

COUPLING MULTIPLE SCALES OF AGENT-BASED MODELS: SUPERSPREADING AND EFFECTS OF TRANSMISSION CHAIN INFORMATION LOSS

Sascha Korf^{1,2}

¹Institute of Software Technology, Dept. of High-Performance Computing, German Aerospace Center, Cologne, GERMANY

²Institute of Bio- and Geosciences, IBG-1: Biotechnology, Forschungszentrum Jülich, Jülich, GERMANY

ABSTRACT

During emerging epidemics, surveillance systems typically detect aggregate case counts but lack detailed transmission chain information (on time), forcing epidemic modelers to make assumptions about initializing their models. This work quantifies how missing transmission chain information affects agent-based model predictions. Our approach couples two agent-based models: Vadere (Rahn et al. 2024) generates detailed superspreading scenarios, providing (synthetic) ground truth data for initialization comparisons, while the MEmilio-ABM (Kerkmann et al. 2025; Bicker et al. 2025) conducts epidemic simulations on a larger scale of districts. We investigate two scenarios representing restaurant and workplace outbreaks. We see that initialization through a detailed micro-simulation creates substantial differences in epidemic trajectories over 10-day simulations in comparison to traditional uniform distributed initialization. Results demonstrate that uniform initialization approaches systematically bias epidemic predictions, with differences up to 46.0% in cumulative infections. This highlights the importance of transmission chain reconstruction in outbreak investigations.

1 PROBLEM DESCRIPTION AND RESEARCH OBJECTIVES

The SARS-CoV-2 pandemic underlined the importance of early-stage epidemic modeling for public health decision-making. Agent-based models serve as versatile tools for analyzing disease spread and evaluating interventions, yet they face several challenges. In particular, when detailed transmission information is unavailable, assumptions about ongoing dynamics have to be made for the initialization. Contact tracing systems can identify outbreak participants but rarely reconstruct complete transmission networks, creating uncertainty about how infections cluster within social groups such as households or workplaces. Current modeling practice typically initializes infections uniformly across the susceptible population, assuming random distribution when precise transmission chains remain unknown. Although initialization sensitivity has been recognized in epidemic modeling (Ódor et al. 2021), existing work has not yet, to our knowledge, thoroughly quantified the specific impact of replacing uniform distribution assumptions with detailed transmission chains in agent-based models. We hypothesize that detailed transmission chain data containing social clustering information lead to systematically different epidemic outcomes compared to uniform initialization, with differences persisting throughout epidemic progression.

2 METHODOLOGY: MODELS AND COMPARATIVE MODELING FRAMEWORK

The Vadere exposure model tracks individual agent positions and movements in spatial environments such as rooms or buildings, where infectious agents emit aerosol clouds containing pathogens that diffuse spatially over time. Susceptible agents become infected based on cumulative pathogen exposure from their precise location relative to these clouds. The MEmilio-ABM simulates agents moving between discrete locations (households, workplaces, schools) in cities or even big regions, where transmission occurs when agents share the same location, based on viral load dynamics and contact patterns. To isolate the effects of missing transmission chain information, we develop a three-stage comparative framework: Stage 1: Vadere

generates detailed superspreading scenarios with complete transmission tracking, capturing precise who-infected-whom relationships during outbreak events. Stage 2: Two initialization approaches extract different information levels from Stage 1 results: transmission-informed initialization preserves exact information, while uniform initialization distributes infections randomly across event participants, simulating typical surveillance limitations. Stage 3: Both approaches initialize identical 10-day MEmilio-ABM epidemic simulations in a synthetic 1000-person German city district. We evaluate two outbreak scenarios: one restaurant event (89 agents) where agents from at most two households sit at the same dining table, and one workplace event (26 agents) with limited mixing from different workplaces. Each scenario begins with one infectious agent, generating complete transmission chains that enable direct comparison of how initialization assumptions affect subsequent epidemic predictions.

3 RESULTS

Infection Curves: Transmission-Informed vs Uniform Initialization

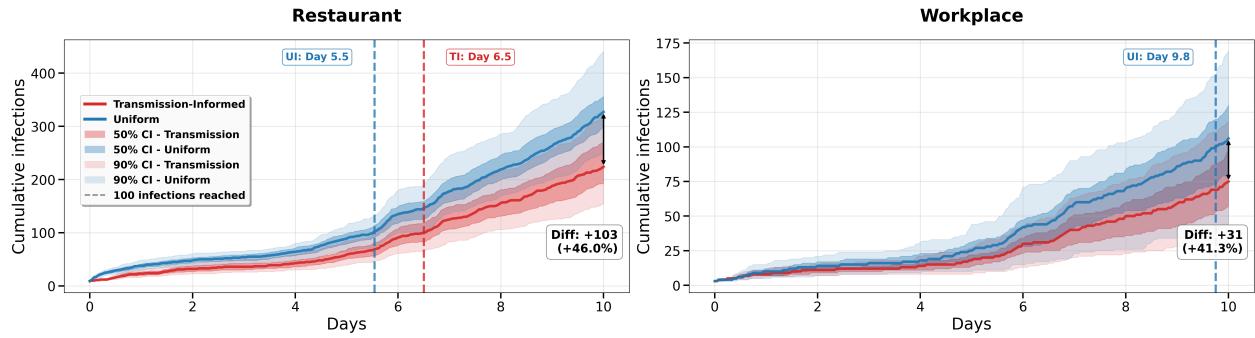


Figure 1: Inflection curves.

For the scenarios, Vadere simulations reveal that infections after the outbreak scenario are highly clustered within households for the Restaurant Scenario and within workplaces for the Workplace Scenario (Figure 1). Now, uniform initialization consistently produced higher cumulative infections than transmission-informed initialization across both scenarios, with differences of 41.3% for the Workplace Scenario and 46.0% for the Restaurant Scenario by day 10. Uniform initialization reached 100 infections 1.0 days earlier in the Restaurant Scenario than transmission-informed approaches. These findings demonstrate that conventional uniform initialization tends to overestimate epidemic spread when transmission exhibits social clustering, with bias magnitude correlating inversely with clustering strength. This implies that surveillance efforts should strengthen transmission chain tracking capabilities to enhance the initialization of ABMs. Alternatively, the potential systematic overestimation from uniform initialization approaches may be considered by modelers. Future research could develop initialization strategies that better preserve transmission network structure when complete contact tracing data is unavailable.

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