# The impact of social networks and coordinated destination choice on the spread of epidemics using Episim

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### SHORT SUMMARY

Person-to-person contact is fundamental to the spread of epidemics. Human mobility is important for understanding the pattern of person-to-person contact. Therefore, understanding human travel behavior is crucial to the understanding of the geographic spread of infectious diseases. Transportation models built to give details on human movement and contact can then be used to simulate epidemic spread. Such has been done in the epidemic model Episim. In addition, there is also research showing people's social networks have strong influence on their travel behavior, such as destination choice. Therefore this study sets out to verify whether adding social network and coordinated destination choice to the epidemic model has impact on the spatio-temporal transmission progression of epidemics. Results show that though the total number of infections do not change, the addition of a social network and coordinated destination help capture during what kind of activities infection events are taking place. Coordinated travel with social networks contribute to a more rapid spread in the beginning. Moreover, results emphasize that social networks should be integrated in conjuncture with joint-travel to better capture social travel behavior and in turn epidemic spread.

**Keywords**: agent-based modeling, epidemic modeling, social networks, transportation network modeling

# **1** INTRODUCTION

Human mobility, like many other aspects of human behavior, is socially driven. In recent years, the transportation modeling field has increasingly tried to capture the undeniable link between social connections and travel behaviorKim et al. (2018). Various elements of travel behavior, including the creation of travel activities, choice of destination and mode of transportation, amongst others, are affected by social connections (Kim et al., 2018). Person-to-person contact is crucial to epidemic spread models. Since social networks can strongly influence travel behavior and contact patterns, it is beneficial to add in social networks when using travel demand models to simulate disease spread.

Previous researchers have used agent-based epidemic models to better understand and predict the spread of infectious diseases in Singapore (Sun et al., 2014; Mo et al., 2021), the Twin Cities (Bóta et al., 2017; Hajdu et al., 2020) or Berlin (Müller et al., 2020). Epidemic transition models varied from the simplest Susceptible-Infected model (SI), in which agents are exposed only while traveling (Hajdu et al., 2020), to the more complex Susceptible-Exposed-Infections-Removed (SEIR) model with exposure while traveling and at destinations (Müller et al., 2020; Mo et al., 2021). On the other hand, travel demand generation was rather simplistic, as it replicated transit trips (Bóta et al., 2017; Hajdu et al., 2020) or smart-card bus trips (Sun et al., 2014; Mo et al., 2021). A notable exception is Müller et al. (2020), who replicated activity-based trajectories from mobile phone data and used traffic and transit assignment in MATSim. Furthermore, Müller et al. (2020) validated the results of Episim with COVID-19 hospital cases in Berlin.

Social connections could potentially affect many aspects of travel behavior and by extension travel demand modeling. Socially connected people may share destinations, which has been seen in the studies by van den Berg et al. (2010) and Moore et al. (2013). Moreover, Ronald et al. (2012), Ma et al. (2011) and Dubernet & Axhausen (2015) presented an agent based system which integrate joint decision-making mechanisms based on rule based simulations of a bargaining process, but none have integrated and implemented a social network in a complete travel demand model framework.

In addition, none of the studies have explicitly considered the impact of social networks in epidemic

spread. This research seeks to fill the gap by adding in a synthesized social network to the process. As a first step, we focus on adding coordinated destination in travel demand generation, and infection rules influenced by social connections in Episim to see the impact of social network on infection spread patterns and rates.

# 2 Methodology

In order to simulate the epidemic spread, we generate travel demand with the open-source microscopic transportation orchestrator (MITO) (Moeckel et al., 2020), which we later assign to the road and transit networks using the Multi-Agent Transport Simulation (MATSim) (Horni et al., 2016). The event files from MATSim are later fed into Episim (Müller et al., 2020) that runs for an entire year.

The base input data for any agent-based model is the synthetic population, specifically, the synthetic population for the Munich metropolitan area. It comprises 4.5 million persons in 2.3 million households, but lacks social networks and group quarters (Moreno & Moeckel, 2018). For this research, a social network and nursing homes are implemented. The social network is built for the Munich metropolitan area. We also utilize the social network in conjunction with rule-based coordinated destination in the travel demand generation to account for joint destination.

This section summarizes the generation of the social network, the incorporation of the social network into MITO for coordinated destination, and the incorporation of the social network into Episim.

#### Geolocation-based social network

We generate a geolocation-based, ego-centric social network for the study area. They are so-called personal social networks or egocentric networks, consisting of an ego or focus point, connected to alters, e.g. family members, co-workers, etc. Due to the lack of relevant collected data on social network structures in the area, the network is currently built on characteristics present in the synthetic population. As such, the generated network reflects a degree of homophily and reciprocity.

Homophily describes how like attracts like, that people tend to be socially connected with those similar to them. Reciprocity is how social connections are bi-directional. If A is friends with B, then B is friends with A. However, it does not take into account the transitivity property of social networks, which means that if A is a friend of B, and B a friend of C, then A would also have a higher chance of being friends with C.

Type of social tie	Edge build criterion	Average degree
Household	From same household	2.2
Neighborhood	Share dwelling location and dwelling type	2.5
Education	Attend same school, same age	9.5
Work	Share job location and job type	5.5
Nursing home	Share nursing home location	10

Figure 1: Network type and build criterion

The social network is currently built on five kinds of relationships, household, neighborhood, education, work and nursing home. Those who reside in the same household are connected to each other. Those who share the same dwelling location and a similar dwelling type, such as single-family-unit, are socially connected. Those who attend the same school and are of the same age are presumed to be socially connected. Those who share a job location and job type have a chance of being socially connected. Residents in the same nursing home also forge social connections with each other. For neighborhood, education, work and nursing home locations, social connections are built using a small-world network algorithm with a maximum clique size of 10. Social connections forged from household, neighborhood, education or work categories are built with the criteria indicated in Figure 1. Figure 1 also shows the average degree forged in each type of social tie using these criteria. For example, a person attending school is on average connected to 9.5 others who attend the school with them. A person's total social connections comprise of connections from all five of these relationship types.

#### Travel demand model and rule-based coordinated destination

The second part of this study uses an agent-based travel demand modeling suite to generate daily movements of individuals. To achieve this, the synthetic population with the geolocation-based social network were fed into MITO (Moeckel et al., 2020). MITO is an agent-based travel demand model that uses econometric statistical models to estimate trip generation, trip distribution, mode choice, and time of day for each individual in the synthetic population. After that, MATSim (Horni et al., 2016) is used as a dynamic traffic assignment model to assign car trips to the road network and simulate public transport trips on the transit system (Swiss Federal Railways, 2020). The individual movements are estimated for a typical 24-hour day for the following trip purposes: home-based work (HBW), home-based education (HBE), home-based shop (HBS), home-based other (HBO), non home-based work (NHBW) and non home-based other (NHBO).

This study extended MITO by adding the rule-based coordinated destination choice. In Figure 2 the modifications to the existing MITO model sequence is shown. After the Trip Distribution step, we add an Arrival Time Choice step in which we compare the trip list of an agent with the trip lists of those in their social network. Compatible trips are defined as trips that have arrival times within six hours of each other, and are of the same purpose. We also give a hierarchy to coordinated trips depending on social network type. Agents prioritize coordinating with household members, then with coworkers or schoolmates and lastly with those from the 'neighbor' social connection type. If compatible trips are found, we then proceed to the next step, Destination Coordination. In this step, the destination and arrival time of the trip belonging to the agent's social connection is set to be the same as the agent's.

After any changes of destination have been made to the trip, the mode choice is ran without any modifications. The departure time can then be calculated based on the chosen mode and projected travel time.



Figure 2: MITO modified model sequence

#### Epidemic spread model Episim

Episim is an infection dynamics model build on top of a person's movement trajectories as developed by the Sebastian Müller et al. at the Technical University of Berlin (Müller et al., 2020). It allows testing of intervention policies such as home-office mandates, mask-wearing mandates, etc. Episim is comprised of several models, the contact model, infection model, and disease progression model (Müller et al., 2020). The contact model defines who comes into contact with whom. Persons at the same location or facility can come into contact and infect each other. These facilities could either be in transit or at an activity location such as home or work. When two persons come into contact, a probability of infection is calculated using the infection model, which gives this probability based on contact intensity, contact duration, viral shedding and intake. If a person becomes infected, the disease progression model then gives the probability that this newly exposed and infected person progresses to the next stage of the disease. The exposed person can become infectious, recover, or get worse. The simulation runs for a year or until no more infections occur. For more details on Episim, please refer to (Müller et al., 2020).

To see the effect of social networks on epidemic spread, we extended the Episim model to account for social networks. Firstly, the contact model was modified. This contact model looks at agents when they leave a facility. Instead of randomly selecting other agents who are at the facility at the same time, we increased the likelihood of being selected if they belong to the same social network. Secondly, we changed the infection model parameters to consider that persons in the same social network may reduce social distancing, and therefore, the viral load may be increased. This is accomplished by increasing the contact intensity factor. For contacts from within the agent's social network, the contact intensity is multiplied by a factor of 10. Short of observed data, this factor is an exogenous assumption that ensures a higher infection rate within social networks. The current contact intensities and infection probabilities are set according to those specified in (Müller et al., 2020) for the COVID 19 virus.

#### Scenarios

By varying the addition of social network and coordinated destination choice, we look at a total of four scenarios, as seen in Figure 3.

Episim rules MITO rules	Randomly selected maximum of three contacts	Selection priority given to social network, maximum three contacts	
No coordinated destination	Base	Base.SocialNetwork	
With coordinated destination	Coordinated	Coordinated.SocialNetwork	

Figure 3: Scenario description



Figure 4: Episim contact rules for different scenarios regarding social network

In the *Base* scenario, for an agent at a certain location/facility, a maximum of three contacts are randomly selected from those who are at the same location and the same time as the agent. This number is the base assumed setting in the calibrated Episim Berlin scenario (Müller et al., 2020). The infection probability is calculated between the agent and each of these three contacts. This is graphically represented in Figure 4, in the left box.

In the *Base.SocialNetwork* scenario, similarly, a maximum of three contacts are selected, but selection priority is given to those within the agent's social network. If there are less than three contacts at the location in the agent's network, then random agents are selected until there are three contacts. This is seen in the right box in Figure 4.

The above scenarios are then repeated, but with a travel demand that now takes into account coordinated destination choice based the social network. To reduce model runtime, all scenarios are ran for a 5% scaled-down population for computational time savings. The social network is generated after scaling down. Episim results are reported after upscaling factors to 100%.

#### 3 Results and discussion

Epidemic spread with and without social networks, with and without coordinated destination are compared. The main hypothesis is that the total number of infected persons would not vary, as agents perform the same number of activities. But the spatial and temporal distribution is expected to be affected by the presence of social networks and coordinated destination choice. For example, we would be able to better capture the outbreak in nursing homes or large employment centers; reducing contact at such hotspots may be more sensitive to interventions than limiting social contacts in general.



Figure 5: Number of infections from day 1 to day 50

In the Figure 5, the Episim total infected curve for the Munich region for each of the four scenarios is shown. As expected, the total number of infections do not vary much between each scenario. The trajectory and the peak of the graph are only slightly staggered. We zoom in on the first 14 days of the epidemic outbreak in Figure 6.



Figure 6: Daily number of infections



Figure 7: Number of infections by infection location and social network status

Figure 6 shows the day-by-day number of infection events for each scenario. In addition, the figure shows the proportion of infection events between socially connected agents (dark gray) and between strangers (light gray). At this more micro-temporal scale, we see that coordinated destination scenarios have a quicker start compared to the base scenarios, with infections in Coordinated.SocialNetwork scenario spreading most rapidly. Within the Base and Coordinated scenarios, the scenario with social-network contact rules also spread faster than scenarios without. This figure also shows that the early disease transmissions tend to be from social contacts. Once the epidemic is more wide spread, infection events between strangers begin to make up the larger proportion. Infections from the social network scenarios with social network contact rules have a higher share of being infected by someone within their social network.

We then break down the infection events by activity type. Figure 7 shows the proportion of infection events from the social network and from strangers. The proportion of infection from social network ties increased for Coordinated Destination scenarios compared to the Base scenarios in the Other, Recreation and Shopping activities. The addition of coordinated destination choice captures how non-essential leisure activities may be conducted together with friends, family and acquaintances, and captures the disease transmission that may happen as a result. Without coordinated destination, agents would seldom meet others in their social network, whereas activities like home, work, education and being in a nursing home usually guarantees that agents are in the same location as someone from their social network.

Figure 8 shows the percentage of infection from social network contacts per total number of infections. The addition of social networks has increased the share of infections that come from social network ties. The Coordinated.SocialNetwork scenario has the highest proportion of social network related infection events.

Scenario	Base		Coordinated	
	Random contacts rule	Social network contact rule	Random contacts rule	Social network contact rule
Home	23.3%	33.3%	22.8%	32.2%
Work	4.0%	7.2%	3.9%	6.9%
Education	1.6%	3.3%	1.6%	3.2%
Nursing	0.2%	0.8%	0.2%	0.8%
Other	0.1%	0.3%	2.3%	5.1%
Public transit	0.0%	0.0%	0.0%	0.0%
Recreation	0.0%	0.0%	0.1%	0.1%
Shopping	0.0%	0.0%	0.0%	0.0%
Total	29.2%	44.9%	30.9%	48.3%

Figure 8: Percentage of infection from social network contacts per total number of infections

The percentage of infection from social network contacts per number of infections varies by activity purpose. For example, in Base.SocialNetwork and Coordianted.SocialNetwork scenarios, social network in nursing homes only account for 0.75% of total infections, because the population of nursing homes is rather small. However, social network ties account for a big proportion of infections occurring in nursing homes, as seen in Figure 6.

# 4 CONCLUSIONS

We combined a simple synthesized social network with an agent-based travel demand model and epidemic spread model to see possible effects on epidemic spread patterns. Our social network and coordinated travel, though simplistic, demonstrate that social networks have some influence on disease spread patterns. It can affect how fast the disease spreads, and where disease is spread.

Future research should focus on implementing more comprehensive joint travel logic based on social network connections in the travel demand model, as the scenarios with coordinated travel showed a marked effect on epidemic spread compared to those without. Another angle for refinement is the social network. Currently the social network is based on shared home, neighborhood, work or education locations in the synthetic population. The next iteration can include social connections outside of household, neighborhood, education and work. These connections can reflect general

friendship and social ties. In addition to homophily and reciprocity, this social network can incorporate the transitivity properties of social connections. Nevertheless, this research presents a novel coupling of synthesized social networks, travel demand modeling and epidemic spread modeling. It demonstrates a way to model human connections in human movement, and how an epidemic travels through the human network.

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