# Temporality is Important for Networks of Hospital Patient Transfers

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## Key Points

- There is a significant amount of patient movement in the Victorian hospital system where the patient returns home for a substantive amount of time between discharge from one hospital and subsequent admission at another hospital.
- This "indirect" movement has implications on the rate of spread of a hypothetical contagion through the hospital system. It causes dispersal of patients to be slower than expected.
- We can recover some of this behaviour by introducing an additional layer in the network to represent indirect movement.

## Introduction

Antimicrobial resistance poses a great threat to human health and development. [1] Globally, it poses a large burden, operationally and economically, on hospital systems. In Australia, we see [significant] economic burden from AMR. this impact could become more significant if we had incursion and subsequent establishment of new [strains] of AMR. One X of interest is carbapenemase-producing enterobacteriacea (CPE). Australia has an endemic strain of CPE – IMP4 – but this is at a relatively low level. This already causes some level of burden, and introduced strains would further multiply this.

Understanding of the spread of AMR through hospital systems has been studied in the past as a network phenomenon. The movement of patients through the hospital systems induced by referrals can be represented as edges between hospital nodes. However, these networks are usually presented as static, where movement over a large period of time has been aggregated to form a single network. It is known, especially in other applications, that temporal networks can display different behaviour than the static equivalents. In this paper, we investigate these differences using the Victorian hospital system as a baseline for comparison. In particular, we investigate the impacts of the inclusion of modelling the period

of time that patients spend at home between admissions, and the effect of approximating the granularity of the temporality]]]]].

# Methods

## Setting and data sources

<- yank from [2]

Admissions data is from the Victorian Admitted Episdoes Dataset (VAED).

Some exploratory analysis was done in by [2]

## Network Modelling

A network or graph $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ is made up of nodes or vertices $\mathcal{V} = \{v_1, v_2, ...\}$ and edges $\mathcal{E} = \{e_{ij} := (v_i, v_j)\}$ that join those nodes. Each edge $e_{ij}$ can be assigned attributes, including an edge weight $w_{ij}$. For our application, this edge weight will typically represent the number of observed movements in a given time period. Thus the network can encode a representation of the movement between hospitals over a given time period.

We can use the network to construct a Markov chain, where the expected rate of movement is governed by the observed movement in the data. For some edge $e_{ij}$ with a number of observed movements $w_{ij}$ over some time period $\tau$, the rate of movement along that edge $\lambda_{ij} = w_{ij}/\tau$, such that the time between movement events along that edge are exponentially distributed $\text{Exp}(\lambda_{ij})$.

[Stuff about previous implementations of this idea]

## Explicitly Temporal Models

Previous analyses of movement and spread of contagions through these networks have made the assumption that the weight $w_{ij}$ for a given edge does not change over time, i.e. the network is static. One advantage that the VAED provide us is the minute-scale granularity of patient admissions, which allows us to construct temporal networks and models of patient movement.

<- Description of temporal networks and models>

<- Description of temporally reductive networks and models>

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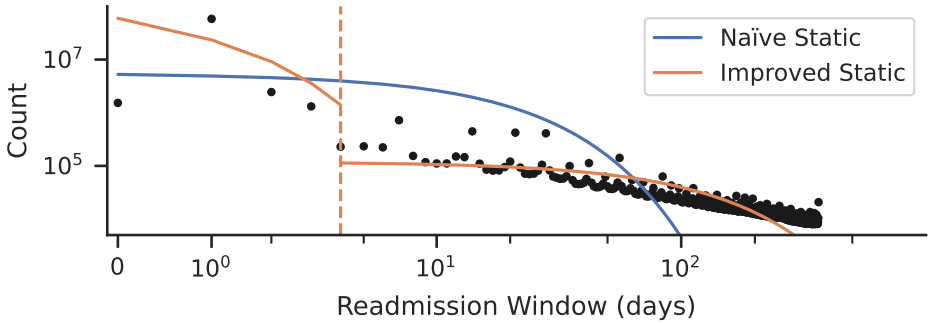


Figure 1: Distribution of readmission time (time between discharge and successive admission of a single patient)

### Networks and Projections

Patient transfers can be considered as edges from some source hospital $x_i$ at some time $t_m$ to a target hospital $x_j$ at some time $t_n$. We could work with the exact times, but this will lead to an overly sparse representation that is difficult to work with. Instead, we discretise time into bins by treating movements involving some arbitrary hospital $x_i$ between times $t_n$ and $t_n + W$ as instead involving a single node at $v_{i,n} := (x_i, t_n)$. Then we can have a temporal network that can be treated as a static network as in Section , i.e. we have edge weights $w_{ij}$ along the edge $e_{ij} := (v_i, v_j)$.

The network analysis of the temporal network as described above is computationally expensive since it is relatively large ($N_x = 388$ hospitals and $N_t = 259$ fortnightly bins, for $\approx 10000$ nodes). We can instead analyse slices of the temporal network, where a slice at $t_n$ consists of nodes at that time discretisation bin, and the related nodes.

### Dynamics

For the temporal network, we can model the number of patients discharged from some given location $(x_i)$ at a given time $(t_n)$ as a Poisson random variable with rate $\gamma(x_i, t_n)$. Some proportion $q(x_i, \emptyset)$ of these individuals will not re-admit at any other hospital, and can be removed from the system; the remaining discharged patients will have some probability $p(x_i, t_n, x_j, t_m)$ to re-admit at location $x_j$ at time $t_m$. These probabilites $p$ wil depend on the edges… Patients that have $t_i \neq t_j$ will be moved into an auxiliary state $z_{i,j}$… Movemnts $z_{ij}$ are distriuted as Uniform(0, W)

# Results

## A Reduced Model

For the naïve and improved static network models, we can compute the hitting times directly and compare them. We can model the dyanmics on these networks as a (continuous time) Markov Chain and extract the mean hitting time to any target hospital from all other hospitals.

A simplistic model of the effect of indirect transfer can be modelled with the following figures:

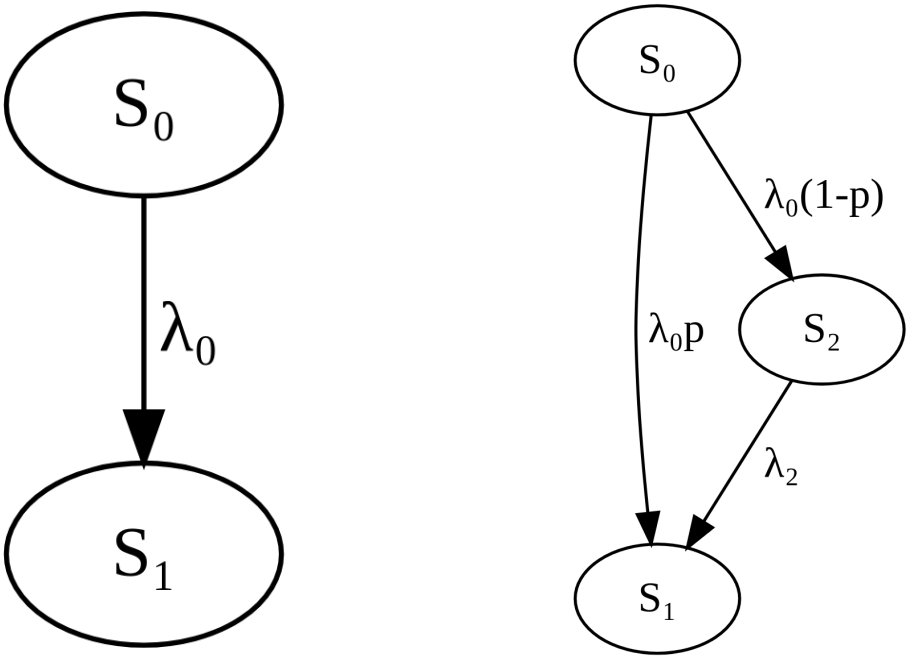


Figure 2: Toy model of the effect of indirect transfer on hitting time

In the model without indirect transfer, we can compute the expected hitting time $k$ from $S_0$ to $S_1$

$$k = {\lambda_0}^{-1}$$

In a model with indirect transfer, we introduce an additional state $S_2$ which represents the indirect pathway. If the probability of direct transfer is $p$ given that an individual will move out of $S_0$, and the average indirect transfer period is $T = \lambda_2^{-1}$, the we can compute the hitting time $k$ of $S_1$ given we start at $S_0$:

$$k = {\lambda_0}^{-1} + \frac{1-p}{\lambda_2}$$

i.e. the hitting time is increased by $\frac{1-p}{\lambda_2}$.

For a larger network, the number of possible paths causes complications for explicit computation of the effect, but we can always expect it to follow a similar principle, where splitting transfers into a direct path and a slower indirect path will add to the expected hitting time. These can be obtained by solving a linear system [3]. For the naïve static network, we can model the rate of movement from hospital $i$ to hospital $j$ as the mean number of observed movements over the observation period (XXX days). For the improved static network, we expand the state by including an additional state for each pair of hospitals, so that the residence time at home (between hospital admissions) for indirect transfers can be modelled. Then as with the naïve model, the movement from $i$ to $j$ directly is the mean observed number of transfers over the observation epriod. The indirect movements from $i$ to the intermediate $i, j$ state are derived from the observed number of movements, and the rate from $i, j$ to $j$ is derived from the mean readmission period (as seed in Figure 1).

Comparing the relative difference in the mean hitting times gives us Figure 3

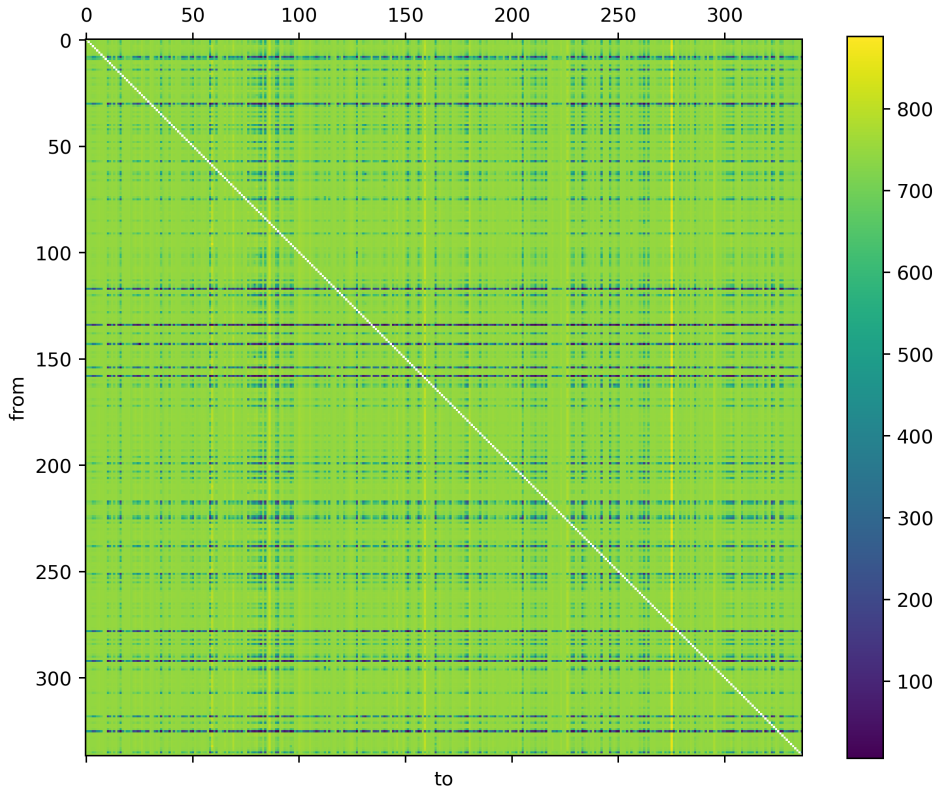


Figure 3: Relative difference between the expected hitting times for the naïve static and improved static models

### Movement Simulation Studies

We define the *extent* of a simulation by the number of facilities that some patient has moved to or through within a given number of days. We see in Figure 4 that we get starkly different distriubtions of extent for the naïve static model, commpared to the other models.

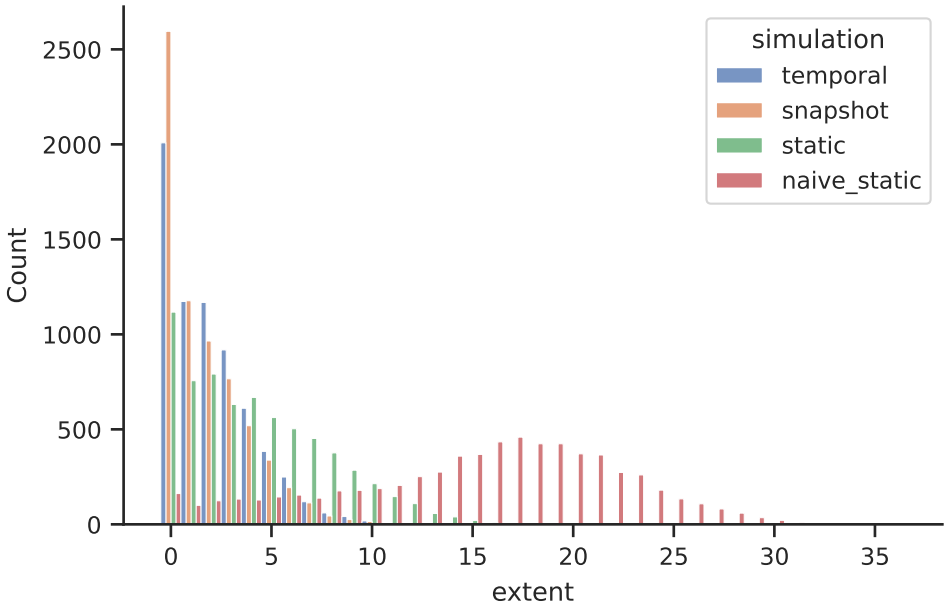


Figure 4: Distribution of 30-day extent in different simulation models on different network types

We can frame the empirical cumulative distribution (ECDF) of hitting times from a given seed hospital to a target hospital in a survival analysis view, and compare different experimental setups by comparing the ECDFs of the combinations of hitting times with log-rank tests. Each pair of hospitals yields a separate log-rank test statistic. Using a crude Bonferroni correction to counteract the multiple comparisons (which occur due to the $N = 338^2$ combinations of seed and target hospitals), we find that there are significant differences between each type of model. We note spikes at very low p-values when comparing the naïve static model to other models.

## Appendix

### Projecting the temporal network

We can project these causal edges by making their effects persistent in a hospital. This reduces the amount of information stored, so in theory should improve performance of simulations.

With a naive approach, an edge $(A, t_1) \to (B, t_2)$ can be decomposed into:

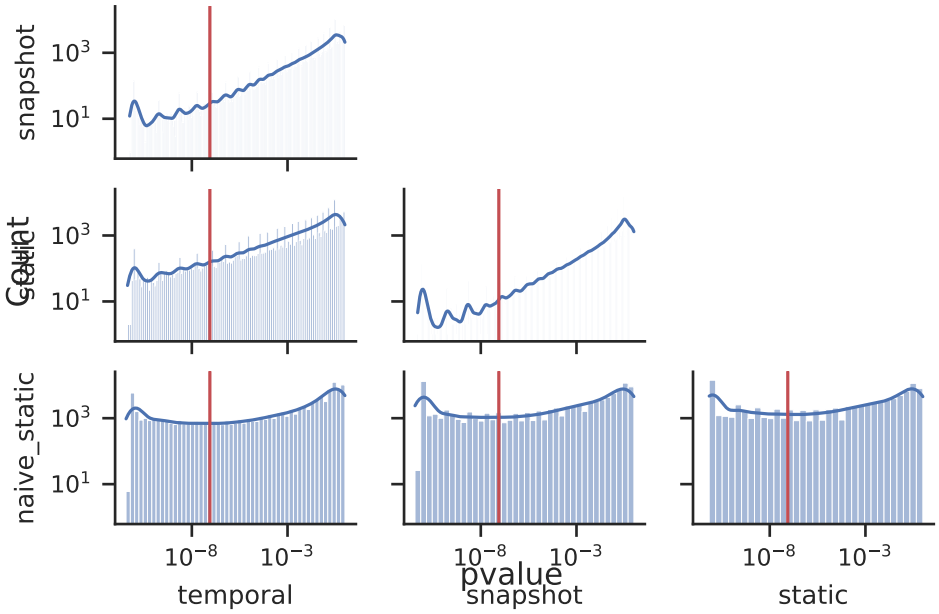


Figure 5: Log-rank test comparisons between experiments

1. $(A, t_1) \to (B, t_1)$ and $(B, t_1) \to ... \to (B, t_2)$
2. $(A, t_1) \to ... \to (A, t_2)$ and $(A, t_2) \to (B, t_2)$

This causes an implied increased infection pressure at certain hospital nodes. This sort of projection also loses specificity of temporal causality. By inspecting the temporal network that results from this projection, you cannot tell if a patient is moving from $t_1$ to $t_2$ or to $t_3$.

There is also a mechanistically distinct projection, where we introduce "home" nodes for each facility. For some facility $A$, the home node is denoted $A'$. Thus we could also project the edge as

- $(A, t_1) \to (A', t_1)$ and $(A', t_1) \to ... \to (A', t_2)$ and $(A', t_2) \to (B, t_2)$.

This is an ideal projection, but is difficult to achieve. Specifically, it is difficult to control the duration that an individual spends in the home node. However, this projection still loses temporal causal specificty, as above.

We project the temporal network into a series of multilayer networks. Instantaneous movements (consisting of direct hospital-hospital transfers) make up one layer; movements from hospital to home make up another layer; and movements from home to hospital make up the third layer. By doing this, we can more accurately capture the time that a patient spends at home between hospital visits, but without explicitly tracking individuals (just the number of patients along each path).

## Simulation Details and Model

We keep records of two sets of states:

1. $n(t, x)$, the current number of infected at location $x$. This represents individuals in hospital.
2. $u(t, x, y)$, the current number of individuals that came from location $x$ and will depart for location $y$ at some point in the future. This represents the number of people at home.

Each snapshot can be considered a graph composed of vertices $V$ that correspond to locations, and have edges $E$.

Edges of the temporal network, $e(x, s, y, t)$ from location $x$ at time $s$ to location $y$ at time $t$ with some weight $w$ can be decomposed:

1. if $s = t$, construct an edge $e(x, y)$ with weight $w$
2. if $s \neq t$ construct two edges:
    1. $e_o(x, y, s)$ if it doesn't exist, and add weight $w$
    2. $e_i(x, y, t)$ if it doesn't exist, and add weight $w$

We can alternatively conceptualise this as decomposing the temporal edges into movements to a "home" node for each pair of hospitals. The edges $e_o(x, y, s)$ can be conceptualised as an edge between $x$ and a new "home" node denoted by the ordered pair $(x, y)$ at time $s$.

## Searching snapshots for information on unlikely paths

We observed some empirical simulated hitting time survival curves that suggested that paths that did exist and were likely on the temporal network did not exist or were very unlikely on the equivalent snapshots. This seems confusing, since the snapshot representation *should* represent a superset of possible movements.

## Approximations made with the Static Network

A standard static network consists of a single layer of nodes and edges. In order to capture patients leaving and then subsequently returning to hospital, we model the network with two layers: a "standard" layer represeting 'direct' transfers, and a secondary layer representing indirect transfers. This secondary layer is bipartite in nature, where each (potential) edge in the primary layer is represented by replacing it with a "home" node, and adding two additional edges to it: one from the original source node to the home node, and another from the home node to the original target node. This is implicitly captured in the network data structure by setting two additional edge attributes that represent the amount of flow on each of the two new secondary layer edges respectively.

We remove self-loops from the static network; we attempt one model without self-loops in only the direct layer (since this does not make physical sense), and another without self-loops

in both the direct layer, and the indirect layer (we uspected that these self-loops slowed the movement of individuals down, but the resulting effect is the explosion of movement in the first simulation step)


1. Murray CJL, Ikuta KS, Sharara F, Swetschinski L, Aguilar GR, Gray A, et al. Global burden of bacterial antimicrobial resistance in 2019: A systematic analysis. The Lancet. 2022;399: 629–655. doi:10.1016/S0140-6736(21)02724-0

2. Lydeamore MJ, Donker T, Wu D, Gorrie C, Turner A, Easton M, et al. Carbapenemase-producing enterobacterales colonisation status does not lead to more frequent admissions: A linked patient study. Antimicrobial Resistance & Infection Control. 2024;13: 82. doi:10.1186/s13756-024-01437-x

3. Norris JR. Markov Chains. Cambridge University Press; 1997.