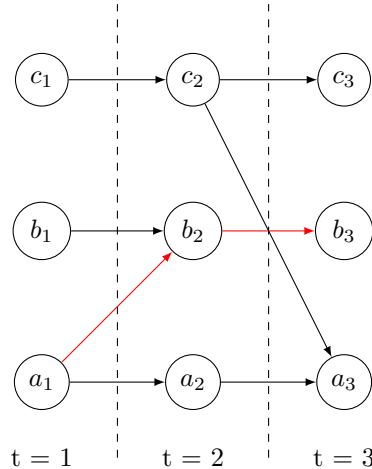

Figure 1: A simple temporal network represented as a digraph. The temporal shortest path from a to b is shown in red.

Temporal Prestige

In this study, I am primarily concerned with the likelihood of infection, which is closely related to the more general notion of prestige. In a directional network, a prestigious node is the object of many ties i.e. has many incoming connections. This is a distinct concept from centrality, which is also concerned with outgoing connections. Many conventional measures of centrality are ill-defined in directional graphs, owing to the fact that directional graphs are not necessarily strongly-connected. Due to this limitation, we usually only consider nodes in the influence domain of node i i.e. the set of all nodes from whom n_i is reachable. Lin (1976) proposed the following measure of prestige for directional relations, called the proximity prestige:

$$P_p(n_i) = \frac{I_i/(g-1)}{\sum d(n_j, n_i)/I_i} \tag{1.}$$

where I_i is the size of the influence domain of node i, and g is the total number of nodes in the network. For temporal networks, I propose a modified version

$$P_p(u_i) = \frac{I_{u/(g-1)}}{\sum_{v \in N} d_{0,i}(v, u)/I_u} \tag{2.}$$

where N is the influence domain of node u at time i. Intuitively, this is the proportion of the network covered by the influence domain, divided by the average temporal distance over the influence domain. When the influence domain is empty, the temporal prestige is 0. Kim and Anderson [2012] proposed temporal closeness, a similar metric which considers all time intervals $[t, i], t \in [0, i-1]$.

$$C_{i,j} = \sum_{i \le t < j} \sum_{u \in V} \frac{1}{d_{t,j}(v, u)} \tag{3.}$$

When u is unreachable from v over [t, j], $d_{t,j}(v, u) = \infty$. We cover cases where the denominator is infinite by assuming that $\frac{1}{\infty} = 0$. Note that as we are considering a directional graph, $d_{t,j}(v, u)$ is not equivalent to $d_{t,j}(u, v)$. To turn (3.) into a prestige measure, we simply reverse the direction of the paths to get:

$$C_{i,j}^P = \sum_{i \le t < j} \sum_{u \in V} \frac{1}{d_{t,j}(u, v)} \tag{4.}$$

We will call this the temporal prestige. The temporal prestige can be normalized by dividing by $(|V|-1)(j-i)$.

Temporal Proximity Prestige

Kim and Anderson (2012) showed that by considering all time-intervals, temporal closeness improves the quality of estimates in some situations. By this same token, we can modify equation (2.) to obtain

$$P_p(u_i) = \sum_{t=0}^{i-1} \frac{I_{t,i,u}/(g-1)}{\sum_{v \in N} d_{t,i}(v, u)/I_{t,i,u}} \tag{5.}$$

where $I_{t,i,u}$ is the influence domain of u over the time interval [t, i]. We will call this the temporal proximity prestige. The temporal proximity prestige can be normalized by dividing by i.

When each edge is associated with a probability of transmission, as is the case with epidemiology models, the probability of a path may be of greater interest than the temporal length. In this case, we can generalize existing methods by considering a digraph where the edge weights are the natural log of the probability. Figure 2 shows a graph of this kind.

In accordance with the specification of the Susceptible-Infected model, the probability of transmission from an individual to them self is assumed to be one, and hence the natural log becomes 0. This representation has several useful mathematical properties. Consider a path, P, starting at v_i and ending at u_j. The probability
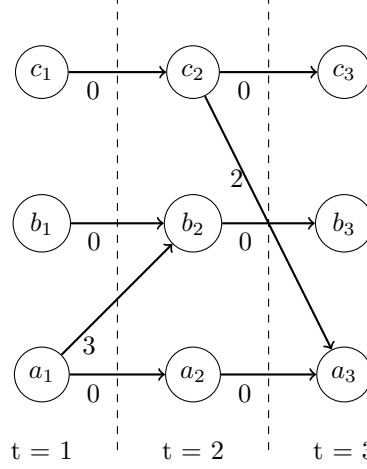
Figure 2: A simple temporal network represented as a digraph

of this path is equal to $\prod_{k=i}^{j} E_k$, where E is the list of transmission probabilities of path P. With edge weights on the log scale, the probability of path P can be calculated by:

$$e^{\sum_{w \in E} log(w)}$$

To generalize conventional notions of centrality, we need to define distance in terms of probability. For this reason, I propose a new measure of distance, which I call the stochastic distance:

$$d^{\mathbf{P}} = 1 - \sum_{w \in E} log(w)$$

Note that the stohastic distance ranges from 1 to ∞, therefore we can adjust equations (4.) and (5.) to get

$$C_{i,j}^{P} = \sum_{i \leq t < j} \sum_{u \in V} \frac{1}{d_{t,j}^{\mathbf{P}}(u, v)} \tag{4.}$$

and

$$P_p(u_i) = \sum_{t=0}^{i-1} \frac{I_{t,i,u}/(g-1)}{\sum_{v \in N} d_{t,i}^{\mathbf{P}}(v, u)/I_{t,i,u}} \tag{5.}$$

where $d_{t,i}^{\mathbf{P}}(v, u)$ is the shortest stochastic path distance between v and u over the time interval [t, i]. Note that the shortest stochastic path is not necessarily equal to the shortest temporal path, and thus we cannot use conventional algorithms for calculating geodesics. Nevertheless, it can be shown that all stochastic shortest paths to u_i can be calculated in $O(i|V|^2)$ time using a modified version of the Reversed Evolution Network (abbreviated as REN) algorithm proposed by Hanke and Foraita (2017).

Absorption Prestige

In this section, I propose an ad-hoc prestige measure for epidemiological study. Without loss of generality, we will consider a temporal network consisting of a set of nodes, N, and positive integer contact times, $t = (1, 2, 3, \cdots, T)$. Let $p_{ijk}(t)$ denote the probability of transmission for the k'th contact between individual i and individual j, at time t. Let $n_{ij}(t)$ denote the number of contacts between i and j at time t. Define the transition probability matrix for each contact time as:

$$\mathbf{B}_{ij}(t) = \begin{cases} 1 & i = j, s_i(t) = 0 \\ 0 & i \neq j, s_{ij}(t) = 0 \\ \prod_{m \in N, m \neq i} \prod_{k=1}^{n_{im}(t)} (1 - p_{imk}(t)) & i = j, s_i(t) > 0 \\ (1 - \mathbf{B}_{ii})(s_{ij}(t)/s_i(t)) & i \neq j, s_{ij}(t) > 0 \end{cases}$$

where $s_{ij}(t)$ and $s_i(t)$ are defined as:

$$s_{ij}(t) = 1 - \prod_{k=1}^{n_{ij}(t)} (1 - p_{ijk}(t))$$

$$s_i(t) = \sum_{j \in N, j \neq i} s_{ij}(t)$$

Denote by $\mathbf{B}_i(t)$ the transition matrix obtained by taking $\mathbf{B}(t)$, and setting all entries in the i'th row to zero, except the diagonal entry (which is necessarily one). The walk $\mathbf{B}_i = (\mathbf{B}_i(1), \mathbf{B}_i(2), \cdots, \mathbf{B}_i(T))$ is an absorbing random walk, and the product $C_i^A(t) = \mathbf{B}_i(1)\mathbf{B}_i(2)\cdots\mathbf{B}_i(t)$ will be called the temporal absorption prestige for individual i, at time t.

Example

A simple example network of five nodes is shown in Example_Network.csv. For simplicity, a constant transmission probability was used for all contact events. In total, 500 simulations were run on this network. The absorption centrality and the number of times infected were calculated for the final contact time. Table 1 shows the correlation between the absorption centrality and the probability of infection by the end of the simulation.

Table 1: Pearson correlation between temporal absorption centrality
and infected proportion over 500 simulations

	Correlation
p = 0.3	0.6649671
p = 0.2	0.6614322
p = 0.1	0.5206837

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