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Quantitative microbial risk assessment of a non-membrane based indirect potable water reuse system using Bayesian networks

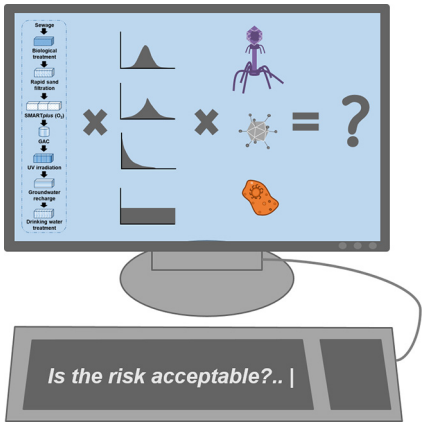
Veronika Zhiteneva [a], Guido Carvajal [b], Omar Shehata [a], Uwe Hübner [a,*], Jörg E. Drewes [a]

[a] Chair of Urban Water Systems Engineering, Technical University of Munich, Am Coulombwall 3, 85748 Garching, Germany
[b] Facultad de Ingeniería, Universidad Andrés Bello, Antonio Varas 880, Providencia, Santiago, Chile

HIGHLIGHTS

- A QMRA for an IPR treatment train featuring SMART*plus* was conducted using a BN.
- Norovirus, *Cryptosporidium*, and *Campylobacter* disease burden lower than 10^{-6} DALYs
- *Cryptosporidium* posed the greatest disease burden to the non-membrane IPR train.
- The BN built in Netica provides easy-to-interpret results for decision-makers.

GRAPHICAL ABSTRACT



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ABSTRACT

Risk-based approaches are used to define performance standards for water and wastewater treatment to meet health-based targets and to ensure safe and reliable water quality for desired end use. In this study, a screening level QMRA for a non-membrane based indirect potable reuse (IPR) system utilizing the sequential managed aquifer recharge technology (SMART) concept was conducted. Ambient removals of norovirus, *Campylobacter* and *Cryptosporidium* in advanced water treatment (AWT) steps were combined in a probabilistic QMRA utilizing Bayesian networks constructed in Netica. Results revealed that all pathogens complied with disease burden at the 95th percentile, and according to the assumptions taken about pathogen removal, *Cryptosporidium* was the pathogen with the greatest risk. Through systematic sensitivity analysis, targeted scenario analysis, and backwards inferencing, critical control points for each pathogen were determined, demonstrating the usefulness of Bayesian networks as a diagnostic tool in quantifying risk of water reuse treatment scenarios.

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Abbreviations: IPR, Indirect potable reuse; DPR, direct potable reuse; SMART, sequential managed aquifer recharge technology; AWT, advanced water treatment; DWT, drinking water treatment; WWTP, wastewater treatment plant; UV, ultraviolet; RSF, rapid sand filtration; MAR, managed aquifer recharge; WSP, Water Safety Plans; CCP, critical control points; QMRA, quantitative microbial risk assessment; DALYs, disability adjusted life years; BNs, Bayesian networks; GAC, granular activated carbon; LRVs, log reduction values; PDFs, probability distribution functions; BP, beta Poisson; CFU, colony forming units; CDFs, cumulative distribution functions; CF, common factor; ARI, annual risk of infection.

* Corresponding author.
E-mail address: u.huebner@tum.de (U. Hübner).

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1. Introduction

Potable reuse has become a more viable option to combat water shortages as an increasing number of projects consistently produce appropriate water qualities (US EPA, 2017; World Health Organization, 2017a). These can be achieved through applying advanced treatment after conventional wastewater treatment by using combinations of oxidative, adsorptive, biological, or physical processes. Potable reuse can be either indirect or direct. In indirect potable reuse (IPR), advanced treated water is introduced into a groundwater aquifer or surface reservoir, where it undergoes further natural transformation processes before abstraction and use as raw water for drinking water treatment (DWT) plants. In direct potable reuse (DPR), advanced treated water is either directly fed into the raw water supply of a DWTP or into the distribution system, where it might be blended with other water sources (World Health Organization, 2017a). Potable reuse is now practiced on nearly every continent and many of these projects favor membrane-based treatment trains (Tang et al., 2018): Europe (Van Houtte and Verbauwhede, 2013), Africa (Ander and Forss, 2011; Khan, 2013; Lahnsteiner et al., 2018), Asia (Ghernaout et al., 2019), Australia (Radcliffe and Page, 2020), and North America (US EPA, 2017).

To reduce energy costs and brine disposal, in particular for inland applications, research groups have begun to explore alternative non-membrane-based treatment systems. Managed aquifer recharge (MAR) has been identified as a multi-objective treatment process, where a combination of different attenuation mechanisms (i.e., biodegradation, sorption, filtration, dilution, die-off) significantly improves the microbiological and chemical quality of the infiltrated water (Regnery et al., 2017a). MAR systems can be optimized by controlling key operational factors such as redox conditions and carbon concentrations in the subsurface, which determine the primarily biological removal efficiency of chemicals and pathogens (Hellauer et al., 2018; Regnery et al., 2016, 2017b; Zhang et al., 2019). Modified engineered biofiltration systems have shown that establishing controlled redox and carbon conditions can be achieved at a much smaller footprint than in conventional MAR systems (Müller et al., 2017). Another engineered solution, the sequential managed aquifer recharge technology (SMART), combines two infiltration systems with intermediate aeration (Hellauer et al., 2017, 2018; Regnery et al., 2016). This was further improved in the SMART*plus* concept, which utilizes high-rate trench infiltration technology and in situ oxygen injection through gas-permeable membranes to optimize flow, carbon concentrations and redox conditions for efficient removal of chemicals and pathogens during short travel times (Karakurt-Fischer et al., 2020). Combining SMART*plus* with subsequent adsorptive or oxidative processes could potentially provide a reliable IPR treatment train at significantly lower energy demand than membrane based systems.

To consistently meeting stringent water quality requirements, preparing Water Safety Plans (WSP) can be used to identify health-based targets, ensure proper surveillance, and determine critical control points (CCP) (World Health Organization, 2017b). Proposed treatment trains can undergo a screening level risk analysis prior to construction, and validation and monitoring after commissioning. One tool used to determine whether health-based targets are met is quantitative microbial risk assessment (QMRA). QMRA is a probabilistic evaluation of the pathogens present at each treatment step, coupled with exposure scenarios and dose-response models, for an ultimate characterization of the risk from exposure to the treated water. This information can be used to analyze the efficacy of a treatment train, as well as to characterize how much the variability and uncertainty of individual treatment steps contribute to overall uncertainty in final water quality, and is particularly useful in the selection and design of multi-barrier reuse approaches. QMRA can be used as part of a WSP and considers local information when quantifying tolerable health burden in terms of disability adjusted life years (DALYs) (World Health Organization, 2016). Screening level QMRAs can evaluate whether a treatment train will be able to reach the health-based target before operation commences. However, a large amount of data is needed for QMRA, which can be difficult, time intensive, and cost-prohibitive to obtain. In these cases, different statistical approaches, such as Bayesian networks (BNs), have been proposed to address the variability associated with environmental datasets and attempt to combat the lack of data.

BNs provide intuitive management of uncertainty and variability when assessing the risk of a system and identifying management strategies (Beaudequin et al., 2016). They are probabilistic graphical models represented as directed acyclic graphs, where direct dependence relationships between variables (nodes) are represented by directed arcs connecting parent and child nodes (Scutari and Denis, 2015). Bayes theorem, the underlying equation behind BNs, allows the estimation of a likelihood of a certain outcome. BNs can be modeled in a probabilistic or a deterministic fashion, with nodes including two or more mutually exclusive states or values, and the reasoning or inference is conducted in the same or opposite direction to the causal arcs or links (depending on the type of inference) (Uusitalo, 2007). Nodes can be discretized using expert knowledge or numerical approaches to set meaningful thresholds relevant for removal verification. Three main types of inferences can be found in BNs, namely causal, diagnostic and intercausal reasoning. In causal reasoning, the information follows the direction of the arcs, whereas in diagnostic reasoning information flows against the direction of the arcs. Intercausal reasoning is also called the 'explaining away effect' and allows inference between competing hypotheses or causes of a common effect (Kjaerulff and Madsen, 2008). Such features are particularly useful when discussing risk scenarios and identifying CCPs. Likewise, since nodes are expressed as probability distributions, BNs are exceptionally suited to quantifying uncertainty, which is especially helpful when assessing risk in a water reuse system. However, BN usage in QMRAs has not been widely explored, with only individual applications in potable reuse practices (Beaudequin et al., 2015, 2016, 2017; Verbyla et al., 2016). More standard approaches for generating samples from probability distributions include Monte Carlo or Latin Hypercube simulations (Zhiteneva et al., 2020). The lack of BNs in published QMRAs could stem either from the difficulty of integrating mathematical equations in a network which includes joint probability distributions of all nodes, or from resolution of the results, because of the exponential growth of the parameters required when many variable states are used. If a large network is constructed with many parameters, the size and processing time is large, a problem not experienced in Monte Carlo simulations. However, the benefits of using BNs in QMRAs warrant further exploration and utilization.

The aim of this study is to assess the operational feasibility of the newly developed SMART*plus* concept as a key process of a non-membrane based IPR treatment train used for subsequent drinking water production. For this purpose, a screening level Bayesian network QMRA for key pathogens using a combination of literature and empirical data was conducted.

2. Methods

2.1. Treatment train of interest

The proposed IPR treatment train is comprised of advanced biological, chemical and physical processes providing a multi-barrier treatment approach for microbial and chemical contaminants (Fig. 1). The starting point was pathogen concentrations in raw sewage, after which a biological wastewater treatment plant (WWTP) was modeled as a conventional activated sludge treatment plant with primary (mechanical) and secondary (biological) treatment for carbon, nitrogen and phosphorus removal. Further turbidity removal occurred during tertiary treatment comprised of rapid sand filtration (RSF). The SMART*plus* treatment step, a technical sand biofilter operated at a 0.58 m/h effective velocity and a hydraulic residence time of 12–13 h, provided 2.2–3.1 ambient log reduction of viruses and phages (Karakurt-Fischer et al., 2021, submitted). The

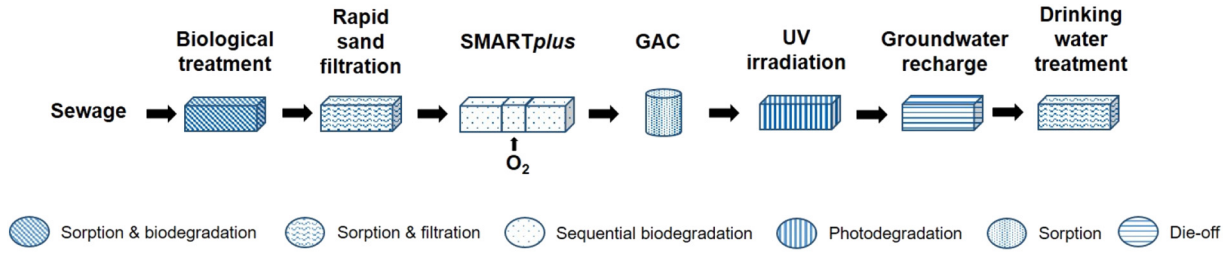


Fig. 1. Investigated IPR treatment train employing sequential managed aquifer recharge technology followed by GAC filtration and UV irradiation prior to groundwater recharge.

SMART*plus* effluent was then fed to a granular activated carbon (GAC) filter contributing to chemical removal. However, as removal of viruses and protozoa in a GAC adsorber is rather low (Smeets et al., 2006), the GAC filter was omitted from the modeling. Subsequent ultraviolet (UV) irradiation at 180 mJ/cm^2 served as an additional pathogen inactivation barrier. Next, the advanced treated effluent was injected into a sandy aquifer with an assumed subsurface residence time between 50 and 120 days. Finally, the abstracted water was subject to conventional drinking water treatment via aeration followed by dual media filtration (sand and anthracite) for iron and manganese removal. Given the long residence time in the subsurface, no additional post-treatment disinfection was considered.

2.2. Risk assessment

2.2.1. Hazard identification

Pathogens of interest in this study were norovirus (virus), *Cryptosporidum* spp. (protozoa) and *Campylobacter* (bacteria), which are recommended by the WHO when assessing potable reuse systems (World Health Organization, 2017a). All three pathogens cause gastroenteritis, warranting them relevant reference pathogens for assessing human risk (NRMMC–EPHC–AHMC, 2006). Although the WHO Guidelines for Drinking-water quality list rotavirus as the reference pathogen (World Health Organization, 2017b), the imminent development of a rotavirus vaccine, in addition to the fact that nearly 20% of acute diarrheal diseases worldwide are caused by norovirus, led the WHO to select norovirus as the reference virus in their potable reuse guidelines (World Health Organization, 2017a). Therefore, norovirus was evaluated in the present study.

2.2.2. Determining source water concentrations and removal efficiencies

As the proposed IPR treatment train was not yet operational at full scale, literature values for distributions and point values of each pathogen concentration in raw sewage, as well as ambient removal in each treatment step, were collected. Studies describing concentrations and removals were obtained by searching for the three aforementioned pathogens in water reuse studies in Scopus. Log reduction values (LRVs) and probability distribution functions (PDFs) from literature were compiled for similar operating conditions of the targeted individual processes to determine which distribution or point value best described performance. When numerous distributions were available, studies or guidelines whose operational parameters most closely matched the desired operational parameters of the current train were selected. Uniform distributions were applied to studies reporting minimum/maximum LRVs.

Only ambient pathogen concentrations studies were used in this analysis, as the focus was on observed removal, not treatment validation. This resulted in very conservative risk assessment, particularly in treatment steps where removal is biologically dominated.

2.2.3. Health effects assessment

Dose-response models were also obtained from literature. As noted in Zhiteneva et al., 2020, dose-response model choice can noticeably affect the final risk, therefore two dose-response models were assessed for each pathogen (Table 1). Reasoning for dose-response model selection can be found in the Supplementary Information (SI).

2.2.4. Exposure assessment

Exposure to pathogens in drinking water varies widely and often represents the greatest source of uncertainty in risk assessments (Haas et al., 2014). Intake via drinking is generally modeled using lognormal distributions (Åström et al., 2007; Barker et al., 2013; Sato et al., 2013; Chaudhry et al., 2017; Pecson et al., 2017). WHO guidelines recommend lognormal PDFs for describing daily high consumption (World Health Organization, 2016), which was the distribution taken for this study ($\mu = 0.65$, $\sigma = 0.53$).

2.2.5. Risk characterization

The pathogen dose at the point of exposure D was calculated using Eq. (1):

$$D = C_{DWT} * V \quad (1)$$

where C_{DWT} is the pathogen concentration after the final drinking water treatment step and V is the volume in liters ingested by an individual. The daily risk of infection P_{inf} was estimated using the dose-response relationships identified for each pathogen.

Table 1
Dose-response models tested in this study.

	Model	Equation	Parameters	Source
Norovirus	Approximate beta Poisson (BP)	$P_{inf} = 1-\left[1+\left\{\frac{\text{dose}}{\beta}\right\}\right]^{-\alpha}$	α =0.104 β = 32.3	Van Abel et al. (2017)
	Fractional Poisson	$P_{inf} = P^*\left(1-e^{-\frac{d}{\mu}}\right)$	P = 0.722 μ = 1106	Messner et al. (2014)
Cryptosporidium	Fractional Poisson	$P_{inf} = P(1 - e^{-D})$	P = 0.737	Messner and Berger (2016)
	Exponential	$P_{inf} = P(1 - e^{-r*D})$	P = 0.737 r = 0.0022	
Campylobacter	Approximate BP	$P_{inf} = 1-\left(1+\frac{N}{\beta}\right)^{-\alpha}$	α = 0.145 β = 7.59	Medema et al. (1996), World Health Organization (2016)
	Exact BP		α = 0.024 β = 0.011	Teunis et al. (2005), World Health Organization (2016)

The annual risk of infection $P_{\inf(ann)}$ was calculated using Eq. (2) (World Health Organization, 2016), assuming that the consumers ingest only drinking water that has been augmented by reclaimed water and are thus exposed to the risk all year long.

$$P_{inf(ann)} = 1-(1-P_{inf})^{365} \quad (2)$$

The annual risk of illness $P_{\mathrm{ill}(ann)}$ was modeled using Eq. (3) (World Health Organization, 2016):

$$P_{ill(ann)} = P_{inf(ann)} R_{ill|inf} \quad (3)$$

where $R_{ill|inf}$ is the probability of illness given an infection. Finally, the annual disease burden of illness of each pathogen, DB_{ann}, expressed as DALYs per person and year, was modeled using Eq. (4) (World Health Organization, 2016):

$$DB_{ann} = DB_{case}\, P_{ill(ann)} \quad (4)$$

where DB_{case} is the pathogen specific disease burden per case of illness. In this study, the entire population was assumed to be susceptible.

2.3. Bayesian network construction and validation

The BN model (Fig. 2) was constructed in Netica 6.07 (Norsys Software Corp., 2019), and comprised a number of variables including the type of pathogen to be analyzed, inlet and outlet concentrations of pathogens, treatment step LRVs, exposures, dose-response outcomes and risks. Netica allows higher resolution analytical and statistical evaluation of the network due to the much greater bin capacity than in Beaudequin et al. (2015), which used GeNIe (BayesFusion). Beaudequin et al. (2015) employed a QMRA model in which 2–4 states were used, which did not display any numerical outputs and only provided information on the probabilities associated with each state. In contrast, Netica features a numerical output on its graphical interface, allowing the user to visualize statistics such as means, standard deviations, and 95th percentiles. Another advantage of Netica is the possibility of selecting a range of values as evidence instead of single states. In this paper, most child nodes were an algebraic transformation of one or more parent nodes: for example, outlet concentration for a particular treatment step was computed from the inlet concentration and the LRV of that step. Parentless nodes were defined using their individual distributions. A screenshot of the model is provided in Fig. SI-3.

The model included an easy option to assess failure of each treatment step (i.e., 0 LRVs) by using selector nodes. Additionally, a second identical model with a common factor was built, which presented a rank correlation of 0.5 between the common factor and the LRV nodes. The idea behind this modification was to assess whether the performance dependency between the barriers would increase or reduce the final risk. The common factor allowed simulation of scenarios where the LRV nodes (WWTP, RSF, SMART*plus*, UV, MAR and DWT) were conditionally correlated, meaning the performance of one LRV node would be correlated by a factor of 0.5 to the other LRV nodes. Haas et al. (2014) indicated that correlations should be considered when modeling risks, and that the existence of correlations between variables will have an impact on the outcomes derived from such variables. Since the impact usually becomes more important at the extremes of the distribution, Haas et al. (2014) presented copulas as a useful methodology to simulate such conditions. The correlation factor was modeled via rank correlation, using normal copulas to define the dependence between the common factor and the correlated LRV nodes, and was incorporated into the model using Uninet (LightTwist Software, 2019). Uninet supports continuous, discrete and function nodes using non-parametric conditional correlations (i.e. conditional rank correlations) to capture dependencies between the variables. For the LRV nodes, data obtained from Uninet was also used when learning the parameters in Netica. Unlike the model without the common factor, in which the parameters were learned only from equations, the parameters were obtained both from equations and the Uninet data in the model with the common factor. A simplified illustration of how the common factor influences the Netica model is depicted in Fig. 2.

Both models were built by evaluating the equations of the network 1,000 times for each combination of parent states without including uncertainty. To obtain numeric data from the nodes, the model was sampled 10,000 times, which allowed precise generation of the marginal distributions from one or more target nodes. Although Monte Carlo

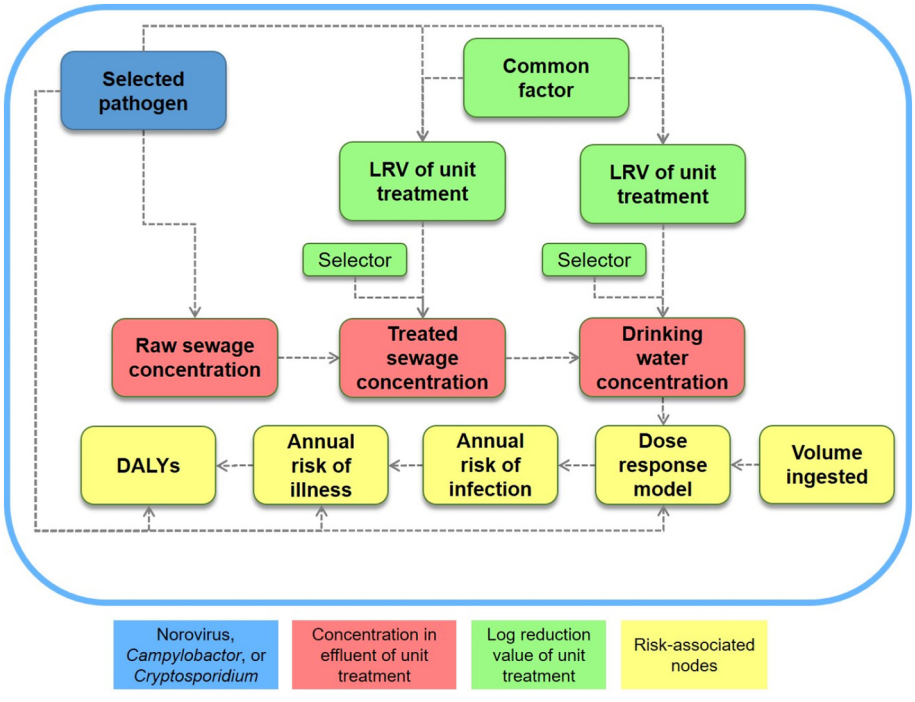


Fig. 2. Simplified information flow within the common factor Netica model (not all LRV nodes shown).

simulations are more suitable for forward prediction due to the continuous nature of distributions used, the benefits of a BN lie in the graphical representation, the large amount of data that can be represented, and the possibility of forward and backward inference, which is particularly useful for determining CCPs and evaluating how unit treatment processes react under particular risk scenarios. Although some model information is likely lost when discretizing continuous distributions, a BN is more suitable for diagnostic inference.

The models presented in this study were constructed following best QMRA modeling practices and their parameters were obtained from relevant published literature. Model validity was verified during the different steps of the model construction including model structure, model discretization, model parameterization and model behavior. Structure was based on the generic mathematical procedure to calculate microbial risks through a QMRA framework (World Health Organization, 2016). Because every node featured an equation, the inputs of such equations dictated the connections from parent nodes. Nodes were discretized using Netica's discretization tool for fixed and logarithmic divisions. Monte Carlo simulations (n = 10,000) of the same models were conducted in the mc2d package in R (R Core Team, 2013) to visually compare the BN results of the cumulative distribution function of the disease burden outcome (Fig. SI-3). Model parameters were obtained from the equations defined in Section 2.2 through the sampling procedure performed by Netica. Model behavior was tested through sensitivity analysis, which allowed all associations between variables to be evaluated for accuracy: for example, increasing the ingested volume of water should increase final risk.

2.4. Evaluation methods and scenario analysis

A sensitivity analysis was conducted to determine which nodes exerted the most influence on final risk and could be considered potential CCPs. The sensitivity analysis was performed by evaluating the change in the 95th percentile values of the DALYs node under minimum and maximum values of the tested node (i.e., raw sewage concentration, WWTP LRV, RSF LRV, SMART*plus* LRV, UV LRV, MAR LRV, DWT LRV, volume ingested, norovirus distribution and common factor nodes) and visualized in a tornado plot. Unless otherwise noted, all numerical results reported in this paper describe the 95th percentile value, which is a conservative value to assess when considering the uncertainty of using literature data for specific treatment trains (World Health Organization, 2016). Finally, numerous scenarios were tested to evaluate the reaction of the model: 1) a high pathogen loading event; 2) SMART*plus* performance failure; 3) MAR failure; 4) experimental norovirus removal; and 5) the effect of the common factor. Additionally, a backwards inferencing exercise was conducted to determine where the likelihood of failure of the treatment scenario is located.

3. Results and discussion

Numerous guidelines, peer-reviewed papers, and grey literature were consulted when deciding upon PDFs. Quite often the most reliable assumption came from guidelines (Table 2), whereas individual studies did not match the operational parameters of the treatment system investigated in this study. Extended reasoning for PDF selection can be found in the SI.

Table 2
Distributions used for pathogen concentrations or presence in the evaluated treatment steps.

Pathogen	Treatment step (units of LRV, unless otherwise noted)	Distribution & parameters	Source
Campylobacter	Raw sewage (colony forming units (CFU)/L)	Triangular (min 10, mode 7000, max 10^5)	Beaudequin et al. (2017), World Health Organization (2017b)
	Secondary treatment	Triangular (min 0.6, mode 2, max 3.5)	Ayuso-Gabella et al. (2011)
	Rapid sand filtration	Uniform (0.6, 2.8)	Mohammed and Seidu (2019)
	SMART*plus*	Uniform (2, 6)	World Health Organization (2017a)
	UV irradiation	Uniform (4, 6)	World Health Organization (2017a)
	Subsurface removal ($\log_{10}$ d^{-1})	Triangular (min 0.02, mode 0.08, max 1.5)	Ayuso-Gabella et al. (2011)
	Dual media filtration	Uniform (0,1)	NRMMC-EPHC–NHMRC (2009)
	Infection: illness ratio	0.3	NRMMC–EPHC–AHMC (2006), World Health Organization (2016, 2017a)
	Disease burden	4.6×10^{-3} DALYs per case	
Cryptosporidium	Raw sewage (oocysts/L)	Triangular (min 0, mode 2700, max 10^6)	Beaudequin et al. (2017), World Health Organization (2017b)
	Secondary treatment	Triangular (min 0.5, mode 1, max 1.4)	Ayuso-Gabella et al. (2011)
	Rapid sand filtration	Triangular (min 0, mode 2, max 3.1)	Smeets et al. (2006)
	SMART*plus*	Uniform (0.3, 6)	World Health Organization (2017a)
	UV irradiation	Uniform (4, 6)	World Health Organization (2017a, 2017b)
	Subsurface removal ($\log_{10}$ d^{-1})	Uniform (0.025,0.082)	Toze et al. (2010)
	Dual media filtration	Uniform (1.5, 2.5)	NRMMC-EPHC–NHMRC (2009)
	Infection: illness ratio	0.7	NRMMC–EPHC–AHMC (2006), World Health Organization (2016, 2017b)
	Disease burden	1.5×10^{-3} DALYs per case	
Norovirus	Raw sewage (units/L)	Triangular (min 0, mode 20,000, max 10^6)	Adapted from World Health Organization (2017b)
	Secondary treatment	Uniform (0.5, 2)	Karakurt-Fischer et al. (2021)
	Rapid sand filtration	Uniform (0.06, 0.3)	
	SMART*plus*	Uniform (2.2, 3.0)	
	UV irradiation	Uniform (3.9, 4)	World Health Organization (2017a)
	Subsurface removal ($\log_{10}$ d^{-1})	Uniform (0.093, 0.174) (MS2 removal)	Regnery et al. (2017a)
	Dual media filtration	Uniform (0.5, 2)	NRMMC-EPHC–NHMRC (2009)
	Infection: illness ratio	0.67	Atmar et al. (2013)
	Disease burden	Uniform (3.71×10^{-4}, 6.23×10^{-3} DALYs)	Barker et al. (2013), Mok et al. (2014)
Volume ingested	Liters (natural log)	Lognormal (0.65, 0.53)	World Health Organization (2017b)
Residence time	Subsurface (d)	115–120	Expert opinion
Tolerable DALYs	$\leq 10^{-6}$	Threshold value	World Health Organization (2016)

3.1. Stochastic sampling of dose-response model scenarios

Two dose-response models per pathogen were tested to determine how model choice affected final risk, with the more conservative dose-response model predicting the closest risk to 10^{-6} DALYs (approximate beta Poisson for norovirus, fractional Poisson for *Cryptosporidium*, and exact beta Poisson for *Campylobacter*) chosen for further analysis. The cumulative distribution functions of the chosen models (with and without the common factor) are displayed in Fig. 3, which shows that all pathogens comply with the DALYs threshold at the 95th percentile. The common factor was modeled to observe how the model would react if barriers were not independent, and although DALYs for all pathogens increased by 0.6–3.5 logs (1.5 log for *Cryptosporidium* and 3.5 for *Campylobacter*), they were still under the 10^{-6} threshold.

However, maximum *Cryptosporidium* DALYs exceeded the 10^{-6} DALYs threshold, and in the model with the common factor node, maximum DALYs for all pathogens exceeded the threshold. This can be explained by the common factor affecting the associations between the unit treatment barriers by causing higher probabilities of exceedance at larger DALYs when compared to the model without a common factor.

Unlike previous studies assessing pathogenic risk in IPR systems (Betancourt et al., 2014, 2019), the pathogen of importance for this treatment train was deemed to be *Cryptosporidium* instead of viruses, which can be attributed to the broad LRV range for the SMART*plus* process (see Table 2 and SI). Prior QMRAs conducted on IPR systems without microfiltration or reverse osmosis also found that greatest disease burden or annual risk of infection (ARI) came from *Cryptosporidium* (Ayuso-Gabella et al., 2011; Soller et al., 2017, 2018a). The treatment trains investigated in Ayuso-Gabella et al. (2011) featured secondary treated effluent introduced via injection, recharge basin, or riverbank filtration into unconfined karstic or sandy aquifers, which was then either directly used for crop irrigation (Nardo, 20–25 days subsurface residence time), was treated with Cl_2 prior to crop irrigation (Shafdan, 270 days subsurface residence time), or underwent UV and Cl_2 disinfection, rapid sand filtration and was then used for urban landscape and crop irrigation (Sabadell, ~7 days subsurface residence time). Despite describing *Cryptosporidium* removal using lower decay rates than in the current paper, protozoan risk was greater than viral risk for Sabadell and Shafdan, and though the median disease burden complied with the 10^{-6} DALYs, greater percentiles clearly above this threshold were not discussed (Ayuso-Gabella et al., 2011). This demonstrates a bias in selecting thresholds when reporting disease burden. Risk is perhaps more intuitively understood by using boxplots such as those in Fig. 4 describing the cumulative LRVs of the treatment train.

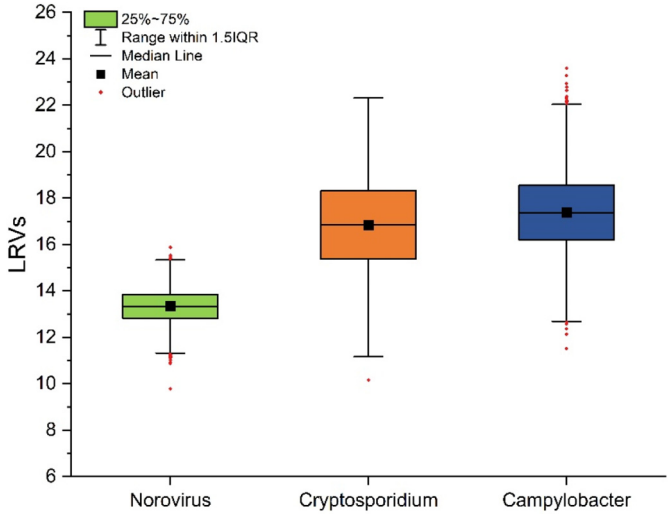


Fig. 4. Box plots of LRVs for the proposed overall treatment train ($n = 10{,}000$).

The treatment trains investigated in Soller et al. (2017, 2018a) included secondary effluent followed by ozonation, biologically active filtration, ultrafiltration, UV irradiation, an engineered storage buffer, and

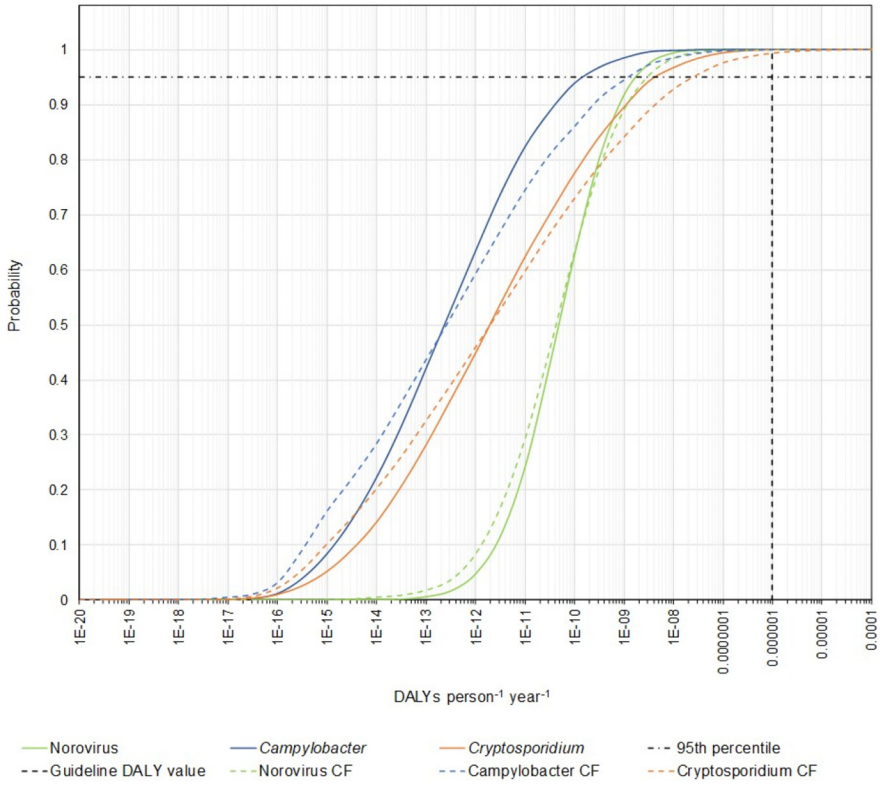


Fig. 3. Cumulative distribution functions (CDFs) of DALYs achieved using the approximate beta Poisson for norovirus, the fractional Poisson for *Cryptosporidium*, and the exact beta Poisson for *Campylobacter*. Solid colored lines denote the results for the models without a common factor (CF), whereas dashed colored lines denote the results for the models with a CF.

Cl_2 disinfection. The train was assessed with LRVs obtained from literature review as well as with regulatory LRVs obtained from Olivieri et al. (2016), demonstrating that predicted risk was substantially higher when using regulatory LRVs (Soller et al., 2018a). Furthermore, after updating the same treatment train investigated in Soller et al. (2017) with the latest dose-response models, raw wastewater pathogen densities, and treatment LRVs from literature, Soller et al. (2018a) observed that not only would the 12/10/10 LRVs required in California for viruses and protozoa no longer meet the 10^{-4} ARI threshold, but that depending on which final risk percentile was reported (i.e. 50th vs 95th vs maximum), the LRVs required to meet the 10^{-4} threshold varied. While differences between the health burden thresholds (10^{-4} ARI vs 10^{-6} DALYs) can be addressed by describing the uncertainty through the use of PDFs, a broader discussion within the water reuse and public health sector is needed to determine which percentile should comply: should the maximum value, i.e., the most conservative estimate, comply or is compliance of the 90th or 95th percentile sufficient?

Another important discussion relates to the LRVs credited to MAR by various guidelines. California regulations require that if 100% of water introduced into the subsurface is disinfected tertiary treated wastewater or advanced treated water and if the underground storage time is at least 6 months (180 days), then subsurface treatment can be credited with 10 LRVs for *Cryptosporidium* and *Giardia* (CDPH, 2014). The regulations also require at least three independent processes in the treatment train to each achieve at least 1 LRV (CDPH, 2014). The Australian guidelines credit a maximum of 6 LRVs to engineered treatment systems as a conservative approach to human health protection (NRMMC-EPHC–NHMRC, 2009). In this study, MAR LRVs were capped at 4 logs due to the assumed subsurface residence time of no greater than 120 days (Regnery et al., 2017a). However, research has demonstrated that subsurface treatment is capable of more than 6 log removal of pathogens. Findings from field studies of bacteriophage or virus infiltration show that up to 8 LRVs have been achieved over a distance of 30 m in about 25 days, and 3–8 LRVs were obtained over distances between 2.4 and 100 m (National Research Council, 2012). Toze et al. (2010) showed a near linear decay for bacteria in MAR, resulting in complete removal within 10 days. The same study described a broken stick model for *Cryptosporidium* decay which resulted in faster protozoa removal than virus removal (Toze et al., 2010). Therefore, site-specificity of MAR removal can be underestimated when maximum removal is capped. If risk assessments should incorporate the most recent peer-reviewed research on raw wastewater pathogen densities and site-specific removals in QMRAs, the guidelines could also be updated and instead of limiting maximum LRVs, provide minimum LRVs along with detailed methods for determining removal on a site-specific basis (Rauch-Williams et al., 2021).

3.2. Sensitivity to findings

A sensitivity analysis, demonstrated for *Cryptosporidium* in Fig. 5, was conducted to identify which parameters were most influential on final risk by observing the changes in the 95th percentile DALYs to the full range of the preceding nodes. The plot colors demonstrate the association between the assessed node and the target, i.e., whether the node change directly or inversely affected the DALYs. This revealed that norovirus was most sensitive to WWTP, SMART*plus* and DWT, *Cryptosporidium* was most sensitive to RSF, SMART*plus* and MAR (Fig. 5), and *Campylobacter* was most sensitive to WWTP, SMART*plus* and MAR. The DALYs range calculated from the range of each unit treatment can be explained by the distributions used in the networks and listed in Table 2, but the order of nodes signifies the importance affected on the DALYs.

Although the tornado plot mostly follows the range of LRVs attributed to each unit treatment for *Cryptosporidium* from Table 2 (only RSF and MAR order is switched), the change in the order of the top 3 and the greater influence of the common factor than of UV irradiation (whose range was 2 LRVs) in Fig. 5a demonstrates that if/when failure is correlated within the model, the relative importance of unit treatment processes in the treatment train changes. A similar trend was observed for *Campylobacter*, where the common factor was more influential than the 2.2 LRVs attributed to UV irradiation (Fig. SI-2). However, for norovirus the findings were very different: SMART*plus* removal mattered more in the sensitivity analysis than could be attributed to its LRVs, and raw sewage concentration was also very influential. In the model with the common factor, SMART*plus* was the most influential and the common factor the second most influential, denoting SMART*plus* as a clear CCP for viruses despite the relatively narrow removal (0.8 LRVs). Nevertheless, the sensitivity analysis determined that SMART*plus* was a CCP for all pathogens, with MAR and WWTP also important for 2 of 3 pathogens, identifying the biological removal steps as most critical, in line with the conservative ranges for biological removal used in this paper. Correlations due to the common factor between the unit treatment barriers also produced larger 95th percentile DALY values, changing the order and magnitude of the estimations. Such results highlight the importance of considering correlated inputs in QMRA models when they exist.

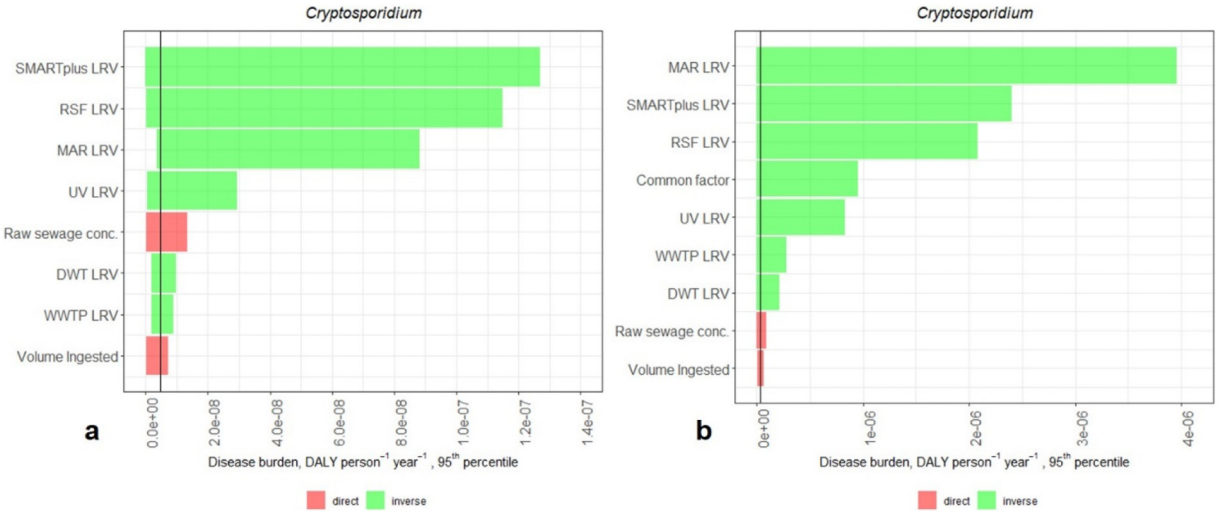


Fig. 5. Tornado plots showing the range of *Cryptosporidium* DALYs achieved when minimum and maximum values of each node were used for the normal model (a) and the common factor model (b). Black vertical line denotes baseline 95th percentile DALYs.

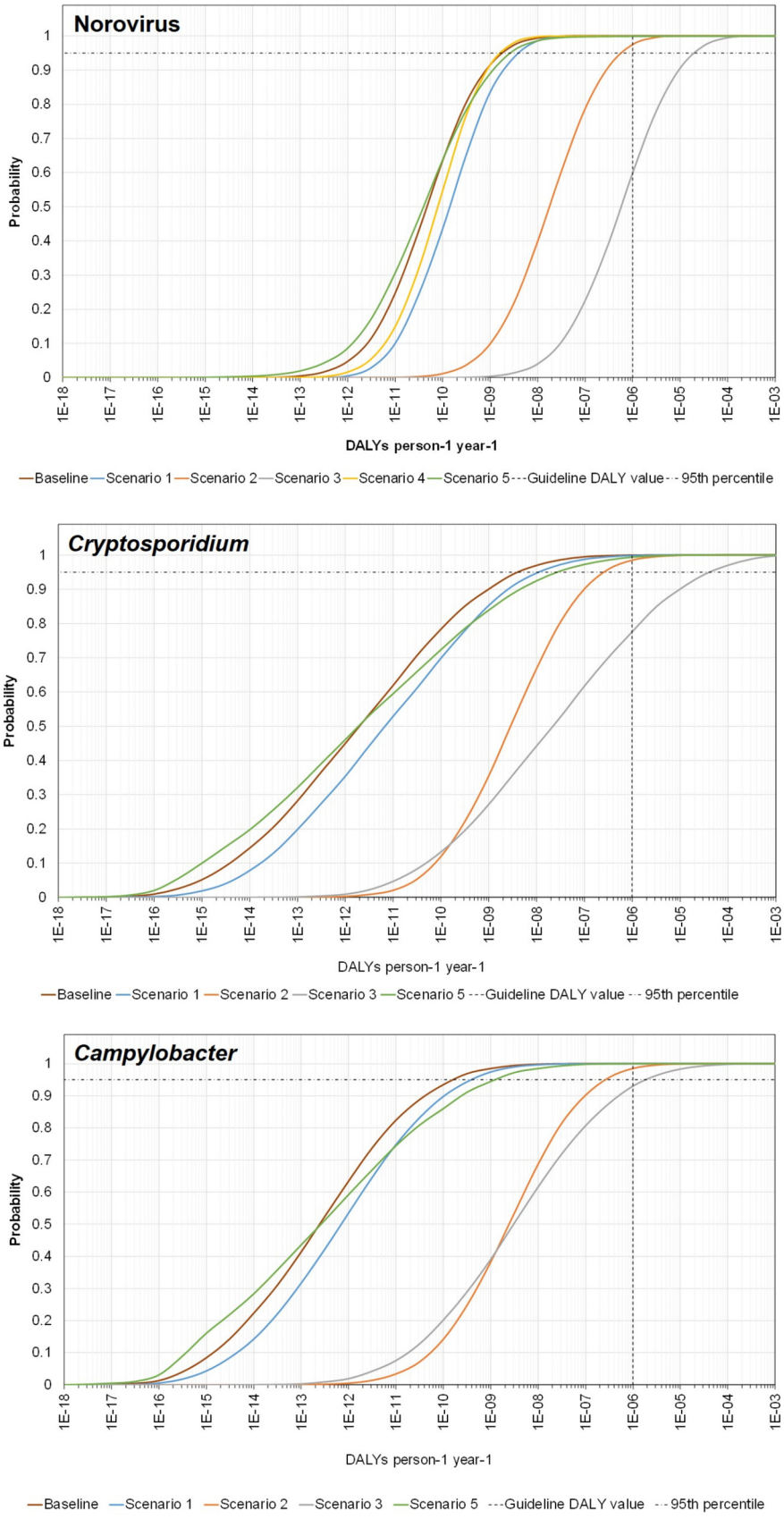


Fig. 6. CDFs of DALYs resulting from scenarios 1, 2, 3, and 5 for all pathogens, with additional DALYs from scenario 4 (experimental data) shown only for norovirus. Results confirm that MAR (scenario 2) and SMART*plus* (scenario 3) performance failure scenarios lead to the highest risk for all pathogens and supports their status as CCPs. Note that scenario 5 shows the same results as CF models in Fig. 3.

3.3. Scenario evaluation

Scenarios to investigate CCP behavior and to determine how failures would affect the final risk were evaluated by comparing the scenario DALYs to baseline DALYs. However, it is worth noting that the scenario evaluations are specific to the thresholds used in the analysis (i.e., norovirus UV LRVs were very narrow). For simplicity this evaluation only included single events, but a combination of events could also be incorporated. Scenarios were evaluated only for the normal model without the common factor, and results of all scenarios are presented in Fig. 6.

3.3.1. Scenario 1: High pathogen loading

For this scenario, the effect of all concentrations greater than the 95th percentile of the raw sewage pathogen concentrations on final DALYs was tested. This corresponded to testing ~10^6 units/L of both norovirus and *Cryptosporidium*, and ~ 10^5 units/L of *Campylobacter*. For all pathogens, only a 0.3–0.5 log increase in final DALYs was observed. This demonstrates that the treatment train successfully buffers higher raw sewage concentrations without any notable effects on disease burden, even for norovirus and *Campylobacter*, which displayed high sensitivity to sewage concentrations.

3.3.2. Scenario 2: SMARTplus performance failure

SMART*plus* performance failure (0 LRVs) affected all pathogens differently. *Cryptosporidium* was least affected, with a DALY increase of 1.8 log, contrary to the sensitivity shown in Section 3.2. This can likely be explained by the fact that the attributed LRV range was already close to zero (0.3, 6). Norovirus DALYs increased by 2.5 log and *Campylobacter* DALYs increased by 3.2 log. This 2–3 log change in DALYs for all pathogens solidifies the status of SMART*plus* as a CCP.

3.3.3. Scenario 3: MAR failure

MAR failure (0 LRVs) caused all pathogen DALYs to be 0.3–1.6 logs greater than the 10^{-6} threshold. This was the only scenario with failure of a biological removal step which resulted in DALYs above the acceptable threshold, and MAR was therefore thought to be a CCP after this scenario analysis, despite its lower rank in the norovirus sensitivity analysis (Fig. SI-1). However, as microbial growth is difficult to monitor and correct at larger scale (Dewettinck et al., 2001), MAR is ultimately not considered a CCP.

3.3.4. Scenario 4: Experimental conditions

This scenario was evaluated only for norovirus by using the ambient human norovirus removals calculated in Karakurt-Fischer et al. (2021). This meant that WWTP removal was set to 0.75–1 LRVs, RSF removal was set to 0.25–0.3 LRVs, and SMART*plus* removal was set to 2.5–2.75 LRVs. This resulted in DALYs nearly identical to the baseline ($2.1 * 10^{-9}$), which can be explained by the relatively narrow ranges taken for all 3 treatment steps from the phage and virus removals reported in Karakurt-Fischer et al. (2021). However, this demonstrates that the model provides a feasible outcome, as the evidence given was within the calibration range of the model and provided results similar to the baseline.

3.3.5. Scenario 5: Common factor effect

The common factor was modeled to determine how the model would react if barriers were not assumed to be independent. For example, a common factor which could be considered is the influence of influent concentration on LRVs (Brown et al., 2019; Hirani et al., 2012). Although Pecson et al. (2017) mentioned that independence of barriers can be assumed, this has not yet been widely accepted, and therefore interdependence was modeled to determine how the model would respond. All DALYs increased by 0.6–3.5 logs but were still within the 10^{-6} threshold. Greatest increases were observed for *Campylobacter* (3.5 LRVs) and *Cryptosporidium* (1.5 LRVs).

3.4. Backwards inferencing

Backwards inferencing can be used to identify the most likely cause of an event and discriminate amongst competing hypotheses. To find the most likely cause, the ratio between the posterior and prior marginal probabilities can be evaluated for a state of a target node, with a larger ratio providing stronger evidence in favor of that particular node being the likely cause for the event. In this model, by switching the probabilities of the selector nodes from equal likelihood of working and not working to 99.9% working and 0.1% not working, a more likely outcome for the treatment train could be modeled. All DALY values ≥10^{-6} were selected to determine how the likelihood of the selector nodes working would change during such a high risk scenario. For all pathogens, as observed in Table 3, WWTP and RSF LRVs were the least likely to not work during a condition of ≥10^{-6} DALYs, but the unit treatment processes exhibiting the greatest change varied for each pathogen. For norovirus, MAR, UV irradiation, and SMART*plus* were most affected (in that order), for *Campylobacter* UV irradiation, MAR, and SMART*plus* were most affected, and for *Cryptosporidium*, UV irradiation, MAR, and DWT were most affected. Although UV failure was not explicitly investigated as a scenario due to the narrow range of norovirus removal during UV irradiation, and did not rank high during the sensitivity analysis for any pathogen, this backwards inferencing determined that it is also a CCP for all pathogens, along with SMART*plus*.

3.5. Additional considerations

When evaluating statistical models, limitations should be made explicit. As only site-specific norovirus removal was available at the time of the study, validation of the model requires more site-specific data, particularly for pathogen removal processes in porous media, which is dependent upon further study of unit treatments where pathogen removal is biologically dominated. This screening level assessment can therefore only give an initial, generic estimate of predicted risk, which is especially useful when designing a new treatment train or system. The BN approach can be easily updated later as empirical data are obtained and additional considerations are identified.

Failure of treatment processes, especially short-term, drives risk (Amoueyan et al., 2019; Smeets et al., 2006; Soller et al., 2018b). This was noted as the DALYs increased the later in the treatment train the failure had occurred, as well as in the common factor model. This demonstrates how QMRA can assist in identifying CCPs and ensuring proper measures are in place to mitigate such failures and prevent compromised water quality prior to commencing full-scale operation.

This QMRA did not account for dilution with native groundwater, which could impact concentrations at the point of abstraction for subsequent DWT. *Cryptosporidium* presence in groundwater is under studied but has been reported in the USA and Canada (Murphy et al., 2016; Rose, 1997; Stokdyk et al., 2019, 2020). A recent global review of *Cryptosporidium* concentrations in groundwater intended for human consumption suggested that it is present in 10–20% of domestic

Table 3
Results of backwards inferencing on the selector nodes. Prior marginal probabilities for the "not working" state were all set to 0.1%, and the ratios between posterior and prior marginal probabilities for each selector node demonstrate the likelihood that the selector node is responsible for the >10^{-6} DALYs.

Barrier selector	Norovirus		*Campylobacter*		*Cryptosporidium*	
	Posterior probability	Ratio	Posterior probability	Ratio	Posterior probability	Ratio
WWTP	0.26%	2.6	0.68%	6.8	0.48%	4.8
RSF	0.12%	1.2	0.45%	4.5	1.0%	10
SMART*plus*	3.47%	34.7	7.50%	75	1.50%	15
UV irradiation	44.1%	441	64.1%	641	30%	300
MAR	52.8%	528	28.8%	288	17.7%	177
DWT	0.26%	2.6	0.16%	1.6	2.4%	24

groundwater supplies (Chique et al., 2020). Hynds et al. (2014) found that nearly 90% of U.S. studies reported enteric viruses in groundwater, and they were detected more often than protozoa or bacteria (both 60%). Needless to say, better estimations of MAR LRVs and decay and retention rates at field scale are urgently required to improve risk assessments and models, and adapt removal observed at lab- to field-scale (Bradford and Harvey, 2017; Gerba et al., 2018).

Additionally, assuming that consumers would ingest up to 2 L of 100% reclaimed water is an extremely conservative exposure estimate. In IPR systems, advanced treated water is blended with native groundwater or surface water before it is abstracted by the DWT plant, which may also blend different source waters together and result in further dilution. Therefore, when considering such a treatment train for field-scale installation, it will be critical to update the assumptions presented in this paper to site-specific raw sewage concentrations, to more accurately quantify subsurface retention time, ideally via tracer tests and hydrogeological models, and to account for dilution in the DWT plant.

4. Conclusions

This study provides a probabilistic, screening level QMRA for a non-membrane based IPR treatment train. It quantified the disease burden for norovirus, *Cryptosporidium* and *Campylobacter* by encoding a number of probability distribution functions and general mathematical operations from QMRA within a BN. Conclusions of the study are:

- The IPR treatment train incorporating SMART*plus* can produce water meeting the tolerable health burden of 10^{-6} DALYs pppy for norovirus, *Cryptosporidium*, and *Campylobacter* at the 95th percentile, even with the conservative LRVs adapted for unit treatment processes with biological removal. The greatest disease burden was posed by *Cryptosporidium*, similar to other non-reverse osmosis based IPR systems.
- Assessing multiple percentiles of disease burden confirms prior work that treatment train LRV requirements vary according to the percentile used for reporting final risk. Evaluation of multiple percentiles in conjunction with a scenario analysis would provide a more comprehensive illustration of risk, which is particularly useful for communicating with stakeholders as well as utilities seeking to make risk-based decisions.
- Assessing different dose-response models was critical to understanding how the choice of model affected calculated risk and whether additional removal would be needed.
- Simulating various plausible operational scenarios, in conjunction with a sensitivity analysis, can reveal which unit treatment processes are critical control points. Using this combination, unit treatment based on biological removal (SMART*plus*) were identified as CCPs in this treatment train. Further backwards inferencing revealed that UV was also a CCP for all pathogens.
- More studies should focus on quantifying removal, retention and/or decay rates of pathogens in field scale applications of subsurface treatment, at minimum for the pathogens investigated in this study, to better characterize subsurface removal for potable reuse systems.
- The benefit of a BN in providing backward and forward diagnosis cannot be underestimated, especially when updating the model with new empirical data and predicting how the model will respond to particular input conditions. The final models achieved their purpose of communicating a large amount of information in a structured and orderly manner, and simulated a number of scenarios which would be impossible to assess in a real setting. A relevant aspect to consider is the possibility of updating the parameters of the BN, employing the current model as starting point for a plant utilizing the proposed treatment train. Therefore, when more recent data become available, for example from challenge testing or ambient microbial analyses, the estimates obtained from literature can be updated using Bayes theorem.
- In comparison to prior BN work done for water reuse treatment trains (Beaudequin et al., 2016), this paper presents a more comprehensive (more variables, multiple dose-response models, failure analysis, more uncertainty) and sensitive (greater discretization) approach for quantifying risk with a more user-friendly interface. The benefit of Netica lies in the easy-to-interpret numerical changes in node probabilities when evidence into the network is given, and communicating the model's results via CDFs or box plots will enable political decision makers to adapt risk-informed policies to solve current and future water management concerns.

CRediT authorship contribution statement

Veronika Zhiteneva: Conceptualization, Methodology, Validation, Formal analysis, Investigation, Writing – original draft, Writing – review & editing, Visualization. **Guido Carvajal:** Methodology, Validation, Formal analysis, Investigation, Writing – review & editing, Visualization. **Omar Shehata:** Methodology, Writing – review & editing. **Uwe Hübner:** Conceptualization, Writing – review & editing, Supervision. **Jörg E. Drewes:** Writing – review & editing, 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.2021.146462.

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