






FacilityEpiSim: an agent-based simulation package for infectious disease transmission in healthcare facilities

Damon J. A. Toth^{1,2}, Willy Ray^{1,2}, Om Sanghvi³, and Karim Khader^{1,2}

¹ University of Utah, United States^{ROR} ² VA Salt Lake City Healthcare System, United States^{ROR} ³ Hillcrest High School, Utah, United States  Corresponding author

DOI: [10.xxxxxx/draft](https://doi.org/10.xxxxxx/draft)

Software

- [Review](#) 
- [Repository](#) 
- [Archive](#) 

Editor: 

Submitted: 06 February 2026

Published: unpublished

License

Authors of papers retain copyright and release the work under a Creative Commons Attribution 4.0 International License ([CC BY 4.0](#)).

Summary

Mathematical modeling of healthcare-associated infection (HAI) epidemiology is a useful tool for addressing infections acquired during medical care, which cause significant morbidity, mortality, and financial strain on health systems worldwide. HAIs arise from complex interactions among patients, healthcare workers, the clinical environment, and microbial evolution. Because these interconnected processes are difficult to observe in real-world or experimental settings, models provide a powerful, risk-free way to understand how infections spread and how interventions may reduce transmission. We developed FacilityEpiSim, a continuous-time, agent-based simulation model of infectious disease transmission in healthcare facilities. The software tool allows modelers and their public health collaborators to run simulations to study transmission dynamics among facility patients and evaluate the utility of patient surveillance strategies before implementing them.

Statement of need

The tool is an agent-based model (ABM) built with Repast Simphony 2.11.0 (North et al. (2013)) for simulating transmission of an infectious organism in a healthcare facility. The model simulates flow of inpatients or residents of the facility over a specified time period, tracking patient admissions, lengths of stay, and discharges, disease importation and transmission dynamics, clinical detection and active surveillance testing with isolation of detected patients serving to partially decrease transmission. Patients in a susceptible state move to a colonized (i.e., infected) state at a rate proportional to the number of colonized patients currently in the facility, with detected colonized patients transmitting at a discounted rate according to the assumed isolation effectiveness. Undetected colonized patients can progress to clinical detection (i.e. a positive test driven by symptomatic, clinical infection) or can spontaneously return to a susceptible state upon decolonization.

The main intervention that can be tested in the simulation is active surveillance, which can occur at admission and/or at regular intervals during a patient's stay in the facility, with configurable adherence rates, test sensitivity, and durations between mid-stay tests. Active surveillance can identify asymptotically colonized patients who would not otherwise have been detected and reduce transmission according to a configurable isolation effectiveness parameter. A non open-source version of our code was used to generate results for three prior publications: Slayton et al. (2015), Toth et al. (2017), and Toth et al. (2020). These studies demonstrated the utility of this simulation model for generating novel insights for public health.

With this open source version of our model, users can now configure simulation settings to particular facilities, infectious organisms, and surveillance intervention strategies of interest (Figure 1). The code generates time series outputs, event logs for admissions, transmissions, detections, etc., and can also perform batch runs with parameter sweeps to test a range of

assumptions or surveillance strategies. We also provide R scripts that analyze raw simulation output to verify model behaviors and view sensitivity analysis results. These capabilities will allow users to extend our prior, published research findings and generate new insights for public health.

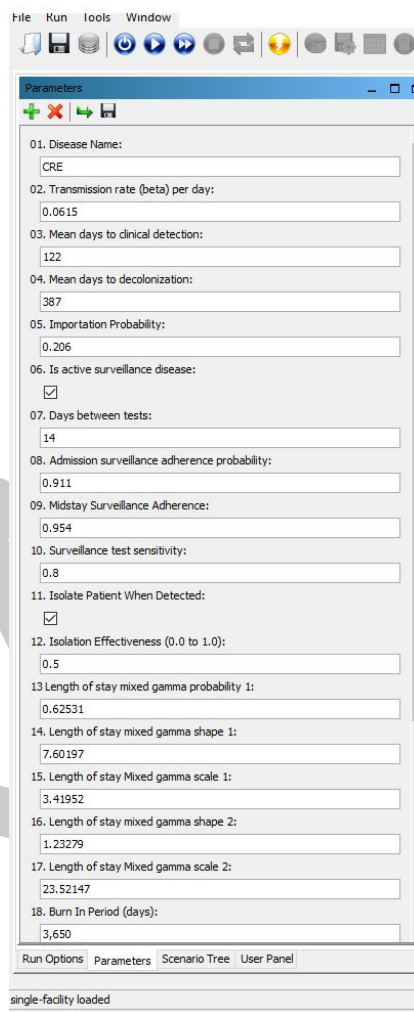


Figure 1: Parameters panel available when running the non-batch version of the simulation in Repast Simphony.

While several open source software packages exist for general infectious disease outbreak simulation (e.g., Jenness et al. (2013), Gozzi et al. (2025), Lorton et al. (2019), Grefenstette et al. (2013), Gallagher et al. (2024), Meyer & Yon (2023)), none of these provide settings specific to healthcare facility epidemiological scenarios without significant customization efforts by the user. We found one public repository, H-outbreak, for spatial-temporal simulation for hospital infection spread (Kim et al. (2023)), which emphasizes modeling spatial hospital layout and staffing rather than transmission dynamics and surveillance. Furthermore, to our knowledge all these existing simulation models use discrete time steps rather than the continuous-time, event-based framework implemented in our model, which obviates the need for choosing a time step frequency that could unintentionally affect simulation dynamics.

AI Usage Disclosure

Generative AI was used in the creation of this project. Tools used include GitHub Copilot, Copilot Agents, and Claude Code. A variety of models were used with each tool, including Sonnet 4.5, Opus 4.5, GPT 4, GPT 5 and GPT-5 mini. These were used primarily in the creation of code and documentation. AI assisted in the generation of code, debugging, bootstrapping data analysis, scaffolding for documentation and some documentation generation. The authors of this paper assert that human authors reviewed, edited and validated all AI-assisted outputs and made the core design decisions.

Acknowledgements

This work was supported by the Centers for Disease Control and Prevention, Modeling Infectious Diseases in Healthcare Network award U01CK000585 and Insight Net award number CDC-RFA-FT-23-0069.

References

- Gallagher, K., Bouros, I., Fan, N., Hayman, E., Heirene, L., Lamirande, P., Lemenuel-Diot, A., Lambert, B., Gavaghan, D., & Creswell, R. (2024). Epidemiological agent-based modelling software (epiabm). *J. Open Res. Softw.*, 12(3).
- Gozzi, N., Chinazzi, M., Davis, J. T., Gioannini, C., Rossi, L., Ajelli, M., Perra, N., & Vespignani, A. (2025). Epydemix: An open-source python package for epidemic modeling with integrated approximate bayesian calibration. *PLoS Computational Biology*, 21(11), e1013735.
- Grefenstette, J. J., Brown, S. T., Rosenfeld, R., DePasse, J., Stone, N. T. B., Cooley, P. C., Wheaton, W. D., Fyshe, A., Galloway, D. D., Sriram, A., Guclu, H., Abraham, T., & Burke, D. S. (2013). FRED (a framework for reconstructing epidemic dynamics): An open-source software system for modeling infectious diseases and control strategies using census-based populations. *BMC Public Health*, 13(1), 940.
- Jenness, S., Goodreau, S. M., Morris, M., Le Guillou, A., & Klumb, C. (2013). *EpiModel: Mathematical modeling of infectious disease dynamics*. The R Foundation.
- Kim, D., Canovas-Segura, B., Jimeno-Almazán, A., Campos, M., & Juarez, J. M. (2023). Spatial-temporal simulation for hospital infection spread and outbreaks of clostridioides difficile. *Sci. Rep.*, 13(1), 20022.
- Lorton, C. W., Proctor, J. L., Roh, M. K., & Welkhoff, P. A. (2019). Compartmental modeling software: A fast, discrete stochastic framework for biochemical and epidemiological simulation. In *Computational methods in systems biology* (pp. 308–314). Springer International Publishing.
- Meyer, D., & Yon, G. G. V. (2023). epiworldR: Fast Agent-Based epi models. *Journal of Open Source Software*, 8(90), 5781.
- North, M. J., Collier, N. T., Ozik, J., Tatara, E. R., Macal, C. M., Bragen, M., & Sydelko, P. (2013). Complex adaptive systems modeling with Repast Symphony. *Complex Adaptive Systems Modeling*, 1(1), 3. <https://doi.org/10.1186/2194-3206-1-3>
- Slayton, R. B., Toth, D., Lee, B. Y., Tanner, W., Bartsch, S. M., Khader, K., Wong, K., Brown, K., McKinnell, J. A., Ray, W., Miller, L. G., Rubin, M., Kim, D. S., Adler, F., Cao, C., Avery, L., Stone, N. T. B., Kallen, A., Samore, M., ... Jernigan, J. A. (2015). Vital Signs: Estimated Effects of a Coordinated Approach for Action to Reduce Antibiotic-Resistant Infections in Health Care Facilities — United States. *Morbidity and Mortality Weekly Report (MMWR)*,

- 100 64(30), 818–822. <https://www.cdc.gov/mmwr/preview/mmwrhtml/mm6430a4.htm>
- 101 Toth, D. J. A., Keegan, L. T., Samore, M. H., Khader, K., O'Hagan, J. J., Yu, H., Quintana,
102 A., & Swerdlow, D. L. (2020). Modeling the potential impact of administering vaccines
103 against *clostridioides difficile* infection to individuals in healthcare facilities. *Vaccine*, 38(37),
104 5927–5932.
- 105 Toth, D. J. A., Khader, K., Slayton, R. B., Kallen, A. J., Gundlapalli, A. V., O'Hagan, J. J.,
106 Fiore, A. E., Rubin, M. A., Jernigan, J. A., & Samore, M. H. (2017). The potential for
107 interventions in a long-term acute care hospital to reduce transmission of carbapenem-
108 resistant enterobacteriaceae in affiliated healthcare facilities. *Clinical Infectious Diseases*,
109 65(4), 581–587.

DRAFT