Travel Demand Models for Micro-Level Contact Network Modeling

Diaoulé Diallo, Jurij Schönfeld, and Tobias Hecking

German Aerospace Center (DLR)
Linder Höhe, Cologne 51147, Germany
`diaoule.diallo@dlr.de`

Abstract. In the pursuit of accurate infectious disease forecasting, micro-level contact modeling in contact networks emerges as a pivotal element. This research delves into the intricacies of nuanced micro-level modeling, presenting adaptable models tailored for specific locations, derived from a refined travel demand model. In our experiments, we observed that varied encounter patterns among individuals directly influence infection dynamics. Additionally, we observe distinct trends in the spreading dynamics between temporal dynamic networks and their static counterparts for certain encounter models. The study underscores the need for a deeper appreciation of micro-level encounter patterns in epidemiological modeling. Such understanding is pivotal in shaping effective interventions and public health strategies during pandemic scenarios.

Keywords: contact networks, micro-level encounter modeling, mobility data, pandemic research, temporal networks

1 Introduction

Mobility is fundamental to epidemic research, as it leads to the formation of complex contact networks through people's spatial encounters at various locations. Such contact networks offer insights into epidemic dynamics and therefore mitigation strategies, and public health policies [1–3, 5].

The significance of contact networks became particularly evident during the global COVID-19 pandemic, where researchers focused intensely on leveraging these networks to both characterize and forecast the spread of the virus [4,15,20]. The essence of interactions was elegantly encapsulated within these networks, providing a macroscopic view of transmission dynamics. It is noteworthy that these networks predominantly operated at a macro scale, often dealing with high-level representations, such as compartments or similar abstractions.

However, mobility data on a microscopic level are hard to obtain especially because of technical difficulties and privacy reasons. Recognizing the need for agile responses, we put forth a range of resource-efficient, adaptable, and parameterizable methods designed for modeling individual encounters within distinct locations as temporal dynamic networks.

We explore techniques for micro-level contact modeling with agent-based simulation based on traffic demand models and conceptualize the underlying techniques. A micro-level contact denotes the actual physical encounter between individuals. In this context, we deploy temporal dynamic networks, grounded by various encounter models and distinct types of locations derived from a travel demand model. Precisely capturing low-level encounters forms a valuable part that seamlessly integrates into comprehensive models, augmenting the precision of epidemic forecasting and characterization. Beyond the global context, this research also opens up promising avenues for individual infection risk approximation. The incorporation of location-induced variations in infection risk into digital contact tracing strategies holds substantial potential, advancing the way we approach contact tracing and containment efforts. In the future, travel demand models may serve as a foundational resource for rapidly generating temporal dynamic networks, enabling their versatile application in pandemic response and related endeavors.

The subsequent sections of this paper unfold as follows: section 2 sheds light on methodologies employed in micro-level encounter modeling. Following this, the methodology section initially explores temporal dynamic networks, then proceeds to introduce general distinct approaches to modeling micro-level contacts. The results section compares the outcomes of the three techniques we have employed. Finally, the conclusion section encapsulates the overarching findings and implications that emerge from our study.

2 Background

Two large pandemic simulation models OpenABM [9] and Covasim [11] use the concept of multi-layer networks to generate contact networks for different daily life scenarios (school, work, household, ...). Both models were used to investigate COVID-19 dynamics and test different intervention strategies. The multi-layer network approach makes use of census data to build a synthetic population on an urban scale. Contacts are generated by different models representing different types of interactions and environments in daily life. Covasim generates fully connected networks within households, small world networks on the community and work level, and disconnected clique networks representing classes. Similarly, OpenABM employs fully connected networks at the household level, random networks for communities, and small-world networks for occupations. Both models understand the necessity for different micro-level approaches in different locations. However, they choose different and quite simplistic approaches in the same scenarios, proving the need for further research on that topic.

A study conducted by [12] harnessed mobility data to construct micro-level person encounters. This approach considers temporal intersections of individuals at locations, as well as the type of location. The authors differentiate three location types with each being associated with three basic transmission probabilities. A final edge transmission weight is computed by combining the location-dependant transmission risk and a score derived from the intersection time of two individuals. However, for any given location, the edge weights are solely dependent on intersection times, overlooking the spatial attributes of the location and individual movement patterns.

Müller et al. [16] used mobile phone data for agent-based epidemiological simulations including factors like masks and air exchange rates. To model micro-level contact encounters, the approach divides locations into subspaces of predetermined capacity, giving rise to a contact network characterized by cliques. While this leads to a sophisticated model for location-based person-to-person encounters, it requires access to mobile phone data and does not fully account for the diverse encounter patterns that different location types exhibit.

The dynamics of disease spreading in various indoor environments has also been explored by several studies using sophisticated simulation techniques [7,13, 17,22]. Notably, these investigations have aimed to provide insights into transmission patterns and infection potentials in specific settings where a high amount of information is available. However, the effectiveness of such approaches relies on available and accurate information, e.g. layout, structure, and architecture of the location under investigation, which limits its applicability to settings with varying spatial configurations.

Up until now, the landscape of micro-level contact modeling has been characterized by two predominant trends: network generators that mainly rely on time spent at locations as well as the associated capacities and complex physical simulations necessitating substantial data and computational resources for agent-based modeling. While the former overlooks important interaction dynamics, the latter is resource and data-intensive and may not be feasible in many scenarios.

In the following section, we outline approaches for capturing location-specific encounter patterns based on traffic-demand models without the need for physical simulations.

3 Methodology

In this section, we detail the methodologies foundational to our exploration of micro-level encounter modeling using temporal-dynamic networks. We begin by illuminating the essence of temporal-dynamic networks. Subsequently, we introduce three distinct approaches for micro-level contact modeling.

3.1 Temporal-dynamic contact networks

Temporal-dynamic networks serve as a sophisticated framework that reveals the ever-changing nature of interactions among individuals [10]. In contrast to static networks, which offer a snapshot of connections, temporal-dynamic networks capture the intricate evolution of relationships over time. This real-time depiction introduces a higher level of realism, as interactions are not treated as fixed entities but rather as dynamic occurrences. Temporal-dynamic networks prove invaluable in epidemiological studies, as they grant insights into the spread of diseases over time [14]. By incorporating time-varying edges, these networks portray the varying transmission potentials at different stages of an epidemic. This precision empowers researchers and policymakers to devise strategies for disease containment and control more effectively.

Temporal-dynamic networks present interactions as evolving sequences, not mere snapshots [19]. While dynamic networks are gaining traction in pandemic research, many studies still rely on static networks due to their computational simplicity. Although static networks can suffice when disease dynamics align with network changes, they can introduce biases. Such biases arise when aggregating variable dynamic contacts, leading to misrepresentations in potential infection paths. It is debated that static networks might intensify infection dynamics. Contrary some cases are known where temporal correlations accelerate the dynamics of stochastic processes in dynamic networks compared to their static equivalent. In [18], SIR simulations were performed on an empirical temporal network of sexual interactions, to investigate the spreading of sexually transmitted infections. Their findings suggest that especially in the early pandemic stage, temporal correlations in the network accelerate infection dynamics leading to higher outbreak sizes, compared to different variations of static network representations. For a deeper understanding, our study examines both dynamic networks and their static counterparts.

In this study, we generate temporal-dynamic micro-level contact networks from mobility data, typically presented as a collection of trajectories that depict the movement of nodes between various locations. Within the realm of contact networks, our focus is on trajectories that conclude at a specific location. We also consider the time elapsed until the subsequent trajectory relocates our node to another location. Based on this, we construct the vector

$$V(t) = (v_1(t), v_2(t), \ldots, v_i(t), \ldots, v_{N_V}(t))^T,$$

representing all nodes, where $v_i(t) = 1$ if node i is present at our location at time t, and $v_i(t) = 0$ otherwise. Here, N_V denotes the total number of nodes.

In the most general description of a micro-level contact model

$$\theta : V(t) \to A(t),$$

one takes $V(t)$, which is modulated by mobility data, and uses the contact network model θ to generate the edges of the dynamic network. $A(t)$ represents the time-dependent adjacency matrix, where $a_{i,j}(t)$ is set to 1 if nodes i and j are connected at time t. The equivalent static network consists only of a single adjacency matrix, where $a_{i,j}$ holds the time fraction nodes i, j where in contact during the day.

In the following, possible realizations of the model θ are introduced. These are based on previous work on micro-level contact networks discussed in section 2, and adapted to data resulting from travel demand models.

3.2 Mobility data

To generate mobility data, we employ the TAPAS (Travel and Activity Patterns Simulation) travel demand model [6]. TAPAS offers a comprehensive framework for simulating future transportation demand scenarios. It takes into account various factors such as demographic changes, income structures, and transportation infrastructure.

The foundation for TAPAS is empirical spatial and structural data, details related to how individuals allocate their time, and specifics regarding transportation mode preferences. This data is drawn from the "Mobility in Germany" (MiD)[1] survey, which collected detailed information from over 316,000 individuals across 156,000 households. This data encompasses activity types, durations, socio-demographic attributes, and household transportation resources. The synthesized data produced by TAPAS results in 24h of data. At each location, individuals are identified along with their arrival and departure times. For our experimental purposes, we selected four specific locations. Two of these locations, A and B, are associated with leisure activities, while location C represents a workplace and location D stands for a school.

To conduct a comprehensive SIR simulation across several days, we address the challenge posed by the availability of accurate mobility data for just one day. Our approach involves stacking the temporal contact network data from this single day to simulate a continuous span of 20 days. While this method doesn't fully capture the stronger fluctuations and long-term spreading potentials that may emerge among communities and individuals over time, it serves our primary purpose effectively. Our main interest lies in uncovering general topological differences exposed by SIR simulations across various modeling approaches. By extending the available data in this manner, we can gain valuable insights into the impact of micro-level encounter modeling on the broader epidemic dynamics.

3.3 Micro-level contact modeling

Baseline approach $\theta_{baseline}$: Our baseline approach builds upon the work of Klise et al. [12]. In essence, this method leverages mobility data and individual-specific time allocations at specific locations to compute intersecting time frames between individuals, subsequently constructing contact networks.

In this approach, individuals present at the same location are linked by edges in a contact network, with edge weights determined by the shared duration of their presence. Transforming this concept into a temporal dynamic network, we establish edges connecting pairs of individuals who coincide at a given point in time within the same location (see 3.1). Under this premise, our approach assumes an equal likelihood of infection for any pair of individuals who share the same duration of stay at a location. In other words $\theta_{baseline}$ constructs a fully connected network between all nodes active at time t. This simplified framework

---

[1] https://bmdv.bund.de/EN/Services/Statistics/Mobility-in-Germany/mobility-in-germany.html

forms the foundation of our exploration, serving as a reference point against which we compare our more intricate modeling techniques.

Random graph-based approach θ_{random}: In our random graph-based approach, similar to [9], every possible edge, meaning that node i, j are present at the location at time t, is selected with probability p_{random}. Additionally, a contact duration is drawn from an exponential distribution with mean β. Contacts, therefore, have a minimum duration of one time step and, in the case of non-consecutive contacts, a mean duration of $1 + \beta$ time steps. This distribution accounts for the variable nature of interaction durations, resulting in a dynamic and realistic representation of human encounters. A possible application would be in locations where interactions are mainly random and short, like in supermarkets, where the case of two individuals being in close proximity for the entire shopping trip is rather unlikely, however frequent but short contacts are to be expected.

Clique-based approach θ_{clique}: This approach capitalizes on the concept of forming cliques to model micro-level encounters, advancing the clique-based strategy of [16]. By grouping individuals into these compact clusters, we create an efficient representation of contact networks within specific environments. This approach is particularly useful for capturing interactions in places with constrained capacity, like offices or classrooms. First, individuals are assigned to spaces within the location, with fixed size $N_{PeoplePerSpace}$. Nodes enter the location and their respective space according to $V(t)$, forming tightly bounded cliques. For contacts between different spaces at every time step, a node changes its space with probability p_{clique} for a duration that is drawn from a normal distribution $\mathcal{N}(\mu, \sigma)$. Afterwards, the node goes back to its default space.

By modeling and tracing movements within these spaces over time, we identify instances of shared occupancy. These instances lead to the formation of cliques, where individuals have pronounced edges connecting them within the clique, reflecting intensive interactions like in shared offices or classrooms. In contrast, connections outside the clique are rare, mirroring more sporadic or distant interactions. The underlying idea of this approach is to encapsulate the nuanced interplay between spatial arrangements and interpersonal encounters. This modeling technique ensures a more comprehensive understanding of how individuals' interactions are influenced by their physical proximity within specific locations.

3.4 Unveiling topological properties with SIR model

To assess the topological differences introduced by our various micro-level contact network modeling approaches, we employ the Susceptible-Infectious-Recovered (SIR) model [8]. The SIR model is a well-established compartmental model used to analyze the spread of infectious diseases within a population. It divides individuals into three compartments: susceptible (S), infectious (I), and recovered (R). The SIR model tracks the transitions of individuals between these compartments based on their interactions and the disease's transmission dynamics. For our evaluation, we utilize a temporal dynamic SIR model implemented using the

Tacoma framework[2]. Tacoma provides a versatile platform for studying epidemic spreading and other dynamical processes on networks utilizing the Gillepsie algorithm [21]. We let the epidemic spreading simulations run for a simulated period of 20 artificial days. During this time, we monitor the progression of the infection within the population and observe how different modeling approaches influence the spread of the disease. This SIR-based evaluation allows us to gain insights into the impact of micro-level encounter modeling on the topological properties of contact networks and the resulting epidemic dynamics. By analyzing the simulated disease propagation under different scenarios, we can draw conclusions about the importance of accurately representing individual interactions for understanding and managing the spread of infections.

In our research, it is crucial to recognize that the distinctive nature of our various approaches inherently results in networks from the same location having varied edge counts but identical node counts. The baseline approach, as described in 3.3, exhibits a markedly higher mean degree. To ensure a valid and unbiased comparison using a SIR model, we assume that the interaction strength is constant across all networks, i.e.

$$\sum_{t,i,j \in E_{baseline}} w_{i,j}(t) = \sum_{t,i,j \in E_{random}} w_{i,j}(t) = \sum_{t,i,j \in E_{clique}} w_{i,j}(t) = 1$$

where E is the respective set of edges generated by the contact network model. This is achieved by normalizing the adjacency matrix $w_{i,j}(t) = \frac{a_{i,j}(t)}{N_E}$ with the total number of edges N_E during the day creating weighted edges. The experimentation involved adjusting the transmission probability parameter to show sufficient infection dynamics across all networks. SIR runs were performed with this transmission probability and with respect to the edge weights. This methodology guarantees a meaningful assessment of the impact of different network topologies on the dynamics of disease propagation, even when the networks exhibit varying edge counts by definition.

4 Results

In this section, we present our results on micro-level contact network modeling using mobility data. We first describe the mobility data utilized and then discuss our experimental results. For all experiments, we selected $N_{PeoplePerSpace} = 15$, $p_{clique} = 0.01$, $\mu = 10$, $\sigma = 5$. These parameter choices were informed by preliminary experiments and explored in Section 4.2.

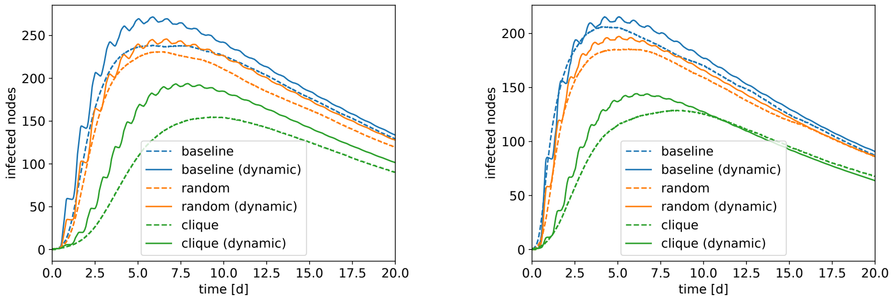
4.1 SIR-based evaluation

The outcomes of the SIR simulation conducted over a span of 20 days are presented in Figure 1. The vertical axis on the graph represents the number of individuals infected per day. Evidently, the baseline approach exhibited the highest

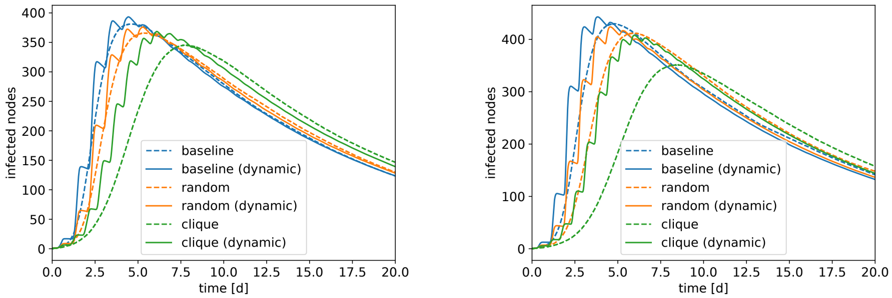
---

[2] https://github.com/benmaier/tacoma

infection count, followed sequentially by the random and clique approaches. This consistent trend was observed across all examined locations. Importantly, the distinctions among the approaches go beyond just the highest infection count, also encompassing differences in the rate of spread. For both, locations A and B, it becomes evident that the peak of the clique approach occurred around days 7-8, whereas the baseline approach reached its highest point at approximately day 5. The work/school locations C and D show similar trends but the difference in infections and speed between the approaches is less emphasized.



(a) Location A. (b) Location B.



(c) Location C. (d) Location D.

Fig. 1: Comparison of infection dynamics in SIR simulation across multiple locations and contact modeling approaches. Number of infected nodes on the y-axis, number of days on the x-axis. $N_{PeoplePerSpace} = 15$, $p_{clique} = 0.01$, $\mu = 10$, $\sigma = 5$.

Essentially, we find variations in the extent and speed of infection dynamics across the selected locations, which can be tied to the nature of each location. For instance, individuals tend to spend less time at locations A and B, which are associated with leisure activities, compared to those representing a school or a workplace. Crucially, the distinct contact models shaping encounter patterns play a significant role in influencing the spreading dynamics within the constructed contact networks.

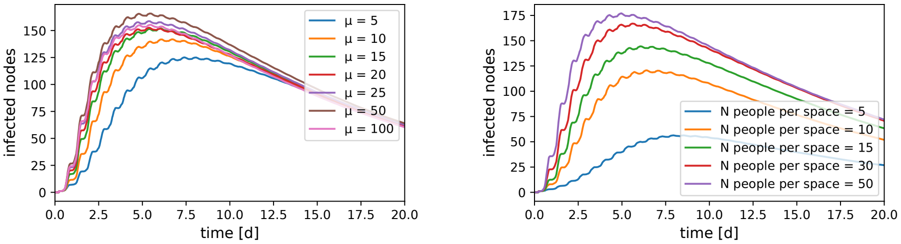
The difference between dynamic and their respective static networks depends on the chosen model. For our baseline, as well as the random approach, we see that both networks behave similarly in terms of infection dynamics. The clique approach instead shows a significant acceleration of the infection dynamic in dynamic networks, resulting in a higher and earlier infection peak as well as a higher outbreak size. This further supports the findings from [18]. Their sexual encounter network is described as a network with many cycles and compact weekly connected cliques, resulting from spatial constraints. This network could be modeled with our clique approach.

The actual efficacy and adaptability of these models necessitate further validation, either through empirical data or simulation studies. Nevertheless, these models serve as starting point and aim to lay the groundwork for fast and adaptable generation of micro-level contact models.

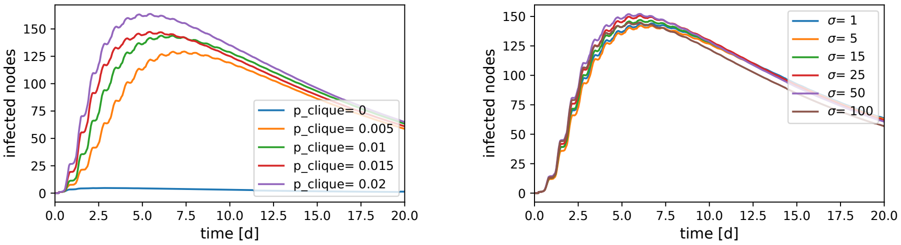
4.2 Effect of hyperparameter settings

Figure 2 demonstrates the effects of various hyperparameters associated with the clique-based approach on the SIR results for location B. Except for the parameter under investigation, we maintain consistency with the experiments detailed in section 4.1. Figure 2a reveals the influence of the mean parameter μ. Elevated μ values correlate with a rise in total infections and a decelerated infection spread. The same trend surfaces when observing the number of individuals per space, $N_{PeoplePerSpace}$. Infections peak around 50 for $N_{PeoplePerSpace} = 5$ and approximately 170 for $N_{PeoplePerSpace} = 50$. Likewise, figure 2b shows that alterations in the probability of space change p_{clique} lead to varying infection outcomes. As expected, larger probability values result in higher infection counts, while minimal space changes yield minimal infections. The absence of space changes restricts inter-clique infections, resulting in substantially lower infection dynamics. Conversely, fluctuations in the σ parameter exhibit minimal impact on infection dynamics, as figure 2d shows. Since this parameter influences the time individuals spend in other spaces without directly affecting encounter numbers, it appears to play a less pronounced role in driving infection dynamics. Upon inspecting the network resulting from θ_{random}, the hyperparameters showcased minimal perturbation on the outcomes. Our experiments revealed negligible effects for β and only minor variations observed in the infection dynamics for p_{random}. When exploring values for p_{random} spanning from 0.001 to 0.5, a notable reduction in infection rate was evident at 0.001, while the remaining values demonstrated relatively comparable results. Notably, $p_{random} = 0.02$ exhibited the highest infection rate, closely followed by 0.3. Neither the contact duration nor the number of edges (under the normalizing factor) appeared to exert a significant impact on the network's topology.

In essence, the results indicate that constrained spaces and diminished interactions among occupants lead to reduced infection propagation. This observation is independent of the sheer edge count since the transmission probability between nodes is normalized as explained above. The deviation in outcomes stems from the unique topological traits of the temporal contact network, reflecting varying encounter dynamics. Our research accentuates the pivotal role of assumptions surrounding encounter patterns and consequent transmission dynamics in dictating infection trajectories. Utilizing contact networks constructed from comprehensive data sources, like mobility data, reveals the importance of real-world contact patterns in epidemiological modeling.



(a) Varying μ (b) Varying $N_{PeoplePerSpace}$



(c) Varying p_{clique} (d) Varying σ

Fig. 2: Parameter exploration for temporal contact network resulting from θ_{clique}

While our study has provided insights into the behavior and characteristics of temporal contact networks, limitations need to be acknowledged. Our current method of stacking these networks doesn't capture long-term dynamics of infection spread. While our choice of an SIR-based evaluation provides a foundation, the process of normalizing temporal networks introduces complexities, as the "overall infection potential" is differently interpreted. Distinct characteristics between temporal and static networks are subject to future investigations and underpin the relevance of temporal dynamic network modeling. While our approach offers promising avenues for future research, its broader applicability needs cautious consideration and further refinement.

5 Conclusion

In this study, we explored micro-level contact network modeling and its implications for understanding disease spread. The goal was to showcase how the choice of micro-level contact models within specific locations influences infection dynamics. Our findings highlight the significance of tailored contact models for different locations and the crucial role of encounter patterns in shaping infection dynamics. Employing travel demand models in understanding infection dynamics paves the way for flexible and modifiable contact models. This research underscores the complexity of real-world contact patterns in epidemiological modeling, emphasizing the need for nuanced approaches to inform public health strategies. The orchestration of multi-tiered contact networks necessitates authentic portrayals of human mobility on both macro and micro scales, enriching our competence in offering precise infection risk assessments to individuals.

Future research directions include refining transmission probability modeling by considering contact distance through human mobility models that emulate actual human movement patterns. Furthermore, analyzing long-term data spanning more than 24 hours can reveal longer-term effects and pave the way for the generation of even more accurate temporal contact networks. Additionally, we aim to develop a versatile, parameterizable model applicable to various location types to enhance its adaptability and usefulness in epidemiological investigations.

References

1. Duygu Balcan, Bruno Gonçalves, Hao Hu, José J. Ramasco, Vittoria Colizza, and Alessandro Vespignani. Modeling the spatial spread of infectious diseases: the GLobal epidemic and mobility computational model. *Journal of computational science*, 1(3):132–145, 2010.
2. Benjamin D. Dalziel, Babak Pourbohloul, and Stephen P. Ellner. Human mobility patterns predict divergent epidemic dynamics among cities. *Proceedings of the Royal Society B: Biological Sciences*, 280(1766):20130763, 2013. Publisher: Royal Society.
3. Stephen Eubank, Hasan Guclu, V. S. Anil Kumar, Madhav V. Marathe, Aravind Srinivasan, Zoltán Toroczkai, and Nan Wang. Modelling disease outbreaks in realistic urban social networks. *Nature*, 429(6988):180–184, 2004. Number: 6988 Publisher: Nature Publishing Group.
4. Josh A. Firth, Joel Hellewell, Petra Klepac, Stephen Kissler, Adam J. Kucharski, and Lewis G. Spurgin. Using a real-world network to model localized COVID-19 control strategies. *Nature Medicine*, 26(10):1616–1622, 2020. Number: 10 Publisher: Nature Publishing Group.
5. Laura M. Glass and Robert J. Glass. Social contact networks for the spread of pandemic influenza in children and teenagers. *BMC Public Health*, 8(1):61, 2008.
6. Matthias Heinrichs. TAPAS: Travel-activity-pattern simulation - parallelisiertes mikroskopisches verkehrsnachfragemodell. In *Next GEneration Forum 2011*, pages 74–74. Deutsches Zentrum für Luft und Raumfahrt e.V., 2011.
7. Arvin Hekmati, Mitul Luhar, Bhaskar Krishnamachari, and Maja Matarić. Simulating COVID-19 classroom transmission on a university campus. *Proceedings of the National Academy of Sciences*, 119(22):e2116165119, 2022.

8. Herbert W. Hethcote. The mathematics of infectious diseases. *SIAM Review*, 42(4):599–653, 2000.
9. Robert Hinch, William J. M. Probert, Anel Nurtay, Michelle Kendall, Chris Wymant, Matthew Hall, Katrina Lythgoe, Ana Bulas Cruz, Lele Zhao, Stewart, and et al. OpenABM-covid19—an agent-based model for non-pharmaceutical interventions against COVID-19 including contact tracing. *PLOS Computational Biology*, 17(7):e1009146, 2021. Publisher: Public Library of Science.
10. Petter Holme and Jari Saramäki. Temporal networks. *Physics Reports*, 519(3):97–125, 2012.
11. Cliff C. Kerr, Robyn M. Stuart, Dina Mistry, , Romesh G. Abeysuriya, Katherine Rosenfeld, Gregory R. Hart, Rafael C. Núñez, and et al. Covasim: An agent-based model of COVID-19 dynamics and interventions. *PLOS Computational Biology*, 17(7):e1009149, 2021. Publisher: Public Library of Science.
12. Katherine Klise, Walt Beyeler, Patrick Finley, and Monear Makvandi. Analysis of mobility data to build contact networks for COVID-19. *PLOS ONE*, 16(4):e0249726, 2021. Publisher: Public Library of Science.
13. Bokyung Lee, Michael Lee, Jeremy Mogk, Rhys Goldstein, Jacobo Bibliowicz, Frederik Brudy, and Alexander Tessier. Designing a multi-agent occupant simulation system to support facility planning and analysis for COVID-19. In *Designing Interactive Systems Conference 2021*, pages 15–30. ACM, 2021.
14. Jack Leitch, Kathleen A. Alexander, and Srijan Sengupta. Toward epidemic thresholds on temporal networks: a review and open questions. *Applied Network Science*, 4(1):105, 2019.
15. Feng Liu, Xin Li, and Gaofeng Zhu. Using the contact network model and metropolis-hastings sampling to reconstruct the COVID-19 spread on the “diamond princess”. *Science Bulletin*, 65(15):1297–1305, 2020.
16. Sebastian A. Müller, Michael Balmer, , William Charlton, Ricardo Ewert, Andreas Neumann, Christian Rakow, Tilmann Schlenther, and Kai Nagel. Predicting the effects of COVID-19 related interventions in urban settings by combining activity-based modelling, agent-based simulation, and mobile phone data. *PLOS ONE*, 16(10):e0259037, 2021. Publisher: Public Library of Science.
17. Mardochee Reveil and Yao-Hsuan Chen. Predicting and preventing COVID-19 outbreaks in indoor environments: an agent-based modeling study. *Scientific Reports*, 12(1):16076, 2022. Number: 1 Publisher: Nature Publishing Group.
18. Luis E. C. Rocha, Fredrik Liljeros, and Petter Holme. Simulated Epidemics in an Empirical Spatiotemporal Network of 50,185 Sexual Contacts. *PLOS Computational Biology*, 7(3):1–9, March 2011. Publisher: Public Library of Science.
19. Kieran J. Sharkey, Carmen Fernandez, Kenton L. Morgan, Edmund Peeler, Mark Thrush, James F. Turnbull, and Roger G. Bowers. Pair-level approximations to the spatio-temporal dynamics of epidemics on asymmetric contact networks. *Journal of Mathematical Biology*, 53(1):61–85, 2006.
20. Stefan Thurner, Peter Klimek, and Rudolf Hanel. A network-based explanation of why most COVID-19 infection curves are linear. *Proceedings of the National Academy of Sciences*, 117(37):22684–22689, 2020. Publisher: Proceedings of the National Academy of Sciences.
21. Christian L. Vestergaard and Mathieu Génois. Temporal gillespie algorithm: Fast simulation of contagion processes on time-varying networks. *PLOS Computational Biology*, 11(10):1–28, 10 2015.
22. Fabian Ying and Neave O’Clery. Modelling COVID-19 transmission in supermarkets using an agent-based model. *PLOS ONE*, 16(4):e0249821, 2021. Publisher: Public Library of Science.