Climate-driven QMRA model for selected water supply systems in Norway accounting for raw water sources and treatment processes

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Abstract

Formulating effective management intervention measures for water supply systems requires investigation of potential long-term impacts. This study applies an integrated multiple regression, random forest regression, and quantitative microbial risk assessment (QMRA) modelling approach to assess the effect of climate-driven precipitation on pathogen infection risks in three drinking water treatment plants (WTPs) in Norway. Pathogen removal efficacies of treatment steps were calculated using process models. The results indicate that while the WTPs investigated generally meet the current water safety guidelines, risks of Norovirus and *Cryptosporidium* infection may be of concern in the future. The pathogen infections attributable to current projections of average precipitation in the study locations may be low. However, the pathogen increases in the drinking water sources due to the occurrence of extreme precipitation events in the catchments could substantially increase the risks of pathogen infections. In addition, without optimal operation of the UV disinfection steps in the WTPs, both the present and potential future infection risks could be high. Therefore, the QMRA models demonstrated the need for improved optimization of key treatment steps in the WTPs, as well as implementation of stringent regulations in protecting raw water sources in the country. The variety of models applied and the pathogen: *E. coli* used in the study introduce some uncertainties in the results, thus, management decisions that will be based on the results should consider these limitations. Nevertheless, the integration of predictive models with QMRA as applied in this study could be a useful method for climate impact assessment in the water supply industry.

Keywords: Quantitative microbial risk assessment, water treatment, climate change, *E. coli*, Norovirus, *Giardia*, *Cryptosporidium*, *Campylobacter*

1. Introduction

Worldwide, microbial contamination of drinking water sources and related public health impacts remains an ongoing challenge for the managers of water supply systems. This challenge is expected to exacerbate in the 21st century due to increased frequency, intensity and duration of climate related events such precipitation, which is known to significantly affect the quality of drinking water sources (Cann et al., 2013; IPCC, 2014). In particular, water supply systems that depend on surface water sources will be the most challenged. Microbial deterioration of surface water sources due to increased precipitation have been directly linked to waterborne disease outbreaks (Curriero et al., 2001; Mann et al., 2007; Nichols et al., 2009; Cann et al., 2013; Tornevi et al., 2015; Beaudeau et al., 2014; Guzman-Herrador et al., 2016; Drayna et al., 2010). In addition, seasonality in sporadic cases of waterborne diseases may be explained by seasonal contamination of surface water bodies (Patz & Han, 2013).

Potential sources of pathogens to surface waterbodies include lateral inputs from pastures and riparian zones, influx of pathogen-contaminated groundwater and faecal matter deposits from livestock and wildlife in catchments (Ram et al., 2007; Pandey et al., 2014). Animal manure provides food and shelter for microorganisms, thereby enhancing the transport of microorganisms in soil (Guber et al., 2005). The fraction of all these potential pathogen sources that reach drinking water sources largely depends on the intensity of precipitation, which can result in increased pathogen loads in runoff within agricultural catchments (Jokinen et al., 2012). In addition, due to increased turbulence in streams during extreme precipitation periods, changes in sedimentation processes and resuspension in stream channels can increase the concentrations of microbial organisms in such streams (Hofstra, 2011; Drummond et al., 2014; Sterk et al., 2015).

Discharge from wastewater treatment systems, leaking sewer pipes, septic tanks and combined sewer overflows (CSOs), which usually occur during intense rainfall are important sources of microbial contaminants to drinking water sources (Grøndahl-Rosado et al., 2014a; Passerat et al., 2011). During extreme rainfall events, new channel flows created in different directions from regular ones (Hunter, 2003) uncover other distant pollutant sources in watershed, further increasing contaminant load in source water. A study that monitored CSO events resulting from precipitations and a mixture of snowmelt and precipitation noted that *E. coli* was mostly associated with raw sewage, and the concentrations remained high throughout each CSO event (Madoux-Humery et al., 2013). FIB and pathogens such as *E. coli*, enterococci, Norovirus and Adenovirus in receiving rivers have surged after CSOs (Passerat et al., 2011; Rodriguez et al., 2012).

In Norway, nearly 90% of the water supply systems depend on surface water sources that are susceptible to point and non-point sources of microbial contamination. It is expected that the quality of these surface water sources will be affected in the future due to projected changes in average precipitation and runoff (Tryland et al., 2011). It has been shown that the concentrations of faecal indicator bacteria occurring at raw water intake zones of Norwegian lakes typically increase during spring and autumn circulation periods when high precipitation occurs in the form of snowmelt and rainfall (Hem, 2008). Mean annual precipitation in the country is projected to increase by 5% - 30% in 2100, with major seasonal variations and increased frequency of torrential rains. Similarly, temperature is projected to increase by 2.3°C - 4.6°C during this period (Ministry of the Environment, 2010). The magnitudes of the projections substantially vary across the different climate regions in the country, implying that the severity of potential effects on the quality of drinking water sources could differ across the country. Water supply systems with inadequate treatment will be particularly challenged by increases in microbial concentrations in their raw water sources during extreme precipitation. Thus, to comprehensively assess the potential effect of the projections and to develop successful adaptation strategies, it is essential to account for the risks of microbial contamination of water sources and treatment needs for different climate regions in the country.

Presently, climate impact assessment of water supply systems in QMRA is often based on simulation of scenarios of high pathogen concentrations in source water and failures on treatment processes. These scenarios are assumed to capture possible changes in climate variables such as precipitation and temperature (Atubo and Mafinejadasl, 2012; Hamouda et al., 2016). Due to the expected increases in average precipitation and temperature in the country and the potential impacts they are likely to have on microbial quality of drinking water resources, efficient management of public health risks associated with treated water consumption requires long-term evaluation of potential risks, and this can be achieved through QMRA. Although some recent studies have developed frameworks to account for this (Schijven et al., 2013a; Smith et al., 2015; Sterk et al., 2015), to the best of our knowledge, no study has particularly integrated the effect of local climate projections from water source to infection risk estimation through QMRA modelling.

The aim of this study was to assess the potential effect of precipitation on the pathogen infection risks associated with the consumption of water consumption from selected treatment plants in Norway. The specific objectives were to: (1) evaluate how current projections of average precipitation can affect *E. coli* and pathogen concentrations in raw water sources; (2) determine the barrier efficacies of the water treatment plants (WTPs) against the pathogenic organisms; (3) evaluate the pathogen infection risk associated with potential changes in pathogen concentration in water sources in relation to projected and assumed increases in precipitation, and (4) evaluate pathogen infection risks associated with optimal and sub-optimal operations in water treatment processes.

2. Materials and methods

2.1. Selected water supply systems and raw water sources

Figure 1 shows the locations of the selected WTPs in Norway. Selection of the WTPs was based on climate zones, the size/capacity of the plants, and the number of people they supply drinking water. They include two plants on the west coast (Ålesund WTP and Svartediket WTP in Bergen), and one in the southern region of the country (Oset WTP in Oslo). The characteristics of the raw water sources, production capacities and the sizes of populations that are connected to the three WTPs are presented in

Table 1.

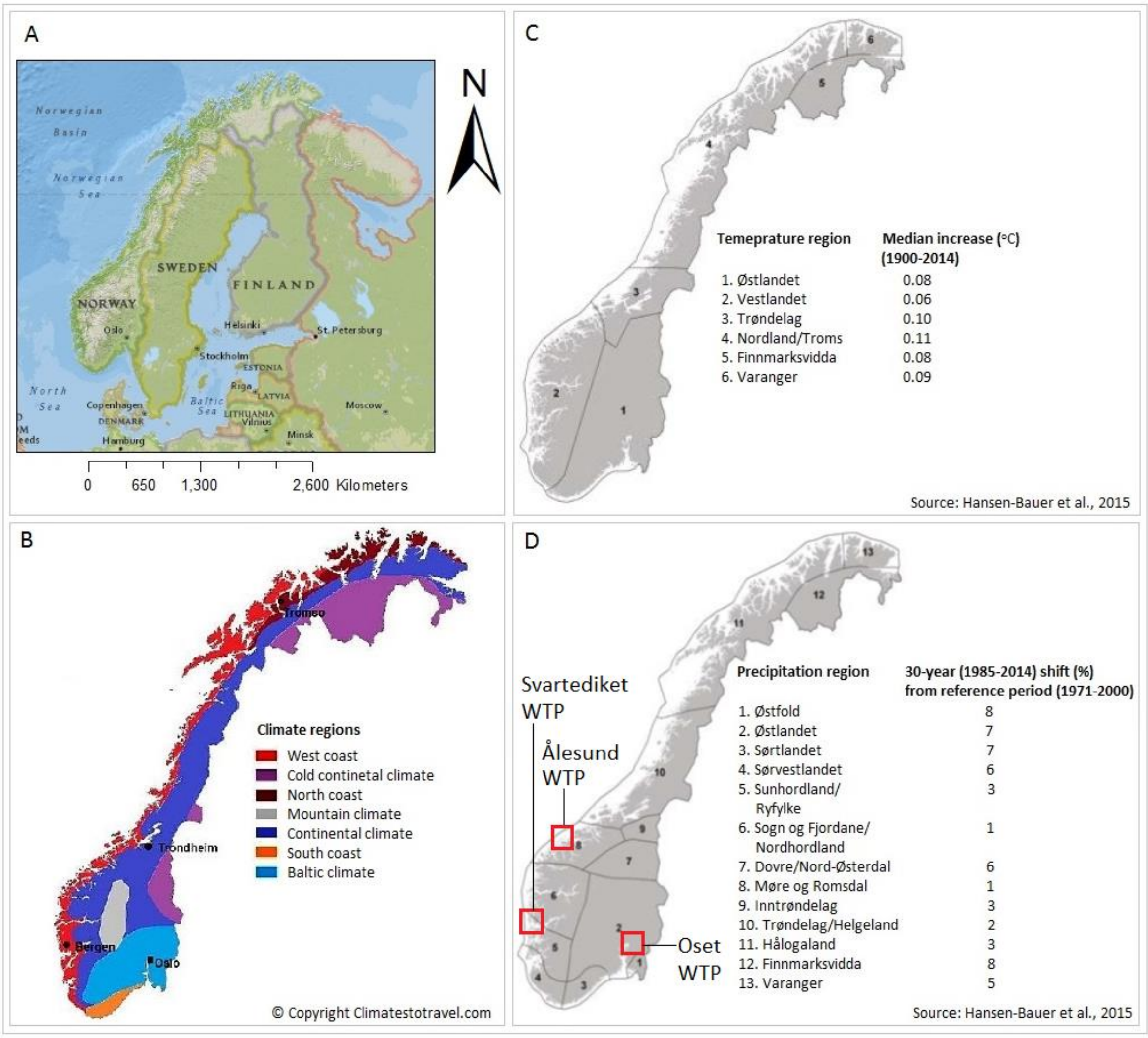

Figure 1. (A) Map of study region, (B) Climate regions of Norway, (C) Temperature zones, and (D) Precipitation zones showing the locations of the WTPs; Ålesund WTP, Svartediket WTP in Bergen, and Oset WTP in Oslo.

Table 1. Water source characteristics and production capacities of the three WTPs.

Water source and production capacity	WTP		
	Ålesund WTP	Oset WTP	Svartediket WTP
Source and location (Lat./Long.)	Lake Brusdalsvatnet (Lat. 62.47, Long. 6.47)	Lake Maridalsvannet (Lat. 59.98, Long. 10.77)	Lake Svartediket (Lat. 60.38, Long. 5.37)
Average surface area (Km^2)	7.3	3.83	0.5
Catchment size (Km^2)	30	252	12.33

Average depth (m)	102	-	-
Raw water intake depth (m)	35	30	30
Production capacity (m^3/day)	55,000	288,000 – 38,4000	40,000 – 80,000
Average population connected	50,000	67,4736	17 1827

Presently, strict regulations are imposed in the catchments of these water sources to regulate activities that can lead to microbial contamination. However, the catchments are composed of forest cover, with substantial numbers of wildlife and birds, which can be major sources of microbial discharge into the water sources. In addition, farm animals such as sheep are located in some of the catchments. For instance, approximately 100 horses have been reported to be in the catchment of Lake Maridalsvannet (Tryland et al., 2015). Moreover, although activities such as bathing, fishing or camping are not allowed within the catchments of the water sources, residents commonly use the areas for recreational walk, and sometimes include their dogs. In addition, onsite wastewater treatment plants and septic tanks located within the catchments may be important sources of microbial contamination. For instance, sewage leakages from residential areas close to Lake Svartediket were implicated in the major waterborne outbreak recorded in the country in 2004 (Tveit et al., 2005), and the leakages may have been triggered by heavy rainfall recorded 2-weeks prior to the event (Johnsen et al., 2005). Results of recent studies that investigated the sources of faecal indicator organisms in the tributaries of major drinking water sources in Norway (including Lake Maridalsvannet and Lake Svartediket) revealed that human faecal contamination occurs mostly in the cold season (November 2014- May 2015), while the contributions of animals were highest in the warm season (June- September 2015) (Paruch et al., 2016a &b).

2.2. Climate-driven QMRA modelling framework and data

Figure 2 presents an overview of the steps applied in the climate-driven QMRA modelling framework used in this study to assess the pathogen infection risks for the selected water treatment plants (WTPs). The framework comprises five sub-modelling processes under historical and climate change scenarios: (A) modelling of the relationships between precipitation and water quality variables (turbidity and color); (B) modelling of the *E. coli* concentration in the raw water sources based on turbidity and color; (C) estimation of selected pathogen concentration from observed (historical) *E. coli* and predicted *E. coli* (under: projected average precipitation for 2045 and 2075; assumed 50% and 100% increases in extreme precipitation events); (D) modelling of the barrier efficacies of the WTPs against the selected pathogens; and (E) modelling pathogen infection risks including sensitivity analysis for the QMRA inputs. Step E also involved calculation of infection risks associated with potential failures in each of the water treatment steps.

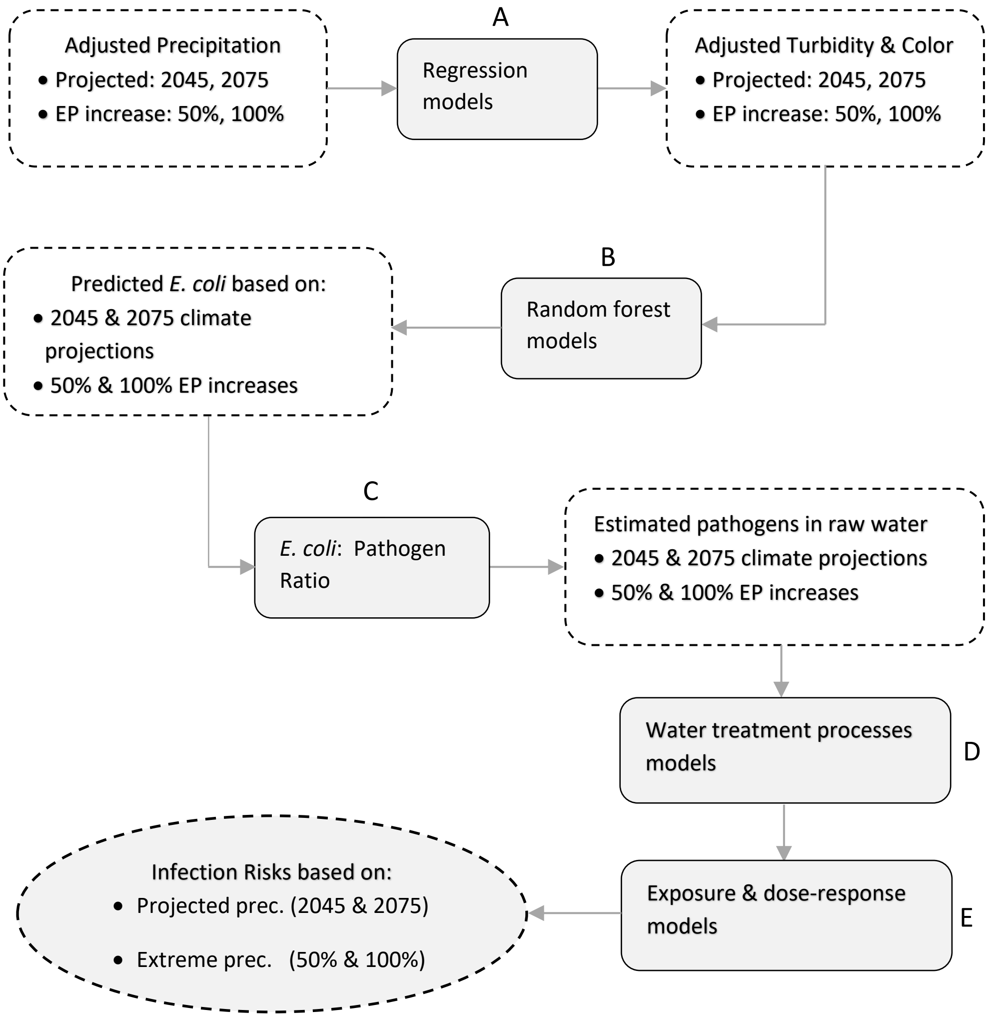

Figure 2. Framework of the modelling steps for prediction of future pathogen infection risks associated with the WTPs. (A) Regression models (prediction of future turbidity and color), (B) Random Forest (RF) models (prediction of future *E. coli*), (C) Estimation of pathogens from *E. coli*, (D) Process models (treatment barrier efficacies), and (E) Dose-response models (pathogen infection risk calculation). EP =

extreme precipitation (Values of average precipitation ≥ 3 times standard deviations of the time series were increased by 50% and 100%).

The water quality data used in this study were taken from the WTPs, and were composed of weekly records of turbidity, color, and *E. coli* measured in the raw water sources between 2009 and 2015. In addition, hourly precipitation measurements in the catchments of the raw water sources for the same period were obtained from weather stations closest to the water sources. From the hourly measurements, total weekly precipitation values were calculated. Further, seasonal mean values of projected precipitation for 2045 and 2075 in the locations of the raw water sources were obtained from the Norwegian Meteorological Institute. The mean projections were first bias-corrected and used to adjust the historical time series of the observed precipitation in the regions. Table 2 shows the bias-corrected projections of precipitation in the study regions for 2045 and 2075.

Table 2. Bias-corrected median projections of precipitation in the regions where the WTPs studied are located.

WTP	Year	Biase-corrected median projected change (%) in average precipitation under RCP8.5 climate scenarios.			
		Winter	Spring	Summer	Autumn
Ålesund	2045	0.16	14.22	9.79	-13.17
	2075	-0.12	17.25	14.26	-10.78
Oset	2045	5.99	22.82	3.19	-8.64
	2075	11.23	20.05	1.76	-5.59
Svartediket	2045	17.51	11.75	21.64	4.33
	2075	22.35	17.31	22.37	10.15

2.2.1. Modelling the relationships between precipitation and water quality

Traditional regression analysis (step A in Figure 2) was used to evaluate the relationships between the measured precipitation in the catchments and levels of turbidity and color measured by the WTPs for the same period. The regression analysis involved various functions including linear, exponential, polynomial and logarithmic. The best models were selected based on coefficient of determination (^{R2}), diagnosis of residuals as well as overall significance levels of the models ($p \leq 0.05$). The regression models were used to predict the values of turbidity and color in the raw water sources based on changes in average precipitation from (1) climate projections, and (2) assumed increases in precipitation. In the first case, the projected changes in average precipitation in the catchments for 2045 and 2075 were used to estimate corresponding changes in the measured turbidity and color through the regression models. These potential change ratios (%) were used to adjust the time series of the two variables to represent future values to be used in predicting *E. coli* in the raw water sources for 2045 and 2075. The precipitation changes factor method as applied in this study is widely used for adjusting historical climate variables in hydrological modelling and climate impact assessment (Teutschbein and Seibert, 2012; Shrestha et al., 2017). The method is based on transforming historically observed time series of climate variables using ratios between mean future and historical climate projections. The seasonal mean values of projections of precipitation used in this study are based on median values derived from ensembles of Representative Concentration Pathways (RCP 8.5) models taken from the Norwegian Climate Service Center. The climate models are composed of 10 different models and calculate the change factors for future years as moving averages. Therefore, the change factor of precipitation used in this study represents expected changes in a 40-year period, with each of the selected years (2045 and 2075) as median. In the second case, values in the records of precipitation (2009 - 2015) that were greater than or equal to three times the standard deviation (σ) of the 7 – year observations were increased by 50% and 100%. This was used to assess the potential effects of extreme precipitation events on the infection risks. Generally, an event of a climate or weather variable such as precipitation is said to be extreme when its occurrence is above or below threshold values near the upper (or lower) ends of their observed ranges (Annex 2012). This is caused by changes in mean total precipitation, which can be accompanied by changes in distribution, frequency, variability and intensity (IPCC, 2001). The new precipitation data (with increases in only the values $\geq 3\sigma$) were applied in the regression models to calculate corresponding changes in turbidity and color under the assumed increases in precipitation. To propagate the uncertainties in the regression model estimates in the subsequent steps of this study, the 95% confidence limits of the regression parameters were used to calculate uncertainty bounds for the predicted water quality variables. Therefore, each prediction was composed of mean, lower 95%CI, and upper 95%CI.

2.2.2. Prediction of future *E. coli* with random forest models

Random forest-based (RF) machine learning models were developed to predict the observed concentrations of *E. coli* in the raw water sources using measured turbidity and color as inputs (step B of Figure 2). Random forest is a tree-based machine learning algorithm developed by Breiman (2001). The model generates multiple decision trees through random data sampling (approximately two-thirds of training data), bootstrapping, and fitting each sample with either a classification or regression trees. Predictions of all the decision trees are aggregated to produce output variables as an average of predictions from the grown trees. The model is designed to prevent overfitting by calculating prediction errors from "out-of-bag samples" (one-third of training data) for each tree, thus obviating the need for additional testing of the model accuracy. Further description of the random forest machine learning and its appropriateness for use in predicting *E. coli* in raw water can be found in the work of Mohammed *et al.* (2018). In this study, weekly measurements of turbidity and color in the water sources from 2009 – 2015 were used to train and test the RF models for predicting *E. coli* in the water sources. The RF models in this study were developed using codes written in MATLAB (version R2017b). Although the RF model has a unique way of assessing the accuracy of predictions, we trained the models with 70% of the data sets, and further assessed the reliability of the models for predicting potential future concentrations of *E. coli* in the water sources by using the remaining 30% of the data for testing. The outputs of both training and testing of the RF models were further regressed to evaluate the performance of each of the models using coefficient of determination (R^2). The time series of turbidity and color adjusted from climate projections of average precipitation and extreme precipitation events were used as inputs to predict potential *E. coli* concentrations (mean, lower and upper 95%CI) in the water sources under the two scenarios described in section 2.2.1. of this study.

2.2.3. Estimation of pathogen concentrations in the raw water sources

For the purpose of modelling pathogen infection risks, the concentrations of pathogens in the water sources are required. For this, the study accounted for Norovirus, *Giardia*, *Cryptosporidium*, and *Campylobacter*. Norovirus is one of the most common causes of non-bacterial gastrointestinal illnesses in Norway, with strong seasonal variations and peaks during winter (NIPH, 2016). In addition, drinking water contamination is considered as a likely cause of between 300- 500 annual reported cases of *Giardia* and *Cryptosporidium* illnesses in the country (Nygård and Blystad, 2005). Amongst the incidences of bacterial gastroenteritis recorded in Norway, cases resulting from *Campylobacter* infections constitute a majority (Kvitsand & Fiksdal, 2010; MSIS, 2015). Further, *Campylobacter* was frequently identified in reported waterborne infections in Norway between 1988- 2002 (Nygård et al., 2003), and has been recognized as the second most common pathogen implicated in reported waterborne outbreaks in Scandinavian countries between 1998 and 2012 (Guzman-Herrador et al., 2015). In addition, consumption of both treated and untreated water have been identified as potential risk factors for incidences of *Campylobacter* infections in Norway (Kapperud et al., 2003; Jakopanec et al., 2008).

However, pathogen concentrations in water sources are rarely monitored, due to complexities in their detection methods. Thus, water quality regulations require targeting faecal indicator bacteria (FIB), which can be easily detected and enumerated in water. Drinking water supply systems in the country heavily rely on surface water sources, which are often subject to contamination from combined sewer overflows (CSOs) and discharges from on-site sanitation (Tryland et al., 2011; Petterson et al., 2016). The ratios used in to estimate the concentrations of pathogens from E. coli concentrations are shown in Table 3. A key limitation of this method is the restriction of the *E. coli* pathogen relationships to that of wastewater, since this may not be the same for other sources in the environment. Therefore, although the observed associations between *E. coli* and the pathogens in wastewater may not necessarily correlate with the situation in the water sources studied, the ratios enabled useful estimates of the concentrations of the pathogens to be obtained. The pathogen concentrations were estimated as time series with their 95% CI. To account for variability and uncertainty in the pathogen concentrations, 95% CI were estimated from the corresponding confidence limits of the predicted *E. coli* concentrations. In addition, the pathogen concentrations were fitted to triangular probability distributions (defined by the minimum, mode and maximum of the time series).

Table 3. Reported average concentrations of pathogens in sewage in Norway and the pathogen: *E. coli* ratios used to estimate pathogen concentrations from the observed and predicted *E. coli* in this study.

Microbe/pathogen (per 100 ml)	Concentration in WWTP influent and sewage system	References	Pathogen: *E. coli* ratio
E. coli	5.9×10^{6}	Grøndahl-Rosado et al., 2014b	
Norovirus	5.1×10^{5}	Myrmel et al., 2015	8.64×10^{-2}
Giardia	7.59×10^{2}	Robertson et al., 2006	1.30×10^{-4}
Cryptosporidium	6.78×10^{2}	Robertson et al., 2006	1.20×10^{-4}
Campylobacter	-	Eregno et al., 2016	2.00×10^{-5}

2.2.4. Modelling of pathogen removal in water treatment processes

Figure 3 shows the main treatment steps involved in the three WTPs included in this study. The treatments steps that serve as barriers to pathogenic organisms in the water are accounted for in this study (Figure 3).

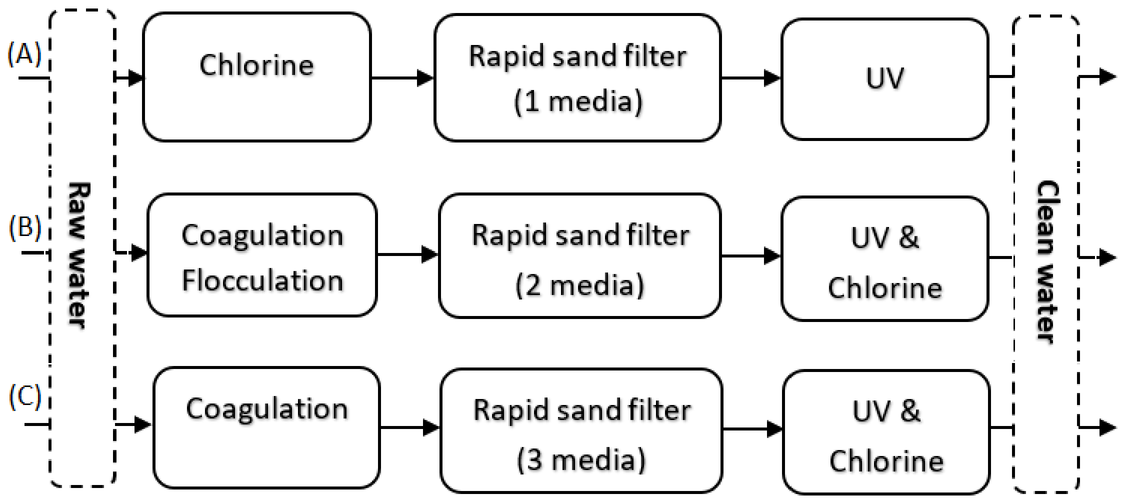

Figure 3. Main treatment steps involved the three water WTPs included in this study (A, B and C for the Ålesund, Oset, and Svartediket respectively).

The models applied in assessing the performances of the different steps in the removal of the selected pathogenic organisms are presented as follows:

The value of C_{out} for each pathogen was calculated as follows (Haas et al., 1999):

$$C_{out} = C_{in} \times \pi_i \times \dots\dots\dots..\pi_n \tag{1}$$

Where C_{in} is the concentration in raw water, π_i is the Log removal (Lr) of treatment step i, and n is the final treatment step. In each treatment step, Lr was calculated as mean (minimum, maximum) by varying one major input parameter. These were fitted to triangular probability distributions to account for the variability in the barrier efficacies. For the WTPs that include coagulation/flocculation and/or sedimentation steps, Lr values were taken from the works of Bell, 2000 and Hijnen & Medema, 2010.

The values of Lr for rapid sand filtration in the WTPs were calculated by applying the colloid filtration theory (Yao et al., 1971). Data on filter dimensions, media characteristics and operation conditions used as inputs to the model were collected from the WTPs. In this model, filter media dimensions were varied to obtain the mean (minimum, maximum) values for Lr. Details of the treatment steps, model equations, and parameters used in calculating the barrier efficacies are presented in Appendix A.

Reduction of pathogens by free chlorine was estimated based on the Ct values for the disinfection contact chambers of each facility, From the Ct values, Lr was calculated using the relation (Ødegaard et al., 2009):

$$Lr = Lr_{req} \times \frac{Ct}{Ct_{req}} \tag{2}$$

where Lr_{req} and Ct_{req} are the required inactivation and Ct values for each pathogen by chlorination for specific water pH and temperature (Ødegaard et al., 2009). To obtain the mean, minimum and maximum values of Lr, corresponding values of the concentrations of total organic carbon (TOC) in the raw water sources used as inputs in the calculation of the Ct values were applied.

For the UV step, disinfection was modelled using the Chick-Watson model (Haas & Karra, 1984), with the disinfectant concentration replaced by the UV intensity as:

$$log_{10}\frac{C_x}{C_0} = -kI^n\tau \quad (3)$$

where I [mJ/cm^2] is the UV intensity, k [cm^{2}W^{-1}s^{-1}] is the inactivation rate constant, τ is the irradiation time [s], and n [-] is an empirical constant. Here, the 95%CI of the values of k were used to calculate the minimum, mean and maximum values of Lr. For Norovirus, the value of k (mean $\pm$ 95%CI) was set at 0.102 ± 0.006, which is based on a study conducted for Rotavirus (Malley et al., 2004), thus, the Rotavirus was assumed as a suitable surrogate for Norovirus. For *Giardia*, *Cryptosporidium*, and *Campylobacter*, a k value of 0.122 ± 0.009 was used (Craik et al., 2000; Malley et al., 2004).

2.2.5. Modelling exposure to pathogens and infection risks

The daily dose of pathogens in the treated water from the respective WTPs consumed per person per day was calculated as follows:

$$d = c \times V \times 10^{-\mathrm{Lr}} \quad (4)$$

where c is the pathogen concentration, V is the mean daily amount of cold water consumed per person (0.74 L), which follows a Log-normal distribution with parameters $\mu = -0.299$ and $\sigma = 0.57$ (Westrell , 2004), and Lr is the total log removal achieved by the different treatment units in the WTP, which were derived from section .2.2.4. To account for variabilities in the dose-response model parameters themselves, the minimum and maximum values shown in Table 4 were fitted to uniform probability distributions. Using the various distributions of the input parameters, Monte Carlo simulations were run with 10 000 iterations, and the resulting data were used for the respective dose-response models. To assess the daily pathogen infection risks associated with the dose, d of pathogens ingested in equation 4, the dose-response models summarized in Table 4 were used for the different pathogens. Although the hypergeometric dose-response for used norovirus has some limitations (Schmidt, 2015; Van Abel et al., 2017), the model was applied in this study under the assumption of a "worst case" scenario for which the populations connected to the water supply systems have no immunity to the virus.

Table 4: Dose-response models and parameters used in calculating the daily infection risks

Pathogen	Model	Parameters *U (min, max)*	References
Norovirus	Hypergeometric	α = U (0.004, 0.005)	Teunis et al., 2008;
		β = U (0.055, 0.063)	Thebault et al., 2013
		a = 0.9997	
Giardia	Exponential	r = U (0.0199, 0.02)	Rose & Gerba, 1991 ;
			Teunis et al., 1996 ;
			Haas et al., 1999 ;
Cryptosporidium	Exponential	r = U (0.004, 0.2)	US. EPA, 2006;
			WHO, 2011
Campylobacter	*Beta-Poisson*	α = U (0.145, 0.15)	Medema et al., 1996
		β = U (7.59, 7.9)	Teunis et al., 1999

U = Uniform distribution

Annual infection risks were calculated from the daily infection risks using the following equation.

$$P_{annual} = 1 - \left(1 - P_{daily}\right)^{n} \quad (5)$$

where P_{daily} is the daily infection risks from the respective dose response models, and n = 365 for annual risk estimation. In this study, median infection risks were calculated and the values were compared with the acceptable infection risk level of 10^{-4} per person per year (pppy), which has been used for surface water treatment requirements in the US (US. EPA, 2006). For drinking water consumption, the WHO recommends the use of Daily Adjusted Life Years (DALYs), with a tolerable disease burden of 10^{-6} DALY ppy (WHO, 2011). However, disease burdens associated with the infection risks were not calculated in this study. The infection risks were calculated using the pathogen concentrations estimated from the historical *E. coli* in the raw water sources, predicted concentrations under climate projections, and the concentrations under extreme precipitation events. Since the pathogen concentrations (from the climate projections and extreme precipitation events) were estimated with their 95%CI (section 2.2.3), the annual median infection risks were separately calculated from the confidence limits and presented as uncertainty bounds.

In the case of the historical infection risks, uncertainty bounds (95%CI) were calculated using the Kolmogorov-Smirnov (K-S) “goodness of fit” test (Hogg and Tanis, 1977). The K-S test determines confidence bands for probability distributions. The QMRA models were implemented and run in R (Ri386 3.5.0).

2.3. Water treatment failure scenarios

After applying the models to estimate the potential future infection risks that are attributable to the projected precipitation and extreme precipitation events in the catchments of the water sources, additional scenarios were performed to investigate the effects of potential failures in each treatment step on the infection risks. These scenarios were meant to determine how safe the treated water can be under events of failures in any of the barriers. This was evaluated by using the 5th percentiles of the calculated barrier efficiency of each treatment step, while all other steps remained unvaried. The resulting median infection risks were compared with the baseline scenarios. By comparing the results of these scenarios with the baseline scenarios, key areas that may be of concern can be identified and prioritized in ensuring the safety of drinking water in the future.

2.4. Sensitivity analysis of QMRA inputs

The main objective of the sensitivity analysis performed in this study was to determine how the various inputs of the QMRA influence the infection risk calculation. For this reason, the pathogen concentrations, water consumption, and dose-response model parameters were varied from their minimum to maximum values, and the infection risk due to each variation was calculated. The sensitivity analysis was performed only for Ålesund WTP, with the assumption that the others would show similar trends. The calculated median infection risks resulting from varying each parameter were averaged and factor sensitivity coefficients (FS_i) were calculated as:

$$FS_i = P_{i,x}/P_{baseline} \tag{6}$$

where $P_{i,x}$ is the averaged median infection risk obtained after varying model input parameter x, and $P_{baseline}$ is the baseline median infection risk. The sensitivity analysis was performed only for the QMRA step, since variabilities in the model input parameters at each step were incorporated using probability distributions.

3. Results

3.1. Dependence of turbidity and color on precipitation

Table 5 summarizes the fitted linear and non-linear relationships between the water quality variables (turbidity and color) in the raw water sources of the three WTPs and the catchment precipitation. For each selected model, the residuals were randomly and symmetrically dispersed from the horizontal, indicating that the linear models adequately describe the data. In addition, the standardized residuals ranged from -0.1 to 0.1 for the turbidity models and -0.4 to 0.4 for the color models. All the models were also significant at $p < 0.05$. The R^2 values for the selected models ranged from 0.28 to 0.37 for turbidity and 0.31 and 0.52 for color, suggesting that catchment precipitation explains less than 40% and 50% of variabilities in the measured turbidity and color respectively. The predicted seasonal averages of the water quality variables and the catchment precipitation are shown in the appendix (Appendix B).

Table 5: Results of the selected regression models fitted to measured turbidity and color in the raw sources and catchment precipitation. The projected seasonal changes in turbidity and color in the water sources are also shown.

Variable	Relationship	R^2	Mean change factor for 2045 and 2075 (%)				
				Winter	Spring	Summer	Autumn
			Ålesund water source				
Turbidity	$y = 0.028 + 0.597x^3$	0.37	2045	2.81	3.01	2.85	2.67
			2075	2.79	3.14	3.01	2.72
Color	$y = 0.106+1.129x-4.277x^2+3.881x^3$	0.52	2045	11.68	19.22	18.01	-12.16
			2075	9.42	19.32	19.22	-7.52
			Oset water source				
Turbidity	$y = 0.083 + 0.091x$	0.28	2045	9.94	10.12	10.31	8.76
			2075	9.95	9.94	10.39	9.31
Color	$y = 0.134 + 0.119x$	0.43	2045	15.48	14.79	15.97	13.92
			2075	16.06	15.46	16.06	14.61
			Svartediket water source				
Turbidity	$y = 0.095exp(x)$	0.29	2045	10.1	11.9	9.8	8.7
			2075	10.7	11.6	9.7	8.9
Color	$y = 0.232 + 0.316x$	0.31	2045	25.1	30.5	24.2	20.4
			2075	26.9	29.5	23.8	21.3

x- catchment precipitation; y-response variables (turbidity or color).

3.2. Historical and predicted concentrations of *E. coli* in the water sources

The seven-year historical observations indicate that the concentrations of *E. coli* are generally low in all the water sources, with seven-year (2009 - 2015) maximum concentrations of 9 CFU/100 ml, 6 CFU/100 ml, and 37 CFU/100 ml in the water sources for Ålesund, Oset, and Svartediket respectively. Higher concentrations occur during winter and autumn seasons in the water sources for Ålesund and Oset WTP, compared to spring and summer. However, the differences are marginal in the Ålesund water source, which has a larger total surface area, and located in an area that receives significantly higher rainfall throughout the seasons (west coast of Norway) than the Oset water source (southern Norway). The pattern of variation was however slightly different in the water source for Svartediket, with higher concentrations occurring mostly in autumn relative to the other seasons.

Figure 4 shows the concentrations of *E. coli* in the raw water sources predicted using the RF models for the two scenarios (average projected precipitation for 2075 and 100% increase in extreme precipitation events). Regression plots comparing the outputs of the RF models with the historical observations of *E. coli* in the water sources are shown in Appendix B. Across the three water sources, R^2 values achieved ranged from 0.71 to 0.89 during model training and from 0.66 to 0.74 during testing. Comparison of the predictions under the two scenarios indicate that the extreme precipitation events may result in higher concentrations of *E. coli* in the raw water sources than the future climate projections.

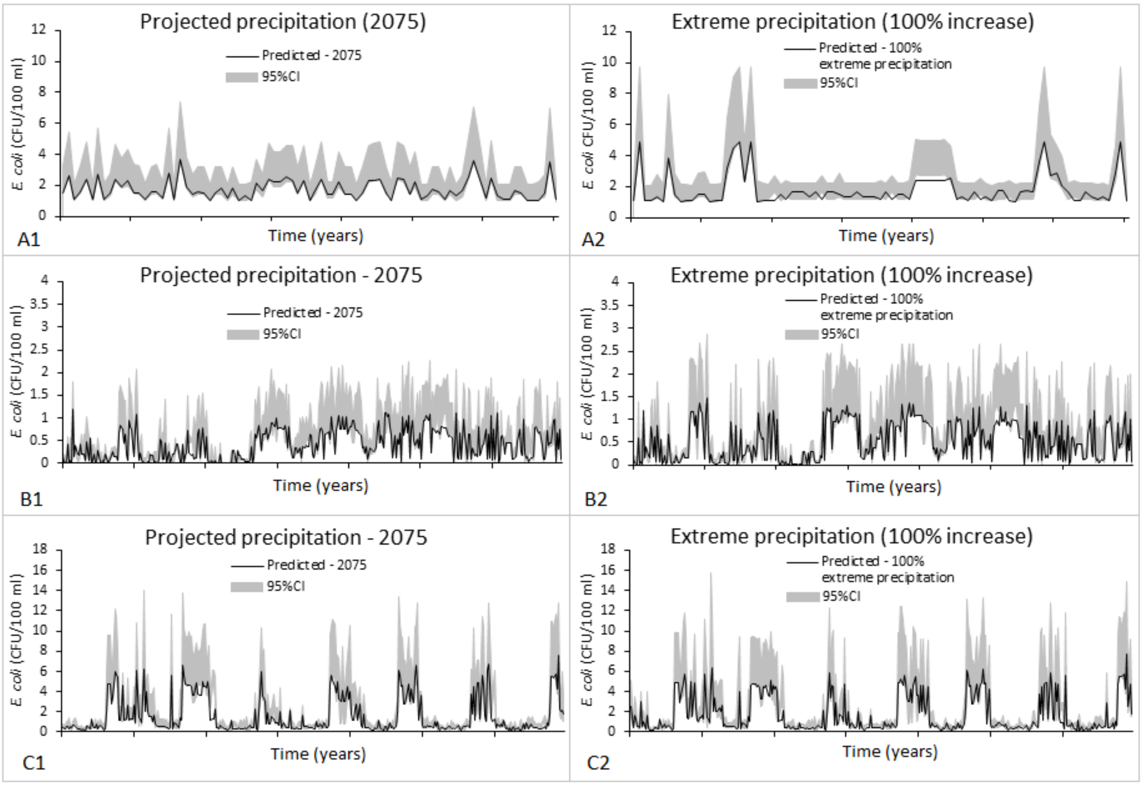

Figure 4. Predicted concentrations of *E. coli* in the raw water sources under climate projections for 2075 and 100% increases extreme precipitation events for Ålesund (A1 & A2), Oset (B1 & B2), and Svartediket (C1 & C2).

3.3. Estimated pathogen concentrations in the water sources

The average and 95% CI of the concentrations of the pathogenic organisms predicted under the two scenarios are shown in Figure 5. As indicated in section 3.2, the concentrations of *E. coli* in the historical observations were generally low in the three lakes. Consequently, the estimated pathogen concentrations in the various raw water sources were generally low. As shown in the figure, the calculated concentrations of Norovirus were higher in the water sources than the other pathogens. The relatively higher concentrations of Norovirus can be attributed to higher ratio of the pathogen to *E. coli* as used in the calculation. Moreover, just as like the predicted *E. coli* concentrations, the increases due to extreme precipitation events were relatively higher than those estimated under the climate projections.

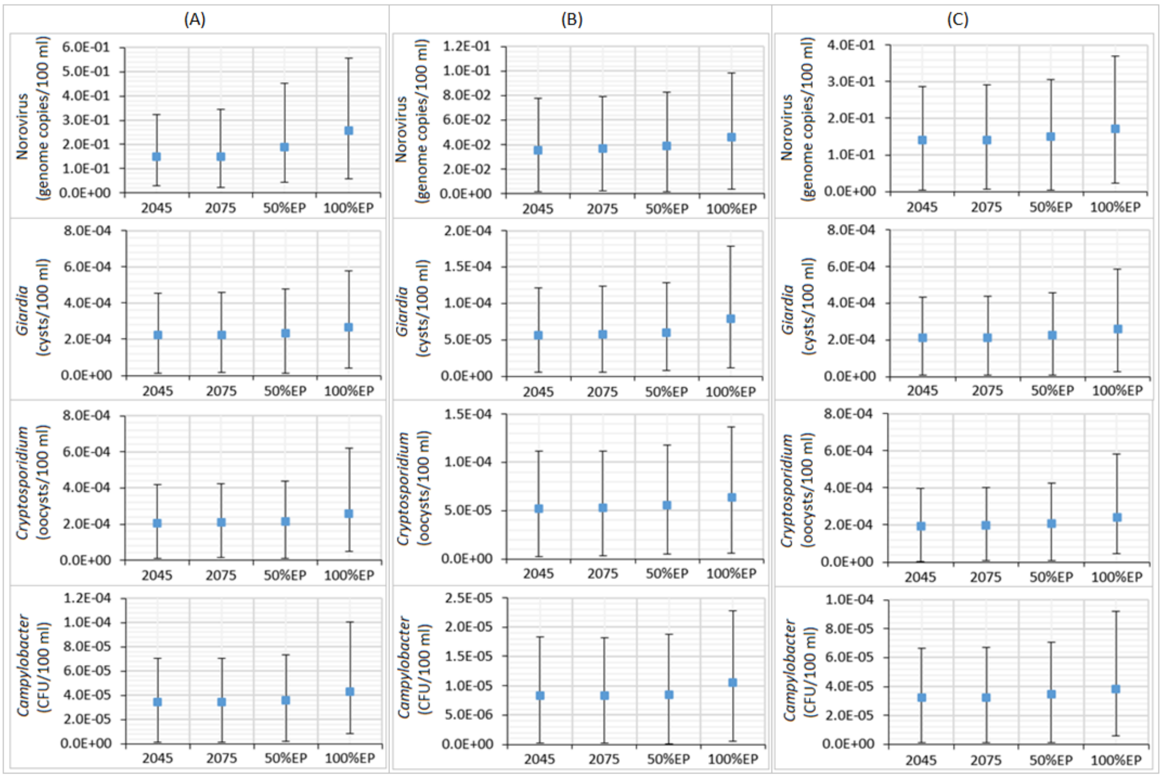

Figure 5. Averages and 95% CI of the concentrations of Norovirus, *Giardia*, *Cryptosporidium*, and *Campylobacter* estimated in the water sources for Ålesund (A), Oset (B), and Svartediket (C) WTPs

3.4. Pathogen removal in the water treatment plants

Table 6 summarizes the results of the model estimates of log removals of the reference pathogens by the treatment processes across the three WTPs. The model results of the rapid sand filters alone generally yielded less than 1 log removal of the pathogens. Across all the WTPs, log removal of Norovirus by filtration was lower than the three other pathogens. This may be partly due to the average size of the pathogen, which is an essential component of the colloid filtration theory applied in this study.

Table 6: Calculated log reductions of pathogens in the various WTPs

Pathogen	Log removal (π) *mean (min - max)*				
	Coagulation/ Flocculation, sedimentation	Rapid sand filtration	Chlorination	UV	Total
		Ålesund WTP			
Norovirus		0.09 (0.06, 0.19)	0.0099(0.0094,0.011)	3.234 (3.095, 3.366)	3.335 (3.164, 3.574)
Giardia		0.174 (0.099, 0.332)	0.00039 (0.00036, 0.00042)	3.646 (3.489, 3.792)	3.819 (3.589, 4.125)
Cryptosporidium		0.253 (0.151, 0.504)	0.00039 (0.00037, 0.00042)	3.646 (3.489, 3.792)	3.898 (3.642, 4.296)
Campylobacter		0.932 (0.566, 1.887)	0.039 (0.037, 0.0415)	3.646 (3.489, 3.792)	4.617 (4.094, 5.722)
		Oset WTP			
Norovirus	1.8 (0.2, 4.3)	0.151 (0.105, 0.218)	0.916 (0.727, 0.959)	3.605 (3.466, 3.736)	6.472 (4.498, 9.215)
Giardia	1.83 (0.30, 2.91)	0.245 (0.177, 0.368)	0.036 (0.029, 0.038)	4.016 (3.861, 4.163)	6.128 (4.367, 7.469)
Cryptosporidium	1.91 (0.4, 3.8)	0.373 (0.269, 0.509)	0.036 (0.029, 0.039)	4.017 (3.861, 4.163)	6.336 (4.559, 8.511)
Campylobacter	1.98 (0.6, 3.7)	1.331 (0.972, 2.058)	3.665 (2.911, 3.839)	4.017 (3.861, 4.163)	10.992 (8.344, 13.762)
		Svartediket WTP			

Norovirus	1.83 (0.2,4.3)	0.199 (0.155, 0.297)	0.982 (0.753, 1.044)	3.234 (3.095, 3.366)	6.244 (4.202, 9.001)
Giardia	2.01 (0.3, 2.9)	0.335 (0.259, 0.498)	0.039 (0.031, 0.042)	3.646 (3.489, 3.792)	6.031 (4.079, 7.233)
Cryptosporidium	2.35 (0.4, 3.81)	0.508 (0.394, 0.755)	0.039 (0.031, 0.042)	3.646 (3.489, 3.792)	6.543 (4.313, 8.388)
Campylobacter	2.07 (0.6, 3.7)	1.784 (1.475, 2.832)	3.925 (3.011, 4.176)	3.646 (3.489, 3.792)	11.425 (8.575, 14.501)

The current drinking water regulation in Norway requires that WTPs reduce bacteria and viruses by a minimum of 99.9% (3 log reduction), and parasites by 99% (2 log reduction) (Norwegian Food Safety Authority, 2005). Based on the Norwegian guideline for microbial barrier analysis in water supply systems, the levels of raw water quality and the population that are connected to the WTPs included in this study require minimum log reductions of 5 for Norovirus, 5 for *Campylobacter*, and 3 for *Giardia* and *Cryptosporidium* (Norwegian Food Safety Authority, 2005; Ødegaard & Østerhus, 2014). The total log reductions calculated in this study (5.28 – 6.85 log for Norovirus; 3.92 – 6.5 log for *Giardia* and *Cryptosporidium*; and 9.39 – 11.91 for *Campylobacter*) suggest that the WTPs studied generally meet the requirements. However, these are purely under the assumption that each of the treatment processes are performing at their optimal capacities.

3.5. Historical and future infection risks

A summary of the annual median infection risks per person per year (pppy) from the historical and predicted concentrations of the pathogens are shown in Table 6. In this table, infection risks that are higher than the acceptable limit of 10^{-4} pppy are shaded in grey color. The annual median infection risks (historical) for the Ålesund WTP were; 3.15 10^{-6} (pppy), 3.33 x 10^{-7}, 2.06 x 10^{-6} (pppy), and 8.76 x 10^{-7} (pppy) for Norovirus, *Giardia*, *Cryptosporidium*, and *Campylobacter* respectively. The respective historical risks for Oset and Svartediket were 9.64 x 10^{-9} (pppy) and 1.03 x 10^{-8} (pppy) for Norovirus, 1.14 x 10^{-8} (pppy) and 5.98 x 10^{-8} (pppy) for *Giardia*, 5.85 x 10^{-10} (pppy) and 1.96 x 10^{-8} (pppy) for *Cryptosporidium*, and 4.76 x 10^{-12} (pppy) and 3.24 x 10^{-10} (pppy) for *Campylobacter*. It can be noted from the above values that the median values for Norovirus, *Cryptosporidium*, and *Campylobacter* in the Ålesund WTP, were high, although they were averagely within acceptable limits of 10^{-4} pppy (US EPA, 2006). Moreover, the 95% CI of the historical risks for Norovirus in this WTP (10^{-4} pppy) suggests that the risk of the virus may have been high. The 95% CI risk values for the other pathogens in the Ålesund WTP and all the pathogens in the Oset and Svartediket WTPs were however < 10^{-5} (pppy).

The results also indicate that under the current projections of average precipitation in the regions where the raw water sources are located, future infection risks may generally remain close to the present levels. However, as shown by the 95% CI values in Table 6 (A), the risk of Norovirus and *cryptosporidium* in the Ålesund WTP may be high in the future. Further, the results shown in Table 6 (B) indicate that the occurrence of extreme precipitation events in the catchments of all the raw water sources may lead to substantial increases the infection risks. The risks of Norovirus and *cryptosporidium* in the three WTPs could be particularly high under these events, with median risk levels > the acceptable limit of 10^{-4} (pppy).

Table 6: Population annual median infection risks from the estimated pathogen concentrations in the water sources; historical and future climate projections (A), historical and increases in extreme precipitation events (B).

(A)	Historical			Predicted-2045			Predicted-2075		
	5%CI	Median	95%CI	5%CI	Median	95%CI	5%CI	Median	95%CI
Ålesund WTP									
Norovirus	6.8E-08	3.2E-06	9.8E-04	2.4E-07	2.5E-05	2.5E-03	2.6E-05	2.7E-04	2.7E-03
Giardia	1.1E-10	3.7E-07	8.0E-06	2.0E-07	2.0E-05	2.1E-04	2.4E-07	2.7E-05	2.9E-04
Cryptosporidium	8.0E-09	2.1E-06	6.3E-05	8.5E-06	8.4E-05	1.6E-04	8.9E-06	8.7E-06	1.8E-03
Campylobacter	3.7E-09	8.8E-07	4.5E-06	6.6E-07	1.4E-06	3.9E-05	4.8E-07	4.8E-06	4.8E-05
Oset WTP									
Norovirus	1.3E-12	9.2E-09	4.1E-05	8.0E-09	9.7E-07	1.3E-05	4.3E-09	6.4E-07	8.5E-05
Giardia	7.3E-11	1.1E-08	3.4E-07	3.3E-10	3.6E-08	4.4E-06	6.8E-09	2.1E-06	2.3E-05
Cryptosporidium	1.1E-12	5.9E-10	9.4E-06	1.1E-09	1.2E-07	1.5E-05	1.6E-09	2.5E-06	3.1E-06
Campylobacter	0.0E+00	4.8E-12	2.6E-09	5.7E-13	6.9E-13	7.3E-08	5.7E-13	7.3E-11	6.9E-09
Svartediket WTP									
Norovirus	1.3E-10	1.0E-08	4.1E-05	2.9E-08	3.3E-05	4.2E-04	3.0E-08	4.0E-05	7.7E-04
Giardia	3.9E-11	6.0E-09	1.0E-06	5.4E-09	2.4E-06	4.6E-05	6.0E-08	1.1E-05	1.8E-05
Cryptosporidium	6.6E-11	2.0E-08	6.9E-06	9.9E-09	1.7E-06	3.1E-05	1.0E-07	1.5E-05	3.4E-05
Campylobacter	0.0E+00	3.2E-10	4.3E-08	1.6E-13	2.0E-10	2.8E-06	1.1E-12	2.0E-09	3.0E-05

(B)	Historical	50% EP increase	100% EP increase

	5%CI	Median	95%CI	5%CI	Median	95%CI	5%CI	Median	95%CI
Ålesund WTP									
Norovirus	6.8E-08	3.2E-06	9.8E-04	2.7E-05	3.3E-04	3.5E-03	4.1E-05	5.4E-04	7.2E-03
Giardia	1.1E-10	3.7E-07	8.0E-06	3.2E-06	3.3E-04	3.4E-04	5.4E-07	8.6E-04	1.4E-03
Cryptosporidium	8.0E-09	2.1E-06	6.3E-05	2.0E-06	2.3E-04	2.6E-03	4.7E-06	7.5E-04	7.1E-03
Campylobacter	3.7E-09	8.8E-07	4.5E-06	3.3E-06	3.3E-06	3.7E-06	7.1E-06	1.3E-05	3.0E-04
Oset WTP									
Norovirus	1.3E-12	9.2E-09	4.1E-05	3.7E-09	4.7E-05	5.4E-04	3.1E-09	3.7E-04	6.8E-03
Giardia	7.3E-11	1.1E-08	3.4E-07	3.2E-09	3.6E-06	4.1E-05	5.2E-09	6.7E-04	1.0E-04
Cryptosporidium	1.1E-12	5.9E-10	9.4E-06	1.5E-09	2.2E-06	2.8E-04	1.1E-09	1.5E-04	2.5E-03
Campylobacter	0.0E+00	4.8E-12	2.6E-09	8.1E-14	1.2E-10	1.2E-07	6.1E-13	8.1E-09	1.3E-05
Svartediket WTP									
Norovirus	1.3E-10	1.0E-08	4.1E-05	2.9E-08	4.4E-04	5.1E-04	3.0E-08	4.6E-04	6.6E-03
Giardia	3.9E-11	6.0E-09	1.0E-06	2.1E-08	3.4E-05	8.5E-04	8.5E-09	1.7E-05	7.2E-04
Cryptosporidium	6.6E-11	2.0E-08	6.9E-06	5.5E-07	8.5E-05	4.1E-04	3.3E-05	6.6E-05	6.0E-03
Campylobacter	0.0E+00	3.2E-10	4.3E-08	1.5E-12	3.7E-08	7.5E-05	1.5E-12	2.4E-06	6.2E-04

EP = extreme precipitation

3.5 Effects of sub-optimal performance of treatment steps on infection risks

Figure 6 shows the results of the additional scenarios performed on the WTPs to investigate potential effects of variations in the performances of the treatment steps on the infection risks. The scenarios were simulated for all the pathogens in each WTP and compared to the baseline scenarios. Results for the Ålesund WTP show that when the UV step performs at its 5th percentile capacity, risk of Norovirus infection can increase from the baseline value of 3.15 10^{-6} (pppy) to 1.02 x 10^{-4} (pppy). However, low performance of the chlorine unit does not appear to affect the infection risks. Similar effects of sub-optimal performance of the UV steps can be seen in the resulting infection risks calculated in the other WTPs. In addition, poor performance of the main treatment step in the Ålesund WTP (1 media filter) had low effect on the risks of infection of Norovirus and *Giardia* in the Ålesund WTP. Despite the relatively low effect of the filter in this WTP on the two pathogens, a poor performing filter implies that water from the filter outlet would contain relatively higher particle concentrations, subsequently reducing UV transmittance and disinfection efficacy. Across all the WTPs, the overall performance of the treatments and disinfections depended on the UV step. It can also be seen that for Oset and Svartediket WTPs, the effects of the chlorine steps on the infection risks were higher compared to the case of the Ålesund WTP. This is due to the relatively higher barrier efficacies calculated for the chlorine steps in these WTPs, compared to the Ålesund WTP.

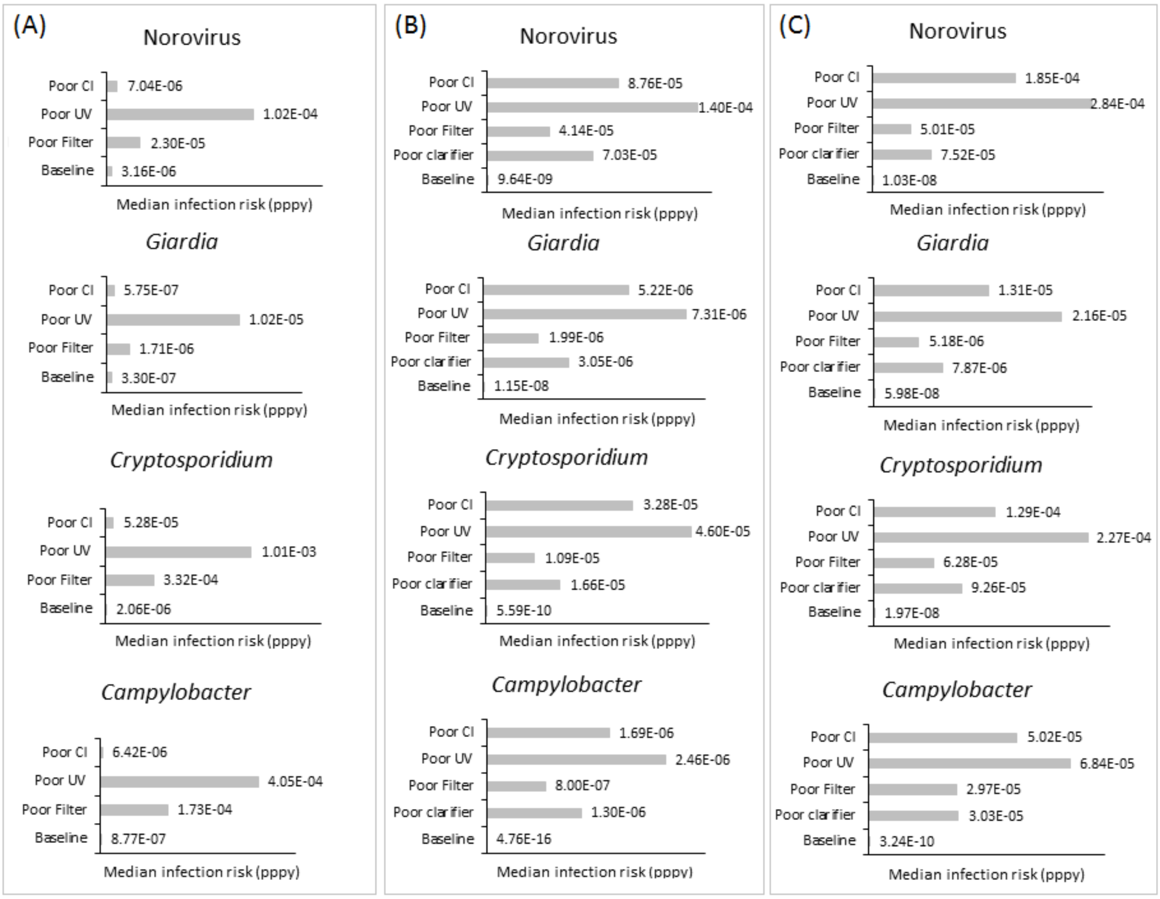

Figure 6. Effects of poor performing treatment steps (5th percentiles of their efficacies) on the infection risks in the Ålesund WTP (A) Oset WTP, (B) and Svartediket WTP (C).

3.6. Parameter sensitivity in the infection risk calculation

Figures 7 shows a plot of the sensitivity ranks of the various inputs of the infection risk calculation in the Ålesund WTP. Varying the model input parameters within their ranges resulted in significant changes in the calculated infection risks. For instance, increasing the concentration of Norovirus in the estimated historical time series from the minimum of 0.086 genome copies/100 ml to the maximum of 0.966 genome copies/100 ml resulted in increasing the infection risk from 3.15 x 10^{-6} (pppy) to 4.73 x 10^{-3} (pppy). Similar increases were noted when the volume of water and the alpha parameter (α) in the model were varied from minimum to maximum values. For the beta parameter however, increasing it from 0.055 to 0.063 resulted in lower infection risks of the virus. The alpha and beta parameters (α, β) determine the infectivity of the virus, and the results in Figure 7 suggest that the choice of values for these parameters can have substantial impact on the final risk estimates. The concentration of Norovirus was the most sensitive parameter to the dose-response model with a sensitivity rank of 1.84, followed by the beta parameter with 1.22. In the exponential model for *Giardia*, water consumption was ranked highest among the input parameters. This parameter also ranked highest in the models for *Cryptosporidium*, followed closely by pathogen concentration in both cases. In the beta-Poisson model for *Campylobacter*, the pathogen concentration achieved the highest ranking (1.82) with the remaining parameters having approximately 1.1.

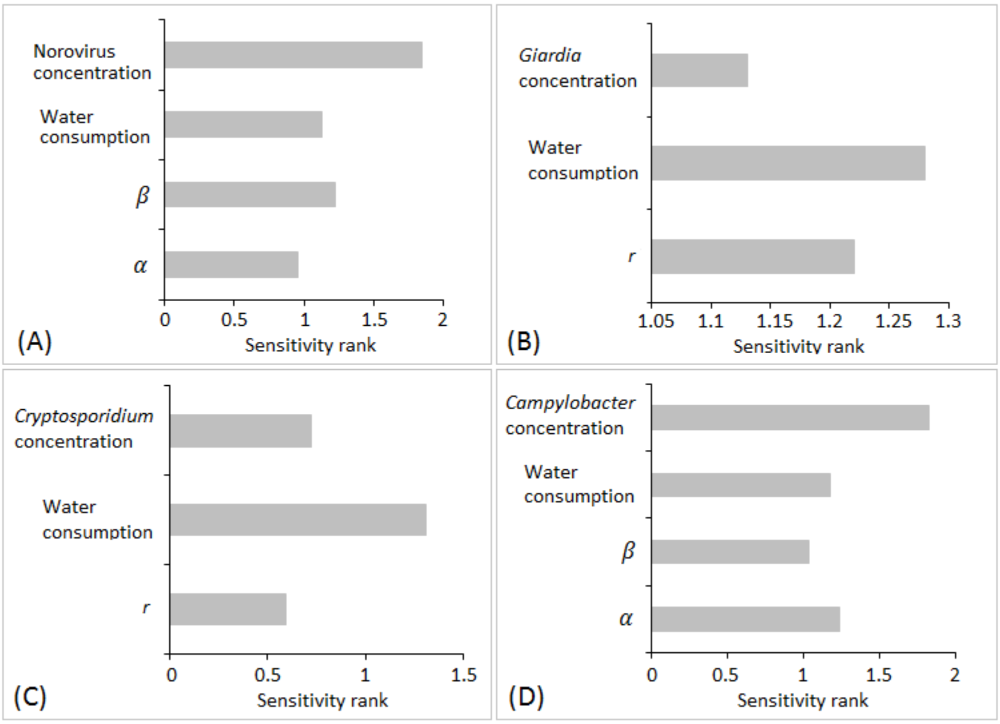

Figure 7. Sensitivity ranks of the infection risk calculation input parameters for Norovirus (A), *Giardia* (B), *Cryptosporidium* (C) and *Campylobacter* (D) in the Ålesund WTP. α, β and r are parameters in the dose-response functions.

4. Discussion

As presented in Table 5 in the results section, catchment precipitation may be expected to result in higher percent increases in the color of the raw water sources than the turbidity. This may be due to the spatial characteristics of the catchments such as soil type, topography, and concentrations of decaying organic matter in the catchments. The expected increase in turbidity in the future may be lower (~ 3%) in Lake Brusdalsvatnet (raw water source of the Ålesund WTP) than the other water sources, apparently due to the relatively larger size of the lake (surface area of ~ 7.2 km^2) and higher mean resident time compared to the other two lakes. Moreover, both turbidity and color displayed different responses to variations in the precipitation observed in the various water source catchments. Therefore, the predicted variations in the water quality variables reflect a combined influence of the respective responses and the varying magnitudes of the projected precipitation in the catchments. It is worth noting that the calculated change factors only account for potential impact of catchment precipitation, as the actual future concentrations of these variables can be affected by other factors such as soil/sediment characteristics and anthropogenic activities within the catchments.

Precipitation in the catchments of the water supply systems in this study comprises rainfall and snow, both of which can affect the turbidity and color of the water sources. In addition, high stream flows from heavy rainfall events and snowmelt cause mixing of stratified drinking water reservoirs such as lakes (Bertone et al., 2016), potentially increasing turbidity and color at the raw water intake zones of WTPs. Studies have found significant positive correlations between precipitation and variations in turbidity and color of drinking water sources (Nilsson & Renöfält, 2008; Whitehead et al., 2009). Moreover, high river flows from intense rainfall in the catchment of water supply systems have been associated with increased sediment load and turbidity of raw water (Göransson et al., 2013; Bertone et al., 2016). Color can be significantly varied by the concentration of dissolved organic and inorganic substances such as humic and fulvic materials, both of which are affected by precipitation through increases in organic matter content of surface water (Delpla et al., 2015; Dieleman et al., 2016).

The R^2 values obtained from regression of the observed *E. coli* in the raw water sources and the outputs of the random forest models were from 0.66 to 0.74 during testing in this study. This indicates that turbidity and color could substantially explain variabilities in the concentrations of FIB in drinking water sources. Other studies that applied multivariate regression models in predicting the concentrations of *E. coli* in surface water resources from water quality variables have reported similar prediction accuracies. For instance, results of a study that predicted the concentrations of FIB in a river from water quality parameters such as turbidity, pH and water temperature reported R^2 of up to 0.82 in in the model for *E. coli* prediction (Herrig et al., 2015). Similarly, when water quality and weather parameters including turbidity, rainfall, and air temperature were applied in predicting *E. coli* in beach water, the models were able to explain approximately 70% of the variations in the FIB (Olyphant & Whitman, 2004). Moreover, the RF model as applied in this study has been demonstrated to have potential for application in predicting water quality variables, including FIB (Rodriguez-Galiano et al., 2014; Mohammed et al., 2018).

Although precipitation and its variability are key drivers of faecal contamination of surface water bodies, precipitation alone rarely predicts the concentrations of FIB in water. Therefore, FIB predictive models rely on additional environmental and water quality parameters. For catchments where precipitation poorly correlates with the occurrence of FIB in surface water, determining the relationships between precipitation and other surrogate variables such as turbidity could offer a means of evaluating the indirect effects of precipitation. The results of this study show that combining this relatively efficient model with multiple regression can allow potential future changes in water quality parameters to be estimated. Although the method as applied in this study neglects the effects of other factors such as future anthropogenic activities in the catchments that may affect the quality of water in the future, it enables the changes attributable to changes in key weather variables to be quantified from climate projections. Instead of only assuming certain future concentrations of pathogens for simulating climate scenarios in QMRA, the method applied in this study relates the concentrations with actual climate projections in the catchments of water sources. Although the method can be applied to other drinking water sources, records of water quality variables and precipitation specific to different water sources are required. Apart from the data inputs, the reliability of this approach depends on the appropriateness of the statistical relations established between the water quality variables and catchment precipitation, as well as the quality of the climate projections. In addition, the pathogen: *E.coli* ratios used to estimate the concentrations of the pathogens may be specific to the study region, and this may not be true for other locations. Moreover, since animals such as horses and dogs have been documented as important sources of microbial discharge into the raw water sources included in this study, estimating pathogen concentrations based on reported ratios in wastewater alone could misrepresent the effects of contributions from other potential sources in the catchments.

Results of a study that examined the filterability of different viruses in water using advection-dispersion models showed that the size was the only factor that influenced the retention of viruses in filter media, and better retention was achieved for larger viruses (Aronino et al., 2009). The least removal efficiency of 0.09 log for Norovirus was calculated for the WTP that uses a one media filter composed of calcium carbonate marbles (Ålesund WTP). In addition, the treatment steps in the WTP does not include clarification by coagulation, although this was not accounted for in the filtration models. A study that investigated the removal of Norovirus in a laboratory scale coagulation-rapid sand filtration set-up observed very low removal was achieved in the absence of a coagulant (Shirasaki et al., 2010). Their results indicated that removal of viruses in rapid granular filtration is greatly dependent on coagulation upstream of the filters. The low virus removal efficacies of the rapid sand filters as calculated in this study are consistent with performances reported in literature. Results of a study that reviewed the performances of various water treatment processes on the removal of microorganisms indicate that rapid granular filtration alone can achieve an average virus removal efficiency of up to 0.6 log (Hijnen et al., 2004).

For the protozoan pathogens, the maximum log removals by the filters were 0.29 log for *Giardia* and 0.45 log for *Cryptosporidium*. These removal efficacies were achieved for the Svartediket WTP that uses a three-media filter. The respective minimum removal efficacies were 0.17 log and 0.25 log, both in the Ålesund WTP, which uses a single-media filter. Compared to the values achieved in this study, higher removal efficacies of these pathogens by rapid granular filters have been reported in literature.

For instance, results of the review performed by Hijnen et al. (2004) showed that up to 1.2 log and 1.1 log removals can be achieved for *Giardia* and *Cryptosporidium* respectively, when the filtration step is not preceded by coagulation. The highest removal efficacies (1.28 and 1.68) were achieved for *Campylobacter* in the Oset and Svartediket WTPs. Efficacies reported in literature typically range from 0.2 log and 1.5 log for granular media filter alone (Hijnen et al. 2004). The calculated pathogen removal by chlorine disinfection ranged from 0.009 log to 0.98 log for Norovirus and from 0.039 log and 3.93 log for *Campylobacter*. The corresponding values achieved for the protozoan pathogens were however very low (0.0004 log to 0.039 log). A review on the efficacies of chlorine disinfection in WTPs revealed that 2.1 log and 4 log removal of viruses could be achieved by free chlorine dose of ~0.5 mg/L in raw water sources with pH of 6.5 - 8 and temperature of < 10 ºC (Petterson and Stenström, 2015). The concentrations of TOC in the water sources for the reviewed studies were not however reported. As described in section 2.3 of this study, calculation of both the initial chlorine oxidation and degradation constant involved the use of TOC in the water sources. This parameter is one of the key determinants of chlorine disinfection units, and the average values in the water sources included in this study was 2.3 to 3.8 mg/l. The calculated log reductions for the protozoan pathogens and *Campylobacter* achieved in this study are consistent with reported values in the literature. For instance, Petterson and Stenström 2015 showed that at an initial chlorine residual of 0.4 mg/L and mean residence time of 12 minutes, up to 0.03 log and 9.1 log reductions can be achieved for *Giardia* and *Campylobacter* respectively for average hydraulic behavior in the tank (with baffling factor of 6) using the disinfectant concentration × time (Ct) approach. UV disinfection resulted in the highest log-reductions for all the pathogens across the different WTPs. The least log removal was 3.23 log for Norovirus, while higher efficacies were calculated for *Giardia* (4.02 log), *Cryptosporidium* (4.02 log) and *Campylobacte*r (4.36 log). The relatively high efficacy of UV in pathogen inactivation is widely reported in literature (Clancy, 2002; Linden et al., 2002; Gerba et al., 2002; Malley et al., 2004). For UV doses within the range of the values applied in the WTPs considered in this study (~ 40 mJ/cm^2), up to 4.8 log of viruses and 3 log of protozoa and bacteria were reported in a review by Hijnen et al. (2006).

The results of the QMRA in this study suggest that the local projections of average precipitation in the country are not likely to substantially increase the risks of pathogen infections due to water consumption from public water utilities. However, the occurrence of extreme precipitation events in the catchments of water sources may be associated with significant increases in the infection risks. This indicates that managers of drinking water supply systems should be more concerned about meeting water quality targets during these rather unpredictable events, instead of climate projections. This further emphasizes the need for protection of drinking water source catchments such that faecal contamination of raw water that may be associated with the occurrence of extreme precipitation events, either as rainfall or snow can be minimized.

The predicted historical and future infection risks in the Ålesund WTP suggest that the WTP will require additional treatment steps such as a coagulation/flocculation unit in order to reduce the potential risks of pathogen infections presently and in the future. In addition, chlorination that is used as the first step in this WTP has a very short effective residence time. This resulted in very low chlorine disinfection efficacies calculated for the WTP. Therefore, it may be necessary to change both the location and design of the chamber such that the residence time can be improved. Moreover, a pH control step (CO_2 unit), which follow the chlorination unit in this WTP reduces the pH of water. This can affect the effectiveness of the chlorine disinfection due to the influence of pH on the type of species formed. Although lower pH (~ < 7) favors the formation of hypochlorous acid (HOCL), which may be a better bactericidal species of chlorine (Le Dantec et al., 2002; Crittenden et al., 2012), at extremely low water pH, other species such as chlorous gas may dominate.

Moreover, results of the scenarios for failures in the treatment steps show that ensuring optimal performances of certain treatment processes such as UV disinfection are more important in ensuring the safety of drinking water than the threats of climate change. Across all the WTPs, the overall performances of the treatment steps depended on the UV step. As indicated in Figure 6, failures in this step could significantly increase the risks of pathogen infection due to consumption of treated water from all the WTPs studied. Therefore, without optimal performance of the UV step during extreme precipitation events, the WTPs may not guarantee safe drinking water to their consumers.

Major potential sources of uncertainties in the calculated pathogen infection risks include the assumed relationships between *E. coli* and the pathogens used in predicting the risks, the climate projections of average precipitation, water consumption pattern, and the dose-response models themselves. Although uncertainties may still be present in the results, considerable reduction in the overall uncertainty can be achieved through extensive pathogen data acquisition in the raw water sources. Improving the uncertainty associated with the pathogen concentrations requires more sampling and analysis of raw water samples such that actual pathogen concentrations can be used in QMRA modelling. While such analysis may not eliminate the uncertainties, more representative pathogen concentrations are still necessary for efficient risk characterization. Estimation of pathogen concentrations from *E. coli* for the purpose of QMRA as applied in this study can either underestimate or overestimate the actual concentrations, and the associated health risks. The use of the results of the assessments for decision support should consider the associated uncertainties. Further, it may be necessary to compare calculated infection risks with actual incidence of pathogen infections in the populations connected to the various WTPs, although limited data exist, often due to under-reporting.

5. Conclusions

The present study investigates the potential impact of climate projections of average precipitation and the occurrence of extreme precipitation events on pathogen infection risks due to treated water consumption from three drinking water facilities in Norway. Regression and random forest machine-learning models were used to predict potential concentrations of pathogens in the raw water sources in the future. Subsequently, dose-response models were applied to calculate present and potential future pathogen infection risks. Based on the calculated median risks of infections, the historical risk levels in the Ålesund, Oset and Svartediket WTPs were generally within acceptable limits. However, risks for Norovirus in the Ålesund WTP were considerably high, and this may be partly attributed to the absence of a coagulation-flocculation unit in the water treatment plant, as well as the relatively low effectiveness of the chlorine system.

Results of the 2045 and 2075 infection risks suggest that under the current projections of average precipitation in the regions where the raw water sources of the WTPs are located, the infection risks may remain close to present levels. However, infection risks that may be associated with the occurrence of extreme precipitation in the water source catchments may be considerably high. This means that the WTPs will require optimization of treatment steps in the facilities to accommodate potential impact of climate change through extreme precipitation events. Further, sub-optimal operation of water treatment processes, particularly the UV steps could significantly increase the pathogen infection risks. The QMRA model results presented in this research provides strong evidence of the need to ensure protection of the raw water sources and ensuring optimal operation of water treatment processes. Estimating pathogen concentrations from FIB introduces uncertainties in the infection risks calculated. However, current limitations of detection methods for pathogenic organisms in water make it difficult to perform QMRA without such relationships. Overall, the study confirms that viral and/or protozoan pathogens may be the key drivers of infections in the populations that are connected to the water supply systems studied, and significant effort needs to be done to reduce these risks and to ensure more resilient water treatment processes under changing climate.

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