JEPIBIO
Journal of Epidemiology and Infection Biology

Research Article

Evaluating Cleaning and Filtration Strategies in Waterborne Escherichia coli Outbreaks Using Agent-Based Modelling

Usama Hanif*

Department of Bio-systems Engineering, Gyeonsang National University, Jinju, 52828, Republic of Korea.

*Corresponding author:

Mr. Usama Hanif
(e-mail: usama@gnu.ac.kr)

Date of Receiving: 21/08/2025
Date of Acceptance 09/11/2025
Date of Publishing 10/12/2025

ABSTRACT Waterborne transmission is still a major public health problem in many contexts especially when shared water sources are widespread. The contaminated water containers can serve as environmental reservoirs and help to spread an outbreak of an enteric pathogen like Escherichia coli. But it is difficult to measure, by field studies alone, the relative effect of environmental cleaning and water filtering measures. The aim of this study was to build an agent-based model for simulating the spread of E. coli through shared water jugs in a community scenario. Individual movement between locations, environmental contamination dynamics, bacterial shedding and dose dependent infection risk were included in the model. Various scenarios of interventions were evaluated such as increasing the frequency of water container cleaning and varying the coverage of filters. The scenarios were simulated more than 50 times, for stochastic variation in outbreak dynamics. The outcomes were attack rate, number of infectives, time to peak, epidemic duration and the probability of outbreaks. Higher frequencies of cleaning significantly lowered attack rates and shortened the course of epidemics. The higher the filter coverage, the more the peak infection was lowered. The intervention scenario that combined both interventions had the greatest decrease in the size and duration of outbreaks. Sensitivity analysis showed that the most important parameters affecting the outcomes of an outbreak were cleaning interval and sensitization probability. These results emphasize the importance of environmental hygiene in controlling waterborne outbreaks. Agent-based modelling is a useful tool for assessing intervention strategies in complex transmission systems. The findings demonstrate the importance of the regular cleaning and better filtering of shared water sources to minimize the risk of a large outbreak.

KEYWORDS Agent-based modelling, Waterborne transmission, *Escherichia coli,* Environmental contamination, Outbreak dynamics

Introduction

Escherichia coli is a major cause of waterborne gastrointestinal disease worldwide (Suleiman and Azlan, 2025). Pathogenic strains can lead to diarrhea, hemorrhagic colitis, and hemolytic uremic syndrome. The global burden of diarrheal diseases remains substantial, particularly in low-resource settings (Mensah *et al*, 2023). Contaminated drinking water is a persistent source of exposure. Shared water containers increase the risk of secondary transmission. Environmental contamination can amplify outbreaks in clustered populations. Poor sanitation and inadequate hygiene practices further contribute to spread. Informal water systems often lack routine monitoring. Outbreak investigations frequently identify water handling as a key risk factor (Sudsandee *et al*, 2026). Climate variability and extreme weather events may increase contamination events. Rapid urbanization adds stress to water infrastructure. Population density enhances exposure probability (Seymour and McLellan, 2025; Wang *et al*, 2025). Though a huge progress has been recorded in water safety but localized outbreaks still continue to occur in Lower Income and Lower Middle-Income Countries (Remfry *et al*, 2021). Therefore, to effectively control and prevent such outbreaks, a clear understanding of environmental transmission dynamics is required. Additionally, quantification of hygiene interventions and their related drivers, that can modify outbreak patterns, remains an important epidemiological challenge (Whiteman *et al*, 2025).
Agent-based modelling (ABM) has become an important tool in infectious disease epidemiology in understanding the disease patterns (Kerkmann *et al*, 2025). It allows simulation

of individual-level transmission processes. Such models capture heterogeneity in exposure and susceptibility at individual levels (Hilton and Hall, 2024; Abed *et al*, 2026). They can represent environmental reservoirs as dynamic components of transmission and their impact in the causation. Dose–response relationships can be further integrated into infection risk along with other drivers (Cascante-Vega *et al*, 2023; Abed *et al*, 2026). This is particularly relevant for waterborne pathogens, soil borne pathogens and zoonotic diseases. Unlike deterministic compartmental models, agent-based approaches incorporate stochastic variability which allows estimation of outbreak probability and distribution of outcomes (Bays *et al*, 2021; Belser *et al*, 2022). Multiple intervention scenarios can also be tested under controlled conditions. On the other hand, repeated simulations generate confidence intervals for epidemiological measures calculated under different scenario conditions (Watson, 2022)(Lymperopoulos, 2021). These methods provide mechanistic insight into outbreak behavior. Agent-based modeling therefore offers a valuable framework for evaluating environmental control strategies.

The objective of this study was to assess how cleaning frequency and filtration coverage influence waterborne outbreak dynamics. The current study developed an agent-based model simulating transmission of *E. coli* through shared water containers. The model incorporated contamination growth, bacterial shedding, incubation, and recovery periods. Multiple intervention scenarios were simulated under stochastic conditions. Each scenario was repeated across multiple iterations to account for variability. Epidemiological outcomes included attack rate, peak prevalence, time to peak, and epidemic duration. Outbreak probability was estimated using predefined thresholds. This study aims to provide quantitative evidence on environmental hygiene interventions. The findings may inform public health strategies for reducing waterborne disease transmission in high-risk settings.

Materials and Methods

Model Structure and Environment

An agent-based model was developed to simulate waterborne transmission of *Escherichia coli* in shared drinking environments. The model was implemented in Python using the Mesa framework. Individuals were represented as autonomous agents. Each agent occupied one of four health states: susceptible (S), exposed (E), infected (I), or recovered (R). Agents moved between shared water containers at each time step. Water containers were modeled as environmental reservoirs. Each container had a dynamic contamination level that evolved over time. Let $C_{j,t}$ denotes the contamination level of container j at time t. Contamination increased due to bacterial shedding and background growth. Background contamination was represented by a constant rate γ. Infectious individuals contributed shedding σ during water consumption events. Contamination was capped at a maximum value Cmax. Cleaning events reset contamination to zero. Filtration, when present, prevented contamination accumulation. The simulation advanced in discrete time steps.

Environmental contamination evolved according to the following equation:

$$C_{j,t+1} = \min\left(C_{max}, C_{j,t} + \gamma + \sum_{i\in I} \sigma_i\right)$$

Here γ represents background growth and σ_i represents shedding from infectious individuals. The summation term captures contamination added by all infectious agents interacting with container j at time t. If filtration was active, contamination accumulation was suppressed. Cleaning intervals were applied deterministically. These mechanisms allowed environmental transmission to emerge dynamically.

Infection Dynamics and Disease Progression

Infection was modelled using a dose-dependent probability function. When a susceptible individual consumed water from container j, exposure was proportional to Cj, t. The probability of infection was defined as:

$$P_{infection} = \min\left(1, \beta C_{j,t}\right)$$

In the above-mentioned equations β shows the infection probability factor and contamination to risk of transmission. The probability was capped at 1 to keep the validity. The infection was induced by random selection. When the person became infected, he/she was classified as an E. If the person got infected, he/she moved from an S to an E. Exposed state was an incubation period. Agents moved from E to I after a certain incubation period and infectious persons were infectious for a fixed recovery time. Once recovered from the illness, people were moved to R. recovered persons were assumed immune for the duration of the simulation. One infected person was added at the beginning. All other people were initialized as susceptible. Transmission could emerge from the interactions between an agent and the environment in these rules.

Simulation Protocol and Intervention Scenarios

A total of 100 individuals were considered as the baseline population. The environment was made up of containers for water at hotel and street stalls. Twenty hundred (200) time steps were simulated. An equal number of stochastic iterations (50) were performed for each scenario. Agents were updated at each step by the random activation method. Four scenarios of intervention were tested. Moderate cleaning and partial coverage of filters was considered as the baseline scenario. The stall hygiene scenario drove a change in the frequency of cleaning which was increased at street stalls. Increased the coverage of the filtration at the hotel locations by using the hotel filter scenario. In the combined scenario both interventions were used at the same time. A fixed time step method for cleaning intervals was used. The coverage of filters was probabilistically determined across locations. This criterion enabled direct comparison of effects of the intervention while stochastic repetition accounted for the variability of outbreaks.

Outcome Measures and Statistical Analysis

Primary outcomes included attack rate and peak infection size. Attack rate was defined as the proportion of individuals ever infected during simulation. Peak infection was defined as the maximum number of infected individuals at any time step.

Time to peak was recorded as the step of maximum infection. Epidemic duration was defined as the final time step with active infection. Outbreak probability was calculated using a predefined attack rate threshold. Mean values were calculated across iterations. Ninety-five percent confidence intervals were computed using standard error. Pairwise scenario comparisons were conducted using independent t-tests. Statistical significance was assessed at a threshold of 0.05. One-way sensitivity analysis was performed by varying key parameters individually. Parameters included infection probability factor, cleaning interval, and filtration coverage. Global sensitivity was assessed using partial rank correlation coefficients. Spearman rank correlation was used to account for nonlinearity. All analyses were conducted using Python statistical libraries.

Results

Epidemic Dynamics Across Scenarios

Distinct epidemic patterns were observed across intervention scenarios. The baseline scenario produced a rapid and intense outbreak. Mean infections peaked early within the first ten-time steps. Peak prevalence exceeded 90 individuals in the baseline setting. The stall hygiene scenario showed a similar early peak. However, infections declined more rapidly afterward. The hotel filter scenario produced a substantially lower epidemic curve. Peak infections were markedly reduced compared with baseline. The combined intervention further reduced peak magnitude. The epidemic curve in the combined scenario was broader but flatter. Infection levels declined gradually over time. Variability across iterations was evident in all scenarios. The hotel filter scenario showed the most visible suppression of early growth. These patterns are illustrated in Fig. 1. Overall, filtration had a stronger effect on peak suppression than cleaning alone.

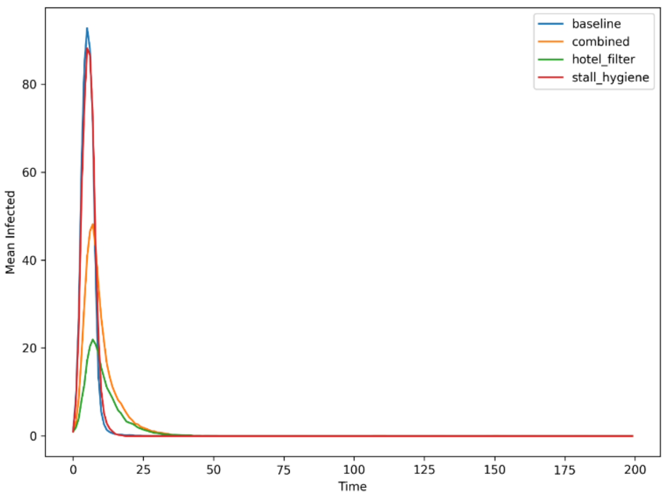

Fig. 1 Mean epidemic curves across intervention scenarios. Lines represent mean infected individuals over time averaged across 50 stochastic iterations. The baseline scenario shows rapid exponential growth. The hotel filter scenario demonstrates marked suppression of peak infection. The combined intervention produces a flatter epidemic curve. Time is shown in simulation steps.

Attack Rate

There was also a significant variation in attack rate between scenarios (Fig 2, Tab 1). An attack rate approaching full population infection was achieved in the baseline scenario. A high attack rate was observed in the stall hygiene scenario as well. There were no differences between the attack rate in either scenario. The intervention had an intermediate effect on attack rate (combined intervention). The combined scenario had the lowest attack rate compared to baseline. The attack rate in the hotel filter scenario was the lowest. In this scenario the mean attack rate was less than 0.5. Wider confidence intervals were created in intervention scenarios. The hotel filter setting has the largest variation. The hotel filter scenario was very different from the "baseline". Both the combined scenario and its relative to baseline were highly significant.

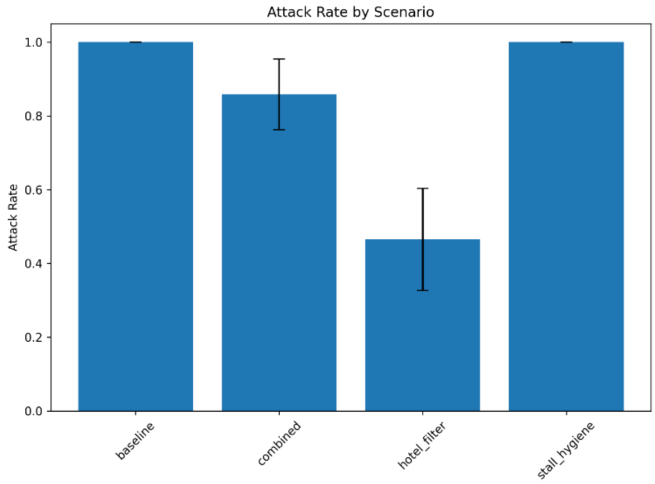

Fig 2. Mean attack rate by scenario with 95% confidence intervals. Bars represent mean proportion of individuals ever infected across 50 iterations. Error bars indicate 95% confidence intervals. The hotel filter scenario shows the largest reduction in attack rate.

Table 1. Pairwise statistical comparisons of attack rate between scenarios using independent t-tests. P-values below 0.05 indicate statistically significant differences.

Scenario 1	Scenario 2	P value
Baseline	Combined	0.004548
Baseline	Hotel filter	1.93E-11
Baseline	Stall hygiene	0.884
Combined	Hotel filter	1.39E-05
Combined	Stall hygiene	0.004548
Hotel filter	Stall hygiene	1.93E-11

JEPIBIO

Peak Infection

There was some variation in peak infection across interventions. The basic case scenario resulted in over 90 people getting infected. In the case of the stall hygiene scenario, peak values were, again, high. The overall intervention was able to bring a big reduction in the peak infection. Combined scenario resulted in about half of the mean infection peak. The lowest peak burden was obtained for the hotel filter scenario. There were virtually no more than about 25 people infected during this period. Confidence intervals ranged from moderate in all scenarios. There was greater variability in the combined and filter scenarios. The results of these findings are indicated on Fig. 3. The peak infection level significantly dropped in the filter at hotel disinfection case compared to baseline. The total scenario also showed considerable decrease. There was no significant difference in peak magnitude when implemented with stall hygiene only.

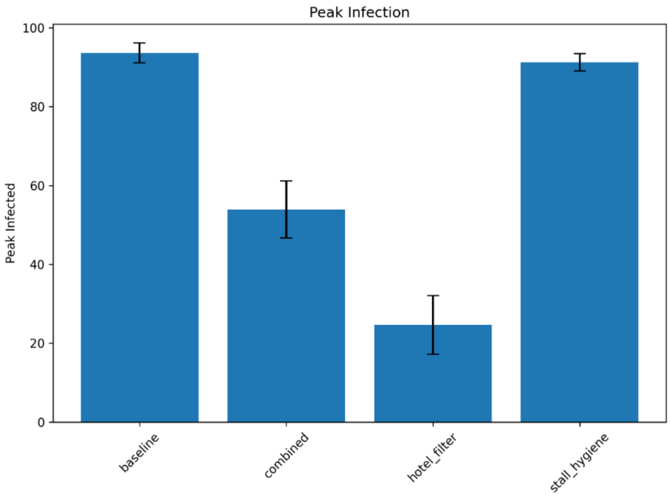

Fig. 3: Peak number of infected individuals by scenario with 95% confidence intervals. Bars represent maximum infected individuals per simulation averaged across runs. The hotel filter scenario shows marked peak suppression.

Epidemic Duration

Different pattern was observed with regard to the duration of epidemic. The overall intervention resulted in the longest outbreaks. The combined scenario resulted in a mean duration more than 35 time steps. The filter scenario with the epidemics also lengthened the time period over which the epidemic continued, compared to baseline. The baseline scenario had short and intense outbreaks. Duration was similar to baseline for stall hygiene. The widest confidence intervals occurred for the combined scenario. Under combined intervention, there was a lot of variation. The results obtained are displayed in Fig. 4. The results of these summary statistics appears in Table 3. Interventions that reduced the level of the infection tended to increase the length of infection. This is a slow-down in the epidemic curve. The results of the combined scenario were increased time for the transmission, but slower and stable. The outbreak was also put off for some time, due to the hotel filter scenario. Overall, interventions decreased in intensity and lengthened the time until extinction.

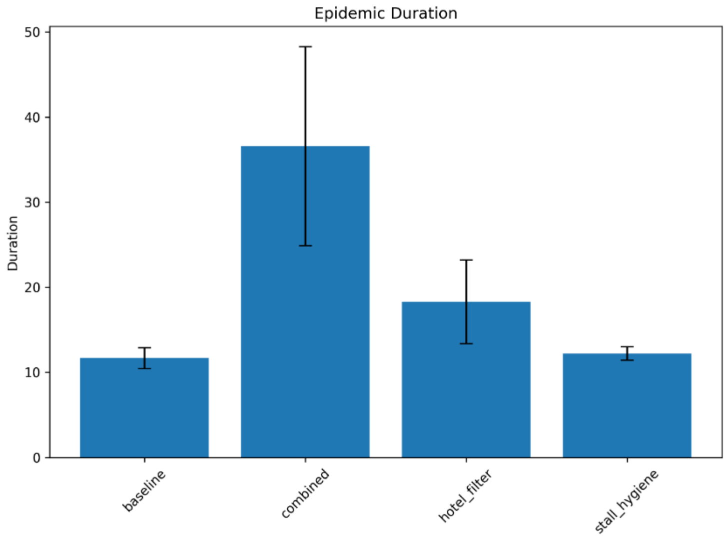

Fig. 4: Epidemic duration by scenario with 95% confidence intervals. Bars represent the final time step with active infection averaged across simulations. The combined intervention shows the longest epidemic duration.

Discussion

The current study considered environmental interventions for a simulated waterborne outbreak scenario. The baseline scenario exhibited fast and high transmission. Under these conditions almost all the population was infected. No significant difference was found in attack rates by correcting only the hygiene of the stalls. In this scenario, peak infection continued to be high. These results indicate that routine cleaning alone might not be enough to stop the transmission of COVID-19. In contrast, attack rate was significantly decreased with increased filtration coverage. The least outbreak size was obtained in the hotel filter scenario. There was also significantly less peak infection with filtration. The results suggest that source control efforts have a significant epidemiological impact consistent with previous findings (Chen *et al*, 2025; Lee *et al*, 2025). The overall intervention was successfully successful in reducing the peak burden, without in turn eradicating transmission. There were fewer attacks, but the attack rate was still high. This study indicated that environmental contamination was a major factor in magnitude of outbreak.

As previous studies indicated differences in intervention effects were found for each epidemiological measures (Romanello *et al*, 2021). There was a reduction in attack rate and peak infection with filtration. But interventions also influenced the length of an epidemic (Kelly *et al*, 2022). The total amount of contributing cases resulted in more extended outbreaks. Epidemics tainted but extended. This is typical of the "flattening" of an epidemic. Reducing transmission intensity may lengthen outbreak duration. Peak burden reduced and time to extinction increased. Moderate duration extension was also observed in the hotel filter scenario. Short, but intense, outbreaks occurred in baseline and stall hygiene situations. These distinctions highlight the considerations of intensity/extensity and duration. Both aspects should be taken into consideration when planning public health (Majeed *et al*, 2022). Minimizing peak burden

can help safeguard health systems. However, if it has been around for longer, it might need continuous monitoring. These results highlight the difficulty in designing environmental control strategies.
The results of the sensitivity analyses also confirmed the significance of contamination dynamics. The parameters of infection probability and the filtration coverage were influential parameters. The smaller effect measured was that of cleaning interval. Partial correlation analysis showed that there were strong correlations with outbreak size. The findings confirm the importance of reducing exposure as a focus area. These results are in agreement with the previous studies (Li *et al*, 2025; Liu *et al*, 2025). Interventions that directly intervene with the contamination seem to be the most effective environmental interventions. Cleaning may lower the bacterial load occasionally. But in areas where there is a high risk of re-contamination, this can happen quickly. Filtration results in continuous suppression of contamination. The results of the two interventions were intermediate. It was able to decrease peak infection – not wipe out long-term transmission. The results obtained show that layering the interventions could optimize control as previously reported (Cascante-Vega *et al*, 2023; Abed *et al*, 2026). Further research is needed to assess the cost-effectiveness of using a combination of strategies. However, the model gives an insight into waterborne transmission control mechanisms.
The results of this study do have limitations. The model adopted the simplified assumptions of contamination dynamics. A linear dose–response model was used for modelling infection probability. The patterns of real-world transmission are not necessarily linear. A population size of 100 individuals were set. Lowering down of the contour interval was not done. Shared containers were the only form of spatial structure modeled, and behavioral differences in hygiene practices were reduced. Immunity is assumed to last for the whole simulation period. Additional environmental parameters (e.g., temperature) were not factorised. No empirical data was used for calibration of parameter values. There was no evaluation of the economic costs of interventions as short-term outbreak model was used. Although there may be restrictions to the use of the framework, it can still give some helpful mechanistic understanding of environmental transmission processes.
Finally, in this study, an agent-based model was adopted to test environmental control measures in E. coli outbreaks in water. With baseline conditions, rapid and widespread transmission occurred. Overall attack rate was barely affected by cleaning. The highest impact was seen for the filtering effect on outbreak size and peak burden. The lowest attack rate and peak attack were obtained in the "hotel" scenario. The joint effort led to a reduction on peak intensity while increasing the length of the epidemic. The results show that contamination at source is important. Cleaning frequency alone is not enough; it seems that environmental filtration is more effective. Outbreak duration may be longer with interventions that reduce intensity of transmission. Public health planners should thus strive for both peak reduction and duration management. The model is useful to illustrate the influence of environmental dynamics in outbreak patterns. Agent-based modelling is a suitable tool to compute these interventions. These findings call for the importance of prioritizing filtration approaches in shared water systems.

Declaration of Competing Interest
The authors declare that they have no competing or conflict of interests.

Author Contributions

UH: Conceptualization, Methodology, formal analysis, Writing—original draft preparation, Writing—review and editing. The author has read and agreed to the published version of the manuscript.

References

1. Abed, A., M. Torabi, and Z. Mashreghi. (2026). *Individual level modeling of infectious disease transmission with reinfection dynamics: Application to Tuberculosis in Manitoba, Canada*. Spat Spatiotemporal Epidemiol 56:100780. doi: 10.1016/j.sste.2025.100780
2. Bays, D., H. Williams, L. Pellis, J. Curran-Sebastian, O. O'Mara, P. J. M. Team, and T. Finnie. (2021). *Insights gained from early modelling of COVID-19 to inform the management of outbreaks in UK prisons*. Int J Prison Health 17(3):380-397. doi: 10.1108/IJPH-09-2020-0075
3. Belser, J. A., J. A. Pulit-Penaloza, N. Brock, H. M. Creager, K. M. Gustin, T. M. Tumpey, and T. R. Maines. (2022). *Inherent Heterogeneity of Influenza A Virus Stability following Aerosolization*. Appl Environ Microbiol 88(4):e0227121. doi: 10.1128/aem.02271-21
4. Cascante-Vega, J., M. Galanti, K. Schley, S. Pei, and J. Shaman. (2023). *Inference of transmission dynamics and retrospective forecast of invasive meningococcal disease*. PLoS Comput Biol 19(10):e1011564. doi: 10.1371/journal.pcbi.1011564
5. Chen, M., Y. Wang, B. Dong, Y. Zhang, L. Feng, H. Zou, Y. Li, Y. Huang, G. Huang, X. Mao, Y. Kang, S. Xu, H. Lin, and P. Sun. (2025). *Epidemiological analysis of human papillomavirus infection in senior women: a hospital-based retrospective study*. BMC Infect Dis 25(1):1378. doi: 10.1186/s12879-025-10836-3
6. Hilton, J., and I. Hall. (2024). *A beta-Poisson model for infectious disease transmission*. PLoS Comput Biol 20(2):e1011856. doi: 10.1371/journal.pcbi.1011856
7. Kelly, S. L., E. A. Le Rutte, M. Richter, M. A. Penny, and A. J. Shattock. (2022). *COVID-19 Vaccine Booster Strategies in Light of Emerging Viral Variants: Frequency, Timing, and Target Groups*. Infect Dis Ther 11(5):2045-2061. doi: 10.1007/s40121-022-00683-z
8. Kerkmann, D., S. Korf, K. Nguyen, D. Abele, A. Schengen, C. Gerstein, J. H. Gobbert, A. Basermann, M. J. Kuhn, and M. Meyer-Hermann. (2025). *Agent-based modeling for realistic reproduction of human mobility and contact behavior to evaluate test and isolation strategies in epidemic infectious disease spread*. Comput Biol Med 193:110269. doi: 10.1016/j.compbiomed.2025.110269
9. Lee, Y., P. K. N. Salonga, C. Son, G. Jang, D. H. Koh, J. H. Kim, and H. Lee. (2025). *Effective strategies for typhoid conjugate vaccine delivery: Health and economic insights from the 2015 Kampala outbreak*. PLoS Negl Trop Dis 19(10):e0013566. doi: 10.1371/journal.pntd.0013566

10. Li, W., Q. Yuan, X. Li, M. Teng, Z. Zhang, Y. Luo, and F. Wu. (2025). *Clostridium perfringens as an alternative fecal indicator bacteria in surface water quality: A national investigation in Chinese rivers*. Water Res 286:124223. doi: 10.1016/j.watres.2025.124223
11. Liu, W., Q. Feng, Y. Liang, Y. Cui, L. Xu, and B. A. Engel. (2025). *Exploring spatiotemporal dynamics of urban flood socioeconomic exposure risk and driving factors under future precipitation change and urbanization scenarios*. J Environ Manage 395:127980. doi: 10.1016/j.jenvman.2025.127980
12. Lymperopoulos, I. N. (2021). *#stayhome to contain Covid-19: Neuro-SIR - Neurodynamical epidemic modeling of infection patterns in social networks*. Expert Syst Appl 165:113970. doi: 10.1016/j.eswa.2020.113970
13. Majeed, B., J. F. David, N. L. Bragazzi, Z. McCarthy, M. D. Grunnill, J. Heffernan, J. Wu, and W. A. Woldegerima. (2022). *Mitigating co-circulation of seasonal influenza and COVID-19 pandemic in the presence of vaccination: A mathematical modeling approach*. Front Public Health 10:1086849. doi: 10.3389/fpubh.2022.1086849
14. Mensah, G. T., P. F. Ayeh-Kumi, A. K. Annang, I. Owusu-Frimpong, S. Niampoma, and C. A. Brown. (2023). *Molecular epidemiology of Cryptosporidium species in Kpong and its environs, Ghana*. PloS one 18(2):e0281216. doi: 10.1371/journal.pone.0281216
15. Remfry, S. E., R. G. Amachawadi, X. Shi, J. Bai, M. D. Tokach, S. S. Dritz, R. D. Goodband, J. M. Derouchey, J. C. Woodworth, and T. G. Nagaraja. (2021). *Shiga Toxin-Producing Escherichia coli in Feces of Finisher Pigs: Isolation, Identification, and Public Health Implications of Major and Minor Serogroupsdagger*. J Food Prot 84(1):169-180. doi: 10.4315/JFP-20-329
16. Romanello, M., A. McGushin, C. Di Napoli, P. Drummond, N. Hughes, L. Jamart, H. Kennard, P. Lampard, B. Solano Rodriguez, N. Arnell, S. Ayeb-Karlsson, K. Belesova, W. Cai, D. Campbell-Lendrum, S. Capstick, J. Chambers, L. Chu, L. Ciampi, C. Dalin, N. Dasandi, S. Dasgupta, M. Davies, P. Dominguez-Salas, R. Dubrow, K. L. Ebi, M. Eckelman, P. Ekins, L. E. Escobar, L. Georgeson, D. Grace, H. Graham, S. H. Gunther, S. Hartinger, K. He, C. Heaviside, J. Hess, S. C. Hsu, S. Jankin, M. P. Jimenez, I. Kelman, G. Kiesewetter, P. L. Kinney, T. Kjellstrom, D. Kniveton, J. K. W. Lee, B. Lemke, Y. Liu, Z. Liu, M. Lott, R. Lowe, J. Martinez-Urtaza, M. Maslin, L. McAllister, C. McMichael, Z. Mi, J. Milner, K. Minor, N. Mohajeri, M. Moradi-Lakeh, K. Morrissey, S. Munzert, K. A. Murray, T. Neville, M. Nilsson, N. Obradovich, M. O. Sewe, T. Oreszczyn, M. Otto, F. Owfi, O. Pearman, D. Pencheon, M. Rabbaniha, E. Robinson, J. Rocklov, R. N. Salas, J. C. Semenza, J. Sherman, L. Shi, M. Springmann, M. Tabatabaei, J. Taylor, J. Trinanes, J. Shumake-Guillemot, B. Vu, F. Wagner, P. Wilkinson, M. Winning, M. Yglesias, S. Zhang, P. Gong, H. Montgomery, A. Costello, and I. Hamilton. (2021). *The 2021 report of the Lancet Countdown on health and climate change: code red for a healthy future*. Lancet 398(10311):1619-1662. doi: 10.1016/S0140-6736(21)01787-6
17. Seymour, J. R., and S. L. McLellan. (2025). *Climate change will amplify the impacts of harmful microorganisms in aquatic ecosystems*. Nat Microbiol 10(3):615-626. doi: 10.1038/s41564-025-01948-2
18. Sudsandee, S., W. Kliengchuay, V. Keawduanglek, A. Hongtong, W. Siriratruengsuk, S. Niampradit, R. Mingkhwan, N. Kiangkoo, N. Precha, and K. Tantrakarnapa. (2026). *Assessment of water quality and associated health risks in community-managed water systems in highland areas: A case study Chiang Rai province, Thailand*. One Health 22:101290. doi: 10.1016/j.onehlt.2025.101290
19. Suleiman, J. B., and M. Azlan. (2025). *Burden and Distribution of Protozoan Pathogens in Diarrhea Cases Worldwide: A Systematic Review and Meta-Analysis, 1999-2024*. Cureus 17(9):e91561. doi: 10.7759/cureus.91561
20. Wang, S., L. Wang, X. Liao, G. Zhou, Y. Huan, S. Li, and T. Liang. (2025). *Impact of residential density on heavy metal mobilization in urban soils: Human activity patterns and eco-health risks in the Beijing-Tianjin-Hebei region*. Ecotoxicol Environ Saf 302:118559. doi: 10.1016/j.ecoenv.2025.118559
21. Watson, L. M. (2022). *Likelihood of infecting or getting infected with COVID-19 as a function of vaccination status, as investigated with a stochastic model for Aotearoa New Zealand for Delta and Omicron variants*. The New Zealand medical journal 135:89-100.
22. Whiteman, D. C., C. M. Olsen, H. Wang, M. H. Law, R. E. Neale, and N. Pandeya. (2025). *A Risk Prediction Tool for Invasive Melanoma*. JAMA Dermatol 161(11):1123-1131. doi: 10.1001/jamadermatol.2025.3028