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Cross-connections in drinking water distribution networks: Quantitative microbial risk assessment in combination with fault tree analysis and hydraulic modelling

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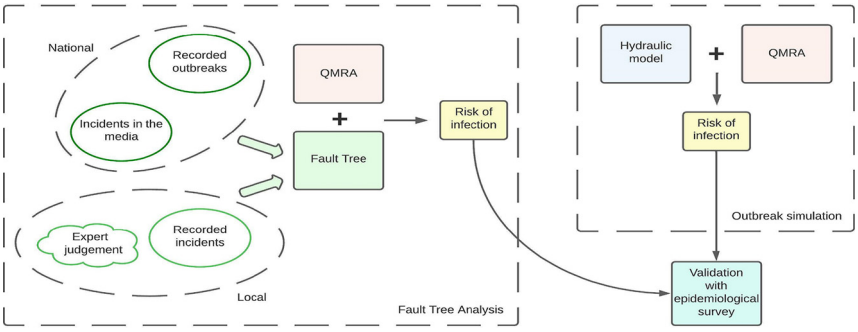
HIGHLIGHTS

- Study of cross-connections and backflows in drinking water distribution networks
- Assessment using national-aggregated data showed high infection risks.
- Assessment using local data showed acceptable infection risks.
- National data can be used for risk assessment, especially if local data are lacking.

GRAPHICAL ABSTRACT



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ABSTRACT

Deficiencies in drinking water distribution networks, such as cross-connections, may lead to contamination of the drinking water and pose a serious health risk to consumers. Cross-connections and backflows are considered among the most severe public health risks in distribution networks. The aim of this paper was to provide a framework for estimating the risk of infection from cross-connection and backflow events. *Campylobacter*, norovirus, and *Cryptosporidium* were chosen as reference pathogens for this study. The theoretical framework was constructed based on the fault tree analysis methodology. National aggregated cross-connection incident data was used to calculate the probability of a contamination event occurring in Swedish networks. Three risk cases were evaluated: endemic, elevated, and extreme. Quantitative microbial risk assessment (QMRA) was used to assess daily risk of infection for average national estimates. The framework was also evaluated using local data from the Gothenburg network. The daily risk of infection from cross-connection and backflow events in Swedish networks was generally above an acceptable target level of 10^{-6} for all reference pathogens and modelled cases; the exception was for the Gothenburg system where the risk was lower than 10^{-7}. An outbreak case study was used to validate the framework results. For the outbreak case study, contaminant transport in the network was simulated using hydraulic modelling (EPANET), and risk estimates were calculated using QMRA. The outbreak simulation predicted between 97 and 148 symptomatic infections, while the epidemiological survey conducted during the outbreak reported 179 cases of illness. The fault tree analysis framework was successfully validated using an outbreak case study, though it was shown on the example of Gothenburg that local data is still needed for well-performing systems. The framework can help inform microbial risk assessments for drinking water suppliers, especially ones with limited resources and expertise in this area.

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1. Introduction

Deficiencies in drinking water distribution networks, such as cross-connections, may lead to contamination of the drinking water and pose a serious health risk to consumers. Cross-connections and backflows are considered one of the most severe public health risks in distribution networks (National Research Council, 2006; WHO, 2014). Cross-connection and backflow events may occur at points in the distribution network where external non-potable water elements can come into contact with the drinking water (USEPA, 2002). When the pressure in the non-potable water source is greater than in the distribution system, and cross-connections controls are inadequate (i.e., absence of backflow prevention device), a backflow can occur (WHO, 2014).

Best practices are already established in the drinking water industry to prevent, detect, and remove cross-connections and backflows into the distribution network. Measures that can be implemented to reduce the risk of contamination of the drinking water include, e.g., supervision of new connections, inspection programs for detection of incorrectly-connected non-drinking water pipes or faulty backflow devices, certification of plumbing personnel, detailed mapping of pipe layout (WHO, 2014). Nevertheless, cross-connections and backflows are still sources of disease outbreaks across the globe (Craun et al., 2010; Guzman-Herrador et al., 2015; Hrudey and Hrudey, 2004; Schuster et al., 2005).

The largest waterborne outbreak reported in Finland was due to a cross-connection inside Nokia's municipal wastewater treatment plant (Laine et al., 2011). Approximately 450,000 L of treated wastewater flowed into the drinking water distribution network due to a cross-connection. A connection was made to the drinking water supply to ensure water availability for the dissolution of chemicals added to the wastewater treatment process even if the access to treated wastewater was disrupted. A valve in this emergency system was left open as an operational error. *Campylobacter*, norovirus, and *Giardia* were considered the main causative agents (Laine et al., 2011; Maunula et al., 2009; Rimhanen-Finne et al., 2010). Another large incident occurred in Belgium, where the firefighters' pressurised storage unit was alternatively refilled by water from fire hydrants and river water (Braeye et al., 2015). Since the fire brigade lacked a backflow prevention device (BPD) for their storage unit, which could have prevented the event, contaminated water then intruded into the drinking water system. The same causative agents as in Nokia were identified in infected patients' stool samples. In Everöd, Sweden, a low reservoir for drinking water storage was contaminated through its overflow function during a heavy storm event where the overflow pipe was flooded by stormwater and wastewater (Kristianstads kommun, 2015). This led to contaminated drinking water being distributed from the reservoir to the drinking water consumers causing a waterborne outbreak. The most likely causative agents were *Campylobacter* and calicivirus; these were detected in infected patients' stool samples during the outbreak. Similar cases have occurred earlier in Sweden, leading to outbreaks in Karlskrona and Sälen (Swedish Public Health Authority, 2021).

These examples show the potential for many more cross-connection events to be expected in the future. Reporting of waterborne disease outbreaks can illustrate impact of incidents in the distribution network on consumer health. There is reason to assume that minor incidents are underreported as currently installed monitoring systems often cannot detect them; also, drinking water suppliers and property owners have little interest in making them public knowledge. The city of Gothenburg, Sweden, has a system for reporting minor incidents to learn from mistakes and as input for risk analyses (Westrell et al., 2003). During a 25-year period for the 1800 km distribution network, this local reporting system revealed two incidents with household wastewater systems being improperly connected to the drinking water system and an incident with a private well pump cross-connected to the drinking water system. There were no indications of people getting ill from any of these incidents.

Microbial risk modelling can also be used to estimate the health effects of distribution network deficiencies. The quantitative microbial risk assessment (QMRA) framework was developed in the 1990s (Regli et al., 1991) and has been adapted into tools used by water suppliers to assess the risks related to the source water and the drinking water treatment processes (e.g., Hamouda et al., 2018; Mohammed and Seidu, 2019; Owens et al., 2020; Petterson and Ashbolt, 2016). The QMRA approach has also been applied to assess risks related to the distribution network (Blokker et al., 2018; Jamal et al., 2020; McInnis, 2004; Mena et al., 2008; Teunis et al., 2010; van Lieverloo et al., 2007; Yang et al., 2011; Yang et al., 2015). Earlier studies applied the QMRA approach to assess the infection risks due to intrusion during regular operation (Teunis et al., 2010; Yang et al., 2011) and during maintenance and pipe repairs (Blokker et al., 2018; Yang et al., 2015), as well as to plan the rehabilitation of the distribution network (Jamal et al., 2020). However, the effect of cross-connections and backflows has so far been studied only from an outbreak perspective (Mena et al., 2008). Our study expands the understanding of cross-connections and backflows by including both outbreak and endemic effects. The previous studies of the risks in the distribution network employed hydraulic modelling to provide input to carry out QMRA . The novelty of our study lies in developing a new approach, which utilises fault tree analysis (FTA) to provide input to QMRA. FTA has been used within a drinking water context (Lindhe et al., 2012; Lindhe et al., 2009; Risebro et al., 2007) as it enables modelling interactions between different events potentially leading to a system-wide failure and can be easily constructed from a combination of experience and literature information.

The aim of this paper was to provide a framework for estimating the risk of infection from cross-connection and backflow events. To estimate the risk of infection, an approach combining FTA and QMRA was developed and then validated using an approach combining hydraulic modelling and QMRA. An example of an actual outbreak was used as a case study. The outcomes of both approaches were compared with the results of an epidemiological survey from the outbreak. The following research questions were formulated:

- How can the available data be used to estimate the infection risks from cross-connection and backflow events?
- What data gaps need to be addressed to achieve reliable estimates of infection risks from cross-connection and backflow events?

2. Methodology

The theoretical framework developed in this study was divided into two main parts: one for calculating the probability of a cross-connection and backflow event in the drinking water distribution network (P) and the other for estimating the infection consequences during contamination events (C) using QMRA. An outbreak case study was used to validate the results obtained with the framework. The number of symptomatic cases due to norovirus infections for the outbreak case study was estimated using results from FTA calculation as well as using hydraulic modelling combined with QMRA. The estimates using these two approaches were eventually compared to the epidemiological survey carried out during the outbreak. Fig. 1 exemplifies the flow process for applying the methodology described in the following sections.

2.1. Fault tree analysis: probability of contamination event (P)

A generic fault tree was constructed to estimate the probability of a contamination event (P) in the distribution network (see Fig. 2). For a cross-connection to happen, two main failures must occur: (i) a non-potable source must be put into contact with the drinking water, and (ii) the competent authority fails to detect it either through having a supervision program with this goal but failing to detect or absence of supervision program (Fig. 2 – cross-connection intermediate event, Misconnection/Detection). The misconnection can be considered to originate from human error, e.g., connecting a wastewater/stormwater pipe to a point in the drinking water distribution network, or a design failure, e.g., connecting drinking water reservoir overflows to non-drinking water drainpipes.

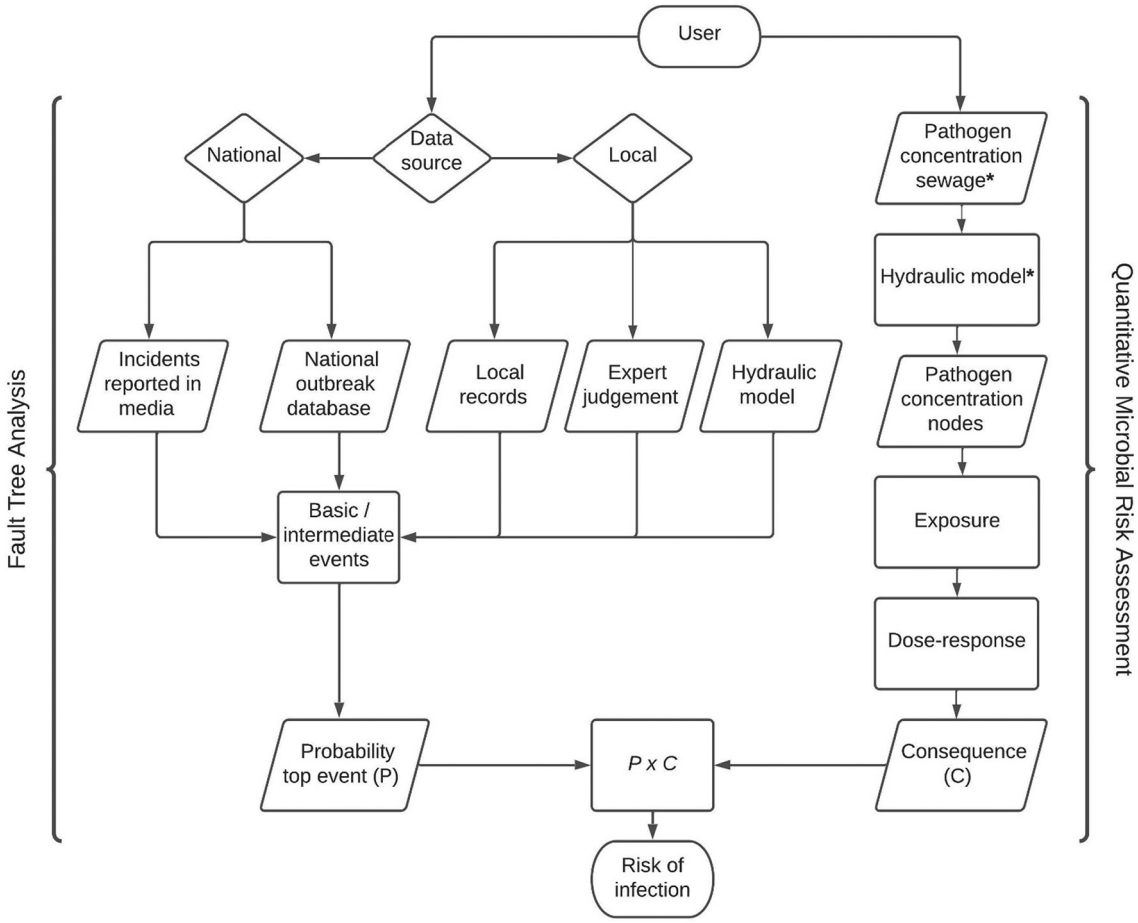

Fig. 1. Flowchart showing the procedure to calculate the risk of infection using the theoretical framework. The fault tree path allows the user to choose between using data at the national level or at the local level. Basic and intermediate events of the fault tree are assigned values and the probability at the top event is calculated. The quantitative microbial risk assessment path allows the user to estimate the infection consequences based on the exposure. The probability at the top event and the infection consequences are combined to calculate the risk of infection. The risk of infection obtained at the end of the process may be used to estimate symptomatic infections. The steps marked with an * may be used at the user's discretion, based on the level of detail needed for their particular assessment.

A backflow event can occur due to a combination of a backflow-prevention device (BPD) failure and adverse pressure conditions in the network (Fig. 2 – BPD intermediate event). The BPD may be missing or, if present, may be damaged. Transient pressure conditions can occur because of various failures in the network (Fig. 2). For a contamination event to occur, there must be both the presence of a cross-connection (source of contamination) and a backflow event (trigger of the event).

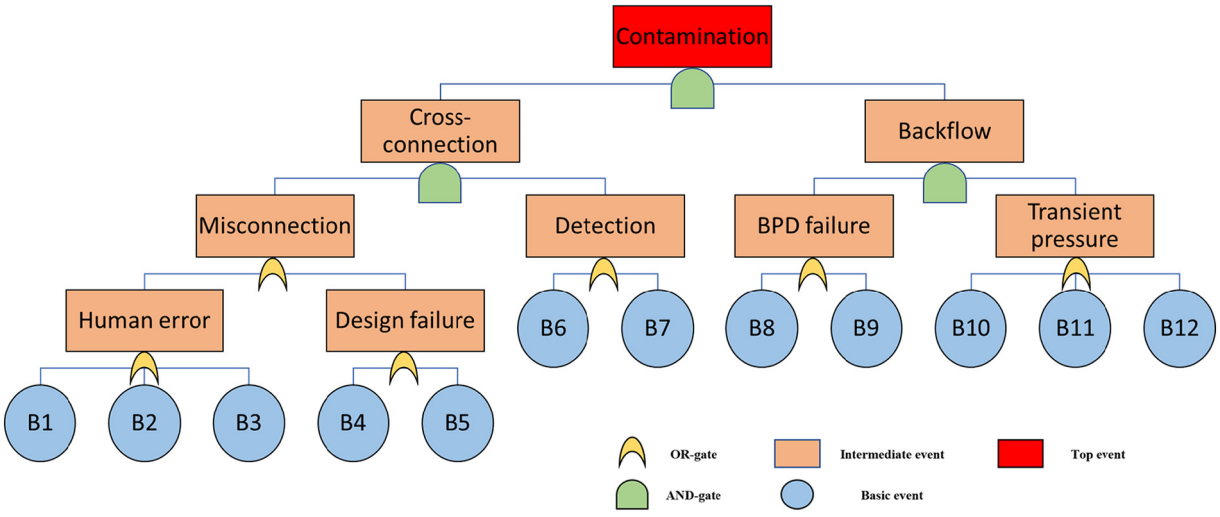

Fig. 2. Cross-connection and backflow fault tree. The probability calculated for the top event represents the likelihood of a contamination event at a given node in the network.

The list of basic events building up the cross-connection fault tree is presented in Table 1. The events are categorised based on the characteristics of the failure. To build this table, failure events suggested in the TECHNEAU Hazard Database checklist were used as well as events from historical outbreaks and previous risk assessments (Beuken and Pettersson, 2009; Braeye et al., 2015; Falco and Williams, 2009; Geldreich et al., 1992; Kristianstads kommun, 2015; Laine, 2014; Mena et al., 2008; Pan et al., 2021; Schoen et al., 2018; Xu et al., 2019). The resulting top event of the fault tree provides the probability of a contamination event occurring at any point in the distribution network.

To test the fault tree developed, the probability (P) at the top event was calculated with national aggregated data and with local system data for the Gothenburg network (see Table 2). Lindberg and Lindqvist (2005), expanded by Malm et al. (2010), compiled statistics on the frequency of reported incidents in the distribution network as published in Swedish media for a 9-year period compared to the reported waterborne outbreaks in Sweden during a 30-year period. It was estimated that for cross-connection and backflow, 0.16 incidents per 1000 km of pipe were reported in the 9-year study period, representing 14% of the total incidents in the media (Malm et al., 2010). However, the contribution of cross-connection and backflow events to outbreaks was 33% (0.13 outbreak incidents per 1000 km). The average length of the Swedish drinking water pipe network was calculated to be 231 km per municipality (total 67,000 km and 290 Swedish municipalities) (Government Offices of Sweden, 2018; The Swedish Water and Wastewater Association, 2000).

Events contributing to the endemic level of disease were estimated to occur at the same frequency as an incident reported in the media (see Table 2). Outbreaks were estimated to occur at the frequency of reported outbreak cases due to cross-connections and backflows. A severe outbreak was five times less frequent than a regular outbreak. This assumption was based on repeated reports of outbreaks caused by wastewater-impacted stormwater or similar; rarely was there a wastewater pipe cross-connected. The average length of distribution networks at a national level was used for national estimates.

The Gothenburg network was selected to test the method with local data. Local network data was available for Gothenburg at the basic event level. Cross-connection incidents recorded in Gothenburg's system, complemented with expert judgement when data was unavailable, were used to generate the basic event values (see Table 1). *B2 – Incorrect connection in-house plumbing* had a likelihood of 0.05; *B3 – Misc. error* was 0.1; and *B12 - Inadequate pressure due to pipe failure* was 0.0011. All other basic events with no records

Table 2
Summary of national estimates and Gothenburg for probability of a contamination event (P) for the different cases.

Parameter	Value	Description
Total length of distribution network in Sweden	67,000 km	The Swedish Water and Wastewater Association, 2000
No. of Swedish municipalities	290	Government Offices of Sweden
Average length of distribution network/municipality	231 km	
No. of disturbances reported 2000–2008	11 incidents	Malm et al. (2010)
No. of disturbances reported 2000–2008 (km^{-1} yr^{-1})	1.82×10^{-5}	Probability of a contamination event for endemic disease
Outbreaks reported 1980–2009	9 outbreaks	Malm et al. (2010)
Outbreaks reported 1980–2009 (km^{-1} yr^{-1})	4.48×10^{-6}	Probability of a contamination event that leads to outbreak
Outbreaks reported 1980–2009 (km^{-1} yr^{-1})[a]	8.96×10^{-7}	Probability of a contamination event that leads to (severe) outbreak
Gothenburg (km^{-1} yr^{-1})	3.31×10^{-8}	Probability of a contamination event for Gothenburg distribution network

[a] A severe outbreak was 5 times less frequent than a normal outbreak.

Table 1
List of basic events for cross-connection and backflow events.

ID	Basic events	Type	Description
B1	Inappropriate maintenance/repair work in the mains	Misconnection: Human error	Inappropriate connection of a non-potable water pipe to drinking water pipe during regular maintenance or repair work
B1	Building of new mains	Misconnection: Human error	Inappropriate connection of a non-potable water pipe to drinking water pipe during construction of new mains
B2	Incorrect connection in-house plumbing	Misconnection: Human error	Inappropriate connection of a non-potable water pipe to drinking water pipe (service lines)
B3	Misc. error	Misconnection: Human error	Other human mistakes
B4	Backflow into reservoir from overflow pipe	Misconnection: Design failure	Overflow in the reservoir connected to a non-potable pipe
B5	Misc. design	Misconnection: Design failure	Other design mistakes
B6	Failure of supervision	Detection	Lack of supervision program during new connections to the network Lack of sufficient staff and/or knowledge about the system Lack of sensors in critical control points
B7	Supervision failure	Detection	Supervision program fails to detect misconnection, e.g., sensor malfunction, human error
B8	BPD failure	Backflow: BPD failure	Faulty backflow-prevention device
B9	Absence of BPD	Backflow: BPD failure	Absence of device to prevent backflow
B10	Pump failure	Backflow: Hydraulic loss	Low pressure in the network due to wrong settings, deficient metering, or deficient control of pumps operation
			Power failure combined with failing back-up supply
			Mechanical malfunctioning/failure
			Damage or destruction of network pipes due to water hammer, caused by absent or malfunctioning surge tanks
			Human-caused accidents (car, truck or aircraft collision, landslides caused by leakage or nearby excavation)
B11	Valve failure	Backflow: Hydraulic loss	Pipe burst due to water hammer caused by wrongful operation
B12	Pipe failure	Backflow: Hydraulic loss	Pipe burst due to increased external stresses on pipe (e.g. traffic, soil movement, etc.) in combination with a reduced pipe condition
			Pipe burst due to deteriorated physical condition of the pipe

were considered to have a likelihood of 0.001 to be able to account for extremely infrequent events. Probabilities were calculated for intermediate and top events. The total length of the network was 1800 km. An example of calculation is provided in Supplementary material S1.

2.2. Quantitative microbial risk assessment: infection consequences (C)

In parallel to calculating the probability of contamination event (P), the magnitude of the infection consequences during contamination events (C) was estimated using QMRA. Three levels of potential contamination scenarios of pathogen load in intruded water were considered: (1) endemic risk case, (2) elevated risk case and (3) extreme risk case. The levels were generated from a study of a new monitoring sensor tested in Swedish networks (Sensation III, Unpublished). The concentrations of the indicator organism *Escherichia coli* assumed to intrude into the distribution network for each case were:

Endemic risk case: 5–50 CFU/100 mL (0.005–0.05% untreated wastewater).

Elevated risk case: 700 CFU/100 mL (0.7% untreated wastewater).

Extreme risk case: 5000 CFU/100 mL (10% treated wastewater).

Endemic risk case (F1 for national estimate; Got1 for Gothenburg estimate) represents the background level of risk present in the distribution network due to minor incidents. The *elevated risk case* (F2; Got2) was an outbreak of the same magnitude of contamination as the Everöd outbreak (Kristianstads kommun, 2015). The *extreme risk case* (F3; Got3) was based on the Nokia outbreak (Laine et al., 2011).

The reference pathogens chosen were *Campylobacter*, norovirus, and *Cryptosporidium*. These are the most relevant enteric pathogens for Swedish networks, representing bacterial, viral, and protozoan organisms (Abrahamsson et al., 2009; WHO, 2014). Concentrations were calculated using ratios of the faecal indicator concentrations, *E. coli*, for each scenario and standard values of pathogens for domestic wastewater and treated wastewater (Henze et al., 2001; Hewitt et al., 2011; Metcalf and Eddy, Inc., 2003) (see Table 3).

To account for the uncertainty, the pathogen concentrations were treated as a triangular distribution (min, mode, max). The minimum and maximum values were taken from the range provided in the literature (when available), and the most likely value was the average of the range. If the pathogen concentration was given in the literature as a point estimate, the maximum value from the less critical scenario was used to generate the range, e.g., minimum concentration for *Campylobacter* in the elevated case was assumed to be the same as the maximum value in the endemic case. The mode was then the average of the range times 1.5 to account for skewness towards the maximum value in wastewater. Pathogen concentrations for each risk case used for the QMRA are shown in Table 3.

These concentrations were used to calculate the probability of infection (P_{inf}) for each reference pathogen using previously established Beta-Poisson dose-response functions: *Campylobacter* ($\alpha = 0.024$, $\beta = 0.011$) (Teunis et al., 2005), norovirus ($\alpha = 0.04$, $\beta = 0.055$) (Teunis et al., 2008) and *Cryptosporidium* ($\alpha = 0.115$, $\beta = 0.176$) (Teunis et al., 2002). The population was assumed to be homogenous, i.e., all consumers would respond according to the chosen dose-response function. Each case was simulated for different durations of contamination incidents: 1 h, 2 h, 4 h, 8 h, 12 h, and 24 h. The daily consumption pattern was a lognormal distribution (mean = 0.87 L, stddev = 0.54 L) taken from Westrell et al. (2006). For durations under 8 h, the lognormal distribution was assumed to have a mean of 200 mL (one standard serving). This was assumed to be a representative volume for hourly consumption. The daily probability of infection with the different durations of incidents was calculated as:

$$C = 1-\left(1-P_{inf}\right)^{n}$$

where C is the daily risk of infection for each case and reference pathogen,

P_{inf} is the hourly probability of infection for each reference pathogen based on dose-response models,

n is the duration of the contamination event (1 h, 2 h, 4 h, 8 h, 12 h, and 24 h) expressed in days.

Finally, the daily risk of infection (R_{daily}) for consumers in Sweden and Gothenburg was calculated by multiplying the probability of a contamination event (P) times the daily infection consequences during contamination events (C) for each case ($R_{daily} = P\,x\,C$). The acceptable target for daily risk of infection was 10^{-6} (Signor and Ashbolt, 2009) since a daily target would be more representative of the risk caused by contamination events in the distribution network than a yearly target. The calculations of R_{daily} were performed using the assumptions on the national level as well as, for the purpose of comparison, on the example of Gothenburg. The calculated R_{daily} for the national level was also used to estimate the number of infected consumers during the outbreak case study presented in the following section for validation purposes.

2.3. Waterborne outbreak case study

A waterborne outbreak in a small municipality in Sweden (undisclosed for security reasons) was used as a case study to validate the framework developed for cross-connections and backflows. Hydraulic modelling was carried out to simulate the pathogen transport in the distribution network during the outbreak. QMRA was used to assess the infection risks during the outbreak. Symptomatic cases were quantified using both the hydraulic modelling and the national FTA infection risks and were compared to the reported cases in the epidemiological survey conducted during the outbreak.

2.3.1. Event description

The first indications of an outbreak were reported on the 4th of July 2010, when multiple gastrointestinal illness complaints reached the drinking water producer (confidential internal report, 2010/2011). The geographic spread of the reported cases led to the suspicion that the drinking water was the source of the illness. A fault investigation was carried out on the 5th of July. One of the households that first reported symptoms had a cross-connection between the municipal distribution network and their private well, which was used as a water source for livestock, with a malfunctioning check valve. The well was impacted by the household's three-chamber septic tank with a ground bed. When the water pressure from the well on the farm's side (which had a hydrophore tank) became higher than in the drinking water distribution network, contaminated water was pumped into the network and distributed to the consumers downstream of the household.

The cross-connection was disconnected immediately after discovery. Water samples were collected from the private well and household tap. Analyses of the water samples showed high levels of faecal indicators, and norovirus GII.4 was detected via PCR analysis. Norovirus GII.4 was

Table 3
Pathogen concentrations assumed to enter the distribution network for each risk case used for the QMRA calculations.

Reference pathogen	Endemic mode (min, max) No./L	Elevated mode (min, max) No./L	Extreme mode (min, max), No./L	Reference
Campylobacter	71.5 (13,130)	1410 (130, 1750)	20,062 (1750, 25,000)	(Metcalf and Eddy, Inc., 2003)
Norovirus[a]	27.5 (5, 50)	577 (70, 700)	600 (500, 700)	(Metcalf and Eddy, Inc., 2003)
Cryptosporidium	2.53 (0.5, 5)	5.78 (0.7, 7)	8.5 (7, 10)	(Henze et al., 2001)

[a] Norovirus is analysed for gene copies, and not only "living" (infectious) pathogens, and assumed to have a reduced infectivity of 1/100, i.e., only 1 organism for every 100 would be capable of infecting the host (Hewitt et al., 2011). Norovirus concentrations in this table were later reduced according to this assumption when carrying out the QMRA.

also detected in stool samples collected from two consumers in the affected area.

Emergency measures taken during the event included: boiling alert issued and communicated through the municipal website, radio, telephone information services, and local press; additional chlorination in the network to achieve a residual disinfectant; hydrant flushing; water trucks deployed to one of the affected neighbourhoods to fill up the reservoir supplying the area.

An epidemiological survey was sent to all 610 households in the affected downstream area on the 22nd of July, and 323 households, with 1297 consumers, responded to the survey. Approximately 14% of the consumers (n = 179) reported symptoms consistent with norovirus infection. The most common symptoms were diarrhoea (n = 141, 79%), abdominal cramps (n = 109, 61%), vomiting (n = 85, 47%), and fever (n = 68, 38%). Fig. 3 shows the time distribution of the reported illness during the outbreak.

2.3.2. Risk assessment

The following steps were taken to assess the number of symptomatic infections for norovirus during the outbreak:

1. Estimation of norovirus load due to contaminated well water being pumped into the distribution network
2. Simulation of the norovirus transport within the distribution network using a hydraulic model in EPANET (Rossman, 2000)
3. Calculation of infection risks using QMRA based on concentrations from the EPANET simulation
4. Calculation of the risk of illness and comparison with the epidemiological survey, and the risk of illness calculated using FTA.

To estimate the norovirus load in step 1, virus shedding in faeces, 10^9 norovirus/g of faeces (min-max: 1×10^5–1.64×10^{12} copies/g of faeces), was taken from a human experimental study (Atmar et al., 2008). The amount of stool produced by a person in one day was 106 g (min-max: 80 g–120 g) (Cummings et al., 1992). The average load at the septic tank outlet was 1.06×10^{11} copies/day; the minimum load was 1.06×10^7 copies/day; the maximum load was 1.74×10^{14} copies/day.

The norovirus load was then applied a reduction factor, ranging between 10^{-6} and 10^{-3} (Åström et al., 2016). The reduction factor represented the transport of pathogens from the septic tank through the soil material to the private well, from which the contaminated water was pumped into the distribution network. Due to the considerable uncertainty associated with the pathogen transport from the septic tank to the well, each reduction factor was considered a different scenario (scenarios C1–C4). For scenario C1, the norovirus load intruding into the network was 73.6 copies/min (55.6–83.33 copies/min), increasing 1-log for each subsequent scenario.

For step 2, a hydraulic model of the affected area in EPANET was used to simulate the downstream transport of the contamination to the consumers' taps. The water supplier provided the network's demand patterns and pressure conditions to recreate the conditions under which the outbreak occurred as accurately as possible. The downstream distribution network was divided into three main zones: Z1, Z2, and Z3. The zones and the cross-connection node in the system are highlighted in Fig. 4. Key zones were selected to represent the contamination transport at the neighbourhood level, i.e., the concentrations of norovirus in the nodes within a zone were assumed to be equal. The contamination node was based on the location of the cross-connection as documented in the outbreak investigation. The cross-connection event was assumed to last for 1 h per day, which the drinking water supplier hypothesised was a reasonable assumption for the outbreak (personal communication). The total length of the network was 39.7 km. In the hydraulic model, the quality time step was set to 1 min, and the simulation ran for 168 h.

For step 3, the concentrations in each node from the hydraulic simulation were used as input data to estimate the infection risks. A triangular distribution with the minimum, mean and maximum concentrations were generated for each zone. The probability of infection was calculated using the dose-response model and consumption pattern as described in section 2.2 on QMRA.

In step 4, the daily risk of infection was used to quantify the number of symptomatic cases during the outbreak. The estimated number of symptomatic cases was then compared to the number of reported cases documented in the epidemiological survey sent to the affected community. Cross-connection duration was assumed to be either 9 or 10 days, considering an incubation time of 1–2 days (Lee et al., 2013) and the date the cross-connection was disconnected. As the affected area had a high number of short-term residents as the outbreak occurred during a holiday period, a range of 3–4 persons per household was used. The proportion of asymptomatic infections due to norovirus GII.4 was assumed to be 40.7% (95% CI: 32.8%–49.0%), taken from an outbreak study in Japan (Miura et al., 2018). Additionally, the number of symptomatic cases was calculated using the national daily risk of infection for norovirus (1 h) – endemic from the FTA (section 2.1) to compare with the epidemiological survey and the estimation based on the EPANET simulation. Finally, the estimates using the hydraulic simulation and using the FTA were compared with the number of reported cases documented in the epidemiological survey.

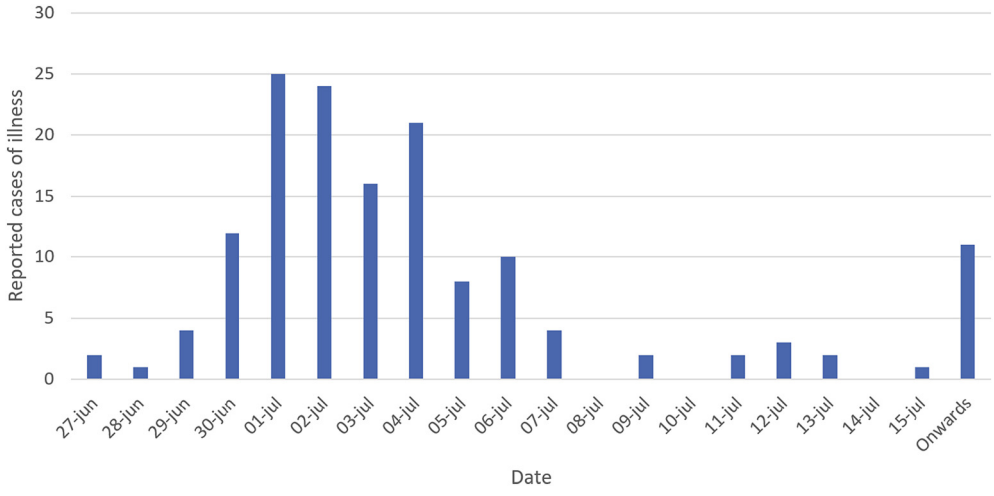

Fig. 3. Number of reported cases of illness per day during the waterborne outbreak (Confidential internal report, 2010/2011). The final reported case occurred on 1 August 2010. The total number of reported cases was 179.

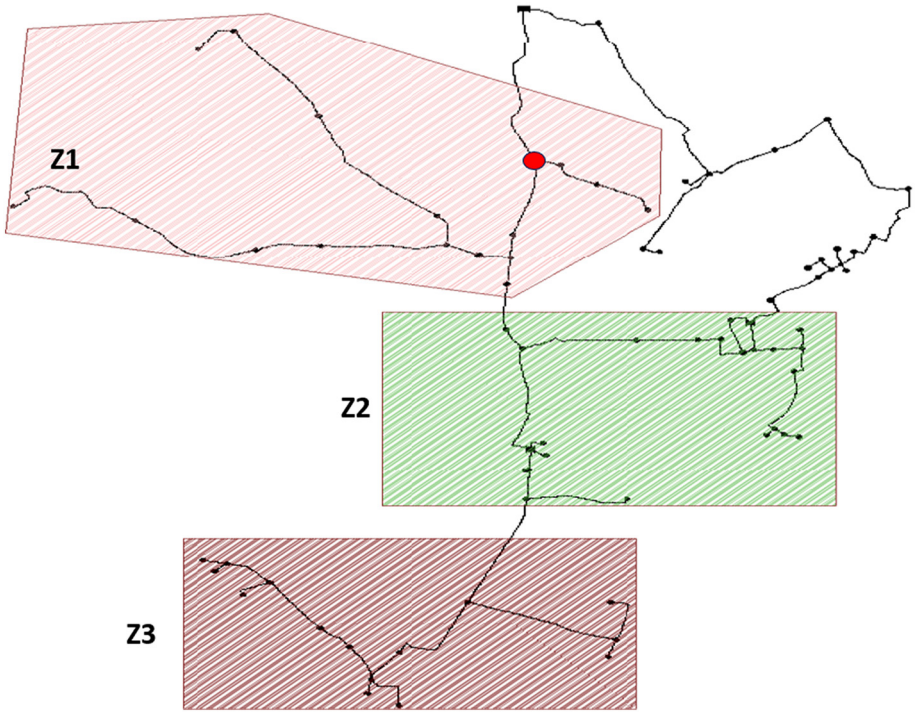

Fig. 4. Schematic representation of the studied distribution network divided in zones Z1, Z2 and Z3. The contamination node (red dot) was located in Z1. The segment of the network not highlighted in any zone was discarded from the analysis, since the contamination did not reach the consumers in that area. For security reasons, the network scale and configuration has been distorted.

3. Results

The estimated national daily risks of infection for the endemic, elevated, and extreme cases are presented in Fig. 5. For all tested cases, the medians were higher than the acceptable target of 10^{-6}. Median values of daily risk ranged between 10^{-4} and 10^{-3} for *Campylobacter;* 10^{-5} and 10^{-3} for norovirus; and 10^{-6} and 10^{-4} for *Cryptosporidium*. Norovirus showed the most extensive spread in all three cases, while *Campylobacter* had the largest proportion of values close to the (absolute) maximum risk of infection. *Campylobacter* also showed the least spread of all the cases studied. In general, the national daily risk of infection was highest for the endemic case (F1) compared to the elevated (F2) and extreme (F3) cases for all reference pathogens (Fig. 5).

The daily risk of infection calculated for the distribution network in Gothenburg is shown in Fig. 6. All values, including maximums, were below the acceptable target of 10^{-6}. The highest risk of infection was for

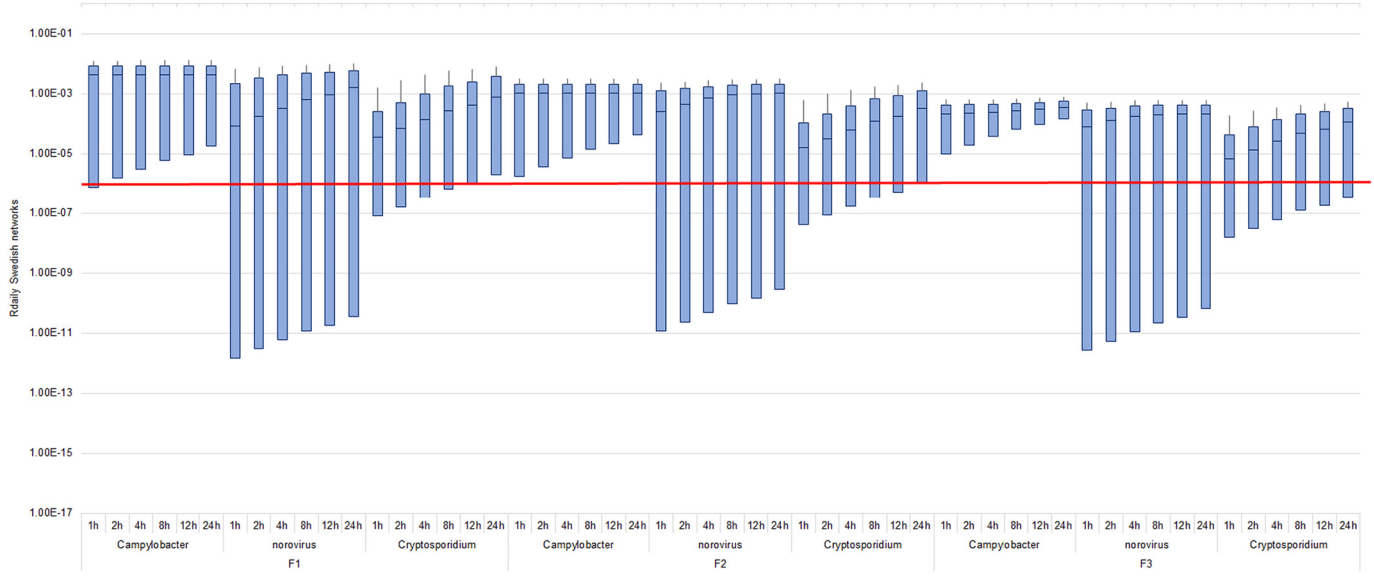

Fig. 5. Box plots for daily risks of infection from cross-connection and backflows in an average Swedish distribution network. The red line is the target value for daily risk of infection (10^{-6}). Times (in hours) on the x-axis represent the different durations of contamination events considered for the calculations, e.g., 1 h is a cross-connection and backflow event lasting 1 h. The bottom and top of the box are the 25th and 75th percentile of the values, respectively. The line inside the box is the median. The upper whisker shows the largest value (excluding outliers) and it is calculated as 1.5*IQR. The value for the bottom whisker is 0 (not shown).

Got3 - *Campylobacter,* while *Cryptosporidium* had, in general, the lowest risks of infection.

For the outbreak case study, the calculated daily risks of infection for the scenarios simulated using hydraulic modelling are shown in Fig. 7. For scenarios C1 and C2, the risk of infection was in the order of 10^{-2} and 10^{-1}, respectively; and for scenarios C3 and C4, the median value for risk of infection was 1 (i.e., 100% infected). Based on the results for scenario C1, the number of symptomatic cases was quantified (Table 4). The number of symptomatic cases, as estimated using hydraulic modelling, varied between 97 and 148, depending on the assumptions about the duration of the contamination event (9 or 10 days) and the number of people per household (3 or 4). The most affected neighbourhood was Z2, with between 41 and 61 symptomatic cases, depending on underlying assumptions (Table 4).

The number of symptomatic cases for the outbreak case study was also estimated using the results from the national FTA. The number of symptomatic cases, as estimated using the infection risk calculated with FTA for 1 h duration, was 87. The epidemiological survey carried out during the outbreak recorded 179 cases of illness.

4. Discussion

The daily risk of cross-connections and backflows was evaluated using the FTA framework for three different cases: endemic, elevated, and extreme; at two different levels: national aggregated networks and the Gothenburg network; and three reference pathogens: *Campylobacter*, norovirus, and *Cryptosporidium*. The national risk estimations showed that all reference pathogens (Fig. 5) had a median risk of infection higher than the acceptable daily target of 10^{-6}. Previous studies have shown high risks for norovirus during simulated intrusion events in other distribution networks (Teunis et al., 2010; Yang et al., 2011) and the contribution of the distribution network to *Campylobacter* infections in Sweden (Nygard et al., 2004). However, data is lacking on the occurrence of *Cryptosporidium* in distribution networks; hence it is not possible to determine the appropriateness of the conclusions for this reference pathogen.

Surprisingly, the endemic case (F1) had a higher daily risk of infection than the elevated (F2) and extreme (F3) cases. This can be explained by the higher frequency of incidents in the network than reported outbreaks, i.e., higher P for incidents that do not seem to cause outbreaks. Furthermore, the infection consequences (C) in the distribution network can be considered more severe than, e.g., when evaluating a water treatment plant, even in the presence of just a small concentration of pathogens, due to lack of microbial barriers to protect the consumers. Recent epidemiological studies, including the ones performed in Swedish networks, have shown that the endemic contribution to the annual burden of gastrointestinal illness could be significant (Ercumen et al., 2014; Nygård et al., 2007; Säve-Söderbergh et al., 2017). This implies that, for a cross-connection and backflow event, the most relevant parameter would be the probability of a contamination event occurring, irrespective of the level of contamination intruding into the network. Therefore, implementing mitigation measures to prevent contamination events entirely, e.g., cross-connection detection programs and proper installations of BPDs, and preserving hydraulic integrity, would be the most effective at reducing the daily risk of infection.

Calculating the probability of occurrence using the length of the network is subjected to confounding with factors, such as the age of the distribution network and the proximity of wastewater networks. For example, ageing infrastructure is prone to higher break rates (Ercumen et al., 2014; Renwick et al., 2019), which would increase the likelihood of inadequate pressure conditions in the network. In addition, local conditions may differ significantly between networks, even if they are of similar size. This is reflected when evaluating the Gothenburg system using FTA, where the infection risks for all scenarios were below the acceptable target of 10^{-6}. This contradicts the expected result from the national estimates as, based on our assumptions, there is a positive correlation between the length of the network and the probability of incidents. Since the national data groups well-functioning networks with poorly performing networks and averages the performance, the distribution networks that are considered well-functioning (such as Gothenburg) would need to carry out local risk assessments to have a realistic outcome from the analysis.

In the outbreak case study, the outcomes for scenario C1 simulated using the hydraulic model were in the same order of magnitude as the result of the epidemiological survey conducted in the area. This implies that the assumptions made for scenario C1 were the most representative of the actual conditions that led to the outbreak in terms of contamination intruding into the network and the duration of the event. One potential limitation was

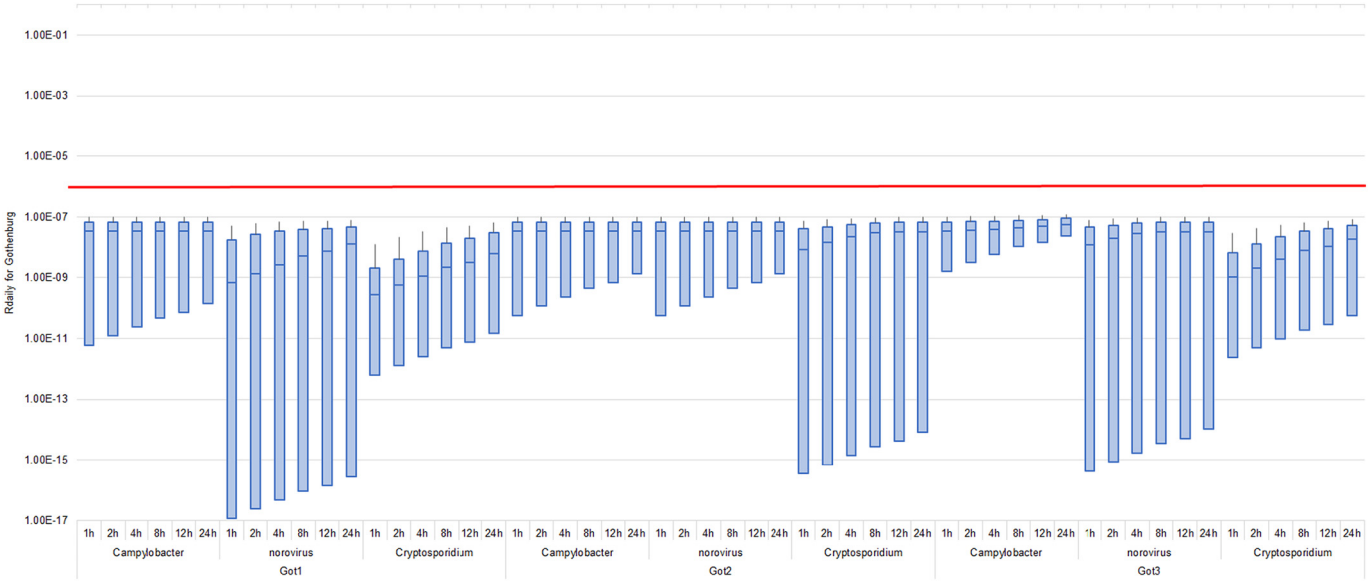

Fig. 6. Box plots for daily risks of infection from cross-connection and backflows in the Gothenburg distribution network. The red line is the target value for daily risk of infection (10^{-6}). Times (in hours) on the x-axis represent the different durations of contamination events considered for the calculations, e.g., 1 h is a cross-connection and backflow event lasting 1 h. The bottom and top of the box are the 25th and 75th percentile of the values, respectively. The line inside the box is the median. The upper whisker shows the largest value (excluding outliers) and it is calculated as 1.5*IQR. The value for the bottom whisker is 0 (not shown).

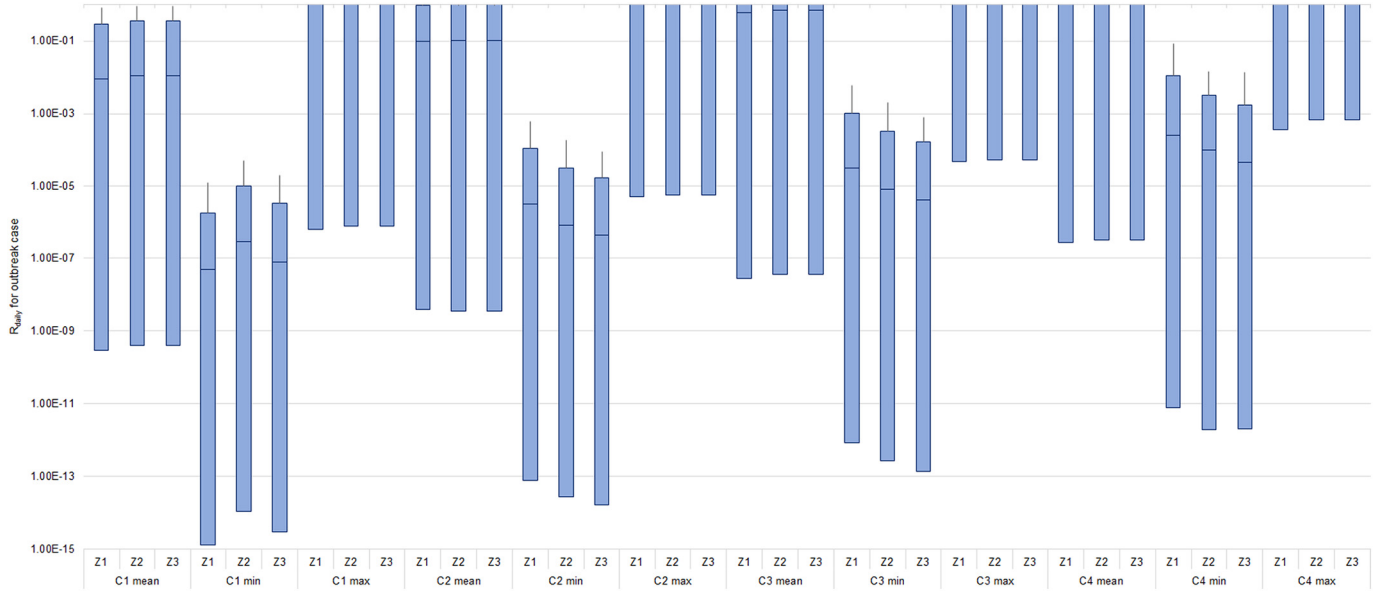

Fig. 7. Daily risk of infection of norovirus during the studied outbreak for each zone (Z1-Z3) and scenario (C1–C4). Mean, min and max refer to the mean, minimum and maximum levels of contamination that intrude the network during the hydraulic simulation. The bottom and top of the box are the 25th and 75th percentile of the values, respectively. The line inside the box is the median. The upper whisker shows the largest value (excluding outliers) and it is calculated as 1.5*IQR. The value for the bottom whisker is 0 (not shown).

the lack of a local consumption pattern to include a time component, which is relevant in QMRA studies (Blokker et al., 2018; Säve-Söderbergh et al., 2018; Westrell et al., 2006). The peak contamination may have occurred during a time of day when most users were irrigating their gardens or filling their pools. This may cause an overestimation of the risk to consumers, considering that not all water used by the household would be for drinking purposes. However, overestimation may not have been a factor in our simulation, considering that the estimated cases were in line with the epidemiological survey.

Mitigation measures implemented during the outbreak were not included in our simulations since the cross-connection had already been disconnected when the measures were carried out. However, including different measures (e.g., flushing, chlorination) is computationally feasible and can be helpful to inform water suppliers on the best approach to take during an ongoing event. Furthermore, the usefulness of testing mitigation measures in the network has been shown in other QMRA studies (Blokker et al., 2018; Yang et al., 2015). Additionally, QMRA, as performed in this study, could be used to inform sensor placement strategies in future distribution networks by identifying the parts of the network with the highest contribution to the infection risks.

In our study, we chose to focus on the risk of infection as the risk measure. However, not all cases of infection lead to illness. This was exemplified in our case study, where we used the estimated infection risks to calculate the number of consumers that would develop symptoms during the outbreak. An additional step was necessary, i.e., assuming that a certain proportion of the infections were symptomatic. It was also assumed that the population was equally susceptible to the reference pathogen, which may not represent sensitive risk groups, e.g., children or immunocompromised populations. An alternative target, such as disability-adjusted life years, would be able to account for this variability, though for our study, it was deemed unnecessary due to the risks already being above the risk target.

Risk estimates using the FTA framework were also used to calculate the predicted number of symptomatic infections during the outbreak. The number of cases estimated with the FTA framework was lower than cases reported in the epidemiological survey and the outbreak simulation. The discrepancy can be attributed to using aggregated national data for Swedish networks, which may not truly represent the network conditions in the outbreak case study. However, the estimation was still within a reasonable range compared to the epidemiological survey, indicating that national estimates can be sufficient for preliminary risk assessments in distribution networks with similar conditions to Sweden.

FTA has several advantages that strengthen its potential use by drinking water suppliers looking to perform risk assessments in their networks. Fault trees can be combined efficiently with other probabilistic methods to address incomplete input datasets better: fuzzy logic (Sadiq et al., 2008; Singer, 1990), Markov approaches (Lindhe et al., 2012; Lindhe et al., 2009), and Bayesian belief networks (Beaudequin et al., 2016; Bobbio et al., 2001). Fault trees allow multiple failures to be analysed simultaneously, which is relevant for cross-connection and backflow events as they are a combination of failures in the network. Local information can be seamlessly included, if, e.g., statistics on duration of low-pressure events are available for the network, as well as information on the physical condition of the network. The simplicity of the FTA framework shown and the seemingly good fit with the outbreak case study indicate that water suppliers can evaluate their networks for risk of cross-connections with little effort. This could provide small suppliers, usually with limited economic

Table 4
Estimation of infected consumers (symptomatic infections) for C1 under different assumptions for the outbreak case study. Total number of persons becoming ill collected in an epidemiological survey and estimation of infected consumers using median risk of infection from F1 – norovirus 1 h is also shown.

Zone	9-days event		10-days event		Reported cases epidemiological survey	Cases using FTA framework
	3 pers. per household	4 pers. per household	3 pers. per household	4 pers. per household		
Z1	26 (23 – 30)	35 (30–40)	30 (25–33)	38 (33–44)	Total: 179	Total: 87
Z2	41 (36–47)	54 (47–62)	45 (39–51)	61 (52–68)		
Z3	30 (25–34)	39 (34–45)	33 (28–37)	49 (38–49)		
Total	97 (84–111)	128 (111–147)	108 (92–121)	148 (123–161)		

resources and expertise to carry out comprehensive assessments, with a reasonable risk assessment tool and estimations of infection risks that can be expected in their networks.

5. Conclusions

The FTA framework developed in this paper is a first step towards a more comprehensive probabilistic risk assessment tool to evaluate infection risks due to distribution network deficiencies. The most sensitive parameter influencing the daily risk of infection for Swedish networks was the probability of a failure event occurring. This implies that mitigation measures should focus on preventing failure events in the network. The FTA framework and the outbreak simulation showed an acceptable prediction of the number of cases expected from a cross-connection and backflow event when compared to the epidemiological survey carried out during the outbreak. The FTA framework can help inform initial microbial risk assessments for drinking water suppliers, especially the ones with limited resources and expertise in this area. However, local data is still necessary to carry out a proper assessment in well-maintained systems.

CRediT authorship contribution statement

Victor Viñas: Conceptualization, Methodology, Formal analysis, Investigation, Writing – Original draft preparation, Visualization. **Ekaterina Sokolova:** Conceptualization, Writing – Review & Editing, Supervision/mentorship. **Annika Malm:** Conceptualization, Supervision. **Olof Bergstedt:** Investigation, Writing – Review & Editing. **Thomas J.R. Pettersson:** Conceptualization, Methodology, Investigation, Writing - Review & Editing, Supervision, Funding acquisition.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.scitotenv.2022.154874.

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