Exploring Vulnerable Nodes, Impactful Viral Intrusion Sites, and Viral Infection Risk Reductions Offered by Chlorine Boosters in Municipal Drinking Water Networks

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Abstract: The effects of drinking water system infrastructure on water quality and health following intrusion events have not been extensively studied. This study proposes a coupling of hydraulic and water-quality modeling with quantitative microbial risk assessment (QMRA) to characterize microbial infection risks. Two networks were considered based on their network configuration. We assumed a continuous intrusion of enterovirus under three scenarios. The location of vulnerable and influential nodes in a looped and a branched network were compared, followed by a comparison of chlorine booster placement to reduce infection risks. The most vulnerable nodes in the branched network were generally downstream of the intrusion site, whereas those for the looped network were in the middle of the network due to tank dynamics. Influential injection nodes for the looped network were also in the middle of the network but mostly located at the upstream nodes for the branched network. A single chlorine booster yielded a risk reduction (47.6%) for the branched network, greater than for the looped network (nearly none). Two chlorine boosters reduced the looped network risks more notably (63%). The generalizability of these results to other networks likely depends upon specific network hydraulics and variability in municipal drinking water use. This work will help public water system managers in identifying vulnerable points in their distribution system and optimal locations for risk reduction strategy implementation. **DOI: 10.1061/(ASCE)WR.1943-5452.0001589.**

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Introduction

Up to 45 million people are impacted annually in the United States by health-related water-quality standards violations, with the most frequent violation pertaining to total coliforms, an indicator of fecal contamination (Allaire et al. 2018). Of these violations, rural areas experience more water-quality violations than urban areas (Allaire et al. 2018; Mueller and Gasteyer 2021). Water quality is of special concern in rural communities because private wells and municipal drinking water distribution systems (WDSs) are often poorly maintained or not routinely monitored (Gall et al. 2015; IAWPRC Study Group on Water Virology 1983; Szewzyk et al. 2000). Of the 42 waterborne disease–related outbreaks associated with drinking water in the United States between 2013 and 2014, over 80% were associated with public drinking WDSs (Benedict et al. 2017), indicating that public drinking WDSs can be a source of contamination and outbreak events. Therefore, ensuring suitable water quality is essential for the health of communities served by WDSs.

Though different water utilities may face different challenges, all water utilities maintain a certain level of water quality. In most cases, chlorine is commonly used for disinfection purposes, and chlorine residual is used as an indicator reflecting the readiness of the system to address microbiological contamination events. In general, chlorine is injected at the source of a WDS. However, there are potential threats of contaminant intrusion, either accidentally or intended, throughout the distribution system, and a single chlorine source may not be sufficient to control all potential intrusion events. In these cases, a secondary chlorine booster may help to control intruded contaminants by injecting additional chlorine into the distribution system. However, not all secondary chlorine boosters are helpful, and they can increase taste and odor complaints (Islam et al. 2017a) and potentially increase disinfectant byproduct concentrations. Therefore, the determination of optimal location(s) for secondary chlorine booster(s) is needed after an investigation of the potential risks of contamination intrusion events.

Municipality-delivered water-quality assessment can be challenging due to variability in water systems, infrastructure, and hydraulic pressure. One method for handling this variability and

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uncertainty is the use of hydraulic and water-quality modeling to estimate the dynamics of water-quality species and concentrations across different municipal WDSs. The USEPA's EPANET, EPANET toolkit, and Multispecies Toolkit (MSX) have been used to model the fate and transport of a number of water-quality species, including arsenic (Burkhardt et al. 2017), chloramines (Ricca et al. 2019), and microorganisms (Propato and Uber 2004; Teunis et al. 2010; Yang et al. 2011). Understanding how health risks may vary from one network to another and elucidating the drivers of these risk differences, such as network configuration and tank dynamics, can inform future network design and placement of microbial risk reduction interventions, such as chlorine boosters.

Linking water-quality assessments to anticipated risk outcomes can contribute to emergency preparedness research and elucidating the risk levels that communities may face. Quantitative microbial risk assessment (QMRA), a framework designed for relating pathogen concentrations to quantified infection risks, has been used to relate network water quality to health risks (Teunis et al. 2010). Within the context of municipal WDSs, QMRA has been utilized to estimate risks related to system characteristics (e.g., biofilm) (Blokker and van der Wielen 2018), system complications (e.g., intrusion events) (Propato and Uber 2004; Schijven et al. 2016), and contamination due to main repairs (Blokker et al. 2014).

Locating chlorine boosters has been demonstrated using EPANET water-quality simulation (Abokifa et al. 2019; Ayvaz and Kentel 2015; Basupi and Nono 2019; Seth et al. 2017; Vrachimis et al. 2021). Among these studies, Seth et al. (2017) and Vrachimis et al. (2021) focused on security concerns and emergency response in addition to secondary chlorine boosters to manage contamination detection issues. Basupi and Nono (2019) accounted for hydraulic uncertainties for the placement of chlorine boosters. Abokifa et al. (2019) highlighted the limitation of the EPANET model especially for water-quality analysis of dead-end pipes and used an advection–dispersion–reaction transport model to solve the chlorine booster location problem. Others have utilized EPANET-MSX for locating ideal placement of chlorine boosters (Islam et al. 2017a, b), and Islam et al. (2017b) also considered risk quantification.

Though infection risks due to enteric virus exposures from municipal drinking water systems have been explored (Teunis et al. 2010), the effect of infrastructure differences (e.g., network configuration) on water quality and health risks following microbial contaminant intrusion events has not been extensively studied. Continued research on differences in anticipated microbial risks between networks with notable differences, such as the extent of looping versus branching and the dynamics of tanks, is needed to better understand how interventions, such as chlorine boosters, may vary in risk reduction efficacy from one network to another. The objective of this study was to compare risk reductions offered by chlorine boosters in two networks: (1) a branched system without a tank; and (2) a looped system with a tank. A scenario assuming a continuous intrusion of enterovirus was used as a worst-case scenario, and risks from drinking municipal water was estimated using a QMRA approach.

Methods

Because the concentrations of multiple parameters (e.g., chlorine and enterovirus) were estimated, the EPANET MATLAB toolkit was used in conjunction with the MSX toolkit to model the hydraulics of distribution networks (Eliades et al. 2016) and changes in chlorine and viral concentrations (Shang and Rossman 2011). This model is similar to those that estimate the fate and transport of two chemical species that interact, as viruses were assumed to not replicate within the network, unlike with bacteria modeling, where growth should be considered.

Two WDSs were considered as case study networks based on network configuration and the existence of a tank in one of the networks: the Oberlin (without a tank) and Bellingham (with a tank) networks. Each network was also partially representative of a rural (Oberlin) or urban (Bellingham) network based on the network structure, providing potential insights into how risks may differ between networks serving different population sizes.

The following workflow was used in this modeling study, divided into three overall steps, described in more detail in the "Case Study Description" subsection:

1. Using EPANET-MSX, the infection risks of each virus intrusion event were first identified deterministically to pinpoint those nodes that were most vulnerable to virus intrusion events and the nodes that posed the greatest risk as intrusion sites. Infection risks were estimated by first estimating a dose and using a pathogen-specific dose-response curve.
2. The addition of a chlorine booster was then explored as an intervention to reduce the infection risk.
3. Lastly, a probabilistic approach based on Monte Carlo simulation (MCS) was used to calculate risk reductions for the worst-case intrusion event scenario and to conduct a sensitivity analysis on the parameters used to simulate water-quality dynamics.

Fate and Transport Modeling of Virus and Chlorine and Risk Assessment

Changes in chlorine concentration in pipes and tanks with respect to time were calculated assuming first-order decay [Eq. (1)] because first-order decay has been assumed for decay the of chlorine and decay of viruses due to inactivation by chlorine [Eq. (1)] (Boccelli et al. 2003; Thurston-Enriquez et al. 2003)

$$\frac{dC_{Cl}}{dt} = -k_A C_{Cl} \tag{1}$$

where C_{Cl} = concentration of chlorine (mg/L); and k_A = chlorine decay constant (per hour).

The change in viral concentrations was calculated assuming first-order decay [Eq. (2*a*)]. As in other models describing viral inactivation by chlorine, the loss of chlorine due to interaction with virus was assumed negligible (Poduska and Hershey 1972). This equation is equivalent to the Chick–Watson model, as follows [Eqs. (2*b*)–(2*d*)]:

$$\frac{dC_V}{dt} = -k_B C_{V,t} C_{Cl,t} \tag{2a}$$

$$\int \frac{dC_V}{C_V, t} = \int -k_B C_{Cl,t} dt \tag{2b}$$

$$\ln(C_{V,t}) - \ln(C_{V,0}) = -k_B C_{Cl,t} t \tag{2c}$$

$$\ln\left(\frac{C_{V,t}}{C_{V,0}}\right) = -k_B C_{Cl,t} t \tag{2d}$$

where $C_{V,t}$ = concentration of virus (viral particles/L) at time t; and k_B = viral decay coefficient (per hour).

Viruses are notoriously difficult to detect in water samples, especially in treated drinking water. However, in other intrusion event risk assessments, the concentrations of enteric viruses in sewage water were used to inform potential intrusion concentrations (Teunis et al. 2010). In samples of municipal wastewater, enterovirus concentrations were detected at concentrations between

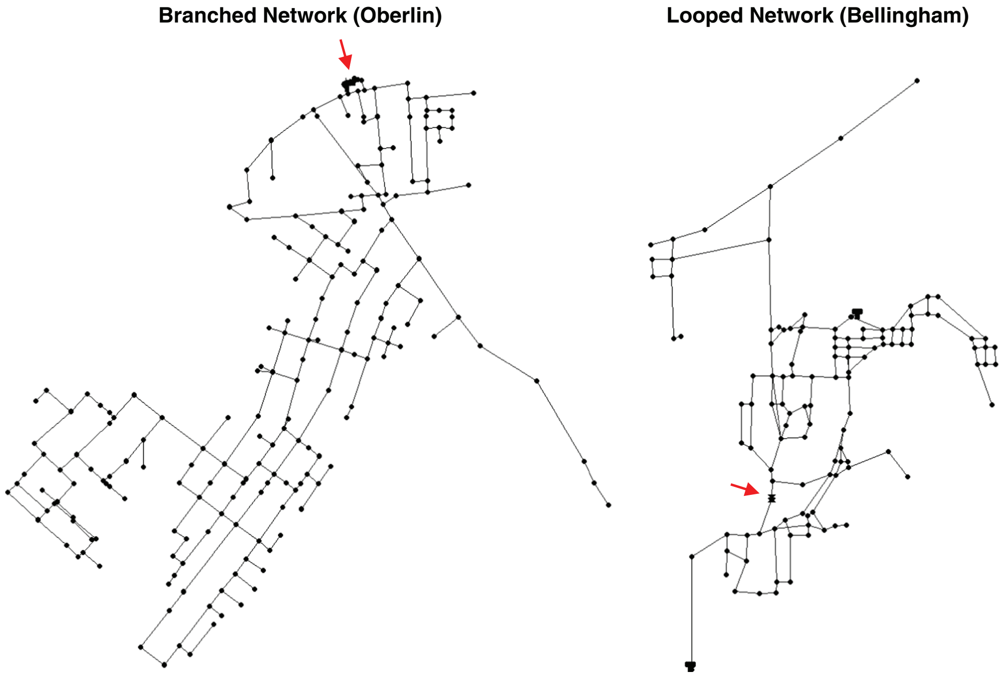

Fig. 1. (Color) Network maps of Oberlin and Bellingham drinking water networks. Arrows indicate locations of chlorine sources.

7.05×10^3 and 8.3×10^5 gene copies/L using reverse transcriptase quantitative PCR (RT-qPCR) (Brinkman et al. 2017). Viruses detected with molecular methods may not be viable, and this should be accounted for when molecular data are used to inform viral concentrations (Van Abel et al. 2017). Therefore, between 1% and 10% of these viral particles were assumed to be infectious, based on variability in this ratio for varieties of viruses and environmental conditions (Rodríguez et al. 2009).

The amount of virus (dose_i) expected at the ith node to be consumed via water over a single day was estimated by multiplying consumption per day ($V_{\text{consumed},i}$) by the maximum enterovirus concentration at that node over a whole simulation period [$\max(C_{V,t,i})$] to estimate viral dose [Eq. (3)]

$$\text{dose}_i = V_{\text{consumed},i} \cdot \max(C_{V,t,i}) \tag{3}$$

A dose-response curve was then used to relate this estimated dose to an infection risk. In the case of enterovirus, the suggested dose-response curve is exponential, as follows [Eq. (4)]

$$P_{\text{infect}} = 1 - e^{-k \cdot \text{dose}} \tag{4}$$

where k = probability that a single organism will survive and arrive at infection site (QMRA Wiki n.d.).

Study Networks

Network Characteristics and Populations

Two networks, Oberlin and Bellingham networks, were chosen based on their configuration and the existence of a tank in the Bellingham network that may influence microbial exposures due to intrusion events. The Oberlin network originates from Oberlin, Ohio, where the population was 8,312 in 2018. This network contains 262 nodes with no tanks and has an average water demand of 130.6 gallons per minute (GPM) with pipes of an average age of at least 50 years. The chlorine source is near the top of the network (near the pump station in Fig. 1). The Bellingham network is in Bellingham, Washington, where the population was 90,665 as of 2018. This network contains a tank and 121 nodes and has an average demand of 2,989.63 GPM, with pipes of an average age of at least 60 years. The chlorine source is from the water treatment plant to the left of the center of the network (marked with a red arrow in Fig. 1). Chlorine decay constants (k_A) for Oberlin and Bellingham have been set as 0.232/day and 0.833/day, respectively (Vasconcelos et al. 1997). These are comparable to other first order decay rates in other networks (Boccelli et al. 2003). Calibrated versions of the input files were archived from the Water Distribution System Research Database operated by the University of Kentucky (Ormsbee et al. 2022). The input files included nodal demand and water-quality data, which were used in the simulations. For both networks, the overall simulation period was set as 35 h, which was sufficient given the initial chlorine concentrations specified within the network model (see Fig. S1 for the representative tank concentrations) and residence time (see Fig. S2; note that most of the red nodes are zero demand nodes). Chlorine levels of the tanks in the looped network over the 35-h period can be seen in Fig. 2.

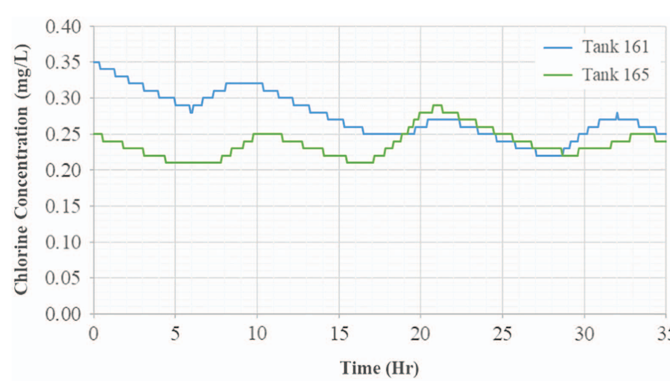

Fig. 2. (Color) Chlorine concentration of tanks for 35 h in looped network.

Branch Index Analysis

Branched index (BI) analysis was done to classify the two networks into either branched or looped systems. In general, rural networks are known to have a more branched configuration, though urban networks show a more looped configuration (Jolly et al. 2014). A threshold of $BI > 0.5$ was used to identify *branched* networks (Hwang and Lansey 2017). The Oberlin network was identified as a branched network ($BI = 0.52$), whereas the Bellingham network was identified as a looped network ($BI = 0.12$), supporting the use of Oberlin as partially representative of a rural, branched network and Bellingham as a looped, urban network.

Case Study Description

Overall Strategy and Risk Metrics

The overall strategy was to identify which nodes were (1) most vulnerable to injections anywhere in the network and (2) most influential on other nodes in the network as a viral intrusion site, and to (3) explore the placement of chlorine boosters to reduce infection risks across the network for any intrusion scenario and for the worst-case scenario intrusion event.

For each strategy, infection risk was quantified by three different definitions: (1) node risk, (2) network risk, and (3) average risk. We defined these three risk components as follows:

- Node risk: the mean infection risk at each node for all virus intrusion scenarios;
- Network risk: mean infection risks across the network for an individual virus intrusion scenario; and
- Average risk: the average of network risks over all intrusion scenarios.

Node risk was used to identify the node that experienced the greatest mean infection risk. The higher the node risk, the more vulnerable the node was to intrusion events. Network risk represented the severity of an individual virus injection scenario. Average risks were used to represent overall risk for a given condition (e.g., chlorine booster locations and virus injection scenarios) to compare the different virus management strategies. To implement this strategy using these three risk metrics, three case studies were used.

Case Study 1

The purpose of the first case study was to identify node risk and network risk for all possible single virus injection scenarios and to identify the most vulnerable nodes. Risks from the virus intrusion events were investigated deterministically by changing the location of the continuous virus injection nodes for both networks, where a single continuous virus injection node was considered at any one time. For a given network condition, chlorine concentrations at the source (following patterns in Fig. S1), viral concentrations at the intrusion site (constant concentration of 8.3×10^5 viral particles/L, set as set point), and chlorine and viral (2.78/min) decay rates were considered. It should be noted that, though a constant concentration of virus leaves the intrusion location, a constant concentration is not added to the system because it depends upon the parcels of water that are entering the system at that point.

Case Study 2

In the second case study, risk reductions following the addition of chlorine booster(s) were explored. For comparison purposes, average risks were calculated for each chlorine booster placement scenario. For example, a chlorine booster was set at Node 1, and the network risk for all potential intrusion sites and an average risk for the network were calculated. Then the chlorine booster location was set to Node 2, and the network risks and average risk were again calculated, and so on, for all potential booster locations.

Following the calculations of network risks for the potential intrusion sites, the chlorine booster scenario that resulted in the network's lowest average infection risk was explored. Note that chlorine boosters were designated as continuous, flow-paced sources with additional chlorine concentrations applied, similar to other source concentrations in the network (Fig. S1). Free residual chlorine concentration was checked for the entire network to make sure it was between 0.2 and 4.0 mg/L, as recommended by the USEPA (USEPA 2005). However, because the primary focus was on comparing chlorine booster placements to reduce risk, specific chlorine concentrations for the chlorine boosters were not explored to maintain a minimum residual concentration need to achieve a given risk target.

Case Study 3

A MCS was applied to estimate average infection risk reduction offered by chlorine booster placement under the worst intrusion scenario, accounting for variability and uncertainty in viral concentrations at the intrusion sites, inactivation rates of chlorine and virus, and daily volume of water ingested by residents at nodes. For viral concentrations at intrusion sites, we randomly sampled from a uniform distribution with a minimum of 7.05×10^3 and a maximum of 8.3×10^5 viral particles/L to determine the concentrations of virus at the intrusion site, and we assumed that between 1% and 10% of these viral particles would be infectious (Rodríguez et al. 2009). Though the ratio of infective virus to genome copies has not been standardized (Sinclair et al. 2008; Ward et al. 1984), the distribution was consistently used for the scenarios with and without a chlorine booster and is therefore unlikely to affect relative risk reductions. The volume of water ingested per day (L/person/day) was randomly sampled from a normal distribution (mean = 0.902, standard deviation = 1.0325, range from 0 to 4 L/day) informed by the USEPA's *Exposure Factors Handbook* (USEPA 2011). Viral inactivation constants were randomly sampled from a uniform distribution with a minimum of 1.41/min and a maximum of 2.78/min (or 2,030 and 4,003/day, respectively), as reported by Poduska and Hershey (1972) for poliovirus I virus.

A sensitivity analysis was conducted to evaluate the effect of randomly sampled inputs on estimated infection risk. Monotonic relationships between stochastic inputs and estimated risks were measured using Spearman correlation coefficients, where a larger magnitude of a Spearman correlation coefficient implies a greater effect on estimated risk, assuming a monotonic relationship. This methodology is consistent with sensitivity analyses in other QMRA studies (Hamilton et al. 2019; Jones 2020). Scatter plots of inputs versus estimated risks were investigated for nonmonotonic relationships.

Results

Identifying Vulnerable Nodes

Fig. 3, summarizing the results of Case study 1, demonstrates the identification of the nodes that were vulnerable to the injection nodes. As shown in Fig. 3, the more vulnerable nodes (higher node risk) in the branched network were generally further downstream of the viral source. Typically, water moves from upstream nodes to downstream nodes in a branched network, and nodes located downstream will have a greater number of upstream nodes. This means that downstream nodes will generally have a greater number of opportunities for viral contamination during intrusion events than

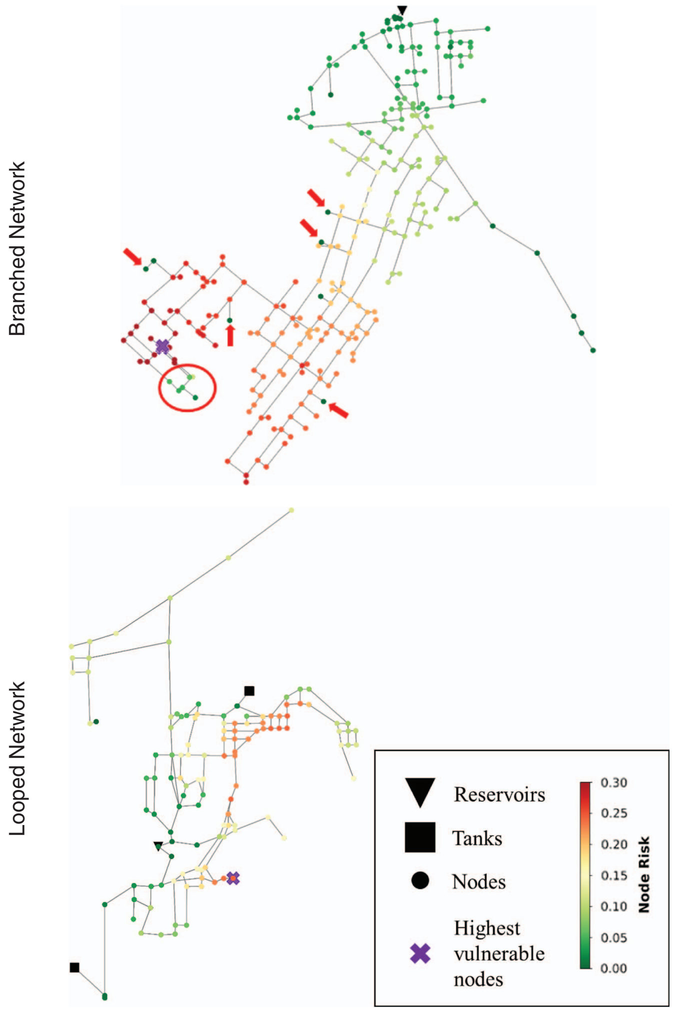

Fig. 3. (Color) Identification of most vulnerable nodes in network (denoted as injection location), where the color of the node indicates the mean risk at that node for all virus intrusion events (node risk). No chlorine boosters were applied. The circled area of the branched network represents locations with residence times long enough to have lower node risk; nodes with arrows illustrate examples of dead-end nodes.

nodes that are upstream in the network. Conversely, upstream nodes will be unaffected by intrusion events at downstream nodes.

For the looped network, the most vulnerable nodes in the network were generally those in the middle (neither upstream nor downstream) of the network close to Tank 165 (the tank on the upper side) (Fig. 3). This area of the network is where flow direction was variable (Fig. S3), a characteristic of looped networks. In this case, the varying flow direction was mainly caused by the behavior of storage facility (i.e., tank). As the flow direction changed, nodes located in the middle experienced a higher chance of viral contamination. Therefore, nodes in this network were generally vulnerable to a greater number of injection sites due to the network structure and flow direction.

In some cases, nodes downstream of the network had lower risks (green nodes) than other network nodes. This was generally due to either (1) zero (or very low) demand (e.g., dead end) (nodes with arrow in Fig. 3) or (2) long residence times and significant inactivation of the virus with transport to downstream nodes (especially in the branched network with a fixed flow direction, nodes in the circled area of Fig. 3). In the case of dead ends, the virus could not reach these nodes because the hydraulic model assumed no flow to the nodes. The limitation of the hydraulic model is addressed further in the section "Discussion."

Average Node Risks

Both the maximum and average node risks were higher for the branched network. Owing to the tank dynamics, the average residence time was longer for the looped network than for the branched network (looped network: 16.13 h, branched network: 12.85 h) (Fig. S2), meaning there was a longer duration over which the virus could be inactivated. For example, in the branched network case, downstream nodes generally reached a high enough virus concentration to affect average infection risk across the network. However, for the looped network, the tank dynamics translated to opportunities for virus spread throughout the network, regardless of the virus injection location, with simultaneous opportunities for viral inactivation due to the longer residence time and inactivation from interaction with chlorine.

Important Injection Locations

In most cases, influential injection sites were distributed over a wider area of the branched network but clustered in the middle of the looped network [Fig. 4(a)]. In the branched network, the most influential intrusion sites followed along the main flow path, upstream of other nodes [Fig. 4(a)]. For the branched network, there were high impact intrusion nodes in the main path leaving the source, with a larger region of more impactful injection locations due to the modified hydraulics from the tank operations. In some cases, some of the upstream injection sites were not identified as influential intrusion sites, potentially because they had little impact on downstream nodes that were dead ends with little to no demand. To explore this hypothesis, additional tracer analysis was conducted for these nodes, and a lower percentage of the water from the nodes in the rectangular box (Fig. 4) reached the vulnerable zone.

Exploring Chlorine Booster Location

Case study 2 was used to evaluate the influence of chlorine booster location for all possible virus injection scenarios [Figs. 4(b and c)]. Note that Fig. 4 only depicts results with the proposed chlorine booster locations that minimized the network risk for each network. More details regarding the specific chlorine booster scenarios that were identified as the most vulnerable can be seen in Figs. S4 and S5. The maximum chlorine concentration was under the maximum concentration of 4.0 mg/L regulated by USEPA (1.03 mg/L for the branched network and 2.10 mg/L for the looped network).

By comparing network risk distributions with and without chlorine booster, evident decreases in network risk were observed. For the branched network, most of the effective chorine booster locations (Fig. S4) were in the middle of the network, along the main flow path, consistent with the higher network risk areas [Fig. 4(a)]. Placement of a single booster effectively reduced risks for the downstream nodes (Fig. S5), where the average network risk for all of the injection scenarios without chlorine booster was 0.813, which was reduced to 0.363 with the addition of a chlorine booster.

For the looped network, effective chlorine booster locations were also located in the middle of the network, where both node and network risks were high for the scenario with no chlorine booster. However, the chlorine booster scenario failed to control the most influential injection scenario, where maximum virus

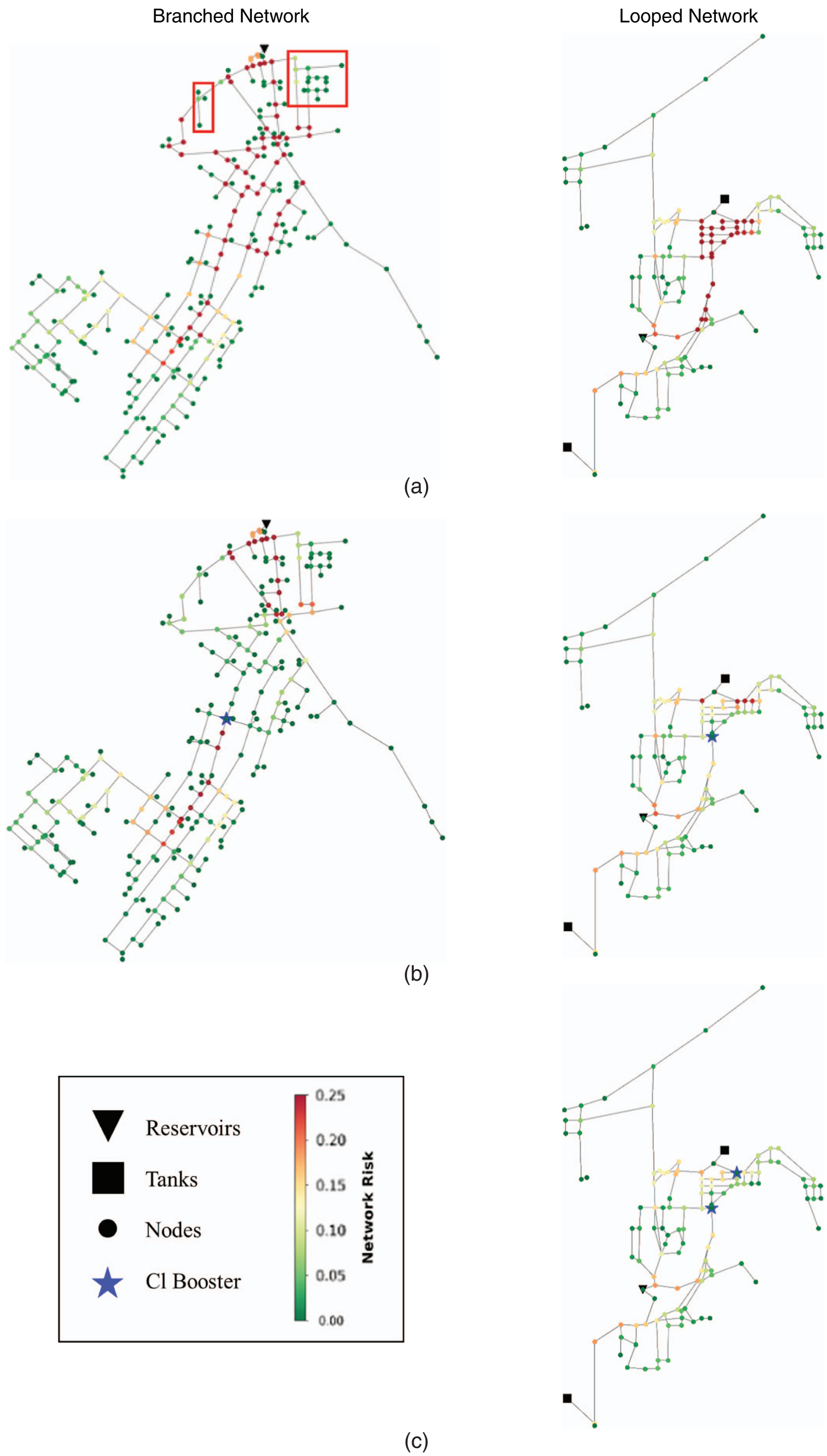

Fig. 4. (Color) Identification of most influential virus injection nodes in network with (a) no booster; (b) one booster; and (c) two boosters, where the color of the node indicates the average risk across the network if an intrusion event occurs at that node (network risk).

concentrations reaching the nodes remained unchanged despite booster placement (Fig. S5). Therefore, the placement of a second chlorine booster was explored for the looped network (Fig. S4). Compared to the single chlorine booster scenario, average risks were generally reduced (no booster: 0.125, single booster: 0.082, dual booster: 0.070; overall 44.2% reduction compared to no chlorine booster), and a visual inspection of network risk for the dual chlorine booster scenario [Fig. 4(c)] shows no high-risk nodes

Table 1. Spearman correlation coefficients for Monte Carlo scenario models

Model scenario		Model variable			
Network	Chlorine booster status	Virus inactivation rate	Virus concentration at intrusion site	Fraction of viral genome copies assumed to be viable	Volume of water consumed per day
Branched network	Without chlorine booster	−0.03	0.58	0.03	0.01
	With chlorine booster	−0.01	0.57	0.05	0.04
Looped network	Without chlorine booster	−0.05	0.65	0.04	0.06
	With chlorine booster	−0.05	0.64	0.04	0.07

Note: Spearman correlation coefficients reflect relationships between model variables and estimated infection risk, where a Spearman correlation coefficient with a greater magnitude indicates a stronger relationship.

(dark red). The network risk for the worst virus injection scenario was also reduced for the most influential injection scenario (0.525 to 0.200) (Fig. S5).

Infection Risk Reductions for a Worst-Case Scenario Intrusion Event

Before chlorine booster placement, average risks for the most influential injection scenario, the worst-case scenario, were higher for the branched network (0.67 ± 0.11) than for the looped network (0.47 ± 0.04). However, placement of a single booster was more effective at reducing average risk in the branched network than in the looped network, where average risk across the network was reduced by 47.6% and nearly not at all in the branched and looped networks, respectively. When a second booster location was selected in the looped network, infection risk reduction was more effective (Fig. S5), with mean infection risk across the network reduced by 63.0% relative to the no booster scenario. This is identical to what was captured from Case studies 1 and 2.

In the sensitivity analysis for the analysis involving Monte Carlo methods, the most influential parameter on infection risk estimation was virus concentration at the intrusion site ($\rho = 0.57$ to 0.65), whereas the least influential parameter was the fraction of genome copies assumed to be infectious for the looped network and either the volume of water consumed per day or the inactivation rate for the branched network scenarios (Table 1). Virus inactivation rate had similar correlation coefficients for the Bellingham network ($\rho = -0.05$ for with and without a single chlorine booster) and the branched network ($\rho = -0.03\,\text{to} - 0.01$) (Table 1).

Discussion

Key Findings

Average estimated infection risk for the most influential intrusion event was higher for the branched network without a tank (Oberlin) than for the looped network with a tank (Bellingham). However, placement of a chlorine booster was more effective at reducing average risk across the branched network for this influential intrusion than for the looped network. This is primarily due to the hydraulics, where the flow direction in the looped network was influenced by tank dynamics, unlike the branched network. The constant flow direction in the branched (Oberlin) network is common among branched networks without tanks. The comparison of these networks implies that chlorine booster placement is likely more complicated for networks with a lower BI. Because rural networks are typically more branched, implying a more consistent flow direction, the ideal placement of a chlorine booster may be easier to determine in these types of municipalities. This may also mean that multiple chlorine boosters for urban, looped networks may be necessary to reduce network-wide average risks below a specific risk threshold, whereas a single booster in a rural, branched network without a tank may be enough, depending upon baseline risks.

Limitations and Future Directions

One of the limitations of this work is the generalizability of our findings to other network types. However, flow direction changes due to the tank dynamics are typical since tanks can have either inflow or outflow. Therefore, the existence of a tank in other networks will likely yield findings similar to those obtained with Bellingham network in this study. Likewise, the lack of a tank in other networks will likely yield findings similar to those for the Oberlin network in this study. Still, more networks with varying configurations should be analyzed to support the generalizability of the findings in this study.

The assumption of a flow-paced injection for chlorine boosters involved a consistent addition of chlorine to the system. Because the focus of this research was on the placement of chlorine boosters, a target concentration to maintain a minimum chlorine residual was not calculated. Future work should expand upon this research by exploring the concentration additions needed and how this relates to specific booster locations within the network.

Another limitation related to the simulation model used is the unrealistic analysis at the zero or very low demand nodes (dead end). As Abokifa et al. (2019) highlighted, dead ends are not pipes without flow but more likely pipes with intermittent low flow and frequent stagnations. However, EPANET and EPANET-MSX cannot accurately estimate water quality at dead ends because the model is based on advection–reaction transport (Rossman et al. 1994). To overcome this limitation, the WUDESIM model developed by Abokifa et al. (2019) can be applied with the model introduced in this study in future work. It should be noted that this limitation is likely less important for a network-scale analysis but more relevant at the household level. It is recognized that continuous virus inputs are unlikely but possible, especially when retrofitting residential plumbing for recycled water and the potential for cross-connecting potable and nonpotable service lines.

The risks estimated in Case study 3 represent risks for a worst-case scenario, not only in terms of location of the intrusion event but also due to the continuous input of high concentrations of virus. These results are conservative insofar as continuous input of virus is unlikely. This assumption was intentionally used as part of a conservative risk approach because of the lack of data describing the timing and concentrations for scenarios in which contamination would enter the system, such as during a backflow event or a pipe break. This explains why daily infection risks, on average, are several orders of magnitude higher (Fig. 5) than the $1/10{,}000$ annual infection risk target used by the USEPA (Bitton 2014). Though the

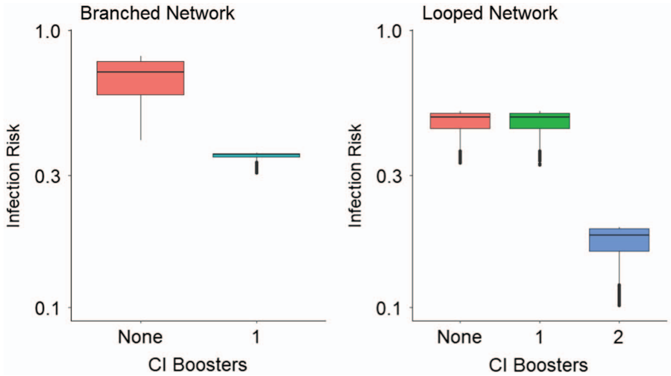

Fig. 5. (Color) Distributions of average infection risks across the network for the branched and looped networks with and without a chlorine booster.

worst-case scenario utilized here may be a highly unlikely event, the relative risk reductions to explore the value of chlorine boosters still allow for useful comparisons between the Oberlin (branched) and Bellingham (looped) networks. Instead, the average risk for the network was used to compare intervention effectiveness between the networks. As seen in Fig. S5, risks are not homogeneously distributed across networks. Thus, protecting a community at a risk threshold level may leave specific areas of a network still vulnerable to unacceptable risk. Considerations of the risk for the most vulnerable nodes can improve a risk assessment approach to the use of risk thresholds for evaluating drinking water safety and protecting the most vulnerable communities served by a network.

Further limitations include uncertainties regarding the volume and everyday behaviors regarding the use of municipal water. Assuming, on average, 0.902 L of drinking municipal water may be an overestimate for communities that prefer bottled water or use private wells or where water consumption occurs more at work or other locations outside the home. For example, in a study of households in Nogales, Arizona, a rural community, municipal water was a primary source of drinking water for only 10% of households, whereas municipal water was the primary source for bathing (95% of households), laundry (85% of households), and cooking (40% of households) (Beamer et al. 2012). In other cases, a volume of 0.902 L may also be an underestimate for communities that rely heavily on municipal water for drinking and that consume greater volumes of water due to living in hot climates. Because uses of municipal water can be community-specific and driven by risk perceptions of the safety of municipal water for drinking (Anadu and Harding 2000), future studies should consider the effects of variability in use across networks to more accurately estimate risk.

Conclusion

This study demonstrates that branched networks may experience greater average risk from a worst-case scenario virus intrusion event compared to looped networks. However, a single chlorine booster was more effective at reducing average risk in a branched network without a tank than in a looped network with a tank. Placement of chlorine boosters in a network with a tank must consider heterogeneous water flow direction. The generalizability of these results to other networks will depend on the specific hydraulics of other looped and branched networks and on the existence of tanks and variability in the use of municipal water for drinking. This work will aid drinking water managers in identifying vulnerable points in their system and the optimal locations for risk reduction strategy implementations, such as chlorine boosters.

Data Availability Statement

All data, models, or code that support the findings of this study are available from the corresponding author upon reasonable request.

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Supplemental Materials

Figs. S1–S5 are available online in the ASCE Library (www.ascelibrary.org).

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